(19) World Intellectual Property Organization International Bureau





(43) International Publication Date 26 July 2001 (26.07.2001)

PCT

(10) International Publication Number WO 01/53312 A1

- (51) International Patent Classification⁷: C07H 21/04, C12N 15/11, 15/63, 15/70, 15/82, 15/85, C07K 14/00
- (21) International Application Number: PCT/US00/34263
- (22) International Filing Date:

26 December 2000 (26.12.2000)

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

09/488,725	21 January 2000 (21.01.2000)	US
09/552,317	25 April 2000 (25.04.2000)	US
09/598,042	9 July 2000 (09.07.2000)	US
09/620,312	19 July 2000 (19.07.2000)	US
09/653,450	3 August 2000 (03.08.2000)	US
09/662,191	14 September 2000 (14.09.2000)	US
09/693,036	19 October 2000 (19.10.2000)	US
09/727,344	29 November 2000 (29.11.2000)	US

(63) Related by continuation (CON) or continuation-in-part (CIP) to earlier applications:

US	09/488,725 (CIP)
Filed on	21 January 2000 (21.01.2000)
US	09/552,317 (CIP)
Filed on	25 April 2000 (25.04.2000)
US	09/598,042 (CIP)
Filed on	9 July 2000 (09.07.2000)
US	09/620,312 (CIP)
Filed on	19 July 2000 (19.07.2000)
US	09/653,450 (CIP)
Filed on	3 August 2000 (03.08.2000)
US	09/662,191 (CIP)
Filed on	14 September 2000 (14.09.2000)
US	09/693,036 (CIP)
Filed on	19 October 2000 (19.10.2000)
US	09/727,344 (CIP)
Filed on	29 November 2000 (29.11.2000)

(71) Applicant (for all designated States except US): HYSEQ, INC. [US/US]; 670 Almanor Avenue, Sunnyvale, CA 94086 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): TANG, Y., Tom [US/US]; 4230 Ranwick Court, San Jose, CA 95118 (US). LIU, Chenghua [CN/US]; 1125 Ranchero Way #14,

San Jose, CA 95117 (US). ASUNDI, Vinod [US/US]; 709 Foster City Boulevard, Foster City, CA 94404 (US). CHEN, Rui-hong [US/US]; 1031 Flying Fish Street, Foster City, CA 94404 (US). MA, Yunqing [CN/US]; 280 W. California Avenue #206, Sunnyvale, CA 94086 (US). QIAN, Xiaohong, B. [CN/US]; 3662 Tumble Way. San Jose, CA 95132 (US). REN, Feiyan [US/US]; 7703 Oak Meadow Court, Cupertino, CA 95014 (US). WANG, Dunrui [CN/US]; 932 La Palma, Milpitas, CA 95035 (US). WANG, Jian-Rui [CN/US]; 744 Stendhal Lane, Cupertino, CA 95014 (US). WANG, Zhiwei [CN/US]; 836 Alturas Avenue, B36, Sunnyvale, CA 94085 (US). WEHRMAN, Tom [US/US]; 3210 CCSR Mol Pharm, 269 W. Campus Drive, Stanford, CA 94305 (US). XU, Chongjun [CN/US]; 4918 Manitoba Drive, San Jose, CA 95130 (US). XUE, Aidong, J. [CN/US]; 1621 S. Mary Avenue, Sunnyvale, CA 94087 (US). YANG, Yonghong [CN/US]; 4230 Ranwick Court, San Jose, CA 95118 (US). ZHANG, Jie [CN/US]; 4930 Poplar Terrace, Campbell, CA 95008 (US). ZHAO, Qing, A. [CN/US]; 1556 Kooser Road, San Jose, CA 95118 (US). ZHOU, Ping [CN/US]; 1461 Japaul Lane, San Jose, CA 95132 (US). GOODRICH, Ryle [US/US]; 4896 Sandy Lane, San Jose, CA 95124 (US). DRMANAC, Radoje, T. [YU/US]; 850 East Greenwich Place, Palo Alto, CA 94303 (US).

- (74) Agent: ELRIFI, Ivor, R.; Mintz, Levin, Cohn, Ferris, Glovsky, and Popeo, P.C., One Financial Center, Boston, MA 02111 (US).
- (81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.
- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:

with international search report

 before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments

[Continued on next page]

(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.

0153312A1 l >

BNSDOCID: <WO

MOO

WO 01/53312 A1



For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. TECHNICAL FIELD

3/

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for example in therapeutic, diagnostic and research methods.

2. BACKGROUND

5

10

15

20

25

30

35

Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs, chemokines, and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, for example, diagnostics, forensics, gene mapping; identification of mutations responsible for genetic disorders or other traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences.

3. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1-1786 and 3573-5358. The polypeptides sequences are designated SEQ ID NO: 2n (wherein n = 1 to 20). The nucleic acids and polypeptides are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, * corresponds to the stop codon.

The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO:1-1786 and 3573-5358 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO:1-1786 and 3573-5358. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO:1-1786 and 3573-5358 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO:1-1786 and 3573-5358. The sequence information can be a segment of any one of SEQ ID NO:1-1786 and 3573-5358 that uniquely identifies or represents the sequence information of SEQ ID NO:1-1786 and 3573-5358.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing

5

10

15

20

25

full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

In a preferred embodiment, the nucleic acid sequences of SEQ ID NO:1-1786 and 3573-5358 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO:1-1786 and 3573-5358 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO:1-1786 and 3573-5358; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO:1-1786 and 3573-5358; and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO:1-1786 and 3573-5358. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO:1-1786 and 3573-5358; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (e.g. orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO:1-1786 and 3573-5358; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (e.g., with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.

5

10

15

2. 20

25

The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, *e.g.*, in situ hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

35

5

10

15

20

25

The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (i.e., increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (e.g., bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound the binds to a polypeptide of the invention is identified.

The methods of the invention also provides methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products. Compounds and other substances can

5

10

15

20

25

30

effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in Table 2); for which they have a signature region (as set forth in Table 3); or for which they have homology to a gene family (as set forth in Table 4). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

10

15

20

25

30

35

5

4. DETAILED DESCRIPTION OF THE INVENTION

4.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule.

Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady

and continuous source of germ cells for the production of gametes. The term "primordial germ cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived. The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonculeotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100 nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30

5

10

15

. 20

25

30

35

۲.

nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NOs:1-20.

Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO:1-1786 and 3573-5358. The sequence information can be a segment of any one of SEQ ID NO:1-1786 and 3573-5358 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NO:1-1786 and 3573-5358. One such segment can be a twenty-mer nucleic acid sequence because the 20 probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 420 possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match (1÷4²⁵) times the increased probability for mismatch at each nucleotide position (3 x 25). The probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

5

10

15

25

30

The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements e.g. repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include the initial methionine residue. The methionine residue may be removed from the protein during processing in the cell. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

5

10

15

20

25

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (e.g., with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

The term "variant" (or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, e.g., recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations

5

10

15

20

25

30

can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, e.g., polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (e.g., nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (e.g., microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (e.g., yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, e.g., E. coli, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use

5

10

15

20

25

30

35

in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed.

20 "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (e.g. Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134-143) and factors released from damaged cells (e.g. Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol.

16:27-55)

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (i.e., hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (i.e., washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

30

35

5

10

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (i.e., the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, e.g., mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more that 5% (95% sequence identity). Substantially equivalent, e.g., mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 90% sequence identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, and most preferably at least about 95% identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (e.g., via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, e.g., using the Jotun Hein method (Hein, J. (1990) Methods Enzymol. 183:626-645). Identity between sequences can also be determined by other methods known in the art, e.g. by varying hybridization conditions.

The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The

5

10

15

-∵20 -≟

25

30

term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

 C_{j}

Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

4.2 NUCLEIC ACIDS OF THE INVENTION

Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358; a polynucleotide encoding any one of the peptide sequences of SEQ ID NO:1787-3572 and 5359-7144; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polypeptides of any one of SEQ ID NO:1787-3572 and 5359-7144. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of SEQ ID NO:1-1786 and 3573-5358; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO:1787-3572 and 5359-7144. Domains of interest may depend on the nature of the encoded polypeptide; e.g., domains in receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

5

10

20

25

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, e.g., cDNA and genomic DNA, and RNA, e.g., mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO:1-1786 and 3573-5358 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO:1-1786 and 3573-5358 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpri, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, e.g., at least about 65%, at least about 70%, at least about 75%, at least about 80%, more typically at least about 90%, and even more typically at least about 95%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, e.g. 15, 17, or 20 nucleotides or more that are selective for (i.e. specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in

5

10

15

:20

25

the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided SEQ ID NO:1-1786 and 3573-5358, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NO:1-1786 and 3573-5358 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NO:1-1786 and 3573-5358, can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altshul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, e.g., by substituting first with conservative choices (e.g.,

5

10

15

20

25

30

hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (e.g., hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., *DNA* 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, *Nucleic Acids Res.* 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., supra, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

5

10

15

...20

25

Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO:1-1786 and 3573-5358, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, e.g., plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following

5

10

15

20

25

30

vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are 15 pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. :20 Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of E. coli 14.4 and S. cerevisiae TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is 25 assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired 30 characteristics, e.g., stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for 35

5

transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

4.3 ANTISENSE

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1-1786 and 3573-5358, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of SEQ ID NO:1787-3572 and 5359-7144 or antisense nucleic acids complementary to a nucleic acid sequence of SEQ ID NO:1-1786 and 3573-5358 are additionally provided.

5

10

15

20

25

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding a nucleic acid disclosed herein (e.g., SEQ ID NO:1-1786 and 3573-5358, antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of a mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of a mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of a mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl2-thiouridine, 5-carboxymethylaminomethyluracil, dibydrouracil, beta D. galactarylamacic

- 25 2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil,
- 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a
 nucleic acid has been subcloned in an antisense orientation (i.e., RNA transcribed from the

5

10

15

inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated in situ such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, e.g., by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, e.g., by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α-anomeric nucleic acid molecule. An α-anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β-units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA -DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

4.4 RIBOZYMES AND PNA MOIETIES

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as a mRNA, to which they have a complementary region. Thus, ribozymes (e.g., hammerhead ribozymes (described in Haselhoff and Gerlach (1988) Nature 334:585-591)) can be used to catalytically cleave a mRNA transcripts to thereby inhibit translation of a mRNA. A ribozyme having specificity for a nucleic acid of the invention can be designed based upon the nucleotide sequence of a DNA disclosed herein (i.e., SEQ ID NO:1-1786 and 3573-5358). For example, a derivative of a Tetrahymena L-19 IVS RNA can be

5

10

15

20

25

30

constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a SECX-encoding mRNA. See, e.g., Cech et al. U.S. Pat. No. 4,987,071; and Cech et al. U.S. Pat. No. 5,116,742. Alternatively, SECX mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, e.g., Bartel et al., (1993) Science 261:1411-1418.

Alternatively, gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region (e.g., promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells. See generally, Helene. (1991) Anticancer Drug Des. 6: 569-84; Helene. et al. (1992) Ann. N.Y. Acad. Sci. 660:27-36; and Maher (1992) Bioassays 14: 807-15.

In various embodiments, the nucleic acids of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, e.g., the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup et al. (1996) Bioorg Med Chem 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, e.g., DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup et al. (1996) above; Perry-O'Keefe et al. (1996) PNAS 93: 14670-675.

PNAs of the invention can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, e.g., inducing transcription or translation arrest or inhibiting replication. PNAs of the invention can also be used, e.g., in the analysis of single base pair mutations in a gene by, e.g., PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, e.g., S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup et al. (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of the invention can be modified, e.g., to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, e.g., RNase H and DNA polymerases, to interact with the DNA portion while the PNA

5

10

15

20

portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (e.g., for targeting host cell receptors in vivo), or agents facilitating transport across the cell membrane (see, e.g., Letsinger et al., 1989, Proc. Natl. Acad. Sci. U.S.A. 86:6553-6556; Lemaitre et al., 1987, Proc. Natl. Acad. Sci. 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, e.g., PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, e.g., Krol et al., 1988, BioTechniques 6:958-976) or intercalating agents. (See, e.g., Zon, 1988, Pharm. Res. 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, e.g., a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

4.5 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express

35

5

the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in coamplification of the desired protein coding sequences in the cells.

The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology* (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, ct al., in Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, Cell 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK,

5

10

15

20

25

30

HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include Saccharomyces cerevisiae, Schizosaccharomyces pombe, Kluyveromyces strains, Candida, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include Escherichia coli, Bacillus subtilis, Salmonella typhimurium, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the

5

10

15

20

25

protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, e.g., inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No.

PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.6 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO:1787-3572 and 5359-7144 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NO:1-1786 and 3573-5358 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NO:1-1786 and 3573-5358 or (b) polynucleotides encoding any one of the amino acid sequences

5

10

15

20

25

30

set forth as SEQ ID NO:1787-3572 and 5359-7144 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO:1787-3572 and 5359-7144 or the corresponding full length or mature protein; and "substantial equivalents" thereof (e.g., with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, typically at least about 95%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NO:1787-3572 and 5359-7144.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., Bio/Technology 10, 773-778 (1992) and in R. S. McDowell, et al., J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (e.g., an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

5

10

15

20

25

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, e.g., Scopes, Protein Purification: Principles and Practice, Springer-Verlag (1994); Sambrook, et al., in Molecular Cloning: A Laboratory Manual; Ausubel et al., Current Protocols in Molecular Biology. Polypeptide fragments that

5

10

15

_ 20

25

30

retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for e.g., small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO:1787-3572 and 5359-7144.

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications, in the peptide or DNA sequence, can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological

5

10

15

20

25

30

methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, Calif., U.S.A. (the MaxBatTM kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearlTM or Cibacrom blue 3GA SepharoseTM; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

5

10

15

20

25

The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, e.g., targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, e.g., antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

15

20

25

30

35

10

5

4.6.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., Nucleic Acids Research 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., J. Molec. Biol. 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., Nucleic Acids Res. vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., J. Comp. Biol., Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, ISMB-97, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference) and the Kyte-Doolittle hydrophobocity prediction algorithm (J. Mol Biol, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., J. Mol. Biol. 215:403-410 (1990).

4.7 CHIMERIC AND FUSION PROTEINS

The invention also provides chimeric or fusion proteins. As used herein, a "chimeric protein" or "fusion protein" comprises a polypeptide of the invention operatively linked to

another polypeptide. Within a fusion protein the polypeptide according to the invention can correspond to all or a portion of a protein according to the invention. In one embodiment, a fusion protein comprises at least one biologically active portion of a protein according to the invention. In another embodiment, a fusion protein comprises at least two biologically active portions of a protein according to the invention. Within the fusion protein, the term "operatively linked" is intended to indicate that the polypeptide according to the invention and the other polypeptide are fused in-frame to each other. The polypeptide can be fused to the N-terminus or C-terminus.

For example, in one embodiment a fusion protein comprises a polypeptide according to the invention operably linked to the extracellular domain of a second protein.

In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide sequences of the invention are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences.

In another embodiment, the fusion protein is an immunoglobulin fusion protein in which the polypeptide sequences according to the invention comprises one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand and a protein of the invention on the surface of a cell, to thereby suppress signal transduction *in vivo*. The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand. Inhibition of the ligand/protein interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, *e,g.*, cancer as well as modulating (*e.g.*, promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies in a subject, to purify ligands, and in screening assays to identify molecules that inhibit the interaction of a polypeptide of the invention with a ligand.

A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, e.g., by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers.

Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for

5

10

15

€20

25

30

example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the protein of the invention.

4.8 GENE THERAPY

5

10

15

20

25

30

Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected ex vivo, in situ, or in vivo by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or ex vivo by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example, Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or artificial chromosomes (stable expression). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered *in vivo* to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in

the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, e.g., inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are

5

10

15

₂ 20

25

30

35

added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.9 TRANSGENIC ANIMALS

In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous

5

10

15

20

25

30

promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development, through, e.g., homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

4.10 USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the

5

10

15

....20

polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or indirectly activate or inhibit the polypeptides of the invention (identified, e.g., via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

4.10.1 RESEARCH USES AND UTILITIES

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

5

10

15

20

25

30

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

4.10.2 NUTRITIONAL USES

Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

4.10.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient

5

10

15

20

25

30

confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK, HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli,

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin-γ, Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 20 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 25 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Aced. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. 30 J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in

35 Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober,

5

10

Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

4.10.4 STEM CELL GROWTH FACTOR ACTIVITY

A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells *in vivo* or *ex vivo* is expected to maintain and expand cell populations in a totipotential or pluripotential state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder

5

10

15

20

25

30

layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotential/pluripotential stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotential/pluripotential mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., Differentiation, 48: 173-182, (1991); Klug et al., J. Clin. Invest., 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering eds.* Lanza et al., Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell

5

10

15

20

25

30

sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support e.g. as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

4.10.5 HEMATOPOIESIS REGULATING ACTIVITY

A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

5

10

15

. 20

25

30

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells 5 with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of 10 stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

15

20

25

30

4.10.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular

5

10

15

.20

25

30

endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

4.10.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes viruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus,

5

10

15

20

25

30

rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof, including antibodies) of the present invention may also to be useful in the treatment of allergic reactions and conditions (e.g., anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by in vivo animals models such as the cumulative contact enhancement test (Lastborn et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxocol. 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high 30 level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic

35

5

10

15

20

25

4.5

composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

5

10

15

20

25

30

PCT/US00/34263 WO 01/53312

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

A polypeptide of the present invention may provide the necessary stimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β₂ microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected turnor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and 30 Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., I. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bowman et al., J. Virology 61:1992-1998; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

35

10

15

...

... 20

25

....

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512,

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

4.10.8 ACTIVIN/INHIBIN ACTIVITY

1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

5

10

15

20

25

A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

4.10.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population.

5

10

15

20

25

30

Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

15

10

5

4.10.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

A polypeptide of the invention may also be involved in hemostatis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

25

20

Therapeutic compositions of the invention can be used in the following:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

30

4.10.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention

may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Karposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine. Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide,

5

10

15

20

25

30

Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (e.g. exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

In vitro models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These in vitro models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wily-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available, e.g. from American Type Tissue Culture Collection catalogs.

4.10.12 RECEPTOR/LIGAND ACTIVITY

A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen

5

10

15

20

25

30

recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or a toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14. Examples of colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

4.10.13 DRUG SCREENING

This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques. The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such

5

10

15

20

25

30

transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (i.e., increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science 282*:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, Curr. Opin. Biotechnol. 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., Mol. Biotechnol, 9(3):205-23 (1998); Hruby et al., Curr Opin Chem Biol, 1(1):114-19 (1997); Dorner et al., Bioorg Med Chem, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding

35

5

10

15

20

25

molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

4.10.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide e.g. a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (i.e., increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The response of the two cell populations to the addition of ligands(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then be assayed for expected modifications i.e. phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

4.10.15 ANTI-INFLAMMATORY ACTIVITY

5

10

15

__20

25

Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflamation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic mylegenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

4.10.16 LEUKEMIAS

Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

30

35

25

5

10

15

20

4.10.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of therapeutic utility, include but are not limited to nervous system injuries, and diseases or

disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

- (i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;
- (ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;
- (iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;
- (iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;
- 20 (v) lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;
 - (vi) neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;
 - (vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and
 - (viii) demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including but not limited to multiple sclerosis, human immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or

5

10

15

25

30

differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

- (i) increased survival time of neurons in culture;
- (ii) increased sprouting of neurons in culture or in vivo;
- (iii) increased production of a neuron-associated molecule in culture or *in vivo*, *e.g.*, choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
 - (iv) decreased symptoms of neuron dysfunction in vivo.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, etc., depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, e.g., weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

4.10.18 OTHER ACTIVITIES

A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or

5

10

15

20

25

30

elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

4.10.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis and treatment. Such polymorphisms may be associated with, e.g., differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides). In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified

5

10

15

. 20

25

30

nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, e.g., by an antibody specific to the variant sequence.

4.10.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis is determined in an experimental animal model system. The experimental model system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et at., 1983, Science, 219:56, or by B. Waksman et al., 1963, Int. Arch. Allergy Appl. Immunol., 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

25

30

5

10

15

20

4.11 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

4.11.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of

administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about 0.01µg/kg to 100 mg/kg of body weight, with the preferred dose being about 0.1µg/kg to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

15 PHARMACEUTICAL FORMULATIONS AND ROUTES OF 4.12 **ADMINISTRATION**

A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable , 20 carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet-derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), insulin-like growth factor (IGF), as well as cytokines described herein.

25

30

5

The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (e.g., at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, e.g., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co- administered with one or more cytokines, lymphokines or other hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic

35

5

10

15

20

25

factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

5

4.12.1 ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

15

10

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

≈20

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

30

35

25

4.12.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be

manufactured in a manner that is itself known, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers

35

5

10

15

20

25

enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, e.g., dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, e.g., gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral administration by injection, e.g., by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, e.g., in ampules or in multi-dose containers, with

5

10

15

20

25

30

an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, e.g., sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, e.g., containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, e.g. polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well

5

10

15

20

25

30

known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent.

Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable

...

5

10

15

-20

25

30

lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about $0.01~\mu g$ to about 100~mg (preferably about $0.1~\mu g$ to about 10~mg, more preferably about 0.1 µg to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions

5

10

15

20

25

30

may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF). platelet derived growth factor (PDGF), transforming growth factors (TGF-α and TGF-β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which

5

10

15

_ 20

25

30

modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either in vivo or ex vivo into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes.

4.12.3 EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate in vitro assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC₅₀ as determined in cell culture (i.e., the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD₅₀ (the dose lethal to 50% of the

5

10

15

20

25

30

population) and the ED₅₀ (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD₅₀ and ED₅₀. Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED₅₀ with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, e.g., Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from *in vitro* data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen which maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about $0.01~\mu g/kg$ to 100~mg/kg of body weight daily, with the preferred dose being about $0.1~\mu g/kg$ to 25~mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

4.12.4 PACKAGING

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the

5

10

15

20

25

invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

4.13 ANTIBODIES

5

10

15

20

25

30

Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} , F_{ab} and $F_{(ab)}$ fragments, and an F_{ab} expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG_1 , IgG_2 , and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, such as an amino acid sequence shown in SEQ ID NO: 1787, and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region of -related protein that is located on the surface of the protein, e.g., a hydrophilic region. A hydrophobicity analysis of the human related protein sequence will indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte

Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, e.g., Hopp and Woods, 1981, Proc. Nat. Acad. Sci. USA 78: 3824-3828; Kyte and Doolittle 1982, J. Mol. Biol. 157: 105-142, each of which is incorporated herein by reference in its entirety. Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, Antibodies: A Laboratory Manual, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

5.13.1 Polyclonal Antibodies

For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and Corynebacterium parvum, or similar immunostimulatory agents. Additional examples of adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the

5

10

15

20

25

30

target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

5

10

5.13.2 Monoclonal Antibodies

The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, 15 hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro. The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin 20 are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. 25 Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT 30 medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego,

California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, <u>J. Immunol., 133</u>:3001 (1984); Brodeur et al., <u>Monoclonal Antibody Production Techniques and Applications</u>, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal. The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin

5

10

15

20

25

30

polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

5 5.13.2 Humanized Antibodies

The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')2 or other antigenbinding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

5.13.3 Human Antibodies

Fully human antibodies relate to antibody molecules in which essentially the entire

sequences of both the light chain and the heavy chain, including the CDRs, arise from human
genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein.

Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell
hybridoma technique (see Kozbor, et al., 1983 Immunol Today 4: 72) and the EBV hybridoma
technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL

Antibodies and Cancer Therapy, Alan R. Liss, Inc., pp. 77-96). Human monoclonal

10

15

20

antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (Bio/Technology 10, 779-783 (1992)); Lonberg et al. (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al., (Nature Biotechnology 14, 845-51 (1996)); Neuberger (Nature Biotechnology 14, 826 (1996)); and Lonberg and Huszar (Intern. Rev. Immunol. 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the XenomouseTM as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

5

10

15

20

25

An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

20 5.13.4 Fab Fragments and Single Chain Antibodies

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see e.g., U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see e.g., Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an $F_{(ab')2}$ fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an $F_{(ab')2}$ fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_{v} fragments.

5.13.5 Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the

5

10

15

25

binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, Nature, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker et al., 1991 EMBO J., 10:3655-3659.

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. F(ab')₂ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate F(ab')₂ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to

5

10

15

20

25

30

stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from E. coli and chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody F(ab')₂ molecule. Each Fab' fragment was separately secreted from E. coli and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., J. Immunol. 147:60 (1991).

Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular

5

10

15

20

defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

5.13.6 Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

5.13.7 Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced antitumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., Anti-Cancer Drug Design, 3: 219-230 (1989).

30

5

10

15

20

25

5.13.8 Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from Pseudomonas aeruginosa), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolaca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include 212 Bi, 131 In, 90 Y, and 186 Re.

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutareldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is in turn conjugated to a cytotoxic agent.

4.14 COMPUTER READABLE SEQUENCES

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon

5

10

15

20

25

30

a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (e.g. text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NO:1-1786 and 3573-5358 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and

35

5

10

15

20

25

software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

30

25

5

10

15

20

4.15 TRIPLE HELIX FORMATION

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA.

Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are

designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

10

15

. 20

25

30

35

5

4.16 DIAGNOSTIC ASSAYS AND KITS

The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification or immunological assay formats can readily be adapted to employ the nucleic acid

probes or antibodies of the present invention. Examples of such assays can be found in Chard, T., An Introduction to Radioimmunoassay and Related Techniques, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., Techniques in Immunocytochemistry, Academic Press, Orlando, FL Vol. I (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

4.17 MEDICAL IMAGING

5

10

15

20

25

5

10

15

20

25

30

The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (e.g., where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, e.g., Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

4.18 SCREENING ASSAYS

Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NO:1-1786 and 3573-5358, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

- (a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and
 - (b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to

activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

10

15

5

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

20

25

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

30

35

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription

from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents which bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

4.19 USE OF NUCLEIC ACIDS AS PROBES

Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NO:1-1786 and 3573-5358. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from of any of the nucleotide sequences SEQ ID NO:1-1786 and 3573-5358 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes in vitro by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of

5

10

. 15

20

25

chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent *in situ* hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

4.20 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, i.e., small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata et al., 1985; Dahlen et al., 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller et al., 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, e.g., Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed Covalink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen et al., (1991) Anal. Biochem. 198(1) 138-42).

5

10

15

20

25

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen et al., (1991). In this technology, a phosphoramidate bond is employed (Chu et al., (1983) Nucleic Acids Res. 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm₇), is then added to a final concentration of 10 mM 1-MeIm₇. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm₇, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphorate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) Science 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) Anal. Biochem. 169(1) 104-8; all references being specifically incorporated herein.

5

10

15

20

25

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

4.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook *et al.* (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schriefer *et al.* (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, $Cvi\Pi$, described by Fitzgerald *et al.* (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation

5

10

15

20

25

of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease CviJI normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (CviJI**), yield a quasi-random distribution of DNA fragments form the small molecule pUC19 (2688 base pairs). Fitzgerald et al. (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a CviJI** digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that CviJI** restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

4.22 PREPARATION OF DNA ARRAYS

Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm², depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane.

5

10

15

. 20

25

30

<u>.</u>_

Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm² and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers e.g. a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

5.0 EXAMPLES

5.1.1 EXAMPLE 1

Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

5

10

15

20

25

5.1.2 EXAMPLE 2

5

10

15

20

25

30

Assemblage of Novel Nucleic Acids

The contigs or nucleic acids of the present invention, designated as SEQ ID NO: 3573-5358 were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST version 114, gb pri 114, and UniGene version 101) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

A polypeptide was predicted to be encoded by each of SEQ ID NO:3573-5358 as set forth below. The polypeptides was predicted using a software program called FASTY (available from http://fasta.bioch.virginia.edu) which selects a polypeptides based on a comparison of translated novel polynucleotide to known polynucleotides (W.R. Pearson, Methods in Enzymology, 183:63-98 (1990), herein incorporated by reference. The predicted polypeptides are shown in Table 7.

5.2.2 EXAMPLE 3

Novel Nucleic Acids

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genebank. Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, ed-ext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS:1- 327.

Table 1 shows the various tissue sources of SEQ ID NO: 1-327.

The nearest neighbor results for SEQ ID NO: 1-327 were obtained by a FASTA version 3 search against Genpept release 117, using FASTXY algorithm. FASTXY is an improved version of FASTA alignment which allows in-codon frame shifts. The nearest neighbor result showed the closest homologue for SEQ ID NO: 1-327 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The nearest neighbor results for SEQ ID NO: 1-327 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the

signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al.. Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

5.3.2 EXAMPLE 4

20 Novel Nucleic Acids

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 117, gb pri 117, UniGene version 117, Genpept release 117). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, edext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 328-1413.

Table 1 shows the various tissue sources of SEQ ID NO: 328-1413.

The nearest neighbor results for SEQ ID NO: 328-1413 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 118, using BLAST algorithm. The nearest neighbor result showed the closest homologue for SEQ ID NO: 328-1413 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in

5

10

15

25

the Sequence Listing. The nearest neighbor results for SEQ ID NO: 328-1413 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

25 **5.3.2 EXAMPLE 5**

Novel Nucleic Acids

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 117, gb pri 117, UniGene version 117, Genpept release 117). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, edext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide sequences, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 1414-1652.

30

5

15

Table 1 shows the various tissue sources of SEQ ID NO: 1414-1652.

The nearest neighbor results for SEQ ID NO: 1414-1652 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 118, using BLAST algorithm. The nearest neighbor result showed the closest homologue for SEQ ID NO: 1414-1652 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The nearest neighbor results for SEQ ID NO: 1414-1652 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

5.4.2 EXAMPLE 6

30 Novel Nucleic Acids

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 118, gb pri 118,

5

10

15

20

UniGene version 118, Genpept release 118). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, edext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide sequences, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 1653-1745.

Table 1 shows the various tissue sources of SEQ ID NO: 1653-1745.

The homology for SEQ ID NO: 1653-1745 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 118, using BLAST algorithm. The results showed homologues for SEQ ID NO: 1653-1745 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The homologues with identifiable functions for SEQ ID NO: 1653-1745 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

5.5.2 EXAMPLE 7

Novel Nucleic Acids

5

10

15

<u>.</u> 20

25

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 119, gb pri 119, UniGene version 119, Genpept release 119). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, ed-

ext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide, including splice variants resulting from

Table 1 shows the various tissue sources of SEQ ID NO: 1746-1768.

these procedures are shown in the Sequence Listing as SEQ ID NOS: 1746-1768.

The homology for SEQ ID NO: 1746-1768 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 119, using BLAST algorithm. The results showed homologues for SEQ ID NO: 1746-1768 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The homologues with identifiable functions for SEQ ID NO: 1746-1768 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the PFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the PFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

5

10

15

20

25

5

10

15

.20

25

5.6.2 EXAMPLE 8

Novel Nucleic Acids

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 120, gb pri 120, UniGene version 120, Genpept release 120). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, edext and gc-zip-2 (Hyseq, Inc.). The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The full-length nucleotide, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 1769-1786.

Table 1 shows the various tissue sources of SEQ ID NO: 1769-1786.

The homology for SEQ ID NO: 1769-1786 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 120 and the amino acid version of Geneseq released on October 26, 2000, using BLAST algorithm. The results showed homologues for SEQ ID NO: 1769-1786 from Genpept. The homologues with identifiable functions for SEQ ID NO: 1769-1786 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by

reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

Table 6 is a correlation table of all of the sequences and the SEQ ID NOS.

TABLE 1

IABLE I			
Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
adult brain	GIBCO	AB3001	9 19-21 50-51 65-66 72 78 80 82
	j		85 87 107-108 113 116 123 138 140 150-152 159 169 177 192-193
			202-203 212-214 225-226 235-236
	ĺ		251 258 268-269 272 280-281 295
			298 301 321 326 331-332 334 356-
	·		357 362 369 379 382-383 416 423
			443 459-460 473 475 477 488 496
			500 503 519 526 547 574 582 587 608-609 613 618 633-634 645-646
			652 657-658 660 669-671 678 687
			695 697 710 715 724 731 775-777
	,		796 804 811 857-859 862 869 899-
			900 912 919 922 924-929 933 936
			962 979 988-989 996 1001 1004-
			1008 1018 1039 1047 1059 1064
1	j		1067 1070 1078 1082 1107 1113 1116-1117 1131 1134-1137 1140
			1149 1151 1157 1180 1206 1229
]	ĺ		1234 1241 1243 1258 1272-1273
	Ì		1279 1288-1290 1294 1307-1308
}	1		1312 1320 1323 1330 1356 1360-
	j	•	1361 1368 1373-1375 1379 1391 1400 1417 1446 1468 1482 1493-
			1494 1501-1503 1506-1507 1512
	ĺ		1517 1522-1524 1530-1533 1537
i i	ł		1549 1565 1578 1598 1606 1608
	i		1623 1625 1627 1639 1643 1648-
1	j		1649 1653 1664 1667 1671 1696
			1734 1741 1743-1744 1760-1761
adult brain	GIBCO	ABD003	3 12-14 18-19 25 30-31 34-36 43-
			45 50-51 56 58 60 65-66 68-69 RA
	1		82 85 87 92 104 107-108 112-113
1	j		115-116 123-124 131-132 135-137 139 142 146 148-149 152 154 157
]	İ		159 163 165 167 169 172 180 192-
	1		193 196-197 199 203 208 210 212-
	Į.		214 223 233 235-237 247 257 259
	1		261 268-269 272 276 280-281 284-
	}		288 291-292 295 297 300-301 304
			307 317 320-321 323 327 329-331 333-334 345-349 356-357 379-381
		1	393 401 408 414 419 424 426-428
			430 433-436 438-439 443 445 449
	l		453-454 459-461 468 471-473 476-
	;		478 483 491 494 496 500 503 507-
		•	508 516 519-520 525-527 534 536- 540 542-543 545 553 555 560 569-
			570 574-576 586-588 593 595 597
ľ		l	601 606-609 616-620 622-623 625
j	Į.	j	628-633 635-636 643 645-649 653
ļ	}	l	655-656 660-665 668-670 676 681
		j	687 701 710 715 717 724-728 735 743 745-746 750 753 759 765-766
	1	1	773 775-778 786 789 796 799-800
1	1	ł	802-803 810-811 815 817 820-821
	Į	j	832 834-836 840 845-847 851 858-
	1	l	861 864 869 874 878 883 897 901-
	ļ	ĺ	902 904-905 908 911-914 916 921-
	1	1	922 924-927 929 932-934 936-939
	}		941-942 945 955-958 963 966-969 977 979-980 985-986 990 992-993
		j	997-1001 1005-1007 1012 1017-
	j	Į.	1020 1023-1024 1029-1031 1034
		ĺ	1036 1039 1050 1059 1063-1066
i i	1	J.	1078 1081-1082 1085-1086 1089

Tissue Origin	RNA Source	Нузед	SEQ ID NOS:
		Library Name	
			1097 1103 1107 1109 1112 1116-
			1117 1119 1121 1124 1127 1130 1134 1144-1145 1149 1151 1157-
	İ		1158 1167 1170 1178 1184 1188
			1190 1193-1194 1200 1202 1215-
			1217 1220 1226-1227 1229 1231
			1241 1243 1247 1252 1258 1263
		}	1267 1269 1279 1281 1284 1286- 1289 1293-1294 1306-1307 1312
	}		1316-1320 1326 1333 1338 1341
	ì	1	1344 1348 1351 1355-1357 1368
	1		1374 1377 1380 1386 1389-1390
}			1394 1400 1409 1414 1422-1423
			1425-1427 1437 1443 1446 1454
	į		1456 1458-1459 1468 1470-1472 1478 1482-1483 1487-1488 1493
	1		1497 1499 1506 1508-1511 1517
			1522-1524 1530-1533 1545-1546
	j		1548-1550 1552 1557-1559-1563
			1565 1567 1569 1571 1586 1588
			1591 1593 1595 1598-1601 1608 1611 1620-1621 1624-1626 1628
	<u> </u>		1630-1632 1636 1640-1641 1644-
	1		1645 1647 1649 1653-1655 1657
			1664 1667 1669 1673 1678-1681
	}		1686 1690 1694-1696 1701 1709
)		1711 1719 1722-1723 1726-1727
			1731-1733 1738 1740 1743-1744 1747 1749 1753 1757-1758 1760-
	j		1761 1765 1771 1785
adult brain	Clontech	ABR001	9 29 68-69 113 115 146 152 206
			223 245 277 307 320 324 330-331
	1		344 348 352 362 379 384 393 404
			408 414 441-442 454 469 481 490
	}		715 799 803 833 865 871 875 880
			882 908 920 937 1000 1005-1006
	•		1027 1036 1041 1043 1075 1107
			1112 1121 1127 1136-1137 1144-
j		,	1147 1231 1238-1239 1280 1293 1320 1345 1355 1361 1383-1384
			1400 1417 1448 1456 1476 1507
			1570 1572 1609-1610 1614 1620
			1626 1645 1653 1754 1759 1770
adult brain	Clontech	ABR006	1786
Luciate Diain	CTOWER	MDRUUB	5-8 15-16 168 212-213 271 278 280-281 291-292 300-301 310 314
			321 326 336-338 341 352 357 359-
			360 362 369 374 379 384 393 396-
		,	397 414 419-420 426-428 430 441-
]			442 453 506 616-617 661 689 785
1			798 845 1018 1109 1113 1124 1148 1167 1187 1207 1227 1252 1265
			1285 1312 131.7-1319 1324-1327
			1344 1369 1381 1400 1416 1421
1			1427 1430-1431 1436 1471 1501
			1557-1559 1586 1588 1651 1653
			1664-1665 1671 1673 1690 1697-
]			1698 1700 1711 1717 1719-1720 1728 1736 1740 1743-1744 1757
			1760-1761
adult brain	Clontech	ABR008	5-10 13-19 22-23 25 29 33 37-39
			43-45 50-51 54-55 57-58 60-66
	ļ		68-70 72 75 77-80 83 85 89-92 94
}			99-105 108-110 112-113 116-117 123 128 133 135-137 139 143 145-
			146 148 152 154-155 157 166 168-
1			172 174-175 181-184 188-190 193-
L			194 196 198-200 202 204-205 207-

Tissue Origin	RNA Source	Urroom	
122000 0219111	KNA SOUICE	Hyseq Library Name	SEQ ID NOS:
			208 210 214-215 218 221-226 229
]			231-232 234-241 245-247 251-253
1			255 257-259 268-269 271 276-281
!			285-286 288 290-292 300-302 304
ł i			307 309-311 313 315 317-318 320-
]			322 325-326 328 330-331 333-338
			341 344-347 349 352 354 356-357
1			362 369-373 376 379-380 382 384
}			387 390-391 393-394 397 399-403
)			405-411 414-415 417-420 426-428
			437-438 440-444 453-455 462 464
			467 469-471 476 478 482-484 488-
			491 497 503 506-513 516-517 520 524-526 528-530 532-534 537-540
			542 544 547-551 553 561 565-567
· I	,		572-574 577 581 585 587-588 590-
	j		591 597 599 601-602 606-610 612
1	Ì		615-617 619-620 622-623 628-629
]	}		631 633-634 636-641 643 645-647
1			651-653 655-664 669-671 673 679
1	1		682 687 689 691-700 702 706 710
1	ł		715-717 720-721 725-734 736-739
1	J		742-743 746 750-752 756 758-759
	Į.		762-764 766 768 773-778 780-782
	. 1		784-785 787-789 794 796 799 802-
1	ł		803 805 811 814-815 818 825-826
1	İ		834-837 839-840 842-843 856-859
1			861-862 865 867-872 874-875 881 883-884 887 889-892 894-895 897-
1	İ		898 901 904 908 910 912 914 917
1			919 921-924 926-927 930-932 935-
1	1		941 943 945 949 953-954 958 961-
1			963 967 969 971 975 977 981-983
1			986 988-990 992 997 999-1002
			1004-1006 1008 1012 1018-1023
1	i		1027 1029-1031 1035-1037 1047-
	į	ì	1048 1053 1057 1059 1063 1068
	1		1070 1072-1075 1077 1081-1083
	1		1085-1093 1095-1096 1108-1112
1		}	1114-1125 1127 1131-1133 1135-
			1138 1142-1145 1148-1158 1160- 1163 1167 1169 1172 1175 1177
!	1		1180 1183-1188 1191-1195 1199-
1			1200 1204 1206 1211 1213-1216
	1		1222-1223 1226-1227 1229-1231
	ļ]	1234-1235 1241-1242 1244-1263
]	Ì	ļ	1266 1269-1271 1276-1277 1279-
1		-	1281 1284-1286 1292 1294-1295
1	İ	ł	1299 1305-1309 1312 1314 1316-
			1319 1322 1324-1327 1330 1332
		1	1334-1335 1339 1344-1346 1351
1		ſ	1354-1355 1357-1358 1365-1367
1			1369-1370 1373-1374 1376-1379
		!	1381-1384 1386-1388 1392 1394 1396-1397 1400 1403-1407 1410
ļ		J	1414 1419-1420 1423 1432-1433
			1435 1437-1438 1440-1442 1446
1	Ì		1448 1453-1455 1457 1461 1463-
]	ļ		1464 1466 1468 1471 1477 1480
			1482-1483 1496 1502-1504 1507-
		.	1509 1513 1519-1520 1524-1526
	-		1536 1547 1549-1552 1567 1573-
	1		1574 1578 1586-1589 1597-1598
	ļ		1601-1602 1605 1607-1609 1611-
	[[1617 1619-1621 1623 1625-1626
	1		1635-1641 1643-1645 1649 1651
1	ļ		1653 1656-1658 1664 1669 1671-
			1674 1676-1684 1686 1689-1690
			1694-1696 1704-1705 1708-1709

Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
	Tour Boarce	Library Name	SEQ ID NOS:
			1720-1724 1726-1728 1730-1733
	ļ	}	1737-1740 1742-1745 1753 1756-
	1		1757 1759-1761 1765 1767 1771-
adult brain	Clontech	ABR011	1772 1776-1777 1779-1780 1786
addit blain	Clontech	ABRULL	24 75 103 186 210 310-31: 364- 365 508 623 710 937 1002-1003
	}		1059 1204 1609 1731-1732
adult brain	BioChain	ABR012	46 182-184 204-205 300 739 767
			1371 1549 1620 1684
adult brain	Invitrogen	ABR013	185 204-205 364-365 393 497 595
1		1	687 692-694 830 845 1068 1320
			1413 1640
adult brain	Invitrogen	ABR014	187 301 357 364-365 375 454 463
			731 859 939 983 1073 1262 1270
			1320 1403 1640 1651 1657 1696
adult brain	Invitrogen	ABR015	1722 1738
addic brain	Invillogen	ABRUIS	119 434-435 441-442 763 789 983
adult brain	Invitrogen	ABR016	312 364-365 379 1320 1334-1335
		1	1674 1722 1785
adult brain	Invitrogen	ABT004	14-16 22-23 25 37-39 43 58 60
	}		70-72 78 86 94 107 113 116 136-
1	Į .)	137 143 146 152 161 173 182-184
<u> </u>	ļ		194 196 198 210 218 229 259 267
			295 298 309-310 320-321 324 336-
			338 346-347 349-350 356-357 362
			371 379-380 382-383 391 393 396 399 401 408 428 438 459 461 476
]			482 490 502 507-509 516 526 531
			557 562 597 602 607-609 624 652
			655 667 669 671-672 687-689 695-
			696 710 712 715 721 732 739 743
			750 753 766 778 780-781 789 803
			814 826 830 837 841 857 869 874
			894-895 925 937 949 954-956 960-
			961 963 968-969 988-989 1000
			1005-1006 1016-1019 1021 1036- 1037 1052 1086 1090 1109 1113
			1115 1120-1121 1123-1124 1136-
 			1137 1140 1144-1147 1151 1167
[,		1170 1174 1188 1193-1194 1205
			1225 1229 1231 1254 1258 1262
			1280 1285 1309 1312 1334-1335
			1341 1343-1344 1356-1357 1370
			1378-1379 1383-1384 1403-1404
		ļ	1423 1429 1434 1442 1448 1451-
	ľ		1452 1454 1470-1472 1482 1499 1525 1528-1529 1532 1536 1547
			1554 1557-1559 1561-1562 1567
			1585 1588 1590 1595 1601-1604
			1608 1610-1613 1615 1619 1624
		1	1627 1640 1644 1647 1660 1664
		1	1666 1670 1675 1696 1704 1715
•			1723 1727 1738 1760-1761 1768
m. 1 h 3	Ob-set		1779 1785-1786
cultured preadipocytes	Strategene	ADP001	5-8 11 17 25 68-69 80 82 87 103
Predationales		ł	105 110 116 136-138 168 171 188- 189 196-198 261 267 276 288 293
,		ì	301 318 331 336-338 379-380 391
		ļ	400 428 430-431 510-512 520 524
			527 549 557 561 602 618 620 622
			631 637 647 670 681-682 710 731
	1		
		İ	748 782 793-794 817 834-836 843
		ļ	845 858-859 879 882 893-895 934
			845 858-859 879 882 893-895 934 960 982 986 995-996 1000 1002
			845 858-859 879 882 893-895 934 960 982 986 995-996 1000 1002 1005-1007 1025 1027-1028 1032
			845 858-859 879 882 893-895 934 960 982 986 995-996 1000 1002

Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
		Library Name	
			1260 1271 1297-1298 1314 1320
			1322 1329 1339 1345 1365-1366
			1370-1371 1398 1408 1423 1431 1437 1466 1468 1533 1539 1594
	·		1602 1608 1614 1631 1649-1650
			1660 1662 1673 1687-1688 1696
			1711 1719-1720 1742 1746 1749
adrenal gland	Clontech	ADR002	1760-1761 1765 1767 1771 1785 4-10 15-16 25 29-31 43-45 47 50-
			51 55 60 62-63 65-66 75 80 102
[116 118 122 126 130 137 150 169-
1			170 181 192 198 201-203 215 227-
}			228 247 251 255 267-269 271 280- 281 285 295 298 311 336-338 342
			349 351-352 354 372-373 383-385
]			391 400 410 415-416 424 426-427
1			431 434-437 439 445 454 461 473
			477 483 491 493 497-498 503 516
1			519 527 535 546 549 552 572-573 581 588 595 600 602 608-610 620
]			628-630 637 645-646 670 679 703
			713 715 719 732 734 744-746 758
[773-778 789 816 829 837 845 848
į į			869 875 883 898 904 912 922-923 930-931 942 948 952 965 967 969
			976-977 981 990 992-993 1001
			1004 1049 1055 1059 1071-1072
			1076 1112-1113 1115 1121 1127
			1134-1135 1151 1158 1163 1175 1181 1188 1209 1218 1224-1225
{			1227 1231 1243 1270-1271 1274
ľ	ľ	,	1280 1285 1290 1293 1307 1324-
}	Į		1325 1327 1330 1342-1343 1345
ļ			1348 1365-1366 1369 1378-1379 1387 1398 1400 1405 1417 1425-
			1426 1436 1440-1441 1444 1454
[ſ		1463-1464 1488 1491 1507 1512
,			1538 1546 1567 1573-1575 1588
	ł		1598 1609 1614 1618 1622 1624 1627 1634 1636 1649 1651 1658
			1671 1674 1678-1679 1691-1692
			1703 1717 1727 1731-1732 1737
adult heart	GIBCO	AITDOOT	1765
addit Heatt	GIBCO	AHR001	4-8 10-11 15-16 18-21 34-39 44- 46, 50-52 57-58 60 62-63 71 75 82
			85 87 89 94 97 100 103-104 108-
	}		110 112 114 116 118-119 122-123
	!		127 130-132 134 136-138 141-144
	J		147-151 153 163-164 168-171 179 186 192 195 197 199 204-205 212-
			215 220 225-226 229-230 232 234-
	[236 251 257-260 262 265 272 274
			277 280-282 285-286 289-292 296
	1		298-301 304 307 309 314 321 324- 325 330 333 336-338 345 349 351-
	Ì	ļ	352 354 358 361 368 370 380 383-
[1		384 387-398 391 393 397 401 406
	ĺ	ſ	408-409 411-412 414-416 430-431
	1	}	433-439 445-446 449 452 454-455 457 459 462 469 472-473 476-480
	ł	1	483-484 487-490 492-493 496-498
1)		503 506 508 510-513 516 519-522
Į			526 534 536-540 542 546 549 553
ĺ	İ	j	560-562 574-577 581-582 584 586-
. [ļ	ł	587 589 593 595 597 604-609 611- 612 615-620 622-623 626 632 637
	į	ł	645-652 656-660 665-666 670-672
1	ł		674-675 683~684 687 692-694 697
			701 709 712 715-716 719-720 725-

Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
		Library Name	JEQ ID NOS.
			726 728 730-732 735 738-739 743-
1			744 746 751 753 759 761 765 770-
1			771 775-780 785 788-790 796 802
1			804 810 812 817 821 826 828 830
}			837 843 845-847 849-853 857-861
			863-864 869 871 875 877-879 881
1			883 887 890-892 894-895 897-898
İ		1	901 903 906-907 911-913 915 919 921-925 927-928 933-935 945 958
1		İ	961-963 967 969-972 975 977-978
}		}	980-986 990 992 999-1002 1005-
	i		1007 1010 1016 1019-1020 1022-
}		}	1023 1025 1028-1037 1039-1040
			1043 1047 1050 1054-1055 1057
}	ł	1	1059 1063-1064 1067-1068 1070
[1	1072 1075-1076 1083 1085-1087
i		1	1089 1093-1094 1104 1106 1108-
		ļ	1109 1113 1116-1117 1119 1121
		1	1124 1126 1128 1131-1134 1144-
)	}	1145 1148-1149 1151 1158 1167
			1169-1170 1175 1177 1192 1196
	J.	1	1199-1200 1202 1206-1208 1211
	[1216 1218 1222 1227-1229 1232-
	1	}	1235 1238-1241 1243-1244 1247-
			1248 1250 1253-1254 1256-1258
ľ	l	!	1261 1268 1270-1271 1277 1280-
			1282 1287 1292 1298-1299 1306
	(1308 1317-1321 1324-1325 1330
			1332 1334-1337 1339 1344-1345
1			1349-1350 1354-1356 1359-1360
į	1	j	1365-1366 1369 1371 1374-1375
			1378-1380 1383-1384 1389 1397
ł			1400 1403 1409 1417 1423-1426
			1437 1439 1442 1444 1446-1447
İ	i i		1450 1453 1468 1470 1473 1479 1481 1488 1490 1501-1504 1519
İ]		1521 1524 1528 1530-1534 1536-
	[1521 1524 1526 1530-1534 1536- 1537 1539 ₁ 1541-1542 1547 1553
			1555 1560 1565 1567-1571 1588
			1591 1597-1598 1601-1602 1605
}			1614-1616 1619-1620 1623-1628
1	İ		1630-1632 1634 1536 1641 1644-
1			1645 1647 1649 1652-1655 1659
			1662 1667 1673-1674 1680-1681
1	(1684 1686-1688 1704-1705 1709
J	j j		1711-1712 1717 1724 1726-1727
[ľ		1731-1733 1737-1738 1741 1743-
	j ļ		1744 1749 1754-1755 1760-1761
2011 + 1-5			1765 1772 1785
adult kidney	GIBCO	AKD001	4-8 10-11 17-21 29-31 35-39 42-
ļ			45 50-51 56-58 60-61 64 68-69 75
			77 80 82 85 87 92-94 97 100 102-
			104 107-108 112 116-117 119 123
	1		127-133 136-137 139-141 143-144
}			147-154 157 161-163 165-166 169
			172 176 178-179 192 194-197 199 201 203-206 209-210 212-213 215-
			216 223-228 234-236 238 247 251-
			253 257-259 261-262 265-269 271-
		Ì	272 274 276-277 279-281 284-286
			290 293 295 298-299 301-302 304
		ì	307 311-313 321 325-326 329-331
	1		333 341 344 348-350 352 356 358-
	[Í	359 362 364-365 368 370-372 374
	j	ļ	376-377 380-382 392 395 398 400-
			401 404 407-409 414-415 423-424
	1	}	430-437 443-444 446 449 451 453-
			455 459 461-462 464 467 469 471-
			474 476-477 480-481 483 487-488

minava Oziai	I DNA Course	11.000	000 ***
Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
	 	DINIGLY Haute	490-491 493 497-505 510-513 516-
]		520 522 524 526-529-534 537-540
	ļ		544 547 549 554-556 560 562 564
}			567 571-576 578 582 586-589 592-
}	}	,	593 598-599 601 604-606 608-613
Ī			615-619 621-626 632-634 637-643
ł.	ì		645-652 655 660-664 669-672 676
l		ì	678-679 688 692-695 698 702 711
1			713 717 719-720 727 731 735-736
ĺ	1		738 743 745-746 751 753 755 762-
1	i	{	763 765 771-773 775-778 780 786
ļ)]	788 793 795-796 800 803 805 808
į	ļ	}	810-812 814-819 821 826 829 832
ſ	ľ		834-838 842-845 848-855 857-861
	<u> </u>		864-865 867 869 871 874 876-883
j		,	886-887 889-891 893-896 898-900
ì	ľ		902 906-908 910-914 918 920 922
			925-927 929-935 937 940-942 945
1	1	1	948-949 951 953-958 960-961 963-
	1		964 969-970 972 976-978 982-986
	[1	988-990 992-993 995-997 999-1002
1	1	1	1004-1008 1010 1012-1013 1016-
Į	1)	1017 1019-1020 1022 1025-1031
Ī	[1035 1038-1040 1042 1044 1047
	[1050 1054-1055 1057-1064 1068
Ì		}	1070-1073 1078 1085-1086 1088-
ļ			1089 1092 1094 1097 1099-1102
			1107 1109-1112 1116-1119 1121
1		ļ	1123-1125 1132-1135 1140 1142-
}		}	1143 1146-1147 1149-1150 1153- 1154 1157 1159 1163 1167 1170
i		İ	1178-1179 1181 1183 1192 1196-
ł			1200 1202-1204 1206-1211 1216-
ĺ	1	ł	1219 1221-1222 1225 1227-1230
			1232-1234 1238-1241 1243-1244
}	}		1246-1247 1253 1257-1258 1260-
			1261 1267-1268 1270 1272-1274
			1281 1283 1287-1289 1293-1295
l		ĺ	1299 1306 1308 1311-1313 1317-
			1320 1323 1329-1330 1334-1335
(1339 1341 1349-1350 1353-1357
}			1359 1367 1369 1373 1375 1378-
j			1379 1394 1397 1400 1403 1405
r		· ·	1407-1409 1417 1419 1423-1424
			1428-1431 1433 1437-1438 1442-
1	}	!	1443 1445-1446 1448-1450 1453-
	1		1454 1459 1461 1465-1468 1474-
	ì		1475 1478 1484-1488 1490 1492-
	(1493 1495 1497-1498 1506-1507
			1509 1512 1518 1521-1522 1525
}			1527-1528 1532-1533 1537 1540-
			1541 1547-1550 1552 1556-1559
			1561 1565-1566 1568 1571 1575 1578-1579 1583 1586-1587 1589
)			1591-1592 1594 1598 1600 1603-
			1604 1606 1608 1611 1613 1615-
	{		1616 1618-1622 1624-1628 1631-
			1632 1634-1636 1638-1639 1641
)		1644 1646-1649 1653-1656 1662
	ļ		1664 1666-1667 1670-1671 1676-
			1679 1683-1684 1686 1691-1692
		İ	1696-1699 1701 1709-1711 1713-
	<u> </u>		1714 1716-1719 1723-1724 1726-
			1727 1733 1737-1738 1741 1743-
]		1744 1748-1749 1751 1760-1761
			1763-1768 1778 1780 1785
adult kidney	Invitrogen	AKT002	20-21 37-39 47 52 57 60 65-66
			68-69 80 104 107-108 122 130 133
			136-137 140 142-143 149 169 174
	L		

Library Name 181 197 227-228 235-236 744 251 261-265 267 280-281 286 290 299 301 304-305 309 312-313 339 341 344-345 349 358 370-372 376 392-303 397 392 401 414 416 421 430 443 445 449 453-454 472 497-488 504 505 513 516 519 522 528 536-540 546 554 585 587 594 598 602 604 695 699 721 735 741 641 642 604 695 699 721 735 741 641 642 604 695 699 721 735 741 641 642 604 695 699 721 735 741 641 642 604 695 699 721 735 741 641 642 604 695 699 721 735 741 641 642 604 695 699 721 735 741 641 642 604 695 699 721 735 741 641 642 604 695 699 692 295 990 3905-907 914 919 9225 977 904 919 9225 977 904 941 949 922 957 960 602 688 970 1000 1008 1029-1030 1044 1052 1055 1063 1067-1068 1073 1085 1099-1102 1107 1110-1111 1131 115 119 1122 1134 1136-1137 1146-1148 1153 1159 1192 1196 1199 1232-1233 1241 1256 1264 1272-1273 1281 1285 1259 1291 1292 1312 1312 1324 1361 137 1446-148 1453 1159 1493 1292 1393 1312 1324 1361 1499 1499 1319 1312 1324 1361 1499 1499 1319 1319 1324 1361 1499 1499 1319 1319 1324 1491 1422-1429 1436 1446 1458 1463-1464 1467-1468 1470 1477-1478 1466 1467-1668 1470 1477-1478 1466 1467-1668 1470 1477-1478 1466 1467-1668 1470 1477-1478 1466 1467-1468 1470 1477-1478 1466 1467-1468 1470 1477-1478 1466 1467-1688 1470 1477-1478 1466 1467-1688 1470 1477-1478 1466 1467-1688 1470 1477-1478 1466 1467-1688 1470 1477-1478 1466 1467-1688 1470 1477-1478 1466 1467-1688 1470 1477-1478 1466 1467-1688 1470 1477-1478 1466 1467-1688 1470 1477-1478 1466 1467-1688 1470 1477-1478 1460 1478-1478 1470 1477-1478 1460 1478-1478 1470 1477-1478 1467 1478 1470 1477-1478 1470 1470 1470 1470 1470 1470 1470 1470	Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
181 187 227-228 238-236 244 251 261-265 267 280-281 286 290 299 301 304-305 309 312-313 339 341 344-345 349 358 370-372 376 382-381 344-345 349 358 370-372 376 382-381 387 392 401 414 416 421 430 443 445 449 483-484 472 487-488 504 506 513 516 519 522 528 536-540 546 554 585 587 587 594 598 602 607 616-617 626-627 636 643 662-646 695 709 721 737 743 761 762 778-779 788 788 804 81-827 837 778-777 788 789 804 81-827 837 785-777 788 789 804 81-827 837 785-777 788 789 804 81-827 837 785-777 788 789 804 81-827 837 785-777 788 789 804 81-827 837 785-777 788 789 804 81-827 837 785-777 788 789 804 81-827 837 839 803-992-898 903-990-907 914 839 925 927 934 941 949 952 987 960 962 968 970 1000 1008 1029-1030 1044 1052 1055 1063 1067-1068 1073 1085 1099-1102 1107 1110-1111 1113 1115 1119 1126 1134 1136-1137 1146-1146 1153 1159 1192 1196 1199 1232-1233 1241 1245 1246 1272-1273 1281 1285 1283-1294 1299 1312 1320 1324-1235 1330 1344 1349 1351 1355-1356 1369 1378-1379 1403 1414 1419 1429 1429-1439 1341 1446 1458 1464 1467-1466 1491 1509 1519 1527 1428 1436 1491 1509 1519 1527 1428 1466 1491 1509 1519 1527 1428 1464 1465 1466 1466 1466 1466 1466 1467 1669-1670 1673 1686 1709 1727 1740 1776 1466 1467 1469-1670 1673 1686 1709 1727 1740 1776 1466 1467 1469-1670 1673 1686 1709 1727 1740 1776 1466 1467 1469-1670 1673 1468 1491 1509 1539 1527 1528 133 140 143 150 152 154 157 162 133 140 143 150 152 154 157 162 133 140 143 150 152 154 157 169 1673 1686 1709 1727 1740 1776 1477 1477 1477 1478 1466 1467 1469 1479 1498 1498 1498 148 147 831-832 837-838 94 164 167 469 471 476-477 88 504 504 504 504 504 504 504 504 504 504	1188ue Origin	KWA SOUICE		SEQ ID NOS:
301 304-305 309 312-313 339 341 344-345 349 358 370-372 376 382-383 387 392 401 414 416 421 430 443 445 449 453-454 472 487-488 504 506 513 516 519 522 528 536-540 546 554 585 587 594 598 602 607 616-617 626-627 636 643 662-664 695 709 721 735 743 761 788 775-777 788 796 804 814 827 837-838 849-870 881 830-692 898 903 905-907 914 919 925 927 934 941 949 952 957 960 962 968 970 1000 1008 1029-1003 1044 1052 1055 1063 1067-1068 1073 1085 1099-1102 1107 1110-1111 1113 1115 1119 1126 1134 1136-1137 1146-1148 1135 1159 1192 1198 1199 1232-1233 1241 1256 1264 1272-1273 1281 1285 1241-121 1215 1216 1134 1326-1346 149 1351 1355-134 1341-141 141 141 141 141 141 141 141 141 1				181 197 227-228 235-236 244 251
344-345 349 358 370-372 376 382-383 383 370-372 376 382-383 387 392 401 441 46 1621 401 413 413 413 413 414 6421 401 413 413 414 6421 401 413 413 414 6421 401 413 415 414 6521 401 415 414 6521 401 415 415 415 415 415 415 415 415 415 41			ĺ	261-265 267 280-281 286 290 299
383 387 392 401 414 416 421 487 488 449 483 -484 472 487 -488 504 506 513 516 519 522 528 536 -540 546 554 585 587 594 598 602 607 616-617 626-627 636 643 662-646 695 709 721 737 743 767 788 796 804 814 827 837 838 049-850 852-853 869-870 818 830-692 898 903 905-907 914 919 925 927 934 941 949 952 577 960 962 968 970 1000 1008 1029-1030 1044 1052 1055 1063 1067-1068 1073 1085 1099-1102 1107 1110-1111 1113 1113 1115 1119 1126 1134 1136-1137 1146-1148 1153 1159 1126 1134 1136-1137 1146-1148 1153 1159 1127 1127 1128 1139 11232-1233 1241 1256 1264 1272-1273 1281 1285 1293 1294 1299 1312 1320 1324-1325 1330 1344 1349 1351 1355-1356 1365 1366 1367-1068 1476 1476 1476 1476 1476 1476 1476 1476				301 304-305 309 312-313 339 341
413 445 449 453-4554 472 87-5 525 58-58- 504 506 513 516 519 522 528 536- 500 546 554 585 587 594 598 602 607 616-617 626-627 636 643 602 664 695 709 721 735 743 761 768 775-777 788 796 804 814 827 37- 838 849-850 852-853 869-870 881 880-892 898 930 950-507 914 919 925 927 934 941 949 952 957 960 962 968 970 1000 1008 1029-1030 1044 1052 1055 1063 1067-1068 1073 1085 1099-1102 1107 1110- 1111 1113 1115 1119 1126 1134 1136-1137 1146-1148 1153 1159 1192 1196 1199 1232-1233 1241 1256 1264 1272-1273 1281 1285 1293-1294 1299 1312 1320 1124- 1325 1330 1344 1349 1351 1355- 1356 1369 1378-1379 1403 1414 1419 1428-1429 1436 1446 1458 1463-1464 1467-1468 1470 1477- 1478 1486 1491 1509 1519 1527 1529 1531 634 1547 1596 1600 1619 1623 1629 1631 1634 1638 1643 1647 1652 1666 1664 1667 1669- 1670 1673 1686 1709 1727 1740 1776 ALG001 ALG00				
504 506 533 516 519 522 528 536 540 516 554 585 585 587 594 598 602 607 516-617 626-627 636 643 662-664 659 57 097 721 735 743 761 768 775-777 788 796 804 814 827 837-838 849-850 852-853 869-870 881 8690-892 898 903 905-907 914 919 925 927 934 941 949 952 957 960 962 968 970 1000 1008 1029-1008 1044 1052 1055 1063 1067-1068 1073 1085 1099-1102 1107 1110- 1111 1113 1115 1119 1126 1134 1136-1137 1146-1148 1153 1159 1192 1196 1199 1292-1233 1241 1256 1264 1272-1273 1281 1285 1293-1294 1299 1312 1320 1124- 1325 1330 1344 1349 1351 1355- 1356 1365 1378-1379 1403 1414 1419 1428-1429 1436 1446 1458 1463-1464 1467-1468 1470 1477- 1478 1486 1491 1509 1519 1527 1529 1534 1547 1596 1600 1619 1623 1629 1631 1634 1638 1643 1647 1652 1660 1646 1667 1669- 1670 1673 1666 1709 1727 1740 1776 adult lung GIBCO ALGOO1 AL			ļ	i e
SAO 546 554 585 587 594 598 602 607 516-627 626-627 636 643 662-664 695 709 721 735 743 761 768 775-777 788 796 804 814 827 837-838 849-650 852-853 869-870 881 890-839 289 809 305-907 914 919 925 927 934 941 949 952 957 960 962 968 970 1000 1008 1029-1030 1044 1052 1055 1063 1067-1068 1073 1085 1099-102 1107 1110-1111 1113 1115 1119 1126 1134 1136-1137 1146-1148 1153 1159 1192 1196 1199 1232-1233 1241 1256 1264 1272-1273 1281 1285 1293-1294 1299 1312 1320 1324-1325 1330 1344 1349 1351 1355-1356 1369 1378-1379 1403 1414 1419 128-1429 1436 1446 1458 1463-1464 1467-1468 1470 1477-1478 1486 1491 1599 1527 1529 1534 1547 1599 1507 1577 1478 1486 1491 159 1519 1527 1529 1534 1547 1596 1600 1619 1623 1623 1623 1639 1374 1370 1324-1325 1330 1344 134 1351 1351 1351 1351 1351 1351				
607 516-627 626-627 636 643 662-626 646 565 709 721 735 743 761 768 766 646 565 709 721 735 743 761 768 775-777 788 796 804 814 827 837-838 49-850 852-853 869-870 881 8690-892 898 903 905-907 914 919 925 927 934 941 949 925 927 960 962 968 970 1000 1008 1029-1008 1044 1052 1055 1063 1067-1068 1073 1085 1099-1102 1107 1110-1111 1113 1115 1119 1126 1134 1136-1137 1146-1148 1153 1159 1129 1196 1199 1292-1233 1241 1256 1264 1272-1273 1281 1285 1293-1294 1299 1312 1320 1124-1325 1330 1344 1349 1351 1355-1356 1365 1378-1379 1403 1414 1419 1428-1429 1436 1446 1458 1463 1463 1463 1463 1463 1463 1463 1643 1652 1650 1645 1667 1673 1666 1709 1727 1740 1777-1478 1486 1491 1509 1519 1527 1529 1534 1547 1556 1600 1619 1623 1629 1631 1634 1638 1643 1647 1652 1660 1646 1667 1669-1670 1673 1666 1709 1727 1740 1776 1776 1776 1776 1776 1776 1776 177		:		
664 595 709 721 735 742 761 768 775-777 788 796 804 814 827 837-838 89-970 881 890-892 889 903 905-907 914 919 925 927 934 941 949 952 957 960 962 986 970 1000 1008 1029-1030 1044 1052 1055 1063 1067-1068 1073 1085 1099-10102 1107 1110- 1111 1113 1115 1119 126 1134 1136-1137 1146-1148 1153 1159 1192 1196 1199 1232-1233 1241 1265 1264 1272-1273 1281 1285 1293-1294 1299 1312 1320 1324- 1325 1330 1344 1349 1351 1355- 1326 1369 1378-1379 1301 3144 1419 1428-1429 1436 1446 1458 1449 1428-1429 1436 1446 1458 1449 1428-1429 1436 1446 1458 1449 1428-1429 1436 1446 1458 1449 1428-1429 1312 1630 1641 1479 1530 1544 1630 1643 1463-1464 1467-1468 1470 1477- 1478 1546 1491 1509 1519 1527 1478 1546 1491 1509 1519 1527 1478 1546 1491 1509 1519 1527 1478 1546 1491 1509 1519 1527 1478 1546 1491 1509 1519 1527 1478 1546 1491 1509 1519 1527 1478 1546 1491 1509 1519 1527 1478 1546 1491 1509 1519 1527 1478 1546 1491 1509 1519 1527 1478 152 1660 1664 1667 1669- 1670 1673 1686 1709 1727 1740 1478 152 1660 1664 1667 1669- 1670 1673 1686 1709 1727 1740 1478 152 1660 1664 1667 1669- 1670 1673 1686 1709 1727 1740 1478 152 1650 1664 1667 1669- 1670 1673 1686 1709 1727 1740 1478 152 1650 1664 1667 1669- 1670 1673 1686 1709 1727 1740 1478 152 1660 1664 1667 1669- 1670 1673 1686 1709 1727 1740 1478 152 1650 1664 1667 1669- 1670 1673 1686 1709 1727 1740 1478 152 1650 1664 1667 1669- 1670 1673 1686 1709 1727 1740 1478 152 1650 1664 1667 1669- 1670 1673 1686 1709 1727 1740 1478 152 1650 1664 1667 1669- 1670 1670 1670 1670 1670 1670 1670 1670				
775-777 788 796 804 814 827 837-883 869-892 838 869-870 881 838 49-850 852-883 869-870 881 850-892 888 903 905-907 914 919 925 97 934 941 949 952 957 960 952 968 970 1000 1008 1029-1020 1044 1052 1055 1063 1067-1068 1073 1085 1099-1102 1107 1110- 1111 1113 1115 1119 1126 1134 1136-1137 1146-1148 1153 1159 1192 1196 1199 1232-2233 1241 1256 1264 1272-1273 1281 1285 1293-1294 1299 1312 1320 1324- 1325 1330 1344 1349 1351 1355- 1356 1365 1378-1379 1403 1414 1419 1288-1429 1346 1446 1458 1463-1464 1467-1468 1470 1477- 1478 1486 1491 1599 1519 1527 1529 1534 1547 1596 1600 1619 1623 1623 1623 1637 1634 1638 1643 1647 1652 1660 1664 1667 1669- 1670 1673 1686 1709 1727 1740 1776 adult lung GIBCO ALGOUI 4-88 93 103-104 113 125 133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 255 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 54 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 719 743-744 767 3766 774 789 803 811 814 817 831-832 837-838 845 852-853 883-859 861 866 880 887 901 905 941 954-957 966 971 977 97 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1059 1064 1072 1080 1066-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1150 1200 1208 1220 1241 1272- 1273 1200 1282 1295 1306 1320 1331-1332 1353 1374 1379 1393- 1364 1407 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1531-1532 1547 1549 1552- 1554 1531-1532 1547 1549 1552- 1554 1531-1532 1547 1549 1552- 1554 1531-1532 1547 1549 1552- 1554 1531-1532 1547 1549 1552- 1573 1573-1573 1788 166 1613 1624 1567 1676-1677 1684 1569 1727 1731-1732 1737-1738 1748-1749 1786 1979h node Clontech ALMO01 42 575-51 82 105 137 153 198 201 223-224 234 268-269 272 280- 281 287 301 312 329 343 362 271				
830 849-850 852-853 869-870 881 890-892 889 893 905-907 914 919 925 927 934 941 949 952 957 960 962 986 970 1000 1008 1029-1030 1044 1052 1055 1063 1067-1068 1073 1085 1099-1102 1107 1110- 1111 1113 1115 1119 1126 1134 1136-1137 1146-1148 1153 1159 1192 1196 1199 1232-1233 1241 1256 1264 1272-1273 1281 1285 1293-1294 1299 1312 1320 1324- 1325 1330 1344 1349 1351 1355- 1356 1365 1378-1379 1403 1414 1419 1428-1429 1436 1446 1458 1463-1464 1467-1468 1470 1477- 1478 1486 1491 1509 1519 1527 1529 1534 1547 1596 1600 1619 1623 1629 1631 1634 1638 1643 1647 1652 1660 1646 1667 1669- 1670 1673 1666 1709 1727 1740 1776 adult lung GIBCO ALGO01 6-8 14 37-39 44-46 50-51 56 62- 63 75 82 88 93 103-104 113 125 133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 255 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 327 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 719 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1089 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1364 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553- 1556 1571 1589 1606 1613 1624 1627-1629 1632 1642 1669 1727 1731-1732 1737-1738 1748-1749 1890 1900 1223 1244 1267-1749 1890 1900 1904 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1290 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1556 1571 1589 1606 1613 1624 1627-1629 1632 1642 1664 1662 1669 1727 1731-1732 1737-1738 1748-1749 1786				
### ### ### ### ### ### ### ### ### ##				1
925 927 934 941 949 952 957 960 962 968 970 1000 1008 1029-1030 1044 1052 1055 1063 1067-1068 1073 1085 1099-1102 1107 1110- 1111 1113 1115 1119 1126 1134 1136-1137 1146-1148 1153 1159 1192 1196 1199 1232-1233 1241 1256 1264 1272-1273 1281 1285 1293-1294 1299 1312 1320 1324- 1325 1330 1344 1349 1351 1355- 1356 1369 1378-1379 1403 1414 1419 1428-1429 1436 1446 1458 1463-1464 1467-1468 1470 1477- 1478 1486 1491 1509 1519 1527 1529 1534 1547 1596 1600 1619 1623 1629 1631 1634 1638 1643 1647 1652 1660 1664 1667 1669- 1670 1673 1686 1709 1727 1740 adult lung GIBCO ALGOOI 4-8 14 37-39 44-46 50-51 56 62- 63 75 82 88 93 103-104 113 125 133 140 143 150 152 154 157 152 1529 1526 256 27 274 280-281 285 252 256 265 272 274 280-281 285 252 256 265 272 274 280-281 285 252 256 265 272 774 280-281 285 252 256 265 273 274 280-281 285 254 256 266 273 75 86 879 1797 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1052 1064 1077 1085 1097 1079 1197 190 992 991 1001 1005-1006 1014 1017 1045 1047 1055 1059 1062 1064 1077 1169 1139 1139 1139 1139 1139 1139 1139				
962 968 970 1000 1008 1029-1036 1044 1052 1055 1063 1067-1068 1073 1085 1099-1102 1107 1110- 1111 1113 1115 1119 1126 1134 1136-1137 1146-1148 1133 1159 1192 1196 1199 1232-1233 1241 1256 1264 1272-1273 1281 1285 1293-1294 1299 1312 1320 1324- 1325 1330 1344 1349 1351 1355- 1356 1369 1378-1379 1403 1414 1419 1428-1429 1436 1446 1458 1463-1464 1467-1468 1470 1477- 1478 1486 1491 1509 1519 1527 1478 1486 1491 1509 1519 1527 1529 1534 1547 1596 1600 1619 1622 1629 1631 1634 1638 1643 1647 1652 1660 1664 1667 1669- 1670 1673 1686 1709 1727 1740 1776 adult lung GIBCO ALG001 4-88 14 37-39 44-46 50-51 56 62-63 75 82 88 93 103-104 113 125 133 140 143 150 152 154 157 126 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251-225 252 256 255 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 445 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-666 450 695 716 719 743-744 763 766 774 789 803 811 814 817 81-831-832 337-838 845 801 901 905 941 987-959 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1364 1104 1409 1409 1423 1434 1436 1442 1474 1478 1494 1509 1552- 1525 1531-1532 1547 1549 1553- 1554 1571 1598 1606 1613 1624 1627-1629 1632 1649 1644 1662 1669 1676-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749 19mph node Clontech ALNO01 4 24 50-51 82 105 137 153 198 201 223-224 234 268-269 272 280-281 285 281 845 466 467 467 475 481-0476 201 223-224 234 268-269 272 280-281 287 301 312 329 343 382 421 1376 1477 1478 1478 1494 1509 1552-1578 1554 1571 1598 1606 1613 1624 1627-1629 1632 1642 1644 1662 1669 1676-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749 1766				
1044 1052 1055 1063 1067-1068 1073 1085 1099-1102 1107 1110- 1111 1113 1115 1119 1126 1134 1136-1137 1146-1148 1135 1159 1192 1196 1199 1232-1233 1241 1256 1266 1272-1273 1281 1285 1291-1294 1299 1312 1320 1324- 1325 1330 1344 1349 1351 1355- 1356 1365 1378-1379 1403 1414 1419 1422-1429 1436 1446 1458 1463-1464 1467-1468 1470 1477- 1478 1486 1491 1509 1519 1527 1529 1534 1547 1596 1600 1619 1623 1629 1631 1634 1638 1643 1647 1652 1660 1664 1667 1669- 1670 1673 1686 1709 1727 1740 1776 adult lung GIBCO ALGOO1 4-8 14 37-39 44-46 50-51 56 62- 63 75 82 88 93 103-104 113 125 133 140 143 150 152 154 157 152 133 140 143 150 152 154 157 152 1529 1529 1536 1547 175 190-191 196 200 211 124 219 223-224 227-228 251 252 252 252 256 265 272 74 280-281 285 310 312 345 351 362 371 381-382 394 408-409 431 436 445 446 459 461 467 469 471 476-477 488 554 564 583 607 616-617 621 622-624 634 645-646 662-664 670 655 71 67 71 719 743-747 788 803 811 814 817 831-832 837-838 854 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 991 987 990 992 991 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383 1344 1404 1409 1429 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553- 1556 1571 1599 1606 1613 1624 1627-1629 1632 1642 1644 1662 1669 1676-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749 19mph node Clontech ALMOO1 424 505-182 105 137 153 198 201 223-224 224 224 2284 2394 330 33 22 421 2373 2373 243 45 14 464 475 481-				1
1073 1085 1099-1102 1107 1110- 1111 1113 1115 1119 1126 1134 1136-1137 1146-1148 1153 1159 1192 1196 1199 122-1233 1241 1256 1264 1272-1273 1281 1285 1293-1294 1299 1312 1320 1324-1325 1330 1324-1325 1330 1344 1349 1351 1355-1356 1365 1378-1379 1403 1414 1419 1428-1429 1436 1446 1458 1463-1464 1467-1468 1470 1477-1478 1486 1491 1509 1519 1519 1478 1486 1491 1509 1519 1519 1527 1478 1486 1491 1509 1519 1519 1527 1529 1534 1547 1596 1600 1619 1623 1629 1631 1634 1638 1643 1647 1652 1660 1664 1667 1669-1670 1673 1686 1709 1727 1740 1478 1486 1368 1709 1727 1740 1478 1486 1368 1709 1727 1740 1478 1486 1368 1709 1727 1740 1478 1486 138 138 139 139 103-104 113 125 133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251-224 227-228 251-224 227-228 251-225 265 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 461 467 469 471 476-477 488 504 513 527 537-540 544 57-548 554 463 465-646 662-664 670 695 716 719 743-744 763 766 774 789 803 811 814 817 831-832 831-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 96 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1069 1062 1064 1072 1080 1086-1089 1094 107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272-1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383-1384 1404 1409 1422 1434 1436 1444 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1552 1526 1531-1532 1547 1549 1552 1527 1531-1532 1547 1549 1552 1528 1531-1532 1547 1549 1552 1528 1531-1532 1547 1549 1552 1528 1531-1532 1547 1549 1552 1526 1531-1532 1547 1549 1552 1527 1531-1532 1547 1549 1552 1528 1531-1532 1547 1549 1552 1528 1531-1532 1547 1549 1552 1528 1531-1532 1547 1549 1552 1528 1531-1532 1547 1549 1552 1528 15				•
1111 1113 1115 1119 1126 1134 1136 1134 1136-1137 1146-1148 1153 1159 1192 1196 1199 1232-1233 1241 1256 1264 1272-1273 1281 1285 1293-1294 1279 1312 1320 1324-1325 1330 1344 1349 1351 1355-1355 1365 1369 1378-1379 1403 1414 1419 1428-1429 1436 1446 1458 1463-1464 1467-1466 1470 1477-1478 1486 1491 1509 1519 1527 1529 1534 1547 1556 1600 1619 1623 1629 1631 1634 1638 1643 1644 1652 1660 1664 1667 1669-1670 1673 1686 1709 1727 1740 1776 1673 1686 1709 1727 1740 1776 1670 1673 1686 1709 1727 1740 1776 1673 1686 1709 1727 1740 1776 1673 1686 1709 1727 1740 1776 1673 1686 1709 1727 1740 1776 1673 1686 1709 1727 1740 1776 1673 1686 1709 1727 1740 1776 1673 1686 1709 1727 1740 1776 1673 1686 1709 1727 1740 1776 1673 1686 1709 1727 1740 1776 1673 1686 1709 1727 1740 1776 1673 1686 1709 1727 1740 1776 1673 1686 1709 1727 1740 1776 1673 1686 1709 1727 1740 1776 1673 1686 1709 1727 1740 1776 1673 1686 1709 1727 1740 1776 1673 1686 1709 1727 1740 1776 1673 1686 1709 1727 1740 1776 1673 1686 1709 1727 1740 1776 1673 1686 1709 1727 1740 1776 1776 1776 1776 1776 1776 1776 177				
1136-1137 1146-1148 1153 1159 1199 1232-1233 1241 1256 1264 1272-1273 1281 1285 1293-1294 1299 1312 1320 1320-1325 1330 1344 1349 1351 1355-1356 1365 1378-1379 1403 1414 1419 1428-1429 1436 1446 1458 1463-1464 1467-1468 1470 1477-1478 1486 1491 1509 1519 1527 1529 1534 1547 1596 1600 1619 1623 1629 1631 1634 1638 1643 1644 1652 1660 1664 1667 1669-1670 1673 1686 1709 1727 1706 1673 1686 1709 1727 1706 1777 1777				L .
1192 1196 1199 1232-1233 1241 1256 1264 1272-1273 1281 1285 1293 1294 1299 1312 1320 1324 1325 1330 1344 1349 1351 1355 1356 1369 1378-1379 1403 1414 1419 1428-1429 1436 1446 1458 1463-1464 1465 1467-1468 1467-1468 1467 1477 1478 1486 1491 1509 1519 1527 1529 1534 1547 1556 1600 1619 1623 1629 1631 1634 1638 1643 1644 1652 1660 1664 1667 1669 1670 1673 1686 1709 1727 1740 1776 1776 1776 1776 1776 1777 1740 1776 1740 1776 1777 1740 1776 1740 1740 1776 1740		'		ł.
1256 1264 1272-1273 1281 1285 1293-1294 1299 1312 1320 1324 1393 1312 1330 1324 1393 1315 1355 1356 1365 1378-1379 1403 1414 1419 1428-1429 1436 1446 1458 1463-1464 1467-1468 1470 1477-1478 1486 1491 1509 1519 1527 1529 1534 1547 1596 1600 1619 1623 1629 1631 1634 1638 1643 1647 1652 1660 1664 1667 1669 1670 1673 1686 1709 1727 1740 1776 1777 1740 1776 1776 1776 1776 1776 1776 1776 1777 1740 1776 1776 1776 1776 1776 1776 1776 1777 1740 1776 1777				
1325 1330 1344 1349 1351 1355- 1356 1369 1378-1379 1403 1414 1419 1428-1429 1436 1446 1458 1463-1464 1467-1468 1470 1477- 1478 1486 1491 1509 1519 1527 1529 1534 1547 1596 1600 1619 1623 1629 1631 1641 1638 1643 1647 1652 1660 1664 1667 1669- 1670 1673 1686 1709 1727 1740 1776 ALGOO1		·		· ·
1356 1369 1378-1379 1403 1414 1419 1428-1429 1436 1446 1459 1463-1464 1467-1468 1470 1477-1478 1486 1491 1509 1519 1527 1529 1534 1547 1596 1600 1619 1623 1629 1631 1634 1638 1643 1647 1652 1660 1664 1667 16659-1670 1673 1686 1709 1727 1740 1776 adult lung GIBCO ALG001 4-8 14 37-39 44-46 50-51 56 62-63 75 82 88 93 103-104 113 125 133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251-252 266 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 445 445 453 464 464-646 662-664 670 695 716 749 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272-1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383-1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1552 1554 1571 1598 1606 1614 1617 1645 167 1771 1773 1773 1773 1773 1773 1773			1	
1419 1428-1429 1436 1446 1458 1463-1464 1467-1468 1470 1477-1478 1486 1491 1509 1519 1527 1529 1534 1547 1596 1600 1619 1623 1629 1631 1634 1638 1643 1647 1652 1660 1664 1667 1669-1670 1673 1686 1709 1727 1740 1776 1767 1686 1709 1727 1740 1776 1768 1689 1709 1727 1740 1776 1774 1776 1774 1776 1774 1776 1774 1775 1775 177			}	
1463-1464 1467-1468 1470 1477- 1478 1486 1491 1509 1519 1527 1529 1534 1547 1596 1600 1619 1623 1629 1631 1634 1638 1643 1667 1652 1660 1664 1667 1669- 1670 1673 1686 1709 1727 1740 1776 ALGOOI			Ţ	
1478 1486 1491 1509 1519 1527 1529 1534 1547 1596 1600 1619 1623 1629 1631 1634 1638 1643 1647 1652 1660 1664 1667 1669 1670 1673 1686 1709 1727 1740 1776 1766 1767 1673 1673 1679 1727 1740 1776 1768 1776 1777 1776 1777 1776 1777 1776 1777 1				
1529 1534 1547 1596 1600 1619 1623 1629 1631 1634 1638 1643 1647 1652 1660 1664 1667 1669 1670 1673 1686 1709 1727 1740 1776 1673 1686 1709 1727 1740 1776 1673 1686 1709 1727 1740 1776 1673 1686 1709 1727 1740 1776 1777 1776 17777 1777 1777 1777 1777 1777 1777 1777 1777 17777 1777 1777 1777 1777 1777 17777				
1623 1629 1631 1634 1638 1643 1647 1652 1660 1664 1667 1669-1670 1673 1686 1709 1727 1740 1776	ı			
adult lung GIBCO ALGOO1 4-8 14 37-39 44-46 50-51 56 62-63 75 82 88 93 103-104 113 125 133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251-252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 719 743-744 766 670 695 716 719 743-744 766 767 74 789 803 811 814 817 831-832 837-838 845 852-853 888-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272-1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383-1554 1571 1598 1606 1613 1624 1627-1629 1632 1644 1662 1669-1676-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749 1786 1876-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749 1786 1876-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749 1786 1876-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749 1786 1878-1878 1878-1878 1878-1879 1878 201 223-224 234 268-269 272 280-281 287 301 312 329 343 382 421 430 433 445 451 461-462 475 481-				
ALGOO1 ALGoo1 ALGoo1 ALGoo1 ALgoo1 ALgoo1 ALgoo1 Algoo1 A				1
adult lung GIBCO ALGOO1 A-8 14 37-39 44-46 50-51 56 62-63 75 82 88 93 103-104 113 125 134 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251-252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 504 504 504 504 504 504 504 504 504				
63 75 82 88 93 103-104 113 125 133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 71,9 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1364 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553- 1554 1571 1598 1606 1613 1624 16627-1629 1632 1642 1644 1662 1669 1676-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749 1786 1ymph node Clontech ALN001 ALN001 Clontech ALN001 AL				
133 140 143 150 152 154 157 162	adult lung ·	GIBCO	ALG001	4-8 14 37-39 44-46 50-51 56 62-
171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 71,9 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553- 1554 1571 1598 1606 1613 1624 1627-1629 1632 1642 1644 1662 1669 1676-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749 1786 lymph node Clontech ALNO01 ALNO	· ·		l .	
211 214 219 223-224 227-228 251- 252 256 265 27 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-646 70 695 716 71,9 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553- 1554 1571 1598 1606 1613 1624 1627-1629 1632 1642 1644 1662 1669 1676-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749 1786 1ymph node		1	i	63 75 82 88 93 103-104 113 125
252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 71,9 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553- 1554 1571 1598 1606 1613 1624 1627-1629 1632 1642 1644 1662 1669 1676-1677 1684 1696 1727 1731 1732 1737-1738 1748-1749 1786 lymph node Clontech ALNO01 4 24 50-51 82 105 137 153 198 201 223-224 234 268-269 272 280- 281 287 301 312 329 343 382 421 430 433 445 451 461-462 475 481-				l .
310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 71,9 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553- 1554 1571 1598 1606 1613 1624 1627-1629 1632 1642 1644 1662 1669 1676-1677 1684 1696 1727 1731 1732 1737-1738 1748-1749 1786 lymph node Clontech ALNO01 4 24 50-51 82 105 137 153 198 201 223-224 234 268-269 272 280- 281 287 301 312 329 343 382 421 430 433 445 451 461-462 475 481-				133 140 143 150 152 154 157 162
394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 71,9 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553- 1554 1571 1598 1606 1613 1624 1627-1629 1632 1642 1644 1662 1669 1676-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749 1786 lymph node Clontech ALN001 4 24 50-51 82 105 137 153 198 201 223-224 234 268-269 272 280- 281 287 301 312 329 343 382 421 430 433 445 451 461-462 475 481-				133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251-
461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 719 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553- 1554 1571 1598 1606 1613 1624 1627-1629 1632 1642 1644 1662 1669 1676-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749 1786 lymph node Clontech ALNO01 ALNO01 ALNO01 A 24 50-51 82 105 137 153 198 201 223-224 234 268-269 272 280- 281 287 301 312 329 343 382 421 430 433 445 451 461-462 475 481-				133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285
S13 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 71,9 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553- 1554 1571 1598 1606 1613 1624 1627-1629 1632 1642 1644 1662 1669 1676-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749 1786				133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382
S64 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 719 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272-1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383-1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553-1554 1571 1598 1606 1613 1624 1627-1629 1632 1642 1644 1662 1669 1676-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749 1786				133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459
634 645-646 662-664 670 695 716 71,9 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553- 1554 1571 1598 1606 1613 1624 1627-1629 1632 1642 1644 1662 1669 1676-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749 1786 lymph node Clontech ALNOO1 ALNOO				133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504
71,9 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553- 1554 1571 1598 1606 1613 1624 1627-1629 1632 1642 1644 1662 1669 1676-1677 1684 1696 1727 1731 1732 1737-1738 1748-1749 1786 lymph node Clontech ALNO01 ALNO0				133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554
B11 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553- 1554 1571 1598 1606 1613 1624 1627-1629 1632 1642 1644 1662 1669 1676-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749 1786 lymph node Clontech ALNO01				133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624
852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272-1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383-1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553-1554 1571 1598 1606 1613 1624 1627-1629 1632 1642 1644 1662 1669 1676-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749 1786 1786				133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716
901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272-1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383-1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553-1554 1571 1598 1606 1613 1624 1627-1629 1632 1642 1644 1662 1669 1676-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749 1786				133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 719 743-744 763 766 774 789 803
979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553- 1554 1571 1598 1606 1613 1624 1627-1629 1632 1642 1644 1662 1669 1676-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749 1786 lymph node				133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 71,9 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845
1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553- 1554 1571 1598 1606 1613 1624 1627-1629 1632 1642 1644 1662 1669 1676-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749 1786				133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 71,9 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887
1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272-				133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 71,9 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977
1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272-				133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 719 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001
1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553- 1554 1571 1598 1606 1613 1624 1627-1629 1632 1642 1644 1662 1669 1676-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749 1786 lymph node				133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 71,9 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080
lymph node Clontech ALN001 ALN001 ALN001 Ala 20 133 123 136 1320 1331 1332 1353 1374 1379 1383 1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531 1532 1547 1549 1553 1554 1571 1598 1606 1613 1624 1627 1629 1632 1642 1644 1662 1669 1676 1677 1684 1696 1727 1731 1732 1737 1738 1748 1749 1786				133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 71,9 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134
1331-1332 1353 1374 1379 1383- 1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553- 1554 1571 1598 1606 1613 1624 1627-1629 1632 1642 1644 1662 1669 1676-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749 1786 1ymph node Clontech ALNO01 4 24 50-51 82 105 137 153 198 201 223-224 234 268-269 272 280- 281 287 301 312 329 343 382 421 430 433 445 451 461-462 475 481-				133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 71,9 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173
1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553- 1554 1571 1598 1606 1613 1624 1627-1629 1632 1642 1644 1662 1669 1676-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749 1786 1ymph node				133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 71,9 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272-
lymph node				133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 71,9 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320
1525 1531-1532 1547 1549 1553- 1554 1571 1598 1606 1613 1624 1627-1629 1632 1642 1644 1662 1669 1676-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749 1786 lymph node				133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 71,9 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383-
1554 1571 1598 1606 1613 1624 1627-1629 1632 1642 1644 1662 1669 1676-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749 1786 lymph node				133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 719 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1384 1404 1409 1423 1434 1436
1627-1629 1632 1642 1644 1662 1669 1676-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749 1786				133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 71,9 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522
1669 1676-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749 1786 1ymph node Clontech ALNOO1 4 24 50-51 82 105 137 153 198 201 223-224 234 268-269 272 280- 281 287 301 312 329 343 382 421 430 433 445 451 461-462 475 481-				133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 71,9 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553-
1731-1732 1737-1738 1748-1749 1786 lymph node Clontech ALN001 4 24 50-51 82 105 137 153 198 201 223-224 234 268-269 272 280- 281 287 301 312 329 343 382 421 430 433 445 451 461-462 475 481-				133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 71,9 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553- 1554 1571 1598 1606 1613 1624
lymph node Clontech ALN001 4 24 50-51 82 105 137 153 198 201 223-224 234 268-269 272 280- 281 287 301 312 329 343 382 421 430 433 445 451 461-462 475 481-				133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 71,9 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553- 1554 1571 1598 1606 1613 1624 1627-1629 1632 1642 1644 1662
lymph node Clontech ALN001 4 24 50-51 82 105 137 153 198 201 223-224 234 268-269 272 280- 281 287 301 312 329 343 382 421 430 433 445 451 461-462 475 481-				133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 71,9 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553- 1554 1571 1598 1606 1613 1624 1627-1629 1632 1642 1644 1662 1669 1676-1677 1684 1696 1727
281 287 301 312 329 343 382 421 430 433 445 451 461-462 475 481-				133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 71,9 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553- 1554 1571 1598 1606 1613 1624 1627-1629 1632 1642 1644 1662 1669 1676-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749
430 433 445 451 461-462 475 481-	lymph node	Clontech	ALN001	133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 71,9 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553- 1554 1571 1598 1606 1613 1624 1627-1629 1632 1642 1644 1662 1669 1676-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749 1786
	lymph node	Clontech	ALN001	133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 71,9 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553- 1554 1571 1598 1606 1613 1624 1627-1629 1632 1644 1644 1662 1669 1676-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749 1786
	lymph node	Clontech	ALN001	133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 71,9 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553- 1554 1571 1598 1606 1613 1624 1627-1629 1632 1642 1644 1662 1669 1676-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749 1786 4 24 50-51 82 105 137 153 198 201 223-224 234 268-269 272 280-
482 503 526 529 537-540 546-547	lymph node	Clontech	ALN001	133 140 143 150 152 154 157 162 171-172 174-175 190-191 196 200 211 214 219 223-224 227-228 251- 252 256 265 272 274 280-281 285 310 332 345 351 362 371 381-382 394 408-409 431 436 445 454 459 461 467 469 471 476-477 488 504 513 527 537-540 544 547-548 554 564 583 607 616-617 621 623-624 634 645-646 662-664 670 695 716 71,9 743-744 763 766 774 789 803 811 814 817 831-832 837-838 845 852-853 858-859 861 866 880 887 901 905 941 954-957 966 971 977 979 981 987 990 992 996 1001 1005-1006 1014 1017 1045 1047 1054 1059 1062 1064 1072 1080 1086-1089 1094 1107 1126 1134 1136-1137 1142 1150 1157 1173 1190 1200 1208 1220 1241 1272- 1273 1280 1282 1295 1306 1320 1331-1332 1353 1374 1379 1383- 1384 1404 1409 1423 1434 1436 1442 1474 1478 1494 1509 1522 1525 1531-1532 1547 1549 1553- 1554 1571 1598 1606 1613 1624 1627-1629 1632 1642 1644 1662 1669 1676-1677 1684 1696 1727 1731-1732 1737-1738 1748-1749 1786 4 24 50-51 82 105 137 153 198 201 223-224 234 268-269 272 280- 281 287 301 312 329 343 382 421 430 433 445 451 461-462 475 481-

Tissue Origin	RNA Source	Hyseq	000 10 100
		Library Name	SEQ ID NOS:
			621 626 649 679 719 725-726 738 793 803 831 834-836 838 844 857-858 866 879 905 913 928 963 976 1005-1006 1012 1038 1050 1116-1117 1151 1199 1204 1226 1243 1265 1274 1324-1325 1339 1353 1374 1377 1440-1441 1447 1504 1549 1600 1618-1619 1631 1641 1644 1653 1687-1688 1691-1692 1741 1771
young liver	GIBCO	ALV001	5-8 11 20-21 46 50-51 58 65-66
			75 79 82 93 97 102-103 108 10 116 139 143-144 148-149 171-172 174 187-189 194-195 198 209 214- 215 230 250 258 267-269 280-281 306 309 342 351 356 359 362 372 374 392 394 398 401 407-408 410 414 431 444 455 459 476 478 483 493 510-512 516 520 522 526 536 549 571 574-577 585 592 601-602 607 621-624 628-630 632-633 637 648 660 666-667 678 697-698 700 717 719 728 730 734 738 744-745 766 770 773 779 788 800 808 812 814 841 849-851 871 874 879 887 893 898-900 902-904 906-907 911 919 922 924 934 953 957 963 965 970 984 986 997 1001 1004 1007 1012 1029-1030 1033-1034 1052 1061 1066 1070 1076 1086 1089 1093 1099-1102 1110-1112 1116- 1117 1119 1121 1125 1136-1137 1144-1145 1156-1157 1159 1196 1199-1200 1209 1211 1219-1220 1241 1244 1262 1270 1275 1279 1283 1295 1317-1320 1332 1339 1344 1359 1362-1363 1379 1383- 1384 1403 1415 1430-1431 1437 1450 1467 1475-1476 1483-1484 1494-1495 1498 1505 1512 1516 1518-1519 1526 1529 1547 1550- 1552 1557-1559 1565 1583 1587 1597 1609 1614 1620 1631 1637 1641 1644 1654-1655 1662 1667 1669 1684 1691-1692 1702 1711 1725 1738 1741 1743-1744 1758 1760-1761 1763-1765 1769
adult liver	Invitrogen		5-8 17 20-21 32-33 41 55 58 64 75 77 86 89 102 108 117 119 175- 176 198 200 209 231 235-236 250 272 275-276 284 306 316 321 325 333 356 359 374 376 398 401 408 414 428 430 433-435 454 476 494 503-505 517-518 528 534 544 552 561-563 567 578 581 608-609 630 632 637 644 650 661 665 672 702 707 710 721-722 750 753 778 782 794 814 820 826 834-837 847 849- 850 858 861 874 879 893 898 904 911 918 921-922 926 946 948 972 978 986 996 1020 1027 1031 1034 1053 1063 1068 1070 1073 1086 1089 1093 1097 1113 1119 1156 1159 1195 1198-1199 1208 1220 1227 1241 1261 1272-1273 1277 1285 1308 1315 1320 1324-1325 1330 1362-1363 1375 1403 1408- 1409 1415 1431-1432 1435 1467 1469 1482 1504 1524 1542

Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
		Library Name	
			1550 1567 1578 1581 1583 1594 1597 1601-1602 1611-1612 1615
			1618-1619 1621 1625 1637 1645
			1647 1652 1654-1655 1660 1666
			1669-1671 1684 1706 1722 1737-
•			1738 1742-1744 1760-1761 1753-
			1765 1772 1774
adult liver	Clontech	ALV003	29 676 997 1063 1119 1536 1766
adult ovary	Invitrogen	AOV001	1 4-18 20-23 29 35-40 42-48 50-
1			51 53-58 61-63 65-66 68-69 73-75
			103-104 106-108 110 113 115 118
	ĺ		122-124 126 128 133-134 136-140
			142 145-147 149-157 161 166 168-
İ	·		170 174 177-178 180 182-186 188-
	Į		189 192-203 207 209 211-215 219
			221-224 229-230 234 242-243 246-
	l		247 255 258 260-262 265-269 271-
1			272 274 277-281 284-286 288 290
[295 299 301-302 304 307 309-311 313-314 316 321 323-326 330 332-
1	{		333 335-338 341 344 349 352-353
		İ	356 358 360 362 370-372 376-377
1 '	1		379-384 387 390-392 394 397-398
1	l		100 103 408-410 412 414-416 423-
			424 426-427 430-435 439 443-446
	1	{	448-449 451 453-455 462-463 468-
İ	j		471 473 476-479 481-484 487 489- 494 496-497 499-501 503-505 509-
			514 516-517 519-520 522 524 526
	i		528-534 541-544 546-547 549 552
		}	554-555 561-564 566-567 569-570
			572-573 575-576 579 581 583 585-
	1		588 590-591 593 595 597 599 601-
	\	į	605 607-613 615 618-622 524-627
, ,	[649-652 654-655 657-665 667-675
			677-678 681 683-684 692-695 697-
			710 714-721 723 725-727 729 732
		Į.	734-735 743-746 750-751 753 758
]	763 765 767 772-773 775-778 780
		1	783-784 786 788 790-791 794-796 800 803 805 809-811 813-815 818-
			819 821-824 826 828-829 831-832
}]	837-838 843-850 852-857 859-864
	1	}	867 869 871-872 874-875 878-883
		[887-888 890-895 898-910 912-914
		j	916 919-922 924 926-927 929-939
			941 943-946 948-951 953 955-958
	1]	961-964 966-967 970-979 981-982 985-986 988-990 992 995-997 999-
		İ	1001 1004-1009 1011-1013 1016
		ĺ	1019-1020 1024-1025 1029-1031
))	1033-1035 1037 1039 1041-1047
			1050-1051 1054-1060 1062-1064
		}	1067-1070 1072-1073 1075-1076
	1	[1078-1079 1085-1086 1089-1090
	1		1094~1096 1098~1103 1106-1108
	1	[1112-1117 1119-1120 1123-1127 1131-1135 1142-1143 1146-1149
			1153 1156 1158 1163 1165-1166
	1	(1169-1171 1173-1175 1177-1178
	,		1180 1183-1185 1190-1191 1195
		(1197-1200 1202 1205-1214 1217-
	Į	1	1219 1221-1226 1232-1235 1238-
			1241 1243-1244 1247 1249 1252-
1	1	(1254 1256-1258 1262 1265 1267-
		1	-1268 1270 1275 1278 1280-1283 1286-1289 1291 1293-1294 1298-
L	<u> </u>	ــــــــــــــــــــــــــــــــــــــ	1200-1283 1731 1533-1534 1538-

Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
118840 0123211	Man Boarde	Library Name	222 25 1105
			1299 1306 1308 1312 1317-1321
			1323 1327 1329-1330 1332-1333
1			1338-1339 1341 1343-1351 1356
ļ .			1359 1361 1365-1366 1371-1375
			1377-1379 1383-1384 1386 1389 1394 1400 1404 1416-1417 1422-
[1427 1429-1431 1435-1436 1439-
}	i	Ì	1443 1445-1450 1453-1456 1459
! !			1463-1464 1466 1468 1470 1474-
1			1481 1484-1485 1488 1491 1493-
1			1494 1496-1498 1501-1504 1506-
}			1507 1511-1517 1519 1521-1524
1 1		Ì	1526-1527 1530-1531 1534-1536 .
1			1538-1539 1541 1546 1548-1550
i l			1553 1555-1559 1561-1563 1566-
,	,	Į	1567 1569-1570 1572 1574-1575
1			1578 1580-1581 1587-1588 1590-
('	1	1591 1595 1597-1598 1600-1606
1		1	1609 1611-1621 1623-1630 1634
			1636 1638 1641 1643 1645 1647-
j			1657 1659-1662 1664 1667 1669- 1671 1673-1674 1676-1681 1683-
1			1690 1699 1702-1707 1710-1711
}			1713-1714 1716-1719 1723-1724
1			1726-1728 1731-1733 1735 1737-
[!		[1738 1740-1741 1743-1744 1748-
}		İ	1751 1753 1755-1756 1760-1762
l I			1765 1767-1768 1770-1771 1776
1			1778-1779 1783-1784 1786
adult placenta	Clontech	APL001	5-8 44-45 90-91 107-108 159 178
			311 351 414 476 503 545 574 624
i '			636 719 755 773 860 890-891 924
[947 955-956 962 990 992 1002
		l	1045 1202 1320 1369 1628 1686
			1 1913 1914 1943 1944
	Taurimmana	NDT 002	1713-1714 1743-1744
placenta	Invitrogen	APL002	14-16 26 29 43 60-61 79-80 103
placenta	Invitrogen	APL002	14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196
placenta	Invitrogen	APL002	14-16 26 29 43 60-61 79-80 103
placenta	Invitrogen	APL002	14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299
placenta	Invitrogen	APL002	14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417
placenta	Invitrogen	APL002	14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857-
placenta	Invitrogen	APL002	14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989
placenta	Invitrogen	APL002	14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064
placenta	Invitrogen	APL002	14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145
placenta	Invitrogen	APL002	14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343
placenta	Invitrogen	APL002	14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482
placenta	Invitrogen	APL002	14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549
placenta	Invitrogen	APL002	14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649
placenta	Invitrogen	APL002	14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730
		APL002	14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649
placenta	Invitrogen GIBCO		14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730
			14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776
			14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99
			14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211
			14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211 215 219 234 253-254 256 258 264
			14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211 215 219 234 253-254 256 258 264 272 280-281 290 295 302 309 312
			14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211 215 219 234 253-254 256 258 264 272 280-281 290 295 302 309 312 325 333 341 349 358 372 382 386-
			14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211 215 219 234 253-254 256 258 264 272 280-281 290 295 302 309 312 325 333 341 349 358 372 382 386- 387 394 406 414 431 434-436 446
			14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211 215 219 234 253-254 256 258 264 272 280-281 290 295 302 309 312 325 333 341 349 358 372 382 386- 387 394 406 414 431 434-436 446 448 451 473 481 490-493 500 503
			14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211 215 219 234 253-254 256 258 264 272 280-281 290 295 302 309 312 325 333 341 349 358 372 382 386- 387 394 406 414 431 434-436 446 448 451 473 481 490-493 500 503 505 517 519 530 534 536-540 547
			14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211 215 219 234 253-254 256 258 264 272 280-281 290 295 302 309 312 325 333 341 349 358 372 382 386- 387 394 406 414 431 434-436 446 448 451 473 481 490-493 500 503 505 517 519 530 534 536-540 547 554 557 574-576 582 592 595 604
			14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211 215 219 234 253-254 256 258 264 272 280-281 290 295 302 309 312 325 333 341 349 358 372 382 386- 387 394 406 414 431 434-436 446 448 451 473 481 490-493 500 503 505 517 519 530 534 536-540 547 554 557 574-576 582 592 595 604 611-612 620-621 623 631-632 642
			14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211 215 219 234 253-254 256 258 264 272 280-281 290 295 302 309 312 325 333 341 349 358 372 382 386- 387 394 406 414 431 434-436 446 448 451 473 481 490-493 500 503 505 517 519 530 534 536-540 547 554 557 574-576 582 592 595 604 611-612 620-621 623 631-632 642 652 659 661 667 671 673-675 684
			14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211 215 219 234 253-254 256 258 264 272 280-281 290 295 302 309 312 325 333 341 349 358 372 382 386- 387 394 406 414 431 434-436 446 448 451 473 481 490-493 500 503 505 517 519 530 534 536-540 547 554 557 574-576 582 592 595 604 611-612 620-621 623 631-632 642 652 659 661 667 671 673-675 684 700 721 728 730 732 738 742-744
			14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211 215 219 234 253-254 256 258 264 272 280-281 290 295 302 309 312 325 333 341 349 358 372 382 386- 387 394 406 414 431 434-436 446 448 451 473 481 490-493 500 503 505 517 519 530 534 536-540 547 554 557 574-576 582 592 595 604 611-612 620-621 623 631-632 642 652 659 661 667 671 673-675 684 700 721 728 730 732 738 742-744 746 762 765 774 780 788-789 794
			14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776 3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211 215 219 234 253-254 256 258 264 272 280-281 290 295 302 309 312 325 333 341 349 358 372 382 386- 387 394 406 414 431 434-436 446 448 451 473 481 490-493 500 503 505 517 519 530 534 536-540 547 554 557 574-576 582 592 595 604 611-612 620-621 623 631-632 642 652 659 661 667 671 673-675 684 700 721 728 730 732 738 742-744

Library Name S84 906-908 912 919 921-923 926-927 914 947 948 948 957-958 963 977-97 978 963 990 992-949 956-997 999 1005-1007 1010 1012 1021 1036 1042-1044 1046 1049 1059 1068 1070 1076 1089-1090 1094 1103 1109 1115 1115 1122 1110 1165 1115 1115 1124 1140 1163 1170 1172 1173 1175 1124 1140 1163 1170 1173 1175 1175 1140 1163 1170 1174 1175 1175 1174 1175 1175 1176 1176 1176 1175 1175 1175				OFFO AD MOS.
### See 306-908 912 919 921-923 926-977 ### See 307 394 92 994 996-997 999 ### See 309 992-994 996-997 999 ### See 309 992-994 996-997 999 ### See 309 992-994 996-997 999 ### See 309 992-994 996-997 999 ### See 309 1005-1007 1010 1012 1013 1036 ### See 309 1005-1007 1010 1012 1013 1016 ### See 309 1005-1007 1010 1012 1013 1016 ### See 309 1019 1019 1019 1019 ### See 309 1019 1019 1019 1019 ### See 309 1019 1019 1019 1019 ### See 309 1019 1019 1019 1019 1019 1019 1019	Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
### Second Control Se			DIDIALY NAME	884 906-908 912 919 921-923 926-
### Section 1978 1983 1990 1992 1994 1997 1999 1008-1007 1010 1010 1031 1036 1002-1044 1046 1049 1059 1068 1070 1076 1089-1090 1094 1103 1109 1113 1115 1124 1140 1163 1170 1174 1177 1190 1196 1219-1220 1226-1227 1229 1236 1241 1246 1258 1269 1271 1274 1295 1301 1320 1322 1330 1334-1335 1339 1349 1351 1333 1359-1360 1364 1369 1374 1346 1377 1431 1436-1447 1439 1468 1474 1437 1436 1437 1431 1446-1447 1439 1468 1474 1477 1430 1445-1447 1439 1468 1474 1477 1430 1445-1447 1498 1551 1560 1567 1591 1600 1631 1636 1561 1564-1655 1658 1662 1670 1674 1678-1679 1644 1686 1700 1772 1731	•			
10.22-1044 10.46 10.49 1059 1056 1070 1076 1089-1090 1094 1103 1109 1113 1115 1124 1140 1163 1109 1119 1119 1129 1219-1220 1226-1227 1229 1236 1241 1246 1225 1256 1259 1271 1274 1295 1301 1320 1322 1330 1334-1335 1339 1349 1351 1235 1351 3159-1360 1364 1369 1374 1386 1397 1413 1417 1434 1436-1437 1439 1468 1474 1437 1430 1485-1487 1498 1512 1522 1525 1544-1549 1553 1560 1567 1591 1600 1631 1636 1651 1656-1655 1656 1662 1670 1674 1678-1679 1684 1686 1700 1727 1733 1738 1740-1741 1760-1761 1774 1779 1781-1782 1728 1739 1739 1739 1730 1730 1730 1730 1730 1730 1730 1730 1730 1730 1730 1730 1730 1730 1730 1730 1730 1730 1730 1730 1730 1730 1730 1730 1730 1730 1730 1730 1730 1730 1730 1730 1730 1730 1730 1730 1730 1730 1730 1730 1730 1730 1730 1730 1730 1730 1730		į		
1.070 1076 1089-1090 1094 1103				1005-1007 1010 1012 1031 1036
1109 1113 1115 1124 1140 1163 1219-				
1170 1174 1177 1190 1196 1219-1220 1226-1227 1229 1236 1241 1246 1258 1269 1271 1274 1295 1201 1220 1322 1330 1334-1335 1339 1349 1351 1353 1359-1360 1364 1369 1374 1386 1397 1413 1417 1434 1436-1437 1439 1468 1477 1480 1485-1487 1439 1468 1477 1480 1485-1487 1439 1468 1512 1522 1525 1544-1549 1553 1560 1561 1567 1591 1600 1631 1636 1651 1654-1655 1658 1662 1670 1274 1773 1738 1740-1741 1760-1771 1773 1773 1778 1778-17782 1778 1778 1778 1778 1778 1778 1778 17		1		
1220 1226-1227 1229 1236 1241 1246 1258 1269 1271 1274 1295 1291 1326 1328 1329 1271 1274 1295 1301 1320 1320 1330 1334-1335 1339 1349 1351 1353 1359-1346 1364 1364 1369 1374 1386 1397 1413 1417 1414 1436-1437 1439 1468 1474 1474 1480 1485-1487 1498 1512 1522 1525 1544-1549 1553 1560 1567 1591 1600 1631 1636 1651 1654-1655 1658 1662 1670 1674 1678-1679 1684 1686 1700 1727 1733 1738 1740-1741 1760-1761 1774 1779 1781-1782 1576 1876 1676 1678-1679 1684 1686 1700 1727 1733 1738 1740-1741 1760-1761 1774 1779 1781-1782 1576 1876 1576		J		
1246 1258 1269 1271 1274 1295 1301 1320 1322 1330 1334-1335 1339 1349 1351 1350 1335 1359-1360 1364 1369 1374 1386 1397 1413 1417 1434 1436-1437 1439 1468 1477 1480 1485-1487 1439 1468 1477 1480 1485-1487 1498 1512 1522 1525 1544-1549 1553 1560 1567 1591 1600 1631 1636 1651 1654-1655 1658 1662 1670 1674 1678-1679 1678 1678 1678 1678 1678 1678 1678 1678		ŀ		
1301 1320 1322 1330 1334-1335 1359-1360 1364 1369 1374 1386 1397 1413 1341 1344 1346-1437 1439 1468 1474 1474 1480 1485-1487 1498 1474 1474 1480 1485-1487 1498 1512 1522 1525 1544-1549 1553 1560 1567 1591 1600 1631 1636 1651 1654-1655 1658 1662 1670 1674 1678-1679 1684 1686 1700 1727 1733 1738 1740-1741 1760-1774 1779 1781-1782 1740-1741 1760-1774 1779 1781-1782 1740-1741 1760-1774 1779 1781-1782 1740-1741 1760-1774 1779 1781-1782 1740-1741 1760-1774 1779 1781-1782 1740-1741 1770-177 192 194 196-187 212-215 1227-228 247 255 258 261 282 285 288-289 301 307 311 316 330 334 3349 370-372 392 398 410 415 426-427 430-431 433 437 446 454 461 4669 473 477 481-482 493 499 502-503 513 522 526 526 555-555 563 564 572-573 578-576 581-582 586 589-602 605 612 615-617 620 631 637 647 649-650 655 656 656 655 670 674-675 712 719-721 723 728 731 736 744 746 773 780 784 788-789 802 804 809 811 814 826 831 837 804 809	ł			
1339 1349 1351 1353 1359-1360 1364 1369 1374 1366 1397 1413 1417 1434 1436-1437 1439 1468 1477 1480 1465-1467 1439 1468 1477 1480 1465-1467 1498 1553 1560 1567 1591 1600 1631 1636 1561 1564-1555 1658 1662 1670 1674 1678-1679 1684 1686 1700 1727 1733 1738 1740-1741 1760-1761 1774 1779 1781-1782 1562 1670 1674 1678-1679 1684 1686 1700 1727 1733 1738 1740-1741 1760-1761 1774 1779 1781-1782 1563 1650 1567 1591 1600 1631 130 130 130 130 130 130 130 130 130 1				
1364 1369 1374 1386 1397 1413 1417 1434 1436-1437 1439 1468 1474 1477 1480 1485-1487 1439 1553 1512 1512 1512 1524 1514 1549 1553 1516 1565 1-1655 1655 1665 1665 1670 1674 1678-1679 1684 1686 1700 1727 1733 1738 1740-1741 1760-1761 1774 1779 1781-1782 Testis GIBCO		1		
1417 1434 1436-1437 1439 1468	}	+		
1474 1477 1480 1485-1487 1498 1553 1550 1567 1591 1600 1631 1636 1561 1654 1655 1544-1549 1653 1650 1667 1657 1658 1652 1670 1674 1678-1679 1684 1686 1700 1727 1733 1738 1740-1741 1760-1761 1774 1779 1731-1732 1733 1738 1740-1741 1760-1761 1774 1779 1731-1732 1733 1738 1740-1741 1760-1761 1774 1779 1731-1732 1735 1568 1659 1659 1659 1659 1659 1659 1659 1659		İ		
1512 1522 1525 1544-1549 1553 1560 1567 1591 1600 1631 1636 1651 1654-1655 1658 1662 1670 1674 1678-1679 1684 1686 1700 1727 1733 1738 1740-1741 1750-1761 1774 1779 1781-1782 158				1
1560 1567 1591 1600 1631 1636 1636 1636 1656 1656 1655 1658 1662 1670 1674 1678 1679 1684 1686 1700 1727 1733 1738 1740-1741 1760-1761 1774 1778 1774 1773 1778 1774-1774 1776 1776 1778 1778 1778 1778 1778 1778				
1651 1654-1658 1688 1662 1670 1674 1678-1679 1684 1686 1700 1727 1733 1738 1740-1741 1760-1761 1774 1779 1781-1782				
testis GIBCO ATSO01 ATSO01 S-8 10 26 30-31 37 30-51 57 68-69 82 84-85 97 102 113 119 137 139 130-130-130 130-130 130 150 152 154 156 163 169 174 176-177 192 194 196-197 212-215 227-228 247 255 258 261 282 285 288-289 301 307 311 313 30 334 349 370-372 392 398 410 415 426-427 430-431 433 417 4454 461 469 473 477 481-482 493 499 502-503 513 522 526 547 552-553 563-564 572-573 575-576 581-582 585 599-602 605 612 615-617 620 631 637 647 649-650 655 660 665 670 674-675 712 719-721 723 728 731 738 474 746 773 780 784 788-789 802 804 809 811 814 826 831 837 843 845 848 859 866 869 877 905 913 916 919 921 926 929 937 950 960 963 971 975 977 981 990 992-993 1007 1016 1029-1030 1034-1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 113 1141 1149 1161-1162 1175 1208-1209 1222 1227 1231 1235 1238-1239 1243 1253 1285 1287-1289 1291-1293 1307 1311 1317-1320 1330 1332 1338 1345 1369 1399-1400 1409 1423-1424 1430 1435-1437 1449 1464 1464 1490 1493 1496-1497 1501 1505 1509-1513 1527 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1777 1724 1730 1737-1738 1752 1776 1777 986 801 180 180 180 180 180 180 180 180 180				
testis GIBCO ATSOUL 5-8 10 26 30-31 47 50-51 57 68-69 82 84-85 97 102 113 119 137 139 150 152 154 156 165 163 169 174 176-177 192 194 196-197 22-215 227-228 247 255 258 268 288 289 301 307 311 316 330 334 349 370-372 392 398 410 415 426-427 430-431 433 437 446 454 461 469 473 477 481-482 493 499 502-503 513 522 526 547 551-525 553 563-564 572-573 575-576 581-522 585 599-602 605 612 615-617 620 631 637 647 649-650 655 660 665 670 674-675 712 719-721 723 728 731 738 744 746 773 780 784 788-789 802 804 809 811 814 826 831 837 843 845 848 859 866 869 877 905 913 916 919 921 926 929 937 950 963 963 971 975 977 981 990 992-993 1007 1016 1029-1030 1034-1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208-1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1238-1239 1244 1430 1435-1437 1443 1459 1484 1466 1490 1493 1496-1497 1501 1505 1509-1513 1527 1536 1591 1513 1527 1536 1591 1519 1627 1506 1629 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1777 1724 1730 1737-1738 1752 1767 1779 Genomic DNA Research BACOOL 686 1352 1412				
Testis GIBCO ATSO01 S-8 10 26 30-31 47 50-51 57 68-69 82 84-85 97 102 113 119 137 139 150 152 154 156 163 169 174 1776-177 192 194 196-197 212-215 227-228 247 255 258 261 282 285 288-289 301 307 311 316 330 334 349 370-372 392 398 410 415 426-427 430-431 433 437 446 454 461 469 473 477 481-482 493 499 502-503 513 522 526 547 552-553 563 563 593-602 605 612 615-617 620 631 637 647 649-650 656 660 665 670 674-675 712 719-721 723 728 731 738 744 76 773 780 784 788-789 802 804 809 811 814 826 831 837 843 845 848 859 866 865 877 905 913 916 919 921 926 929 937 950 960 963 971 975 979 81 990 992-993 1007 1016 1029-1030 1034-1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208-1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1248 1253 1248 1253 1248 1253 1248 1253 1248 1253 1248 1253 1248 1253 1248 1253 1248 1253 1248 1253 1248 1253 1248 1253 1248 1253 1248 1253 1248 1253 1248 1257 1259 1503 1350 1351 1351 1357 1364 1599 1602 1625 1628 1630-1632 1636 1639 1649 1649 1669 1699 1705 1712 1717 1724 1730 1737-1738 1752 1676 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1776 1777 1767 1779 1689 1642 1669 1669 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1776 1779 1880 1686 1686 1686 1686 1686 1686 1686				
### Table				1
69 82 84-85 97 102 113 119 137 139 150 152 154 156 163 169 174 176-177 192 194 196-197 212-215 227-228 247 255 258 261 282 285 288-289 30. 307 311 316 330 334 349 370-372 392 398 410 415 426- 427 430-431 433 437 446 454 461 469 473 477 481-482 493 499 502- 503 513 522 526 547 552-553 563- 564 572-573 575-576 581-582 585 599-602 605 612 615-617 620 631 637 647 649-650 565 660 665 670 674-675 712 719-721 723 728 731 738 744 746 773 780 784 788-789 802 804 809 811 814 826 831 837 843 845 848 859 866 869 877 905 913 916 919 921 926 928 937 950 960 963 971 975 977 981 990 992- 999 1007 1016 1029-1030 1034- 1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208- 1238-1239 1243 1253 1285 1287- 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1466 1450 1493 1496-1497 1501 150 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 6169 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA from BAC 63118 Genetics (CITB BAC (CITB BAC (CITB BAC	tootio	GTRCO	ATS001	
139 150 152 154 156 163 169 174 176-177 192 194 196-197 212-215 227-228 247 255 258 261 282 285 288-289 303 307 311 316 330 334 349 370-372 392 398 410 415 426-427 430-431 433 437 446 454 461 469 473 477 481-482 349 502-503 513 522 526 547 552-553 563-564 572-573 575-576 581-582 585 564 572-573 575-576 581-582 585 599-602 605 612 615-617 620 631 637 647 649-650 656 660 665 670 674-675 712 719-721 723 728 731 738 744 746 773 780 784 788-789 802 804 809 811 814 826 831 837 843 845 848 859 866 869 877 905 913 916 919 921 296 299 337 950 960 963 971 975 977 981 990 992- 993 1007 1016 1029-1030 1034- 1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208- 1229 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287- 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1561-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA Genetics CITB BAC CITB CAC CITB CAC CITB CAC CITB CAC	cestis	GIBCO	112007	
176-177 192 194 196-197 212-215 227-228 247 255 258 261 282 285 288-289 301 307 311 316 330 334 349 370-372 392 398 410 415 426-427 430-431 433 437 446 454 461 469 473 477 481-482 493 499 502-503 513 522 526 475 552-553 563-564 5772-573 575-576 581-582 585 599-602 605 612 615-617 620 631 637 647 649-650 656 660 665 670 674-675 712 719-721 723 728 731 738 744 746 773 780 784 788-789 802 804 809 811 814 826 831 837 843 845 848 859 86 865 877 905 913 916 919 921 926 929 937 950 960 963 971 975 977 981 900 992-993 1007 1016 1029-1030 1034-1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1099-1102 1104 1118 1113 1141 1149 1161-1162 1175 1208-1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287-1289 1291-1293 1307 1311 1317-1320 1330 1332 1331 81345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1464 1468 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1597 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1664 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 686 1350 1698 1772 1777 1774 17730 1737-1738 1752 1767 1779 686 1352 1412 686-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 686 1352 1412 686-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 686 1352 1412 686-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 686 1352 1412		}		
227-228 247 255 258 261 282 285 288-289 301 307 311 316 330 334 349 370-372 392 398 410 415 426- 427 430-431 433 437 446 454 461 469 473 477 481-482 493 499 502- 503 513 522 526 547 552-53 563- 564 572-573 575-576 581-582 585 585- 564 572-573 575-576 581-582 585 599-602 605 612 615-617 620 631 637 647 649-650 656 660 665 670 674-675 712 719-721 723 728 731 738 744 746 773 780 784 788-789 802 804 809 811 814 826 831 837 843 845 848 859 866 869 877 905 913 916 919 921 926 929 937 950 960 963 971 975 977 981 990 992- 993 1007 1016 1029-1030 1034- 1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208- 1209 1222 1227 1229 1231 1235 1228-1239 1243 1253 1285 1287- 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1464 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1664 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA from BAC 63118 Genetics (CITB BAC Library) Genomic DNA from BAC 39316 Research Genetics (CITB BAC CITB BAC CITB BAC	1			
349 370-372 392 398 410 415 426- 427 430-431 433 437 446 454 461 469 473 477 481-482 493 499 502- 503 513 522 526 547 552-553 553- 564 572-573 575-576 581-582 585 599-602 605 612 615-617 620 631 637 647 649-650 656 660 665 670 674-675 712 719-721 723 728 731 736 744 746 773 780 784 788-789 802 804 809 811 814 826 831 837 843 845 848 859 866 869 877 905 913 916 919 921 926 929 937 950 960 963 971 975 977 981 990 992- 993 1007 1016 1029-1030 1034- 1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208- 1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287- 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 Genomic DNA from BAC 63118 Genetics (CITB BAC Library) Genomic DNA Research Genetics (CITB BAC CITE BAC				
427 430-431 433 437 446 454 461 469 473 477 481-482 493 499 502- 503 513 522 526 547 552-553 563- 564 572-573 575-576 581-582 585 599-602 605 612 615-617 620 631 637 647 649-650 656 660 665 670 674-675 712 719-721 723 728 731 736 744 746 773 780 784 788-789 802 804 809 811 814 826 831 837 843 845 848 859 866 869 877 905 913 916 919 921 926 929 937 950 960 963 971 975 977 981 900 992- 993 1007 1016 1029-1030 1034- 1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208- 1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287- 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA from BAC 39316 Genetics (CITB BAC Library) Genomic DNA Research Genetics (CITB BAC CITB BAC CITB BAC	l			
469 473 477 481-482 493 499 502- 503 513 522 526 547 552-553 563- 564 572-573 575-576 581-582 585 599-602 605 612 615-617 620 631 637 647 649-650 656 660 665 670 674-675 712 719-721 723 728 731 736 744 746 773 780 784 788-789 802 804 809 811 814 826 831 837 843 845 848 859 866 869 877 905 913 916 919 921 926 929 937 950 960 963 971 975 977 981 990 992- 993 1007 1016 1029-1030 1034- 1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208- 1209 1222 1227 1229 1231 1235 1238-1239 1231 1235 1238-1239 1231 1235 1238 1385 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA from BAC 63118 Genetics (CITB BAC Library) Genomic DNA Research Genetics (CITB BAC Library) Genomic DNA Research Genetics (CITB BAC Library) Genomic DNA From BAC 39316	1]		
503 513 522 526 547 552-553 563- 564 572-573 575-576 581-582 585 599-602 605 612 615-617 620 631 637 647 649-650 655 660 665 670 674-675 712 719-721 723 728 731 738 744 746 773 780 784 788-789 802 804 809 811 814 826 831 837 843 845 848 859 866 869 877 905 913 916 919 921 926 929 937 950 960 963 971 975 977 981 990 992- 993 1007 1016 1029-1030 1034- 1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208- 1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287- 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1464 1466 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA Research Genetics (CITB BAC Library) Genomic DNA Research BAC001 686 1352 1412				
564 572-573 575-576 581-582 585	ł			
S99-602 605 612 615-617 620 631 637 647 649-650 656 660 665 670 637 647 649-650 656 660 665 670 674-675 712 719-721 723 728 731 738 744 746 773 780 784 788-789 802 804 809 811 814 826 831 837 843 845 848 859 866 869 877 905 913 916 919 921 926 929 937 950 960 963 971 975 977 981 990 992-993 1007 1016 1029-1030 1034-1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208-1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287-1289 1291-1293 1307 1311 1317-1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1531 1537 1546 1549 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA Research BAC001 Genetics		,		
637 647 649-650 656 660 665 670 674-675 712 719-721 723 728 731 738 744 746 773 780 784 788-789 802 804 809 811 814 826 831 837 843 845 848 859 866 869 877 905 913 916 919 921 926 929 937 950 960 963 971 975 977 981 990 992- 993 1007 1016 1029-1030 1034- 1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208- 1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287- 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA from BAC 63118 Research Genetics (CITB BAC Library) Genomic DNA Research From BAC 39316 Genetics (CITB BAC Library) Genomic DNA Research From BAC 39316				
674-675 712 719-721 723 728 731 738 744 746 773 780 784 788-789 802 804 809 811 814 826 831 837 843 845 848 859 866 869 877 905 913 916 919 921 926 929 937 950 960 963 971 975 977 981 990 992- 993 1007 1016 1029-1030 1034- 1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208- 1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287- 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1777 17724 1730 1737-1738 1752 1767 1779 Genomic DNA from BAC 63118 Research Genetics (CITB BAC Library) Genomic DNA From BAC 39316 Research Genetics (CITB BAC Library) Genomic DNA From BAC 39316	į.	\		
738 744 746 773 780 784 788-789 802 804 809 811 814 826 831 837 843 845 848 859 866 869 877 905 913 916 919 921 926 929 937 950 960 963 971 975 977 981 990 992- 993 1007 1016 1029-1030 1034- 1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208- 1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287- 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1446 1490 1493 1496-1497 1501 1505 1509-1513 15527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1771 1724 1730 1737-1738 1752 1767 1779 Genomic DNA from BAC 63118 Genetics (CITB BAC Library) Genomic DNA Research From BAC 39316 Genetics (CITB BAC	}	}		
B02 804 809 811 814 826 831 837		Ì		
B43 845 848 859 866 869 877 905				1 1 5 7 1 5 1
913 916 919 921 926 929 937 950 960 963 971 975 977 981 990 992- 993 1007 1016 1029-1030 1034- 1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208- 1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287- 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA from BAC 63118 Genetics (CITB BAC Library) Research From BAC 39316 Genetics (CITB BAC CITB BAC CITB BAC				
960 963 971 975 977 981 990 992- 993 1007 1016 1029-1030 1034- 1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208- 1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287- 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 14409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA from BAC 63118 Genetics (CITB BAC Library) Genomic DNA from BAC 39316 Genetics (CITB BAC CITB BAC CITB BAC CITB BAC Genetics (CITB BAC CITB BAC CITB BAC CITB BAC CITB BAC 1411-1412	J	}		
993 1007 1016 1029-1030 1034- 1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208- 1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287- 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA from BAC 63I18 Genetics (CITB BAC Library) Genomic DNA from BAC 393I6 Genetics (CITB BAC CITB BAC CITB BAC CITB BAC CITB BAC CITB BAC	· ·			960 963 971 975 977 981 990 992-
1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208- 1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287- 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA Research BAC001 Genetics (CITB BAC Library) Genomic DNA Research Genetics (CITB BAC CI			İ	
1097 1099-1102 1104 1108 1113				1035 1038-1039 1045 1059-1060
1141 1149 1161-1162 1175 1208- 1209 1222 1227 1229 1231 1235 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA Research BAC001 from BAC 63I18 Genetics (CITB BAC Library Genomic DNA Research from BAC 393I6 Genetics (CITB BAC CITB			}	1064 1070 1072-1073 1087 1089
1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287- 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779	· ·	\		
1238-1239 1243 1253 1285 1287- 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA from BAC 63I18		1 .	ſ	
1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA Research BAC001 686 1352 1412 Genomic DNA Genetics (CITB BAC Library) Cenomic DNA Genetics (CITB BAC CITB BA	1	}	1	
1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779			[
1373-1374 1379 1389 1399-1400		İ	1	
1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779	1	Į	ł	
1443 1459 1484 1486 1490 1493			1.	1
1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA Research BAC001 686 1352 1412 Genetics (CITB BAC Library) Genomic DNA Research Genetics (CITB BAC CITB BAC CITB BAC (CITB BAC CI	1		1	
1527 1530-1531 1533 1537 1546	1	1	1	
1549 1563 1565 1567 1569 1571	1	1	1	
1577 1586 1591 1599 1602 1625		1	1	
1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA Research BAC001 686 1352 1412 Genetics (CITB BAC Library) Genomic DNA Research BAC002 1411-1412 from BAC 39316 Genetics (CITB BAC CITB BAC CITB BAC from BAC 39316 Genetics (CITB BAC CITB BAC CITB BAC from BAC 39316 Genetics (CITB BAC CITB BAC CITB BAC from BAC 39316 Genetics (CITB BAC CITB BAC CITB BAC from BAC 39316 Genetics (CITB BAC CITB BAC CITB BAC from BAC 39316 Genetics (CITB BAC CITB BAC CITB BAC CITB BAC from BAC 39316 Genetics (CITB BAC CITB		1	[
1649 1661-1662 1666-1667 1670	}		}	
1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA Genetics (CITB BAC Library) Genomic DNA Research BAC001 686 1352 1412 Genetics (CITB BAC Library) Genomic DNA Research BAC002 1411-1412 from BAC 39316 Genetics (CITB BAC (CITB BAC) Genetics (CITB BAC)	1		}	
1717 1724 1730 1737-1738 1752 1767 1779 Genomic DNA from BAC 63I18 Genetics (CITB BAC Library) Genomic DNA Research from BAC 393I6 Genetics (CITB BAC CITB BAC CITB BAC CITB BAC CITB BAC CITB BAC CITB BAC CITB BAC Genetics (CITB BAC CITB BAC CITB BAC Genetics (CITB BAC CITB BAC CITB BAC Genetics (CITB BAC CITB BAC CITB BAC Genetics (CITB BAC CITB BAC CITB BAC CITB BAC Genetics (CITB BAC CITB B	1			
Genomic DNA Research BAC001 686 1352 1412 from BAC 63I18 Genetics (CITB BAC Library) Genomic DNA Research BAC002 1411-1412 from BAC 393I6 Genetics (CITB BAC	1	1		# - · · · - · · · · · · · · · · · · · ·
Genomic DNA Research from BAC 63118 Genetics (CITB BAC Library) Genomic DNA Research From BAC 39316 Genetics (CITB BAC GENETICS (CITB BAC GENETICS (CITB BAC GENETICS (CITB BAC GENETICS (CITB BAC GENETICS (CITB BAC GENETICS GENETICS (CITB BAC GENETICS GENETICS GENETICS (CITB BAC GENETICS GE	1	}	1	1 = · · · ·
from BAC 63I18 Genetics (CITB BAC Library) Genomic DNA Research from BAC 393I6 Genetics (CITB BAC (CITB BAC	Genomic DNA	Research	BAC001	
(CITB BAC Library) Genomic DNA Research BAC002 1411-1412 from BAC 39316 Genetics (CITB BAC		,		
Library) Genomic DNA Research BAC002 1411-1412 from BAC 39316 Genetics (CITB BAC		l .	Į.	1
Genomic DNA Research BAC002 1411-1412 from BAC 39316 Genetics (CITB BAC		I '		
from BAC 39316 Genetics (CITB BAC	Genomic DNA		BAC002	1411-1412
(CITE BAC		1 .		1
			1	
		Library)		

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
Genomic DNA	Research	BAC003	1352
from BAC 39316	Genetics		Ì
	(CITB BAC Library)		·
adult bladder	Invitrogen	BLD001	5-8 17-18 22-23 33 37-39 56-57
			80 93 100 120-121 169 201 237
			251-252 272 278 311 348 363 382
			413 415 424 430 443 483 502 542-
			543 562 564 607 616-617 626 635
•			652 667 671 710 727 755-756 762 773 786 788 837 840 866 893 898
			909 918 929 966 977 983 1016
			1025 1055 1073 1082 1140 1167
Ì			1185 1189 1199 1270 1369 1481
]			1536 1560 1573 1596 1614 1636-
]	İ		1637 1649-1650 1654-1655 1658 1669 1671 1690 1719 1727 1731-
			1732 1739 1741 1760-1761 1779
bone marrow	Clontech	BMD001	3-8 11 13 18 29-31 33 35-36 40
1			43-45 47-48 50-51 57 60 65-66 75
}]		80 82 85 88-89 94 100 103 107
			110 115 118-119 124-125 133-134 136-137 139-141 146 150 152-153
1			155 161 163 168-170 172 178-180
	İ		187 192-193 197-198 203-205 210-
			213 215 217 219 222 224-226 233
			235-237 242-244 255 258 260 263- 264 266 273 276 278 283 286 290
			295 301-302 307 312-313 321 330
			333 339 343 352 357-358 370-371
			382 384-385 387 389 394 408 410
			412 416 421 424-427 429-431 436- 437 439 441-442 445 447 454-456
1	1		461-462 471-472 475 477-479 481-
1			482 485 488 493 498 500 503-506
	1		513 516 519 523-524 526 530 535-
			540 542 544-545 549 555 565 567 569-577 581 583-586 588 593 601
1	l l		603-604 608-609 613-619 621-622
			632-633 636-637 642 649-650 656-
			560 666 670 672 674-675 679 683 701 708 716 718-720 731 735-736
	1		740-742 744-745 752 761 765 772-
		İ	773 775-778 780 785-786 789-791
i	1		796 798 802 810-812 823-824 826
1	ł		830 832-833 837-838 843-844 848- 855 858-859 866-867 869 878-880
]	ļ		883 890-892 896 903 905 908 912-
}	j		914 922-924 927 930-931 937 939-
			941 952-953 955-958 963 969 973
1	1		976 981 985 987 990 992 995 1000 1002 1005-1007 1013 1016 1025
1	1		1028-1031 1033 1035 1037 1039
1			1042 1044 1047 1050 1053-1054
}	j	j	1059 1061 1063 1066 1070-1071
			1079 1106 1110-1113 1115-1117 1124 1126 1134-1135 1142 1144-
		. {	1145 1163 1172 1178 1197 1199-
	1		1200 1202 1216-1217 1224 1227-
	1		1228 1240 1246 1254 1261 1266
	1	1	1270 1278 1281 1295 1287 1290- 1291 1293 1299-1301 1308 1314
]	}		1317-1320 1327 1331 1339 1343
	1		1346 1349 1353 1356 1361 1367
		1	1369 1372-1374 1379-1380 1394
	ĺ	Ì	1400 1403 1406 1408 1413 1417 1419 1423 1425-1427 1430-1431
	ļ		1433 1439 1443 1446-1449 1459
L			1463-1464 1482 1486 1493-1494

Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
}		Library Name	1506 1509 1513 1521-1522 1524
			1526 1528 1531 1536-1537 1543
1			1546 1548-1549 1552 1554-1555
}			1557-1559 1571-1572 1581 1589-
			1592 1597-1600 1609 1614 1621
i i			1626-1628 1630-1632 1634 1636
1			1638-1639 1641 1646-1647 1651
ļ			1653-1655 1661-1662 1676-1681
1			1684 1686 1690 1702 1707 1711
]			1713-1714 1717 1720 1722-1723
ĺ			1727 1737-1738 1740 1758 1767
			1772 1781-1782 1785-1786
bone marrow	Clontech	BMD002	11 15-16 19 30-31 35-36 68-69 75
1	!		83-84 93 99 103 108-109 118 137
}			139 169-170 174 177 180 190 193
			212-213 219 222 225-226 232 237
ĺ			255 259 264 273-274 284 286 290-
]			292 295 301 303-304 307 312-313
			316 324 326 330 334-335 348 352- 353 357 360 370-373 384 386-387
1			397 403~404 414-416 421 425-427
			429-430 433-436 440 444 451 454
			465-466 472 475 478 491 493 516
1			520 523 525 531 545 548 552 566
]			569-570 581 583 590-591 597-598
			601 616-617 621 641 650 652 656
}		}	659 671 674-675 679 684 710 718-
		1	719 728 734 737-738 742 761 765
1		i	774-778 790 811 814 818 830 834-
) 1]	836 854-855 859 866 869 871 878-
,			879 884 889 892 904 922-923 932
ì			990 992 998 1001 1004 1016 1036
}		j	1042 1048 1051 1054-1055 1058
1			1088-1089 1106 1112-1114 1155
}		ł	1157 1192 1200 1223 1227-1228
Į.		ļ	1236~1237 1260-1261 1282-1283
1			1285 1287 1295 1314 1317-1321
1			1324-1327 1330 1333 1341 1343
			1347 1350 1353 1355-1357 1367
		Į	1369-1370 1373 1377 1379 1381
]	1383-1384 1394 1397 1400 1406
			1413 1417 1425-1427 1438 1442
1	}	ŀ	1446 1459-1460 1470 1493 1505
]			1521 1536 1546-1549 1560 1573- 1574 1578 1598-1600 1621 1626
			1631 1634 1646 1649 1653 1656
	,	i	1658 1669-1670 1683-1684 1687-
		j	1688 1690-1693 1696 1699 1702
			1704 1707-1709 1711 1720 1722-
			1723 1725 1727 1729 1731-1733
			1738-1740 1743-1746 1752 1755
			1760-1761 1767 1777 1781-1782
			1786
bone marrow	Clontech	BMD004	73-74 503 922 1036 1711
bone marrow	Clontech	EMD007	95-96 866 1320 1475
adult colon	Invitrogen	CLN001	17 56-58 103 110 117 144 150 171
	_	l	179 185 188-189 201 204-206 210
		1	218-221 225-226 231 237 251 277
		1	288 310 312 320 333 359 386 388
		1	394 408 420 455 481 485 503 510-
	J	1	512 590-591 615 635 647-648 665
		1	672 684 697 710 725-726 743 780
1	<u> </u>	j	
1			786 788 826-827 848-850 854-855
			786 788 826-827 848-850 854-855 858 866 872 898 918 921-923 953
			786 788 826-827 848-850 854-855 858 866 872 898 918 921-923 953 976 983 993 1005-1006 1017 1020
			786 788 826-827 848-850 854-855 858 866 872 898 918 921-923 953 976 983 993 1005-1006 1017 1020 1025 1027 1054-1055 1063 1068-
			786 788 826-827 848-850 854-855 858 866 872 898 918 921-923 953 976 983 993 1005-1006 1017 1020 1025 1027 1054-1055 1063 1068- 1069 1140 1153 1170 1185 1196
			786 788 826-827 848-850 854-855 858 866 872 898 918 921-923 953 976 983 993 1005-1006 1017 1020 1025 1027 1054-1055 1063 1068-

Tissue Origin	RNA Source	Hyseq	CEO ID WOO
		Library Name	SEQ ID NOS:
			1462-1464 1512 1556 1583 1587
			1594 1596 1614 1625-1626 1631
(1639 1645 1650 1675-1677 1687-
1			1688 1701 1713-1714 1724 1740
Mixture of 16	Various	CTL016	401 1490 1686
tissues -	Vendors		
mRNAs	 		
Mixture of 16 tissues -	Various	CTL021	312 782 1132-1133 1403 1712 1715
mRNAs*	Vendors		
adult cervix	PieChain	OUNIO OL	
addic cervix	BioChain	CVX001	1 4-8 11 13 18-21 25-26 30-31 33
			37-39 43 46-47 58 61 64-66 71
			73-74 82 85 94 100 103-104 113 118 122 126 130 134 140 147 153-
			156 163 170 179 181 186 192 195-
1			196 198 201-202 218-219 222 229-
	1		231 257 266 276-277 285-286 288
		•	298 301-302 304 307 312-314 324
1 1	l		326 329-330 332 335 342 352 358
}		•	362 371-372 376 379 381-382 384
	1		388 398 400 410 414 416 419-420 426-427 430-431 433-436 439 446
1	Ì		448 461-462 464 471-477 479 482-
1.	1		483 491 493 496 503 506 510-513
]			516-517 526 530 535 542-544 546-
1 1	1	ĺ	547 557 561 572-573 575-577 581-
·	,		582 585-586 588-589 593-594 600
[]		j	602 604-605 607-609 612 615-619
l i			623 644 650 654 657-658 662-665 670 672 680 683 691-694 698 706
1			708-709 711 713 720-721 727 729
}			731-732 737 745-747 753-754 760
			765 771 774-777 780 790 793 796
l l	ĺ		798 800 803 805 818 826 828 831-
1	ì		832 834-836 843 847-848 851-855
!	}		857-860 864-866 869 871 876 878-
j j]	}	880 882 887 890-891 897 899-902 905-908 912-913 916 918-919 922
.		İ	927 932 934-938 944 948 955-956
!	i	i	958 963-964 967 969-970 972 976
)	}		978-979 983 985 990 992 1000
ļ		Ì	1005-1007 1016-1017 1024 1027
Í		(1033 1036 1038 1045 1047 1053-
	ļ		1056 1066-1067 1071 1073 1075 1079 1082 1098 1113 1124 1129
	}		1134 1139 1146-1149 1163 1167
		[1170 1173 1175 1177 1181 1197
		1	1200 1202 1211 1214 1216 1221-
	}		1222 1225 1227 1232-1234 1240-
			1241 1243 1258 1264-1265 1268
	- 1	1	1270 1279 1287-1290 1308 1310-
}	}	ł	1311 1316 1320 1323 1327 1345
	• }	j	1349 1353-1354 1360 1372-1374
		L	1383-1384 1386 1394 1397 1405-

^{*}The 16 tissue-mRNAs and their vendor source, are as follows: 1) Normal adult brain mRNA (Invitrogen), 2) normal adult kidney mRNA (Invitrogen), 3) normal adult liver mRNA (Invitrogen), 4) normal fetal brain mRNA (Invitrogen), 5) normal fetal kidney mRNA (Invitrogen), 6) normal fetal liver mRNA (Invitrogen), 7) normal fetal skin mRNA (Invitrogen), 8) human adrenal gland mRNA (Clontech), 9) human bone marrow mRNA (Clontech), 10) human leukemia lymphablastic mRNA (Clontech), 11) human thymus mRNA (Clontech), 12) human lymph node mRNA (Clontech), 13) human spinal cord mRNA (Clontech), 14) human thyroid mRNA (Clontech), 15) human esophagus mRNA (BioChain), 16) human conceptional umbilical cord mRNA (BioChain).

Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
110000 0119111	MA SOULCE	Library Name	OBQ ID NOS.
···			1406 1416 1425-1427 1431 1436-
			1437 1442 1446 1448 1453 1459
			1466 1472 1478 1482 1496 1501-
			1503 1506 1512 1522 1527-1528
			1531 1533 1541 1547 1569 1571
			1585 1589 1597-1598 1600 1608-
	!		1609 1614-1616 1620 1623-1624
			1626-1628 1630 1638 1641 1643
ļ			1649 1653 1656 1662 1667 1669
Ì			1674-1675 1683 1685-1688 1699 1702 1709-1710 1715 1717 1722
j .		,	1702 1709-1710 1715 1717 1722
			1741 1743-1744 1748-1749 1755
			1760-1762 1767 1773 1778 1785-
			1786
diaphragm	BioChain	DIA002	137 282 289 730 780 986 1409
	2100111111	221.002	1478 1599 1614
endothelial	Strategene	EDT001	3 5-10 13 15-21 24-26 29 34 37-
cells			39 42 44-45 50-51 53-55 57-58
			60-61 65-66 68-69 73-74 77-78 80
		}	82-83 85 87 89 93-96 101-105 108
			110 112-114 116 118-122 124 128
	!		133-134 137-142 147-150 152-153
<u>J</u>			161-163 166-172 176-179 187 190
	i		192 194 196-201 204-207 210 212-
1			214 220 224 229-230 233 235-236
)			240-241 251-252 258 261-262 265
			267-269 272 276-277 279-281 284-
[285 288 290 295-296 301-302 310-
·	!		311 313 316 321 325 329 331-333
}			335 340-342 351-355 360 371 375
1			380-382 384 387 390 392 397 400
1			407-408 410 412 414 416 425-427
ì			431 434-436 439 444-445 449 454
			463-464 472-475 477-479 486 488-
			490 497-498 500-504 510-513 516-
{			519 522 524 526-528 532-534 536-
)			540 542-546 548 561-563 566-567
			572-576 579 581 585-586 589 593 595 597 599 603 607-612 615-617
1			620 622 626 630 632-634 638-641
į.			644 647 656-660 662-664 670 673
i			678 680-682 692-697 707 709-710
			712-713 719 730 732 734 736 738
			743-746 751 759 768 771 773 775-
1			778. 783 786-789 793 800 803 805-
			807 810-811 814 816-818 821-822
			824 826 828-829 832 834-838 842-
			845 848-850 854-860 862 864 869
			871 874 876-879 883 885 887 890-
(891 894-895 898-900 903 908 910-
]			913 916 919-922 924 926-928 930-
(İ		935 939 943 948-949 951-954 957
ļ			959-961 964 969-970 973 975-978
]			983-984 988-990 992-993 996-997
ļ			1000 1002 1004-1013 1016-1020
			1022-1025 1028 1031 1033-1034
			1038-1046 1050 1055-1056 1059-
			1060 1062-1064 1067-1070 1072-
			1074 1076 1078 1082 1086-1087
			1089-1090 1093-1097 1099-1103
			1107 1109-1113 1116-1117 1124-
			1126 1128-1131 1134-1135 1138
ļ			1140 1144-1145 1148-1149 1153 1157 1160 1163 1171 1183-1184
[[1198-1199 1202 1205-1207 1211
1			1216-1217 1219 1221 1225 1229
			1232-1235 1238-1241 1243-1244
			1246 1250 1253 1257-1258 1261
<u> </u>			T-40 1400 1400 1401 1401

			SEQ ID NOS:
Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
		Library Name	999 1001 1005-1006 1008 1013
1			1016 1022 1024 1029-1030 1032
	,		1035 1042 1047-1048 1052 1056
i i	ł		1065 1067 1070 1082 1089 1109
i	ì		1114-1115 1119 1131 1143-1149
į	į.		
ì	j		1151 1153-1156 1160 1163 1167
			1172-1173 1178 1184 1186 1188
ł	i		1190-1200 1211 1216 1222-1223
			1226-1227 1229 1231 1236 1245
(ſ		1253-1255 1258 1260 1262 1266
j	}		1270-1273 1281 1287 1308-1309
			1314 1317-1320 1326 1334-1335
ì	l		1339 1341 1344 1350 1356 1369-
1	Į.		1371 1373 1376 1379 1381-1382
1	•		1386 1392 1396-1398 1419 1423
·	1		1425-1426 1428-1429 1432 1437
	ļ		1440-1441 1448 1466 1470 1482
1	Ì		1502-1503 1507 1511 1513 1516
			1519 1536 1544 1549-1550 1557-
į i			1559 1573 1589-1590 1598 1608
]		1611-1614 1619 1621 1625-1626
l .			
			1640 1651 1657-1658 1676-1679
			1693 1696 1703-1704 1713-1714
			1718 1720 1722 1724 1726 1728
			1730-1733 1735-1736 1738-1739
1			1742 1745 1755 1759-1761 1765
}			1767 1771-1772 1777 1779-1780
			1786
fetal brain	Clontech	FBRs03	235-236 520 864 1068 1188 1587
fetal brain	Invitrogen	FBT002	15-18 20-21 24-25 29 34 43 61-63
			77-78 98 101 103 107-108 128 130
1			136 146 148 165-166 171 174 181
Ĭ .	l		
i l	l I		185 196-198 204-205 208 223 230 i
	ļ		185 196-198 204-205 208 223 230 235-236 251 253 261 268-269 280-
			235-236 251 253 261 268-269 280-
			235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329
			235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-
			235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381- 383 390 407 418-419 430 434-435
			235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381- 383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490
			235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381- 383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561-
			235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381- 383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561- 562 572-573 590-591 595 597 623
			235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381- 383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561- 562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672
			235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381- 383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561- 562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736
			235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381- 383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561- 562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825
			235-236 251 253 261 268-269 280-281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561-562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858
			235-236 251 253 261 268-269 280-281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561-562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946
			235-236 251 253 261 268-269 280-281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561-562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970
			235-236 251 253 261 268-269 280-281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561-562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012
			235-236 251 253 261 268-269 280-281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561-562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1055
			235-236 251 253 261 268-269 280-281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561-562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012
			235-236 251 253 261 268-269 280-281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561-562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128
			235-236 251 253 261 268-269 280-281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561-562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085
			235-236 251 253 261 268-269 280-281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561-562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128
			235-236 251 253 261 268-269 280-281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561-562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156-
			235-236 251 253 261 268-269 280-281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561-562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1055 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156-1157 1193-1195 1198 1204-1205
			235-236 251 253 261 268-269 280-281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561-562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156-1157 1193-1195 1198 1204-1205 1220 1222 1234 1257 1262 1271 1274-1275 1280 1285-1286 1294
			235-236 251 253 261 268-269 280-281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561-562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156-1157 1193-1195 1198 1204-1205 1220 1222 1234 1257 1262 1271 1274-1275 1280 1285-1286 1294 1312 1314 1317-1320 1330 1342
			235-236 251 253 261 268-269 280-281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561-562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 966 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156-1157 1193-1155 1198 1204-1205 1220 1222 1234 1257 1262 1271 1274-1275 1280 1285-1286 1294 1312 1314 1317-1320 1330 1342 1344-1345 1349-1350 1355-1356
			235-236 251 253 261 268-269 280-281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561-562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156-1157 1193-1195 1198 1204-1205 1220 1222 1234 1257 1262 1271 1274-1275 1280 1285-1286 1294 1312 1314 1317-1320 1330 1342 1344-1345 1349-1350 1355-1356 1358 1364 1369 1379 1383-1384
			235-236 251 253 261 268-269 280-281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561-562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156-1157 1193-1195 1198 1204-1205 1220 1222 1234 1257 1262 1271 1274-1275 1280 1285-1286 1294 1312 1314 1317-1320 1330 1342 1344-1345 1349-1350 1355-1356 1358 1364 1369 1379 1383-1384 1431 1435 1476 1507 1519 1532
			235-236 251 253 261 268-269 280-281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561-562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156-1157 1193-1195 1198 1204-1205 1220 1222 1234 1257 1262 1271 1274-1275 1280 1285-1286 1294 1312 1314 1317-1320 1330 1342 1344-1345 1349-1350 1355-1356 1358 1364 1369 1379 1383-1384 1431 1435 1476 1507 1519 1532 1536 1547 1554 1564 1567 1578
			235-236 251 253 261 268-269 280-281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561-562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156-1157 1193-1195 1198 1204-1205 1220 1222 1234 1257 1262 1271 1274-1275 1280 1285-1286 1294 1312 1314 1317-1320 1330 1342 1344-1345 1349-1350 1355-1356 1358 1364 1369 1379 1383-1384 1431 1435 1476 1507 1519 1532 1536 1547 1554 1564 1567 1578 1582 1587 1593 1595 1601 1608
			235-236 251 253 261 268-269 280-281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561-562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156-1157 1193-1195 1198 1204-1205 1220 1222 1234 1257 1262 1271 1274-1275 1280 1285-1286 1294 1312 1314 1317-1320 1330 1342 1344-1345 1349-1350 1355-1356 1358 1364 1369 1379 1383-1384 1431 1435 1476 1507 1519 1532 1536 1547 1554 1564 1567 1578 1582 1587 1593 1595 1601 1608 1615 1619-1621 1638 1644 1661
			235-236 251 253 261 268-269 280-281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561-562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 966 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156-1157 1193-1159 1198 1204-1205 1220 1222 1234 1257 1262 1271 1274-1275 1280 1285-1286 1294 1312 1314 1317-1320 1330 1342 1344-1345 1349-1350 1355-1356 1358 1364 1369 1379 1383-1384 1431 1435 1476 1507 1519 1532 1536 1547 1554 1564 1567 1578 1582 1587 1593 1595 1601 1608 1615 1619-1621 1638 1644 1661 1665-1666 1673 1687-1688 1690
			235-236 251 253 261 268-269 280-281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561-562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156-1157 1193-1195 1198 1204-1205 1220 1222 1234 1257 1262 1271 1274-1275 1280 1285-1286 1294 1312 1314 1317-1320 1330 1342 1344-1345 1349-1350 1355-1356 1358 1364 1369 1379 1383-1384 1431 1435 1476 1507 1519 1532 1536 1547 1554 1564 1567 1578 1582 1587 1593 1595 1601 1608 1615 1619-1621 1638 1644 1661 1665-1666 1673 1687-1688 1690 1715 1723 1728 1749 1753 1757
			235-236 251 253 261 268-269 280-281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561-562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156-1157 1193-1195 1198 1204-1205 1220 1222 1234 1257 1262 1271 1274-1275 1280 1285-1286 1294 1312 1314 1317-1320 1330 1342 1344-1345 1349-1350 1355-1356 1358 1364 1369 1379 1383-1384 1431 1435 1476 1507 1519 1532 1536 1547 1554 1564 1567 1578 1582 1587 1593 1595 1601 1608 1615 1619-1621 1638 1644 1661 1665-1666 1673 1687-1688 1690 1715 1723 1728 1749 1753 1757 1759-1761 1765 1771 1774 1776
			235-236 251 253 261 268-269 280-281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561-562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156-1157 1193-1195 1198 1204-1205 1220 1222 1234 1257 1262 1271 1274-1275 1280 1285-1286 1294 1312 1314 1317-1320 1330 1342 1344-1345 1349-1350 1355-1356 1358 1364 1369 1379 1383-1384 1431 1435 1476 1507 1519 1532 1536 1547 1554 1564 1567 1578 1582 1587 1593 1595 1601 1608 1615 1619-1621 1638 1644 1661 1665-1666 1673 1687-1688 1690 1715 1723 1728 1749 1753 1757
fetal heart	Invitrogen	FHR001	235-236 251 253 261 268-269 280-281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561-562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156-1157 1193-1195 1198 1204-1205 1220 1222 1234 1257 1262 1271 1274-1275 1280 1285-1286 1294 1312 1314 1317-1320 1330 1342 1344-1345 1349-1350 1355-1356 1358 1364 1369 1379 1383-1384 1431 1435 1476 1507 1519 1532 1536 1547 1554 1564 1567 1578 1582 1587 1593 1595 1601 1608 1615 1619-1621 1638 1644 1661 1665-1666 1673 1687-1688 1690 1715 1723 1728 1749 1753 1757 1759-1761 1765 1771 1774 1776
fetal heart	Învitrogen	FHR001	235-236 251 253 261 268-269 280-281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561-562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156-1157 1193-1195 1198 1204-1205 1220 1222 1234 1257 1262 1271 1274-1275 1280 1285-1286 1294 1312 1314 1317-1320 1330 1342 1344-1345 1349-1350 1355-1356 1358 1364 1369 1379 1383-1384 1431 1435 1476 1507 1519 1532 1536 1547 1554 1564 1567 1578 1582 1587 1593 1595 1601 1608 1615 1619-1621 1638 1644 1661 1665-1666 1673 1687-1688 1690 1715 1723 1728 1749 1753 1757 1759-1761 1765 1771 1774 1776 1778 1781-1782 1786
			235-236 251 253 261 268-269 280-281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561-562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156-1157 1193-1195 1198 1204-1205 1220 1222 1234 1257 1262 1271 1274-1275 1280 1285-1286 1294 1312 1314 1317-1320 1330 1342 1344-1345 1349-1350 1355-1356 1358 1364 1369 1379 1383-1384 1431 1435 1476 1507 1519 1532 1536 1547 1554 1564 1567 1578 1582 1587 1593 1595 1601 1608 1615 1619-1621 1638 1644 1661 1665-1666 1673 1687-1688 1690 1715 1728 1748 1749 1755 17759-1761 1765 1771 1774 1776 1778 1781-1782 1786
fetal heart	Învitrogen Clontech	FHR001 FKD001	235-236 251 253 261 268-269 280-281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381-383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561-562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156-1157 1193-1195 1198 1204-1205 1220 1222 1234 1257 1262 1271 1274-1275 1280 1285-1286 1294 1312 1314 1317-1320 1330 1342 1344-1345 1349-1350 1355-1356 1358 1364 1369 1379 1383-1384 1431 1435 1476 1507 1519 1532 1536 1547 1554 1564 1567 1578 1582 1587 1593 1595 1601 1608 1615 1619-1621 1638 1644 1661 1665-1666 1673 1687-1688 1690 1715 1723 1728 1749 1753 1757 1759-1761 1765 1771 1774 1776 1778 1781-1782 1786

Tissue Origin	RNA Source	Hyseq	000
122220 0229111	MA Source	Library Name	SEQ ID NOS:
	<u> </u>		258 277 280-281 307 310 314 330
		•	371 387 392 395 403 422-423 431
1 .	İ		436 443 455 469 500 519 522 542
}	}	1	563 572-573 585 600 619 623 650 654 657-658 660 679 719 731 780
	1		798 821 833 844 854-855 857 864
',	Î		868 878 911 929 958 960 969 990
	(992 1007 1046 1087 1103 1129
	1		1139 1285 1312 1331 1355 1369
}	1	ļ	1371 1376 1391 1422 1425-1426 1440-1441 1470 1543 1598 1601
}]	1618 1631 1651 1654-1655 1669
			1678-1679 1691-1692 1733 1785
fetal kidney	Clontech	FKD002	352 384 426-427 440 583 602 1060
fetal kidney	Invitrogen	FKD007	1131 1324-1325 1636 20-21 82 163 335 679 988-989
	anviorogen.	110007	1000 1227 1230 1320 1554
fetal lung	Clontech	FLG001	35-36 94 323 371 398 426-427 445
]	J .		473 549 560 604 616-617 626 631
			649 651 719 746 786-787 832 842 849-850 864 894-895 1075 1178
[1	'	1182 1200 1206 1309 1311 1345
			1429 1493 1567 1576 1620 1686
fetal lung	Invitrogen	FLG003	9 15-16 29 41 47 68-69 83 88-89
			102 124 137 152-153 165 196 224
			229 231 249 254 256 267 291-292 300 325 333 344-345 352 373 376
			379 384 408 425-427 430 432 467-
			468 475 483 488 493 516 531 535
)			545 547 549 564 582 602 623 644
			660 662-664 670 673 725-726 728 761 766-767 774 805 830 852-853
[864 875 921 932 937 946 949 963
1			988-989 1014 1016-1017 1024 1027
}			1090 1097 1170 1185 1200 1215-
	}		1216 1224 1258 1290 1309 1320
	1		1342 1347 1355 1369 1381 1413- 1414 1431 1438 1449 1491 1512
	{		1536 1547 1557-1560 1567 1590
			1601 1636 1644 1653-1655 1662
1			1667 1671 1675 1680-1681 1706
fetal lung	Clontech	FLG004	1739 1760-1761 1769 103 276 334 465-466 737 843 1131
			1614 1658
fetal liver-	Columbia	FLS001	3-11 13 15-21 25 30-39 41-48 50-
spleen	University		51 54 56-58 60-66 68-69 72 75
]			77-80 82-83 85 87 89 92-103 105- 110 112 116-124 126-127 130 133
1			135-139 141 144 147-149 152-153
1	}		157 163-165 167-172 174 176-178
			180 186 188-190 193-194 196 198-
[1	l	200 202-206 210-214 219 221-231
		1	233-236 240-244 246-247 250-251 255-256 258 261-265 268-269 272
	1	j	274 276-278 280-281 284-286 288
j			293 295 299-301 304 306-307 309
	f	[311 314 316 318 320-321 326 329-
	1	ĺ	332 342 344-345 350 352-353 356- 358 360 362 370-374 376 378-384
	1	ļ	386-387 390 392-393 400-401 403
		ļ	406 408 410-412 415 417 419 422-
	j	{	437 439-442 444-445 448 452-454
		İ	456 459 461-470 472-479 481-483
	-		487-488 490-491 493 500-501 503- 506 509-513 515-520 522-524 526-
			529 531 534 536-540 542 547-549
	1		553-554 561-562 564 567-568 571-
1	1	l l	576 579 581 583 585-597 599-605

			GEO TO YOU.
Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
		Library Name	607 610-613 615-621 623-624 626
i			628-634 636-640 644 647-650 655-
			660 665 669-670 672 674-675 678
			681-682 684 690-695 697 702 708-
			710 713-714 716-719 725-728 730-
			731 734 736 738 740-741 743-746
			748 750-751 759-766 768 772 774-
			777 779 783-788 793 796 798 800-
	į į		805 808 810-812 814 818-819 821-
	j		824 826-832 834-837 843-847 849-
•			867 869-876 878-883 887 889~895
			897-898 902 904-914 916 919 921-
	1		928 930-937 939 945-950 953-958
	1		960-961 963-965 967 969 971 974-
	į į		978 980-983 986 988-990 992-993
	1		995-997 1000-1002 1004-1008 1012
	1		1014 1016-1019 1025-1026 1028-
	[1031 1033 1035-1036 1039-1044
1	Į l		1047 1049-1050 1053-1056 1058-
	(1059 1061-1064 1067-1070 1072-
1	1		1074 1076 1078 1082 1085-1087
\	1		1089-1090 1097 1099-1103 1107-
1	1		1113 1115-1119 1121-1123 1125
	1		1127-1128 1131-1134 1136-1137
	1		1170 1175 1177-1178 1188 1190-
) !		1192 1195-1200 1202 1206 1208-
(1		1211 1214 1216 1218 1221-1222
]	}		1225 1227 1234 1237 1241 1244
			1246-1247 1251 1254 1258 1261
ì			1266 1268 1270-1273 1277-1282
1			1284-1285 1287-1290 1294 1299-
1	1		1300 1306-1308 1313-1320 1324-
1			1325 1327 1330 1332-1333 1338
1	1		1341 1343 1345-1347 1349-1350
}			1353-1360 1362-1363 1365-1367
}	Į į		1369-1370 1372-1374 1376 1378-
ł	1		1381 1383-1384 1386 1389-1391
1	1		1400 1402-1403 1405-1410 1413
(1		1415 1417-1419 1422-1429 1431
1	1		1435-1437 1439-1442 1445-1446
			1448-1449 1454 1458-1459 1466-
1	l l	•	1470 1472 1474 1477-1478 1480
	1	i	1482 1485 1491-1493 1496-1498 1501-1507 1509 1511-1512 1516-
-{	1		1519 1524-1526 1529 1532 1536-
	, j		1541 1546-1547 1549-1550 1552-
1	1		1554 1562 1564 1569 1572 1574-
1	}		1575 1578 1581 1583 1587-1588
	1		1591-1592 1594-1595 1597-1598
	ì		1600-1604 1611-1612 1614-1615
1			1617-1618 1620-1622 1624-1625
1			1627-1628 1630-1632 1634-1639
}			1645-1651 1653-1662 1664 1667-
			1669 1671 1673-1674 1676-1688
1		}	1690 1696 1701-1703 1706-1709
		\	1711 1713-1714 1718-1719 1722
1	l	1	1724-1727 1731-1733 1738 1740-
Ì			1741 1743-1744 1746 1748 1751-
1	1		1752 1754 1760-1765 1767-1773
			1780 1783-1786
fetal liver-	Columbia	FLS002	3-11 13 15-21 26 29 32 35-39 42
spleen	University	1	44-45 48 50-51 54-55 57-58 61 64
{		1	68-69 73-75 78 80 82 84 87 95-98 100 103 105 107-108 110 112-113
1		(116-119 122-125 128 130 137-138
		1	116-119 122-125 128 130 137-136
1	Į	1	166 168 171-172 174-175 177 181
}			188-189 193-194 196-198 200-203
\	_ 1	<u></u>	100-109 193-194 190-190 200 200

Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
1		Library Name	
			206 212-215 219-221 223 225-229
			231-232 240-244 246-247 250-251
			258-259 262 264 268-269 272 275
			277 280-281 284 286 288 290-292 295 298-299 301-304 306 308-310
			318 320-321 323 325 329 331 334
			342 348-349 352-353 356 359 368
			371 374 376-379 381-384 386-387
			392-393 397-398 400-401 403 410-
			413 421 423 426-427 429-430 433-
			436 438 440 443 445 448 451-452
			454-455 460-463 465-467 469 471-
	ĺ		473 475-476 478-479 481-483 487 490-491 493-494 497 500-501 503-
}	ļ		505 509-513 515-517 519-520 524
j]	526-531 534 537-542 544 547 552-
	ļ		554 556 558 561-562 564-567 571-
	[577 583-587 590-591 593 595 597
Ì	(601 604-606 608-613 616-617 619-
			624 626-632 634 637-642 644 647
}		j	649-652 654-659 662-665 669-672
1		1	698 700-703 707 709-710 713 717
1			719-721 723-724 728 731-732 734
		1	737-738 742-745 748 752 754 759
1	1	1	763-766 768 770 773-777 780 782
			784 786 791 795-798 801-802 805
	l	1	808 811-812 818 823-824 826-827
			832 834-837 839 843 846 848-856 858-861 865 867 869 871 873-874
		ł	876 878 881-882 887 889 892 894-
		ļ	898 901-902 904 906-908 913-915
·			919 921-924 926-932 934-935 937
		ļ	939-941 943 946-947 950 953 958
·	ĺ		961 965-967 971 973-975 977-979
	ł		981 984-985 990 992-993 995-997
	ł		999 1001 1004-1007 1009-1011
	ļ	}	1031 1033-1035 1039-1042 1044-
	ļ		1045 1049 1053 1055-1056 1058-
	(1059 1062 1064-1065 1067-1070
1]		1072-1074 1079 1082 1087 1089
1			1093 1097 1099-1103 1105-1107
]	}		1109-1114 1123 1125-1127 1132-
}			1156 1158 1160 1163 1172-1173
	1	1	1177-1178 1181-1184 1190-1192
1			1195-1197 1199 1204 1206 1208
1	ļ		1211 1214 1216 1219 1227 1230
1	1		1234-1235 1237 1240-1241 1243
}			1245 1247 1256 1258 1260-1261
(1		1264 1268 1270-1271 1275 1278- 1279 1284-1286 1288-1289 1299-
(1301 1306 1308 1312 1314 1317-
	1		1319 1323-1325 1327-1330 1334-
1	1	ļ	1335 1339 1343-1347 1349-1350
		\	1354-1355 1357 1360 1362-1363
			1365-1367 1369 1372 1376 1378-
			1380 1386 1389-1391 1394 1400
1	}	1	1403 1406 1409 1416-1419 1422- 1427 1429 1435 1437-1438 1440-
)	1427 1429 1435 1437-1438 1440-
	1	1	1461 1468 1470 1472 1474-1475
1		1	1478 1482 1486 1490-1493 1496
		}	1498 1500-1504 1506 1508-1509
Į.		1	1511-1512 1516 1518-1519 1521
1			1524-1528 1531 1536-1538 1543
		{	1547 1550 1554 1556 1564 1567-
L	.1	<u> </u>	1569 1580 1587-1588 1591-1592

Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
		Library Name	1597-1598 1600-1601 1611-1612
			1618-1628 1630-1631 1635-1638
İ	1		1641 1646-1649 1652 1654-1659
{			1661-1662 1664 1667-1669 1674
1	ĺ		1676-1679 1683-1684 1686-1688
1	1		1691-1692 1699 1702 1707 1711
1	i		1713-1714 1717 1719 1722 1726-
Į	j		1727 1730-1733 1738 1740 1743-
Į.	į		1744 1748-1752 1758 1760-1761
			1763-1764 1767 1769 1772-1773
	İ		1776 1779 1783-1786
fetal liver-	Columbia	FLS003	103 300 318 321 352 372 379 381
spleen	University		384 392-393 403 422 424 429 434-
spiech	0		435 440 444 453 503 515 544 592
{	ĺ		978 1064 1324-1325 1327 1333
			1357 1369 1378 1418 1424 1622
			1646 1649 1680-1681 1689-1690
		1	1717 1743-1744 1769
fetal liver	Invitrogen	FLV001	15-16 26 34 58 61 64 70 75 78 89
TCCGT TIACT	3		98 105 112 116 120-121 123 133
			151 166 176 180 194-196 198 200
			204-206 210-211 220 225-226 230
			235-236 239 247 259 261 267 272
1			277 280-281 303 310 313 317 320-
1			321 329 344 356 371 374 376 379-
1	})	382 395 408 412 414 419 429 434-
İ	!		435 441-442 465-466 490 494 504-
1	j		506 509 522 527 534 552-553 562
ĺ			567 569-570 572-574 607 631 657-
ì	İ		658 667 669 672 685-686 702 717
1			725-726 732 748 759 761 778 784
]	1	}	786 809 817 829 837 857 861 872-
	1		873 875 881 889 894-895 909 911
			916 954 963 967 974 977 986 988~
1			989 993 995 997 1000 1005-1006
ì	Į.		1008 1014-1015 1020 1042-1043
ĺ			1070 1086-1087 1089-1090 1118-
j	}]	1119 1122 1144-1145 1148 1153
(1		1157 1159 1183 1195-1196 1227
ļ		}	1250 1257-1258 1262 1267 1280
ì	1	\	1285 1307 1312 1314 1317-1320
ł	1	1	1344-1345 1349-1350 1355 1362-
İ		1	1363 1403 1405 1415 1419 1425-
1		1	1426 1429 1431 1442 1448 1463- 1464 1469-1470 1489 1528 1536
1			1464 1469-1470 1489 1528 1536 1539 1549-1550 1557-1562 1577
		1	1539 1549-1550 1557-1562 1577 1583 1598 1601 1611 1615 1622
			1583 1598 1601 1611 1615 1622 1544 1649 1666 1674 1706 1721
	1	1	1738 1746 1763-1765 1774 1776 1738 1746 1763-1765 1774 1776
			1779 676 998 1719
fetal liver	Clontech	FLV002	93 133 214 301 355 374 379 555
fetal liver	Clontech	FLV004	581 601 679 837 847 859 1123
	1		1236 1270 1313 1324-1325 1327
1	1	1	1355 1367 1425-1426 1536 1690
1			
L			1733 1760-1761 26 37-39 50-51 58 84 86 89 98
fetal muscle		FMS001	113 128 131-132 139 155 172 186
	Invitrogen		
2000	Invitrogen		104 108 201 206 211 230-231 256
	Invitrogen		194 198 201 206 211 230-231 256
	Invitrogen		194 198 201 206 211 230-231 256 261 276 282 286 302 325 359 361
	Invitrogen		194 198 201 206 211 230-231 256 261 276 282 286 302 325 359 361 376 379 383 398 412-413 419 430
	Invitrogen		194 198 201 206 211 230~231 256 261 276 282 286 302 325 359 361 376 379 383 398 412-413 419 430 436 448 452 462~463 473 477 503
	Invitrogen		194 198 201 206 211 230-231 256 261 276 282 286 302 325 359 361 376 379 383 398 412-413 419 430 436 448 452 462-463 473 477 503 519 529 561 569-570 590-591 597
	Invitrogen		194 198 201 206 211 230-231 256 261 276 282 286 302 325 359 361 376 379 383 398 412-413 419 430 436 448 452 462-463 473 477 503 519 529 561 569-570 590-591 597 607 623 626 635 647 660 672 715
	Invitrogen		194 198 201 206 211 230-231 256 261 276 282 286 302 325 359 361 376 379 383 398 412-413 419 430 436 448 452 462-463 473 477 503 519 529 561 569-570 590-591 597 607 623 626 635 647 660 672 715 725-726 730 733 761 775-777 788
	Invitrogen		194 198 201 206 211 230-231 256 261 276 282 286 302 325 359 361 376 379 383 398 412-413 419 430 436 448 452 462-463 473 477 503 519 529 561 569-570 590-591 597 607 623 626 635 647 660 672 715 725-726 730 733 761 775-777 788 826 837 860 874 913 915 921 935
	Invitrogen		194 198 201 206 211 230-231 256 261 276 282 286 302 325 359 361 376 379 383 398 412-413 419 430 436 448 452 462-463 473 477 503 519 529 561 569-570 590-591 597 607 623 626 635 647 660 672 715 725-726 730 733 761 775-777 788 826 837 860 874 913 915 921 935 970 980 986 988-990 992 1000-
	Invitrogen		194 198 201 206 211 230-231 256 261 276 282 286 302 325 359 361 376 379 383 398 412-413 419 430 436 448 452 462-463 473 477 503 519 529 561 569-570 590-591 597 607 623 626 635 647 660 672 715 725-726 730 733 761 775-777 788 826 837 860 874 913 915 921 935

			, - · · · · · · · · · · · · · · · · · ·
Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1099-1102 1116-1117 1121 1164
			1173 1198 1208 1228 1240 1258
			1266 1270 1277 1298 1317-1320
			1324-1325 1329 1336-1337 1369
			1383-1384 1399-1400 1403 1409
			1433 1505 1514 1542 1551 1554
	1		1557-1559 1562 1589 1599 1620
			1632 1644 1650 1652 1671 1675
			1712 1725-1726 1743-1744 1754
			1766
fetal muscle	Invitrogen	FMS002	119 221 273 402 426-427 463 547
			599 736 869 1000 1033 1083 1266
			1431 1440-1441 1468 1545 1599
			1673 1678-1679 1687-1688 1710
			1712-1714 1723 1725 1731-1733
			1743-1744 1760-1761 1767
fetal skin	Invitrogen	FSK001	1 4-11 15-16 20-23 25 29 33 40
	1		43 46 56-57 60-61 64-66 75 82 87
	1		97-98 105 107-108 113 118-119
	ļ		123 133 135-137 139 144 146 148
			151~153 156 163 170 176 180 188-
	1	1	189 197-198 200 202-203 210 218
]			222 231 246-247 261 263 265-270
	1		277 285-286 290 293 299 301 307 311 321 325 328 330 333-335 339
i			311 321 325 328 330 333-335 339
1		·	362 368 370 372 376 379-382 384
1	ĺ		388 394 404-405 408-409 411-412
}	}	}	419-420 424 426-427 436 441-442
			445 448-449 454 462 465-466 472
Ĺ			476 490 493 504 506 509 515-517
}	}]	1 519 526 531 537-540 547 549 560-
		1	561 567 572-573 581 584 589 611-
1			612 615 623 630-631 635 647 649
]	}	}	651 657-658 660 662-665 667 669
1	ļ		672 676 678 681 688 701 704-705
ł			709-710 713 717 720-721 725-726
J]	728-729 732 748 750 753 759 764
			766 770 775-777 780-781 786 788-
· ·	{		789 798 809 811 814 816-817 822
<u> </u>	}]	824-826 831 842 857 859 861 863-
Ì			864 881 894-895 908 910-911 916
	l .		918 922-923 928 932-933 935 937
	1	1	946 948-949 953 960-961 966-967
1			970 975 977 986 990 992-993 999-
ł	1	i	1000 1004 1007 1013 1018 1025
			1027 1032 1035 1041-1043 1054
1	į.		1057-1058 1060 1062-1064 1069
	1	i	1072 1077 1090-1091 1097 1099-
			1103 1108 1113 1119 1123 1128
[1	l	1131 1134 1140 1148-1149 1152-
1			1153 1156 1163 1167 1178 1182
•	1		1189 1192 1195-1196 1198 1201-
1	ſ		1205 1208 1211-1212 1216 1219-
}	,	}	1220 1222 1225 1240 1243 1258
			1266-1267 1274 1277 1280 1282-
	1		1285 1299 1310 1317-1322 1324-
1	1	l	1325 1329-1330 1342 1344 1346
1			1349-1351 1354-1357 1365-1366
1	1	1	1369 1371 1373 1376 1378 1380
1	1		1383-1384 1387 1399-1400 1405
1			1410 1427 1429 1431 1433-1435
1	1	1	1439-1441 1448-1449 1454 1457
1	1]	1468 1470 1472 1475 1480-1481
[1	1487 1490-1491 1493 1498 1509
	ł	1	1512 1521 1525-1526 1529 1535-
1			1536 1547 1549 1557-1559 1588
Ī		{	1592 1595 1597-1598 1601 1603-
	<u> </u>	L	1604 1608 1611 1614 1618 1624-

Library Name Li	Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
1626 1632 1635 1636 1641 1643- 1644 1646 1655-1657 1660-1662 1665 1666 1675 1685 1687-1689 1702-1703 1709-1710 1716 1719 1724 1727 1731-1732 1737-1740 1716 1719 1724 1727 1731-1732 1737-1740 1742 1747 1749 1755 1760-1761 1765 1772 1776-1777 1779-1780 1786 1786 1772 1776-1777 1779-1780 1786 1786 1772 1776-1777 1779-1780 1786 1786 1787 1776-1777 1779-1780 1786 1786 1787 1787 1787 1787 1787 1787	lissue origin	RIA SOURCE		SEQ IS NOS.
1665 1668 1675 1685 1687-1689 1702-1703 1709-1701 0716 1719 1724 1727 1731-1732 1737-1740 1719 1724 1727 1731-1732 1737-1740 1742 1747 1749 1755 1760-1761 1765 1772 1776-1777 1779-1780 1786 1786 1786 1786 1786 1786 1786 1787 1779-1780 1786 1786 1787 1779-1779 1780 1786 1786 1786 1787 1779-1780 1786 1786 1787 1787 1789 1786 1887 1789 1887 1789 1887 1789 1887 1789 1887 1789 1887 1888 1893 1887 1888 1893 1887 1888 1893 1888 1893 1888 1893 1893 1893				1626 1632 1634 1636 1641 1643-
1702-1703 3709-1710 1716 1719 1724 1727 1731-1732 1737-1740 1742 1747 1749 1755 1760-1761 1765 1772 1776-1777 1779-1780 1786				1
True True				1665 1668 1675 1685 1687-1689
fetal skin	·			1702-1703 1709-1710 1716 1719
Fetal skin Invitrogen FSK002				
Tree				1
Fetal skin	}			
339 341 354 370 372 385 400 402 408 414 426-427 433 436 480 454 515 544 585 598 767 810 845 939 1076 109 1155 1317-1120 1326 1331-1331 1343 1347 1350 1369- 1371 1377-1378 1391 1397 1422 1466 1647 1656 1678-1679 1687- 1688 1693 1718 1721 1725 1731- 1732 1739 1755 fetal spleen BioChain FSP001 BioChain FUC001 BioChain FUC001 BioChain FUC001 BioChain FUC001 FUC001 BioChain FUC001 BioChain FUC001 BioChain FUC001 A-8 10 12 14 17 33-36 44-46 57 64 66-69 75 82 85 101 104 113- 144 116 119 122-124 133 137 153- 154 115 161 163 166-160 72 212- 215 230 234 246-247 251 256 263 267 271-272 280-288 280 221 212- 215 230 234 246-247 251 256 263 267 271-272 280-288 283 283 283 283 283 283 283 283 283			707000	1
408 414 426-427 433 416 450 454 515 544 585 598 767 810 845 939 1076 1109 1155 1317-1320 1326 1331-1331 1343 1347 1350 1369- 1371 1377-1378 1391 1397 1422 1466 1647 1656 1678-1679 1687- 1688 1693 1718 1721 1725 1731- 1732 1739 1755 fetal spleen BioChain FSP001 BioChain FUC001	fetal skin	Invitrogen	FSK002	,
Sis 544 585 598 767 810 845 939 1076 1109 1155 1317-1320 1326 1333-1335 1342 1347 1350 1369 1371 1377-1376 1391 1397 1432 1466 1647 1656 1676-1679 1687 1688 1693 1718 1722 1725 1731-1732 1739 1755 1731 1732 1739 1755 1731 1732 1739 1755 1731 1732 1739 1755 1732 1739 1755 1731 1732 1739 1755 1731 1732 1739 1755 1732 1739 1755 1732 1739 1755 1732 1739 1755 1732 1739 1755 1732 1739 1755 1732 1739 1755 1732 1739 1755 1732 1739 1755 1732 1739 1755 1732 1739 1755 1732 1739 1755 1732 1739 1755 1732 1739 1755 1732 1739 1735 1731 1731 1731 1731 1731 1731 1731				1
1076 1109 1155 1317-1320 1326 1333-1335 1343 1347 1350 1369-1371 1377-1378 1391 1397 1422 1466 1647 1656 1678-1679 1687-1688 1639 1718 1721 1725 1731-1732 1731 1732 1731 1732 1731 1732 1731 1732 1731 1732 1731 1732 1731 1732 1731 1732 1731 1732 1731 1732 1731 1732 1731 1732 1731 1732 1731 1732 1731 1732 1731 1732 1731 1732 1731				1
1333-1335 1342 1347 1350 1369-1371 1377-1376 1391 1397 1422 1466 1647 1656 1676-1679 1687-1679 1688 1693 1718 1721 1725 1731-1732 1739 1755 17618 1698 1693 1718 1721 1725 1731-1732 1739 1755 17618 1732 1739 1755 17618 1732 1739 1755 17618 1732 1739 1755 17618 1732 1739 1755 17618 1732 1739 1755 17618 1732 1739 1755 17618 1732 1739 1755 17618 1732 1739 1755 17618 175)			· ·
1371 1377-1378 1391 1397 1422 1466 1647 1656 1678-1679 1687 1687 1688 1693 1718 1721 1725 1731 1732 1739 1755 1732 1739 1755 1639 1771 1732 1733 1755 1639 1771 1732 1733 1755 1639 1771 1732 1733 1755 1639 1771 1732 1733 1755 1639 1771 1732 1735 1755 1639 1771 1732 1735 1755 1639 1771 1732 1735 1755 1639 1771 1732 1736 44-46 57 64 68-69 75 62 85 101 104 113-	['		
1466 1647 1656 1678-1679 1687- 1688 1693 1718 1721 1725 1731- 1688 1693 1718 1721 1725 1731- 1732 1739 1755 110 137 211 353 589 927 1108 1639 1771 373 36 44-46 57 4-8 10 12 14 17 33-36 44-46 57 4-8 6-69 75 82 85 101 104 113- 114 116 119 122-124 133 .37 151- 154 116 119 122-124 133 .37 151- 154 116 119 122-124 133 .37 151- 154 166 192 197-198 200-202 122- 215 230 234 246-247 251 256 263 267 271-272 280-281 284 295 301 314 317 321 326 333-335 345 351 356 368 371-373 379-380 386 399 392 394 406 408-410 412 414 416 420 424 427 430-436 438 444-446 454 459 461 463 467 473 482-483 486 488 490 495 504 509 524 526 537-540 547 555 561 574-577 588- 591 593 606 615 620-621 632 637 645-647 650 659 7-60 662-664 667- 668 674-675 684 687 696 698 701 703-705 709 711 714 719-720 725- 777 780 789-791 793 798 802-803 814-817 822 333 843 465 848 859 879 899 992 998 1000-1001 1005- 1007 1016 1023 1025 1037 1046- 1047 1059 1061-1065 1073 1076- 1077 1089 1094-1097 1112-1113 115 1134 1144-1148 1151 1154 1156 1163 1171 1197 1204-1205 124 124-125 1241 1241 1341 1434 124 1427-1428 1431 133 1440-144 1446 1446 1446 1446 1454 1458 1459 1459 1459 1459 1459 1459 1459 1459	}			
1688 1693 1718 1721 1725 1731- 1732 1739 1755 fetal Epleen BioChain FSP001 110 137 211 353 589 927 1108 1639 1771 1639 1771 umbilical cord BioChain FUC001 4-8 10 12 14 17 33-36 44-46 57 64 68-69 75 82 85 101 104 113- 114 116 119 122-124 133 .37 153- 154 157 161 163 166-167 175 181- 184 186 192 197-198 200-202 212- 215 230 234 246-247 251 256 263 267 271-272 280-281 284 295 301 314 317 321 326 333-335 345 351 356 368 371-373 379-380 386 390 392 394 406 408-410 412 414 416 420 424 427 430-436 484 44-446 454 459 461 463 47 473 482-483 486 488 480 495 504 509 524 526 537-540 547 555 561 574-577 588- 591 593 606 615 620-621 632 637 645-647 650 659-660 652-664 667-668 674-675 684 687 696 698 701 703-705 709 711 714 719-720 725-727 732 749-750 762 765 771 775-777 780 789-791 793 796 802-803 814-817 822 833 843 848 848 858 861 864 807 879 888 894-895 897-900 903 906-907 911-912 925 930-933 936 940 948 953 960 966 977 984 990 992 998 1000-1001 1005-1007 1016 1023 1025 1037 1046-1047 1059 1061-1063 1073 1076-1077 1089 1094-1097 1122-113 1115 1134 1144-148 1151 1154 1156 1163 1171 1197 1204-1205 1208 1216 1218 1224 1234-1235 1243-1244 1246 1279 1283 1266-1287 1298 1316 1320 1344 1340-1442 1446 1446 1435 1459 1492-1493 1504-1505 1513 1525 1527 1536 1538 1536 1556 1658 1661-1662 1672 1675 1675 1675 1575 1575 1576 1578 1575 1575 1576 1578 1675 1675 1675 1675 1575 1575 1575 1575	ļ			
### Spleen BioChain FSP001 110 137 211 353 589 927 1108		1		
1639 1771				1732 1739 1755
1639 1771	fetal spleen	BioChain	FSP001	110 137 211 353 589 927 1108
64 68-69 75 82 85 101 104 113- 114 116 119 122-124 133 137 153- 154 157 161 163 166-167 175 181- 184 186 192 197-198 200-202 212- 215 230 234 246-247 251 256 263 267 271-272 280-281 284 295 301 314 317 321 326 333-335 345 351 356 368 371-373 379-380 386 390 392 394 406 408-410 412 414 416 420 424 427 430-436 438 444-446 454 459 461 463 467 473 482-483 486 488 490 495 504 509 524 526 537-540 547 555 561 574-577 588- 591 593 606 615 620-621 632 637 645-647 650 659-660 662-664 667- 668 674-675 684 687 696 697 698 701 703-705 709 711 714 719-720 725- 727 732 749-750 762 765 771 775- 777 780 789-791 793 796 802-803 814-817 822 833 843 845 848 858 861 864 875 879 888 894-895 897- 900 903 906-907 911-912 925 930- 933 936 940 948 953 609 566 977 984 990 992 988 1000-1001 1005- 1007 1016 1023 1025 1037 1046- 1047 1059 1061-1063 1073 1076- 1077 1089 1094-1097 1112-1113 1115 1134 1144-1148 1151 1154 1156 1163 1171 1197 1204-1205 1208 1216 1218 1224 1234-1235 1243-1244 1246 1218 1224 1334-1235 1243-1244 1246 1218 1224 1334-1235 1243-1244 1246 1454-1455 1479 1482 1442 1446 1454-1455 1479 1482 1442 1446 1454-1455 1479 1482 1442 1446 1454-1455 1479 1482 1442 1446 1454-1455 1479 1482 1464-1455 1489 1492-1493 1504- 1505 1513 1525 1527 1536 1538 1546 1563 1567 1571 1573 1575- 1576 1578-1579 1591 1595 1600- 1601 1608 1612 1615 1621 1624 1626 1636-1637 1647-1648 1651 1653 1656 1658 1669 1661-1662 1672 1675 1662 1668 1666-1668 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1750-1761 1768	i -			1639 1771
114 116 119 122-124 133 137 153- 154 157 161 163 166-167 175 181- 184 186 192 197-198 200-202 212- 215 230 234 246-247 251 255 263 267 271-272 280-281 284 295 301 314 317 321 326 333-335 345 351 356 368 371-373 379-380 386 390 392 394 406 408-410 412 414 416 420 424 427 430-436 438 444-446 454 459 461 463 473 482-483 486 488 490 495 504 509 524 526 537-540 547 555 561 574-577 588- 591 593 606 615 620-621 632 637 645-647 650 659-660 662-664 667- 668 674-675 684 687 696 698 701 703-705 709 711 714 719-720 725- 727 732 749-750 762 765 771 775- 777 780 789-791 791 714 719-720 725- 727 732 749-750 762 765 771 775- 777 780 789-791 791 396 802-803 814-817 822 833 843 845 848 858 861 864 875 879 888 894-895 897- 900 903 906-907 911-912 925 930- 933 936 940 948 953 960 966 977 984 990 992 998 1000-1001 1005- 1007 1016 1023 1025 1037 1046- 1047 1059 1061-1063 1073 1076- 1077 1089 1094-1097 1112-1113 1115 1134 1144-1148 1151 1154 1156 1163 1171 1197 1224-1205 1208 1216 1218 1224 1234-1235 1243-1244 1246 1279 1283 1286- 1287 1298 1316 1320 1344 1346 1350 1357 1359 1371 1373 1375 1381 1398 1400 1403 1408 1414 1424 1427-1428 1431 1433 1440- 1442 1446 1454-1455 1479 1482 1448-1485 1489 1492-1493 1504- 1505 1513 1525 1527 1536 1538 1546 1565 1567 1571 1573 1575- 1576 1578-1579-1579 1595 1600- 1601 1608 1612 1615 1621 1624 1626 1636-1637 1647-1648 1651 1653 1656 1658 1668 1668 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768	umbilical cord	BioChain	FUC001	4-8 10 12 14 17 33-36 44-46 57
154 157 161 163 166-167 175 181- 184 186 192 197-198 200-202 212- 215 230 234 246-247 251 256 263 267 271-272 280-281 284 295 301 314 317 321 326 333-335 345 351 356 368 371-373 379-380 386 390 392 394 406 408-410 412 414 416 420 424 427 430-436 438 444-446 454 459 461 463 467 473 482-483 486 488 490 495 504 509 524 526 537-540 547 555 561 574-577 588- 591 593 606 615 620-621 632 637 645-647 650 659-660 662-664 667- 668 674-675 684 687 696 698 701 703-705 709 711 714 719-720 725- 727 732 749-750 762 765 771 775- 777 780 789-791 793 796 802-803 814-817 822 833 843 845 848 858 861 864 875 879 888 894-895 897- 900 903 906-907 911-912 925 930- 903 906-907 911-912 925 930- 903 906-907 911-912 925 930- 903 906-907 911-912 925 930- 903 906-907 911-113 1131 1115 1134 1144-1148 1151 1154 1156 1163 1171 1197 1204-1205 1208 1216 1218 1224 1234-1235 1243-1244 1246 1218 1224 1334-1235 1243-1244 1246 1218 1224 1334-1235 1243-1244 1246 1218 1224 1334-1235 1381 1398 1400 1403 1408 1414 1442 1442-1428 1431 1433 1340- 1442 1446 1454-1455 1479 1482 1448 1446 1454-1455 1479 1482 1448 1464 1454-1455 1479 1482 1449 1446 1454-1455 1479 1482 1468 1488 1489 1492-1493 1504- 1505 1513 1525 1527 1536 1538 1546 1566 1567 1571 1573 1575- 1576 1578-1579 1591 1595 1600- 1601 1608 1612 1615 1621 1624 1662 1636-1637 1647-1648 1651 1663 1668 1661-1662 1672 1675 1662 1668 1666-1668 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1750-1761 1768	}	1		1
184 186 192 197-198 200-202 212- 215 230 234 246-247 251 256 263 267 271-272 280-261 284 295 301 314 317 321 326 333-335 345 351 356 368 371-373 379-380 386 390 392 394 406 408-410 412 414 416 420 424 427 430-436 438 444-446 454 459 461 463 467 473 482-483 486 488 490 495 504 509 524 526 537-540 547 555 561 574-577 588- 591 593 606 615 620-621 632 637 645-647 650 659-666 662-664 667- 668 674-675 684 687 696 698 701 703-705 709 711 714 719-720 725- 727 732 749-750 762 765 771 775- 777 780 789-791 793 796 802-803 814-817 822 833 843 845 848 858 861 864 875 879 888 894-895 897- 900 903 906-907 911-912 925 930- 933 936 940 948 953 960 966 977 984 990 992 998 1000-1001 1005- 1007 1016 1023 1025 1037 1046- 1047 1059 1061-1063 1073 1076- 1077 1089 1094-1097 1112-1113 1115 1134 1144-1148 1151 1154 1156 1163 1171 1197 1204-1205 1208 1216 1218 1224 1234-1235 1243-1244 1246 1279 1283 1286- 1287 1298 1316 1320 1344 1346 1350 1357 1359 1371 1373 1375 1381 1398 1400 1403 1403 1404 1442 1446 1454-1455 1479 1482 1484-1485 1489 1492-1493 1504- 1505 1513 1525 1527 1536 1538 1546 1565 1567 1571 1573 1575- 1576 1578-1579 1591 1595 1600- 1601 1608 1612 1615 1621 1622 1626 1636-1637 1647-1648 1651 1653 1656 1658 1661-1662 1672 1675 1682 1684 1667-1688 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768	ļ			
215 230 234 246-247 251 256 263 267 271-272 280-281 284 295 301 314 317 321 326 333-335 345 351 336 368 371-373 379-380 386 390 392 394 406 408-410 412 414 416 420 424 427 430-436 438 444-446 454 459 461 463 467 473 482-483 486 488 490 495 504 509 524 526 537-540 547 555 561 574-577 588- 591 593 606 615 620-621 632 637 645-647 650 659-660 662-664 667- 668 674-675 684 687 696 698 701 703-705 709 711 714 719-720 725- 727 732 749-750 762 765 771 775- 777 780 789-791 793 796 802-803 814-817 822 833 843 845 848 858 861 864 875 879 88 894-895 897- 900 903 906-907 911-912 925 930- 933 936 940 948 953 960 966 977 984 990 992 998 1000-1001 1005- 1007 1016 1023 1025 1037 1046- 1047 1059 1061-1063 1073 1076- 1077 1089 1094-1097 1112-1113 1115 1134 1147-118 1151 1154 1156 1163 1171 1197 1224-1225 1208 1216 1218 1224 1234-1235 1243-1244 1246 1279 1283 1286- 2287 1298 1316 1320 1344 3346 1350 1357 1359 1371 1373 1375 1381 1398 1400 1403 1408 1414 1424 1427-1428 1431 1433 1440- 1442 1446 1454-1455 1571 1573 1575- 1576 1578-1579 1591 1595 1600- 1601 1608 1612 1615 1621 1624 1626 1636-1637 1647-1648 1651 1653 1655 1663 1661-1662 1672 1675 1662 1684 1661-1668 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768				
267 271-272 280-281 284 295 301 314 317 321 326 333-335 345 351 336 368 371-373 379-380 386 390 392 394 406 408-410 412 414 414 420 424 427 430-436 438 444-446 454 459 461 463 467 473 482-483 486 488 490 495 504 509 524 526 537-540 547 555 561 574-577 588- 591 593 606 615 620-621 632 637 645-647 650 659-6662-664 667- 668 674-675 684 687 696 698 701 703-705 709 711 714 719-720 725- 727 732 749-750 762 765 771 775- 777 780 789-791 793 796 802-803 814-817 822 833 845 848 858 861 864 875 879 888 894-895 897- 900 903 906-907 911-912 925 930- 933 936 940 948 953 960 966 977 984 990 992 998 1000-1001 1005- 1007 1016 1023 1025 1037 1046- 1007 1016 1023 1025 1037 1046- 1007 1016 1023 1025 1037 1046- 1007 1016 1023 1071 112-1113 1115 1134 1144-148 1151 1154 1156 1163 1171 1197 1204-1205 1208 1216 1218 1224 1234-1235 1243-1244 1246 1279 1238 1286- 1287 1298 1316 1320 1344 1346 1350 1357 1359 1371 1373 1375 1381 1398 1400 1403 1403 1404 1442 1447-1428 1431 1433 1440- 1442 1446 1454-1455 1479 1482 1484-1485 1489 1492-1493 1504- 1505 1513 1525 1527 1536 1538 1546 1565 1567 1571 1573 1575- 1576 1578-1579 1591 1595 1600- 1601 1608 1612 1615 1621 1622 1626 1636-1637 1647-1648 1651 1653 1652 1668 1661-1662 1672 1675 1682 1684 1667-1688 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768	1			
314 317 321 326 333-335 345 351 356 368 371-373 37380 386 390 392 394 406 408-410 412 414 416 420 424 427 430-436 438 444-446 454 459 461 463 467 473 482-483 486 488 490 495 504 509 524 526 537-540 547 555 561 574-577 588-591 593 606 615 620-621 632 637 645-647 650 659-660 662-664 667-668 674-675 68 674-675 68 687-667 668 674-675 68 687 696 698 701 703-705 709 711 714 719-720 725-727 732 749-750 762 765 771 775-777 780 789-791 793 796 802-803 814-817 822 833 843 845 848 858 861 864 875 897 999 999 999 898 1000-1001 1005-903 909 909 999 998 1000-1001 1005-1007 1016 1023 1025 1037 1046-1047 1059 1061-1063 1073 1076-1077 1089 1094-1097 1112-1113 1115 1134 1144-1148 1151 1154 1156 1163 1171 1197 1204-1205 1208 1216 1218 1224 1234-1235 1243-1244 1244 1279 1283 1286-1287 1298 1316 1320 1344 1346 1350 1357 1359 1371 1373 1375 1381 1398 1400 1403 1408 1414 1424 1427-1428 1431 1433 1440-1442 1446 1454-1455 1479 183 1575-1576 1576-1579 1591 1595 1600-1601 1608 1612 1615 1621 1624 1624 1626 1636-1637 1647-1648 1651 1653 1656 1656 1567 1571 1573 1575-1576 1576-1579 1591 1595 1595 1600-1601 1608 1612 1615 1621 1624 1626 1636-1637 1647-1648 1651 1653 1655 1658 1666-1668 1669 1670-1710 1722 1727 1729 1735-1738 1740-1711 1760-1761 1768 1661 1768 1679 1778 1778 1778 1778 1778 1778 1778 17	ł i			
356 368 371-373 379-380 386 390 392 394 406 408-401 412 414 416 420 424 427 430-436 438 444-446 454 459 461 463 467 473 482-483 486 488 49 495 504 509 524 526 537-540 547 555 561 574-577 588- 591 593 606 615 620-621 632 637 645-647 650 659-660 662-664 667- 668 674-675 684 687 696 699 701 703-705 709 711 714 719-720 725- 727 732 749-750 762 765 771 775- 777 780 789-791 793 796 802-803 814-817 822 833 843 845 848 858 861 864 875 879 888 894-895 897- 900 903 906-907 911-912 925 930- 933 936 940 948 953 960 966 977 984 990 992 998 1000-1001 1005- 1007 1016 1023 1025 1037 1046- 1047 1059 1061-1063 1073 1076- 1077 1089 1094-1097 1112-1113 1115 1134 1144-1148 1151 1154 1156 1163 1171 1197 1204-1205 1208 1216 1218 1224 1234-1235 1243-1244 1244 1245 1237 1346 1350 1357 1359 1371 1373 1375 1381 1398 1400 1403 1408 1414 1424 1427-1428 1431 1433 1440- 1442 1446 1454-1455 1479 1482 1484-1485 1489 1492-1493 1504- 1505 1513 1525 1527 1536 1538 1546 1565 1567 1571 1573 1575- 1576 1576-1579 1591 1595 1600- 1601 1608 1661 1615 1621 1624 1626 1636-1637 1647-1648 1651 1653 1656 1658 1661-1662 1672 1675 1682 1684 1686-1688 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768 fetal brain GIBCO HFB001 4 9 11-13 17-18 22-23 25 37-39	j l			
392 394 406 408-410 412 414 416 420 424 427 430-436 438 444-446 454 459 461 463 467 473 482-483 486 488 480 490 55 04 509 524 526 537-540 547 555 561 574-577 588- 591 593 606 615 620-621 632 637 645-647 650 659-660 662-664 667- 668 674-675 684 687 696 698 701 703-705 709 711 714 719-720 725- 727 732 749-750 762 765 771 775- 777 780 789-791 793 796 802-803 814-817 822 833 843 848 888 884-885 8861 864 875 879 888 894-895 897- 900 903 906-907 911-912 925 930- 933 936 940 948 953 960 966 977 984 990 992 998 1000-1001 1005- 1007 1016 1023 1025 1037 1046- 1047 1059 1061-1063 1073 1076- 1077 1089 1094-1097 1112-1113 1115 1134 1144-1148 1151 1154 1156 1163 1171 1197 1224-1205 1208 1216 1218 1224 1234-1235 1243-1244 1246 1279 1283 1286- 1287 1298 1316 1320 1344 1346 1350 1357 1359 1371 1373 1375 1381 1398 1400 1403 1408 1414 1424 1427-1428 1431 1433 1440- 1442 1446 1454 1455 1479 1482 1464-1485 1489 1492-1493 1504- 1505 1513 1525 1527 1536 1538 1546 1565 1567 1571 1573 1575- 1576 1578-1579 1591 1595 1600- 1601 1608 1661 1615 1621 1624 1626 1636-1637 1647-1648 1651 1653 1656 1658 1667-1662 1672 1675 1682 1684 1686-1688 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768	{			
420 424 427 430-436 438 444-446 454 459 461 463 467 473 482-483 486 488 490 495 504 509 524 526 537-540 547 555 561 574-577 588- 591 593 606 615 620-621 632 637 645-647 650 659-660 662-664 667- 668 674-675 684 687 696 698 701 703-705 709 711 714 719-720 725- 727 732 749-750 762 765 771 775 777 780 789-791 793 796 802-803 814-817 822 833 843 845 848 858 861 864 875 879 888 894-895 897- 900 903 906-907 911-912 925 930- 933 936 940 948 953 960 966 977 984 990 992 998 1000-1001 1005- 1007 1016 1023 1023 1025 1037 1046- 1047 1059 1061-1063 1073 1076- 1077 1089 1094-1097 1112-1113 1115 1134 1144-1148 1151 1154 1156 1163 1171 1197 1224-12205 1208 1216 1218 1224 1234-1235 1243-1244 1246 1279 1283 1286- 1287 1298 1316 1320 1344 1346 1350 1357 1359 1371 1373 1375 1381 1398 1400 1403 1408 1414 1442 1442-1445 1489 1492-1493 1504- 1402 1446 1454-1455 1479 1482 1484-1485 1489 1492-1493 1504- 1505 1513 1525 1527 1536 1538 1546 1565 1567 1571 1573 1575- 1576 1578-1579 1591 1595 1600- 1601 1608 1612 1615 1621 1624 1626 1636-1637 1647-1648 1651 1663 1656 1658 1661-1662 1672 1675 1682 1684 1686-1688 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768	Ì			
454 459 461 463 467 473 482-483 486 488 490 495 504 509 524 526 537-540 547 555 561 574-577 588- 591 593 606 615 620-621 632 637 645-647 650 659-660 662-664 667- 668 674-675 684 687 696 698 701 703-705 709 711 714 719-720 725- 727 732 749-750 762 765 771 775- 777 780 789-791 793 796 802-803 814-817 822 833 843 845 848 858 861 864 875 879 888 894-895 897- 900 903 906-907 911-912 925 930- 933 936 940 948 953 960 966 977 984 990 992 998 1000-1001 1005- 1007 1016 1023 1025 1037 1046- 1047 1059 1061-1063 1073 1076- 1077 1089 1094-1097 1112-1113 1115 1134 1144-1148 1151 1154 1156 1163 1171 1197 1204-1205 1208 1216 1218 1224 1234-1235 1243-1244 1246 1279 1283 1286- 1287 1298 1316 1320 1344 1346 1350 1357 1359 1371 1373 1375 1381 1398 1400 1403 1408 1414 1424 1427-1428 1431 1433 1440- 1442 1446 1454-1455 1479 1482 1484-1485 1489 1492-1493 1504- 1505 1513 1525 1527 1536 1538 1546 1565 1567 1571 1573 1575- 1576 1578-1579 1591 1595 1600- 1601 1608 1612 1615 1621 1624 1626 1636-1637 1647-1648 1651 1653 1656 1658 1661-1662 1672 1675 1662 1684 1666-1668 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768) .)
## 486 488 490 495 504 509 524 526 \$37-540 547 555 561 574-577 588-591 593 606 615 620-621 632 637 645-647 650 659-660 662-664 667-668 674-675 684 687 696 698 701 703-705 709 711 714 719-720 725-727 732 749-750 762 765 771 775-777 780 789-791 793 796 802-803 814-817 822 833 843 845 848 858 861 864 875 879 888 894-895 897-900 903 906-907 911-912 925 930-933 936 940 948 953 960 966 977 984 990 992 998 1000-1001 1005-1007 1016 1023 1025 1037 1046-1047 1059 1061-1063 1073 1076-1077 1089 1094-1097 1112-1113 1115 1134 1144-1148 1151 1154 1156 1163 1171 1197 1224-1205 1208 1216 1218 1224 1234-1235 1243-1244 1246 1279 1283 1286-1287 1298 1316 1320 1344 1346 1350 1357 1359 1371 1373 1375 1381 1398 1400 1403 1408 1414 1424 1427-1428 1431 1433 1440-1442 1446 1454-1455 1479 1482 1484-1485 1489 1492-1493 1504-1505 1513 1525 1527 1536 1538 1546 1565 1567 1571 1573 1575-1576 1578-1576 1578-1579 1591 1595 1600-1601 1608 1612 1615 1621 1624 1626 1636-1637 1647-1648 1651 1655 1658 1658 1661-1662 1672 1675 1682 1684 1686-1688 1690 1709-1710 1722 1727 1729 1735-1738 1740-1741 1760-1761 1768				
591 593 606 615 620-621 632 637 645-647 650 659-660 662-664 667-668 674-675 684 687 696 698 701 703-705 709 711 714 719-720 725- 727 732 749-750 762 765 771 775- 777 780 789-791 793 796 802-803 814-817 822 833 843 845 848 858 861 864 875 879 888 894-895 897- 900 903 906-907 911-912 925 930- 933 936 940 948 953 960 966 977 984 990 992 998 1000-1001 1005- 1007 1016 1023 1025 1037 1046- 1047 1059 1061-1063 1073 1076- 1077 1089 1094-1097 1112-113 1115 1134 1144-1148 1151 1154 1156 1163 1171 1197 1204-1205 1208 1216 1218 1224 1234-1235 1243-1244 1246 1279 1283 1286- 1287 1298 1316 1320 1344 1346 1350 1357 1359 1371 1373 1375 1381 1398 1400 1403 1408 1414 1424 1427-1428 1431 1433 1440- 1442 1446 1454-1455 1479 1482 1484-1485 1489 1492-1493 1504- 1505 1513 1525 1527 1536 1538 1546 1565 1567 1571 1573 1575- 1576 1578-1579 1591 1595 1600- 1601 1608 1612 1615 1621 1624 1626 1636-1637 1647-1648 1651 1655 1668 1668 1669 1669 1679 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768 fetal brain GIBCO HFB001 4 9 11-13 17-18 22-23 25 37-39	1			l :
645-647 650 659-660 662-664 667-668 674-675 686 487 696 698 701 703-705 709 711 714 719-720 725- 727 732 749-750 762 765 771 775- 777 780 789-791 793 796 802-803 814-817 822 833 843 845 848 858 861 864 875 879 888 894-895 897- 900 903 906-907 911-912 925 930- 933 936 940 948 953 960 966 977 984 990 992 998 1000-1001 1005- 1007 1016 1023 1025 1037 1046- 1047 1059 1094-1097 1112-1113 1115 1134 1144-1148 1151 1154 1156 1163 1171 1197 1204-1205 1208 1216 1218 1224 1234-1235 1243-1244 1246 1279 1283 1286- 1287 1298 1316 1320 1344 1346 1350 1357 1359 1371 1373 1375 1381 1398 1400 1403 1408 1414 1424 1427-1428 1431 1433 1440- 1442 1446 1454-1455 1479 1482 1484-1485 1489 1492-1493 1504- 1505 1513 1525 1527 1536 1538 1546 1565 1567 1571 1573 1575- 1576 1578-1579 1591 1595 1600- 1601 1608 1612 1615 1621 1624 1626 1636-1637 1647-1648 1651 1655 1666 1658 1661-1662 1672 1675 1682 1684 1686-1688 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768				
668 674-675 684 687 696 698 701 703-705 709 711 714 719-720 725- 727 732 749-750 762 765 771 775- 777 780 789-791 793 796 802-803 814-817 822 833 843 845 848 858 861 864 875 879 888 894-895 897- 900 903 906-907 911-912 925 930- 933 936 940 948 953 960 966 977 984 990 992 998 1000-1001 1005- 1007 1016 1023 1025 1037 1046- 1047 1059 1061-1063 1073 1076- 1077 1089 1094-1097 1112-1113 1115 1134 1144-1148 1151 1154 1156 1163 1171 1197 1224-1205 1208 1216 1218 1224 1234-1235 1243-1244 1246 1279 1283 1286- 1287 1298 1316 1320 1344 1346 1350 1357 1359 1371 1373 1375 1381 1398 1400 1403 1408 1414 1424 1427-1428 1431 1433 1440- 1442 1446 1454-1455 1479 1482 1484-1485 1489 1492-1493 1504- 1505 1513 1525 1527 1536 1538 1546 1565 1567 1571 1573 1575- 1576 1578-1579 1591 1595 1600- 1601 1608 1612 1615 1621 1624 1626 1636-1637 1647-1648 1651 1653 1656 1658 1661-1662 1672 1675 1682 1684 1686-1688 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768]	591 593 606 615 620-621 632 637
703-705 709 711 714 719-720 725- 727 732 749-750 762 765 771 775- 777 780 789-791 793 796 802-803 814-817 822 833 843 845 848 858 861 864 875 879 888 894-895 897- 900 903 906-907 911-912 925 930- 933 936 940 948 953 960 966 977 984 990 992 998 1000-1001 1005- 1007 1016 1023 1025 1037 1046- 1047 1059 1061-1063 1073 1076- 1077 1089 1094-1097 1112-1113 1115 1134 1144-1148 1151 1154 1156 1163 1171 1197 1204-1205 1208 1216 1218 1224 1234-1235 1243-1244 1246 1279 1283 1286- 1287 1298 1316 1320 1344 1346 1350 1357 1359 1371 1373 1375 1381 1398 1400 1403 1408 1414 1424 1427-1428 1431 1433 1440- 1442 1446 1454-1455 1479 1482 1484-1485 1489 1492-1493 1504- 1505 1513 1525 1527 1536 1538 1546 1565 1567 1571 1573 1575- 1576 1578-1579 1591 1595 1600- 1601 1608 1612 1615 1621 1624 1626 1636-1637 1647-1648 1651 1653 1656 1658 1661-1662 1672 1675 1682 1684 1686-1688 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768		1		645-647 650 659-660 662-664 667-
727 732 749-750 762 765 771 775- 777 780 789-791 793 796 802-803 814-817 822 833 843 845 848 858 861 864 875 879 888 894-895 897- 900 903 906-907 911-912 925 930- 933 936 940 948 953 960 966 977 984 990 992 998 1000-1001 1005- 1007 1016 1023 1025 1037 1046- 1047 1059 1061-1063 1073 1076- 1077 1089 1094-1097 1112-1113 1115 1134 1144-1148 1151 1154 1156 1163 1171 1197 1204-1205 1208 1216 1218 1224 1234-1235 12243-1244 1246 1279 1283 1286- 1287 1298 1316 1320 1344 1346 1350 1357 1359 1371 1373 1375 1381 1398 1400 1403 1408 1414 1424 1427-1428 1431 1433 1440- 1442 1446 1454-1455 1479 1482 1484-1485 1489 1492-1493 1504- 1505 1513 1525 1527 1536 1538 1546 1565 1567 1571 1573 1575- 1576 1578-1579 1591 1595 1600- 1601 1608 1612 1612 1612 1624 1626 1636-1637 1647-1648 1651 1653 1658 1658 1661-1662 1672 1675 1682 1684 1686-1688 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768	4	ı		
777 780 789-791 793 796 802-803 814-817 822 833 843 845 848 858 861 864 875 879 888 894-895 897- 900 903 906-907 911-912 925 930- 933 936 940 948 953 960 966 977 984 990 992 998 1000-1001 1005- 1007 1016 1023 1025 1037 1046- 1047 1059 1061-1063 1073 1076- 1077 1089 1094-1097 1112-1113 1115 1134 1144-1148 1151 1154 1156 1163 1171 1197 1204-1205 1208 1216 1218 1224 1234-1235 1243-1244 1246 1279 1283 1286- 1287 1298 1316 1320 1344 1346 1350 1357 1359 1371 1373 1375 1381 1398 1400 1403 1408 1414 1424 1427-1428 1431 1433 1440- 1442 1446 1454-1455 1479 1482 1484-1485 1489 1492-1493 1504- 1505 1513 1525 1527 1536 1538 1546 1565 1567 1571 1573 1575- 1576 1578-1579 1591 1595 1600- 1601 1608 1612 1615 1621 1624 1626 1636-1637 1647-1648 1651 1653 1656 1658 1661-1662 1672 1675 1682 1684 1686-1688 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768 fetal brain GIBCO HFB001 4 9 11-13 17-18 22-23 25 37-39]			IL I
814-817 822 833 843 845 848 858 861 864 875 879 888 894-895 897- 900 903 906-907 911-912 925 930- 933 936 940 948 953 960 966 977 984 990 992 998 1000-1001 1005- 1007 1016 1023 1025 1037 1046- 1047 1059 1061-1063 1073 1076- 1077 1089 1094-1097 1112-1113 1115 1134 1144-1148 1151 1154 1156 1163 1171 1197 1204-1205 1208 1216 1218 1224 1234-1235 1243-1244 1246 1279 1283 1286- 1287 1298 1316 1320 1344 1346 1350 1357 1359 1371 1373 1375 1381 1398 1400 1403 1408 1414 1424 1427-1428 1431 1433 1440- 1442 1446 1454-1455 1479 1482 1484-1485 1489 1492-1493 1504- 1505 1513 1525 1527 1536 1538 1546 1565 1567 1571 1573 1575- 1576 1578-1579 1591 1595 1600- 1601 1608 1612 1615 1621 1624 1626 1636-1637 1647-1648 1651 1653 1656 1658 1661-1662 1672 1675 1682 1684 1686-1688 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768	1			
861 864 875 879 888 894-895 897- 900 903 906-907 911-912 925 930- 933 936 940 948 953 960 966 977 984 990 992 998 1000-1001 1005- 1007 1016 1023 1025 1037 1046- 1047 1059 1061-1063 1073 1076- 1077 1089 1094-1097 1112-1113 1115 1134 1144-1148 1151 1154 1156 1163 1171 1197 1204-1205 1208 1216 1218 1224 1234-1235 1243-1244 1246 1279 1283 1286- 1287 1298 1316 1320 1344 1346 1350 1357 1359 1371 1373 1375 1381 1398 1400 1403 1408 1414 1424 1427-1428 1431 1433 1440- 1442 1446 1454-1455 1479 1482 1484-1485 1489 1492-1493 1504- 1505 1513 1525 1527 1536 1538 1546 1565 1567 1571 1573 1575- 1576 1578-1579 1591 1595 1600- 1601 1608 1612 1615 1621 1624 1626 1636-1637 1647-1648 1651 1653 1656 1658 1661-1662 1672 1675 1682 1684 1686-1688 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768 fetal brain GIBCO HFB001 4 9 11-13 17-18 22-23 25 37-39	1			l l
900 903 906-907 911-912 925 930- 933 936 940 948 953 960 966 977 984 990 992 998 1000-1001 1005- 1007 1016 1023 1025 1037 1046- 1047 1059 1061-1063 1073 1076- 1077 1089 1094-1097 1112-1113 1115 1134 1144-1148 1151 1154 1156 1163 1171 1197 1204-1205 1208 1216 1218 1224 1234-1235 1243-1244 1246 1279 1283 1286- 1287 1298 1316 1320 1344 1346 1350 1357 1359 1371 1373 1375 1381 1398 1400 1403 1408 1414 1424 1427-1428 1431 1433 1440- 1442 14427-1428 1431 1433 1440- 1442 1446 1454-1455 1479 1482 1484-1485 1489 1492-1493 1504- 1505 1513 1525 1527 1536 1538 1546 1565 1567 1571 1573 1575- 1576 1578-1579 1591 1595 1600- 1601 1608 1612 1615 1621 1624 1626 1636-1637 1647-1648 1651 1653 1656 1658 1661-1662 1672 1675 1682 1684 1686-1688 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768	l I		}	
933 936 940 948 953 960 966 977 984 990 992 998 1000-1001 1005- 1007 1016 1023 1025 1037 1046- 1047 1059 1061-1063 1073 1076- 1077 1089 1094-1097 1112-1113 1115 1134 1144-1148 1151 1154 1156 1163 1171 1197 1204-1205 1208 1216 1218 1224 1234-1235 1243-1244 1246 1279 1283 1286- 1287 1298 1316 1320 1344 1346 1350 1357 1359 1371 1373 1375 1381 1398 1400 1403 1408 1414 1424 1427-1428 1431 1433 1440- 1442 1446 1454 1455 1479 1482 1484-1485 1489 1492-1493 1504- 1505 1513 1525 1527 1536 1538 1546 1565 1567 1571 1573 1575- 1576 1578-1579 1591 1595 1600- 1601 1608 1612 1615 1621 1624 1626 1636-1637 1647-1648 1651 1653 1656 1658 1661-1662 1672 1675 1682 1684 1686-1688 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768 fetal brain GIBCO HFB001 4 9 11-13 17-18 22-23 25 37-39]			
984 990 992 998 1000-1001 1005- 1007 1016 1023 1025 1037 1046- 1047 1059 1061-1063 1073 1076- 1077 1089 1094-1097 1112-1113 1115 1134 1144-1148 1151 1154 1156 1163 1171 1197 1204-1205 1208 1216 1218 1224 1234-1235 1243-1244 1246 1279 1283 1286- 1287 1298 1316 1320 1344 1346 1350 1357 1359 1371 1373 1375 1381 1398 1400 1403 1408 1414 1424 1427-1428 1431 1433 1440- 1442 1446 1454-1455 1479 1482 1484-1485 1489 1492-1493 1504- 1505 1513 1525 1527 1536 1538 1546 1565 1567 1571 1573 1575- 1576 1578-1579 1591 1595 1600- 1601 1608 1612 1615 1621 1624 1626 1636-1637 1647-1648 1651 1653 1656 1658 1661-1662 1672 1675 1682 1684 1686-1688 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768 fetal brain GIBCO HFB001 4 9 11-13 17-18 22-23 25 37-39			ļ [*]	
1007 1016 1023 1025 1037 1046- 1047 1059 1061-1063 1073 1076- 1077 1089 1094-1097 1112-1113 1115 1134 1144-1148 1151 1154 1156 1163 1171 1197 1204-1205 1208 1216 1218 1224 1234-1235 1243-1244 1246 1279 1283 1286- 1287 1298 1316 1320 1344 1346 1350 1357 1359 1371 1373 1375 1381 1398 1400 1403 1408 1414 1424 1427-1428 1431 1433 1440- 1442 1446 1454-1455 1479 1482 1484-1485 1489 1492-1493 1504- 1505 1513 1525 1527 1536 1538 1546 1565 1567 1571 1573 1575- 1576 1578-1579 1591 1595 1600- 1601 1608 1612 1615 1621 1624 1626 1636-1637 1647-1648 1651 1653 1656 1658 1661-1662 1672 1675 1682 1684 1686-1688 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768 fetal brain GIBCO HFB001 4 9 11-13 17-18 22-23 25 37-39				
1047 1059 1061-1063 1073 1076- 1077 1089 1094-1097 1112-1113 1115 1134 1144-1148 1151 1154 1156 1163 1171 1197 1204-1205 1208 1216 1218 1224 1234-1235 1243-1244 1246 1279 1283 1286- 1287 1298 1316 1320 1344 1346 1350 1357 1359 1371 1373 1375 1381 1398 1400 1403 1408 1414 1424 1427-1428 1431 1433 1440- 1442 1446 1454-1455 1479 1482 1484-1485 1489 1492-1493 1504- 1505 1513 1525 1527 1536 1538 1546 1565 1567 1571 1573 1575- 1576 1578-1579 1591 1595 1600- 1601 1608 1612 1615 1621 1624 1626 1636-1637 1647-1648 1651 1653 1656 1658 1661-1662 1672 1675 1682 1684 1686-1688 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768 fetal brain GIBCO HFB001 4 9 11-13 17-18 22-23 25 37-39	1		}	
1077 1089 1094-1097 1112-1113 1115 1134 1144-1148 1151 1154 1156 1163 1171 1197 1204-1205 1208 1216 1218 1224 1234-1235 1243-1244 1246 1279 1283 1286- 1287 1298 1316 1320 1344 1346 1350 1357 1359 1371 1373 1375 1381 1398 1400 1403 1408 1414 1424 1427-1428 1431 1433 1440- 1442 1446 1454-1455 1479 1482 1484-1485 1489 1492-1493 1504- 1505 1513 1525 1527 1536 1538 1546 1565 1567 1571 1573 1575- 1576 1578-1579 1591 1595 1600- 1601 1608 1612 1615 1621 1624 1626 1636-1637 1647-1648 1651 1653 1656 1658 1661-1662 1672 1675 1682 1684 1686-1688 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768 fetal brain GIBCO HFB001 4 9 11-13 17-18 22-23 25 37-39]			
1156 1163 1171 1197 1204-1205 1208 1216 1218 1224 1234-1235 1243-1244 1246 1279 1283 1286- 1287 1298 1316 1320 1344 1346 1350 1357 1359 1371 1373 1375 1381 1398 1400 1403 1408 1414 1424 1427-1428 1431 1433 1440- 1442 1446 1454-1455 1479 1482 1484-1485 1489 1492-1493 1504- 1505 1513 1525 1527 1536 1538 1546 1565 1567 1571 1573 1575- 1576 1578-1579 1591 1595 1600- 1601 1608 1612 1615 1621 1624 1626 1636-1637 1647-1648 1651 1653 1656 1658 1661-1662 1672 16675 1682 1684 1686-1688 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768 fetal brain GIBCO HFB001 4 9 11-13 17-18 22-23 25 37-39	1			
1208 1216 1218 1224 1234-1235 1243-1244 1246 1279 1283 1286- 1287 1298 1316 1320 1344 1346 1350 1357 1359 1371 1373 1375 1381 1398 1400 1403 1408 1414 1424 1427-1428 1431 1433 1440- 1442 1446 1454-1455 1479 1482 1484-1485 1489 1492-1493 1504- 1505 1513 1525 1527 1536 1538 1546 1565 1567 1571 1573 1575- 1576 1578-1579 1591 1595 1600- 1601 1608 1612 1615 1621 1624 1626 1636-1637 1647-1648 1651 16653 1656 1658 1661-1662 1672 1675 1682 1684 1686-1688 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768 fetal brain GIBCO HFB001 4 9 11-13 17-18 22-23 25 37-39	1			1115 1134 1144-1148 1151 1154
1243-1244 1246 1279 1283 1286- 1287 1298 1316 1320 1344 1346 1350 1357 1359 1371 1373 1375 1381 1398 1400 1403 1408 1414 1424 1427-1428 1431 1433 1440- 1442 1446 1454-1455 1479 1482 1484-1485 1489 1492-1493 1504- 1505 1513 1525 1527 1536 1538 1546 1565 1567 1571 1573 1575- 1576 1578-1579 1591 1595 1600- 1601 1608 1612 1615 1621 1624 1626 1636-1637 1647-1648 1651 16653 1656 1658 1661-1662 1672 1675 1682 1684 1686-1688 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768 fetal brain GIBCO HFB001 4 9 11-13 17-18 22-23 25 37-39	1			1156 1163 1171 1197 1204-1205
1287 1298 1316 1320 1344 1346 1350 1357 1359 1371 1373 1375 1381 1398 1400 1403 1408 1414 1424 1427-1428 1431 1433 1440- 1442 1446 1454-1455 1479 1482 1484-1485 1489 1492-1493 1504- 1505 1513 1525 1527 1536 1538 1546 1565 1567 1571 1573 1575- 1576 1578-1579 1591 1595 1600- 1601 1608 1612 1615 1621 1624 1626 1636-1637 1647-1648 1651 1653 1656 1658 1661-1662 1672 1675 1682 1684 1686-1688 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768 fetal brain GIBCO HFB001 4 9 11-13 17-18 22-23 25 37-39			Į	
1350 1357 1359 1371 1373 1375 1381 1398 1400 1403 1408 1414 1424 1427-1428 1431 1433 1440- 1442 1446 1454-1455 1479 1482 1484-1485 1489 1492-1493 1504- 1505 1513 1525 1527 1536 1538 1546 1565 1567 1571 1573 1575- 1576 1578-1579 1591 1595 1600- 1601 1608 1612 1615 1621 1624 1626 1636-1637 1647-1648 1651 1653 1656 1658 1661-1662 1672 1675 1682 1684 1686-1688 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768 fetal brain GIBCO HFB001 4 9 11-13 17-18 22-23 25 37-39		1		1
1381 1398 1400 1403 1408 1414 1424 1427-1428 1431 1433 1440- 1442 1446 1454-1455 1479 1482 1484-1485 1489 1492-1493 1504- 1505 1513 1525 1527 1536 1538 1546 1565 1567 1571 1573 1575- 1576 1578-1579 1591 1595 1600- 1601 1608 1612 1615 1621 1624 1626 1636-1637 1647-1648 1651 1653 1656 1658 1661-1662 1672 1675 1682 1684 1686-1688 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768 fetal brain GIBCO HFB001 4 9 11-13 17-18 22-23 25 37-39				1.
1424 1427-1428 1431 1433 1440- 1442 1446 1454-1455 1479 1482 1484-1485 1489 1492-1493 1504- 1505 1513 1525 1527 1536 1538 1546 1565 1567 1571 1573 1575- 1576 1578-1579 1591 1595 1600- 1601 1608 1612 1615 1621 1624 1626 1636-1637 1647-1648 1651 1653 1656 1658 1661-1662 1672 1675 1682 1684 1686-1688 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768 fetal brain GIBCO HFB001 4 9 11-13 17-18 22-23 25 37-39]	
1442 1446 1454-1455 1479 1482 1484-1485 1489 1492-1493 1504- 1505 1513 1525 1527 1536 1538 1546 1565 1567 1571 1573 1575- 1576 1578-1579 1591 1595 1600- 1601 1608 1612 1615 1621 1624 1626 1636-1637 1647-1648 1651 1653 1656 1658 1661-1662 1672 1675 1682 1684 1686-1688 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768 fetal brain GIBCO HFB001 4 9 11-13 17-18 22-23 25 37-39	[1
1484-1485 1489 1492-1493 1504- 1505 1513 1525 1527 1536 1538 1546 1565 1567 1571 1573 1575- 1576 1578-1579 1591 1595 1600- 1601 1608 1612 1615 1621 1624 1626 1636-1637 1647-1648 1651 1653 1656 1658 1661-1662 1672 1675 1682 1684 1686-1688 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768 fetal brain GIBCO HFB001 4 9 11-13 17-18 22-23 25 37-39	1		ļ	
1505 1513 1525 1527 1536 1538 1546 1565 1567 1571 1573 1575- 1576 1578-1579 1591 1595 1600- 1601 1608 1612 1615 1621 1624 1626 1636-1637 1647-1648 1651 1653 1656 1658 1661-1662 1672 1675 1682 1684 1686-1688 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768 fetal brain GIBCO HFB001 4 9 11-13 17-18 22-23 25 37-39			1	ł
1546 1565 1567 1571 1573 1575- 1576 1578-1579 1591 1595 1600- 1601 1608 1612 1615 1621 1624 1626 1636-1637 1647-1648 1651 1653 1656 1658 1661-1662 1672 1675 1682 1684 1686-1688 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768 fetal brain GIBCO HFB001 4 9 11-13 17-18 22-23 25 37-39]	
1576 1578-1579 1591 1595 1600- 1601 1608 1612 1615 1621 1624 1626 1636-1637 1647-1648 1651 1653 1656 1658 1661-1662 1672 1675 1682 1684 1686-1688 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768 fetal brain GIBCO HFB001 4 9 11-13 17-18 22-23 25 37-39			ļ	
1601 1608 1612 1615 1621 1624 1626 1636-1637 1647-1648 1651 1653 1656 1658 1661-1662 1672 1675 1682 1684 1686-1688 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768 fetal brain GIBCO HFB001 4 9 11-13 17-18 22-23 25 37-39			1	i :
1626 1636-1637 1647-1648 1651 1653 1656 1658 1661-1662 1672 1675 1682 1684 1686-1688 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768 fetal brain GIBCO HFB001 4 9 11-13 17-18 22-23 25 37-39	j			t e
1653 1656 1658 1661-1662 1672 1675 1682 1684 1686-1688 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768 fetal brain GIBCO HFB001 4 9 11-13 17-18 22-23 25 37-39			I	
1675 1682 1684 1686-1688 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768 fetal brain GIBCO HFB001 4 9 11-13 17-18 22-23 25 37-39			1	
1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768 fetal brain GIBCO HFB001 4 9 11-13 17-18 22-23 25 37-39	}			
1738 1740-1741 1760-1761 1768 fetal brain GIBCO HFB001 4 9 11-13 17-18 22-23 25 37-39				1
	{		1	I I
42-47 50-51 54-55 58 60-61 65-66	fetal brain	GIBCO	HFB001	4 9 11-13 17-18 22-23 25 37-39
				42-47 50-51 54-55 58 60-61 65-66

Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
		Library Name	
			72 75 77 80 82 85 90-91 94 100-
			102 107 110 112-116 118-119 122-
			123 126 128 134 136-140 147-148
			153-155 157 161 165 169-172 175 181 186 188-189 197-198 204-206
			208 210 215 222-223 225-226 230
			235-238 240-241 247 253 256-258
			260-262 267-269 276 279-281 284
			286 289 298 300-302 307 310 318
			321-323 325 330-331 339 341 346-
1		ĺ	349 352 354 356-359 362 364-365
			371-372 377 379-380 382 384 387
			434-435 438 441-443 449 451 453-
			455 457-463 470 472-473 475 477-
			478 482-483 486-488 490-491 493
			496 499-500 502-504 506-507 509-
]			512 516 519-520 522 525-526 529-
1		Į	530 537-540 543-544 546-547 566-
			567 569-570 572-582 585 588 590- 591 593 595 599 601 604 606-609
	}	÷	611-612 614-620 622-624 630 632
			636 643 645-647 650-652 654 659
			661 665 667-668 670-672 676 678
		{	681 687 689 692-694 697 699 710
			714 717 721 727 729-732 734 736
			738 743-746 750-751 759 763 766
			770 772 775-777 784 789 791 796 799 802-805 810-811 814 819-821
ł		Ì	824 826 830 834-837 839-850 854-
' '		ļ	856 858-860 862 864 869 871 876-
			877 879 883 886-887 890-891 893-
[İ	[895 898-901 905 908-910 912-916
	1	Ì	919 922-923 925 927 930-933 935-
ł		1	938 948 952-960 963-964 967 969- 972 975 978-979 981 983 986-987
)			990 992 995 997 999-1002 1005-
	1		1009 1011-1013 1016 1018-1019
	l	1	1023 1026 1029-1031 1033-1035
		ļ	1038 1041 1047 1050 1053 1057
			1059 1064 1068 1070 1072-1073
	1		1078-1079 1081-1082 1086 1089
{			1094 1097 1103 1107-1109 1113- 1115 1121-1122 1127 1134-1135
			1138 1140 1143 1148-1151 1153
		1	1156-1157 1159 1167 1170 1175
<u> </u>			1193-1194 1200 1202 1207-1209
[1211 1216 1219-1220 1226-1227
}		}	1229 1232-1234 1240-1241 1243
}	})	1246 1249-1251 1253-1254 1258 1267-1268 1271 1276 1279 1282
		1	1285-1289 1293-1294 1305 1307-
1	1		1308 1312 1316 1320 1327 1338-
			1339 1341-1344 1346 1349 1355-
]	1357 1359 1365-1366 1369-1370
•			1373-1375 1379 1386 1389 1394
<u> </u>	1		1398 1409 1413-1414 1416-1417
1	}		1420-1421 1425-1427 1430 1433 14437 1439 1442 1445-1452 1454-
l			1457 1459 1463-1464 1468 1470
	· ·		1474 1477-1479 1489 1492 1494
	ļ		1497-1498 1501-1503 1507 1509
	ļ		1511-1513 1517 1520-1521 1524-
			1526 1531-1533 1535 1537-1538
	ĺ		1547 1554 1556-1559 1564-1567
			1571 1584 1587 1589 1594 1599-
			1601 1611-1612 1614-1616 1619- 1620 1625-1628 1630-1631 1634
			1637-1638 1640-1643 1645 1648-
L	 _	L	1

Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
		Library Name	SEQ ID NOS:
			1649 1651 1653-1655 1657-1658
			1664-1665 1667 1669 1673 1678-
1			1679 1683-1684 1686 1693 1701
]			1704-1705 1709 1713-1714 1717-
1	1		1720 1724 1727-1728 1731-1733
1	İ		1737-1738 1743-1744 1752 1754- 1755 1757 1760-1761 1765 1772
1			1779 1785
macrophage	Invitrogen	HMP001	5-8 110 204-205 503 634 678 859
	•		878 933 988-989 1379 1448 1504
infant brain	Columbia	IB2002	10 12-13 15-18 22-23 25 29 34
· }	University		37-39 43 47 50-51 54-56 58 60-63
1			65-66 68-69 72-74 80 82-83 86
1	l		88-92 97 100 102-104 106-108 110
			112-113 115-116 118 123 128 130
	į		134-136 138-139 143 147-149 151-
,			152 154-155 163 165-167 169 172-
1	[175 181-184 186 193-196 198 201
			203-205 209-210 214-215 222 224- 226 231-232 235-236 239 246-247
			252 257 260 268-269 272 276-277
1	1	İ	279-281 286 288 291-292 295 298
1	}	j	300-301 304 307 310 313 321-323
			330-331 333-334 339 346-347 349
[1		352 356-357 362 371-372 377 379-
]			380 383-384 392 397 401 406 408
1	ĺ		411 413-414 416 418-419 422 428
!!!	į		430-431 434-435 438 443 449 453-
1			454 461 464-466 469-470 472-473 475-476 478 482-483 487 490 492
[[1	ł	494 497 503 507-508 510-513 516
1		}	519-520 524-526 530-534 536-540
1		1	547 550-551 561 563-564 566-567
ł l	į	1	572-576 579 581-582 584-587 590-
j j			591 593 595-597 607-609 611-613
ĺ	ľ	i	616-617 620 622-624 627 631 637
]	1	j	641 645-647 650-655 657-658 660-
j ł	İ		665 667-675 689 691 695 697 699 703 707 713-715 717 721 728-731
	ì		733-736 739 743 745 751 755 759
}			763 769-770 772 778 780-781 785
		ľ	788-789 793-794 799 803 808 811
1	!	•	814 825-826 830 834-836 840-843
	j	1	845 848-850 854-855 860 862 864-
	1	1	865 870 872 875-876 878 886 888
		1	890-891 894-896 898 903-904 916-
	1	{	917 919 922-925 927-928 930-932
			934-936 938 941 945-946 948-950 953-954 959-962 966-969 977 979
		İ	981 986-990 992 997 999-1000
	1		1004-1006 1014 1016 1018-1019
	}		1024-1025 1033 1036 1047 1051-
1	1	1	1052 1054-1055 1057-1059 1063-
1	1	1	1064 1068-1070 1073 1081-1082
ļ		! :	1085 1089 1108-1113 1118-1120
1	1		1123-1124 1130 1132-1138 1140
ļ	į		1149 1151 1153-1154 1163-1170
1	ĺ		1172 1174-1175 1183-1184 1188
j	ļ	1:	1190 1193-1194 1196-1197 1199
			1204 1208-1209 1211 1218-1222 1226-1227 1229 1231 1234 1241
i	ļ		1247 1249 1251 1256 1258 1261-
	j		1262 1269 1274 1279 1281 1283
Ĭ		:	1285 1287-1289 1294-1295 1305
	1		1307 1313-1314 1316-1320 1329
		-	1332 1341-1342 1345 1349 1356
1			
	1	{ 3	1362-1363 1365-1366 1368-1370
ŀ	1	3	1362-1363 1365-1366 1368-1370 1374 1381 1383-1384 1388 1400 1403 1406-1407 1413 1417 1420

Γ	Tissue Origin	RNA Source	Hyses	
-			Hyseq Library Name	
	·		SIDIATY NAME	1423 1429-1431 1435-1436 1439- 1441 1443 1447-1449 1451-1452 1454-1455 1457 1459 1463-1465 1468 1470-1471 1475 1479 1482- 1483 1485 1493-1494 1496 1498- 1499 1502-1503 1505-1507 1509 1522-1523 1525 1528 1531-1533 1542 1546-1547 1549-1550 1554- 1555 1563 1565-1567 1569 1575 1580 1583-1586 1588 1590 1592- 1593 1595 1598 1600-1601 1608- 1610 1612 1614-1616 1619 1621 1624 1626-1627 1630-1633 1637 1639-1640 1642 1644 1647 1652 1654-1655 1658-1659 1664-1665 1672-1673 1676-1681 1685-1688 1693-1695 1701-1702 1704 1708 1717-1720 1723-1724 1726-1728
				1733 1735-1741 1743-1744 1752 1755-1758 1762 1765 1771 1774
	infant brain	Columbia University Columbia University	IB2003	1777-1778 1786 17-18 20-23 29 34 43 60 68-69 78-80 88 100-101 107 110 112 118 123 128 133 135-137 146 148 152 159 166 169 174 194 198 203 215 223 225-226 229 235-236 247 250 276-281 286 290-292 295 300-301 310 322 324 331 334 339 346-347 349-350 352 357 371 376-377 382 384 403 408-409 414-415 453-455 472 476 478-479 490 503 507 516 520 530 534 536-540 551 563 572- 576 585 587 590-591 593 595-596 601 606 612 616-617 620 622-624 650 652-653 661 665 670-671 674- 675 678 689 715 717 727-728 730 734 759 775-777 780-781 785 796 806-807 811 824 845-846 864 869 875 882 889 894-895 898 904 917 919 921-923 932 935-936 946 950 954 962 977 979 997 999-1000 1005-1006 1009 1011 1017 1024 1033 1037 1043 1055 1057 1109 114-1115 1120 1123 1127 1144- 1145 1149 1151-1153 1260 1267 1170 1174 1193-1194 1196 1199 1202 1206 1209 1220-1221 1226 1229 1240-1241 1251 1258 1284 1288-1289 1305 1314 1327 1333 1344 1347 1350 1356-1357 1365- 1366 1378-1379 1388 1400 1403 1421 1423 1431 1436 1440-1441 1446-1447 1457 1459 1471 1499 1503 1507 1509 1536 1546 1557- 1559 1567 1572 1587 1595 1598 1610-1612 1615 1631 1639 1644 1647 1657-1658 1673 1678-1681 1683-1684 1701-1702 1708-1709 1713-1714 1719 1757 1760-1761 1765 1771 1778 101 113 139 152 260 279 290-292 374 377 551 563 608-609 653 659 814 954 1005-1006 1029-1030 1130 1164 1209 1258 1294 1305 1320
			Í	1327 1397 1431 1498 1507 1615 1640 1694-1695 1763-1764 1767
- ;	nfant brain	Columbia University	IBS001	1779 10 12 119 175 279-281 321 334
		OWTACTRICA		371 446 551 563 623 652 667 669

Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
		Library Name	
			671-672 819 949 966 1113 1130
			1151 1188 1193-1194 1196 1229 1258 1265 1271 1287 1317-1319
			1324-1325 1342 1423 1440-1441
			1448 1471 1482 1525 1532 1546
			1562 1569 1588 1591 1610 1618
			1647 1649 1658
lung,	Strategene	LFB001	5-9 17 20-21 25 68-69 82 94 105
fibroblast			153 157 197-198 203 207-208 212-
			213 223 262 266 283 302 321 326
			333 356 370 427 430 436 446 462
	ł i	l.	472 493 498 503 516 519 527 535
	ļ		537-540 542-544 562 565 567 586
			599-600 607 615 630 647 662-664 692-694 712 719 745 748 775-777
			794-796 810 837 843-847 849 854-
	}		856 869 876 903 934 953 955-956
	Î Î		964 975-976 984 1000 1005-1007
	1		1024-1025 1033 1039 1053 1064
			1070 1072 1082 1112-1113 1134
			1136-1138 1140 1195 1223 1232-
			1233 1246 1279 1285 1295 1311
	1		1320 1334-1335 1343 1427-1428
	1		1446 1478 1482 1493 1504 1537
			1552 1555 1567 1575 1582 1598
	į		1620 1625 1632 1638 1645 1654-
	}		1655 1662 1680-1681 1684 1686 1690 1696 1702 1711 1733 1741
ļ		j	1760-1761 1778 1785
lung tumor	Invitrogen	LGT002	5-10 18 20-21 29 33-36 40 43 52
Tung Cumor	inviewoge		54-55 61 65-66 68-70 73-75 80 85
	1	}	88-89 93-94 100 103 106-108 112-
<u> </u>		ļ	113 115-116 118-119 123-124 126
			130-132 135-137 139-141 143-144
ł		ĺ	147-148 151-153 155-156 159 161
	j	i	164 169 171 179-180 185 190 192
'		ļ	194 196-199 203-208 210 212-214 216-217 219 222 233 240-241 244
	ĺ	1	246 251-252 255-256 261-262 266.
	ł	1	272 276-277 279-281 284 286 288
	1	ļ	290 295 298 301-302 309-312 317
			321 329 332 341-342 344-345 348
	1	1	352 358-360 363 368 370-371 376
)		}	380-381 384 389-390 398 400 409
		1	414 423 426-427 430 432-436 443-
	ł	1	444 450-451 454 462 468 472-477
	1	ľ	480-483 487-488 490-491 493 496-
1	1	1	498 500 503-506 509-512 515-516 519 521-523 526 530 534 541 544
1	l .	T .	
1	i	1	
I			547 554 557 564 566-567 572-576
I .			1
			547 554 557 564 566-567 572-576 585-586 588-589 595-596 601 607
			547 554 557 564 566-567 572-576 585-586 588-589 595-596 601 607 611-612 615 619 621 623 626 630 632-633 644 647 649 651 655-656 660 662-665 667 669 672 683-684
			547 554 557 564 566-567 572-576 585-586 588-589 595-596 601 607 611-612 615 619 621 623 626 630 632-633 644 647 649 651 655-656
			547 554 557 564 566-567 572-576 585-586 588-589 595-596 601 607 611-612 615 619 621 623 626 630 632-633 644 647 649 651 655-656 660 662-665 667 669 672 683-684 696 700 706 710 713 716 718-719 722-723 728 734-739 743 750 752
			547 554 557 564 566-567 572-576 585-586 588-589 595-596 501 607 611-612 615 619 621 623 626 630 632-633 644 647 649 651 655-656 660 662-665 667 669 672 683-684 696 700 706 710 713 716 718-719 722-723 728 734-739 743 750 752 763 765-766 773-778 784-785 787-
			547 554 557 564 566-567 572-576 585-586 588-589 595-596 601 607 611-612 615 619 621 623 626 630 632-633 644 647 649 651 655-656 660 662-665 667 669 672 683-684 696 700 706 710 713 716 718-719 722-723 728 734-739 743 750 752 763 765-766 773-778 784-785 787- 789 791 800 802-803 809-812 814
			547 554 557 564 566-567 572-576 585-586 588-589 595-596 601 607 611-612 615 619 621 623 626 630 632-633 644 647 649 651 655-656 660 662-665 667 669 672 683-684 696 700 706 710 713 716 718-719 722-723 728 734-739 743 750 752 763 765-766 773-778 784-785 787- 789 791 800 802-803 809-812 814 824 826 828-829 832 838-839 841-
			547 554 557 564 566-567 572-576 585-586 588-589 595-596 601 607 611-612 615 619 621 623 626 630 632-633 644 647 649 651 655-656 660 662-665 667 669 672 683-684 696 700 706 710 713 716 718-719 722-723 728 734-739 743 750 752 763 765-766 773-778 784-785 787- 789 791 800 802-803 809-812 814 824 826 828-829 832 838-839 841- 845 849-850 852-855 857-861 864
			547 554 557 564 566-567 572-576 585-586 588-589 595-596 601 607 611-612 615 619 621 623 626 630 632-633 644 647 649 651 655-656 660 662-665 667 669 672 683-684 696 700 706 710 713 716 718-719 722-723 728 734-739 743 750 752 763 765-766 773-778 784-785 787- 789 791 800 802-803 809-812 814 824 826 828-829 832 838-839 841- 845 849-850 852-855 857-861 864 866 874 878-880 882 887 890-891
			547 554 557 564 566-567 572-576 585-586 588-589 595-596 601 607 611-612 615 619 621 623 626 630 632-633 644 647 649 651 655-656 660 662-665 667 669 672 683-684 696 700 706 710 713 716 718-719 722-723 728 734-739 743 750 752 763 765-766 773-778 784-785 787- 789 791 800 802-803 809-812 814 824 826 828-829 832 838-839 841- 845 849-850 852-855 857-861 864 866 874 878-880 882 887 890-891 897-898 902 904 906-907 910 916
			547 554 557 564 566-567 572-576 585-586 588-589 595-596 501 607 611-612 615 619 621 623 626 630 632-633 644 647 649 651 655-656 660 662-665 667 669 672 683-684 696 700 706 710 713 716 718-719 722-723 728 734-739 743 750 752 763 765-766 773-778 784-785 787- 789 791 800 802-803 809-812 814 824 826 828-829 832 838-839 841- 845 849-850 852-855 857-861 864 866 874 878-880 882 887 890-891 897-898 902 904 906-907 910 916 918-920 922 924-925 927 930-932
			547 554 557 564 566-567 572-576 585-586 588-589 595-596 601 607 611-612 615 619 621 623 626 630 632-633 644 647 649 651 655-656 660 662-665 667 669 672 683-684 696 700 706 710 713 716 718-719 722-723 728 734-739 743 750 752 763 765-766 773-778 784-785 787- 789 791 800 802-803 809-812 814 824 826 828-829 832 838-839 841- 845 849-850 852-855 857-861 864 866 874 878-880 882 887 890-891 897-898 902 904 906-907 910 916 918-920 922 924-925 927 930-932 934-935 937 947 950 953 955-956
			547 554 557 564 566-567 572-576 585-586 588-589 595-596 601 607 611-612 615 619 621 623 626 630 632-633 644 647 649 651 655-656 660 662-665 667 669 672 683-684 696 700 706 710 713 716 718-719 722-723 728 734-739 743 750 752 763 765-766 773-778 784-785 787- 789 791 800 802-803 809-812 814 824 826 828-829 832 838-839 841- 845 849-850 852-855 857-861 864 866 874 878-880 882 887 890-891 897-898 902 904 906-907 910 916 918-920 922 924-925 927 930-932 934-935 937 947 950 953 955-956 961 963 966-967 969 971 977-979
			547 554 557 564 566-567 572-576 585-586 588-589 595-596 601 607 611-612 615 619 621 623 626 630 632-633 644 647 649 651 655-656 660 662-665 667 669 672 683-684 696 700 706 710 713 716 718-719 722-723 728 734-739 743 750 752 763 765-766 773-778 784-785 787- 789 791 800 802-803 809-812 814 824 826 828-829 832 838-839 841- 845 849-850 852-855 857-861 864 866 874 878-880 882 887 890-891 897-898 902 904 906-907 910 916 918-920 922 924-925 927 930-932 934-935 937 947 950 953 955-956
			547 554 557 564 566-567 572-576 585-586 588-589 595-596 601 607 611-612 615 619 621 623 626 630 632-633 644 647 649 651 655-656 660 662-665 667 669 672 683-684 696 700 706 710 713 716 718-719 722-723 728 734-739 743 750 752 763 765-766 773-778 784-785 787- 789 791 800 802-803 809-812 814 824 826 828-829 832 838-839 841- 845 849-850 852-855 857-861 864 866 874 878-880 882 887 890-891 897-898 902 904 906-907 910 916 918-920 922 924-925 927 930-932 934-935 937 947 950 953 955-956 961 963 966-967 969 971 977-979 981 984 986-987 990 992-993 995

Tissue Origin	RNA Source	Hyseq	CEO TO NOC.
		Library Name	SEQ ID NOS:
			1045 1047-1050 1052 1054-1055
			1059 1063-1064 1067-1071 1073-
	1		1074 1078 1085 1087 1089 1095-
			1097 1104 1106-1107 1109 1112
	l		1116-1117 1119 1126 1134-1135
	[1139 1141-1142 1144-1145 1148
		•	1152-1153 1156-1158 1167 1170 1172 1178 1195-1196 1198-1200
			1202 1204 1208 1214 1216 1219
1			1222 1227 1234 1241 1247 1252
1			1257-1258 1265 1267-1270 1276
			1278 1280-1281 1283 1285 1288-
1			1289 1295 1300 1305 1308 1312
-			1317-1321 1329 1338-1339 1341
1	Í		1344-1346 1349-1351 1353-1355
}			1357 1365-1366 1369 1378-1379
1	i		1383-1385 1394 1397 1400 1402-
i			1403 1408 1417 1419 1423-1426
}	Į į		1431 1433-1436 1438 1444 1446-
1	[<u> </u>	1448 1454-1455 1460 1466 1468
}			1470 1474 1480-1481 1483 1486-
		1	1488 1490-1491 1494-1496 1506
			1508-1509 1511-1512 1515-1516 1519 1523-1524 1528-1529 1536-
ļ			1540 1546 1549-1550 1555 1560-
			1561 1565 1567 1569 1575 1588
1			1591 1593-1594 1596-1598 1600-
ļ ·			1602 1608 1614-1616 1618 1620
Ì			1624-1625 1627-1632 1636 1639
			1644-1645 1647-1649 1652-1653
1			1656-1662 1664 1666-1667 1670-
1			1671 1673-1675 1678-1679 1683
			1685-1688 1690-1692 1696-1699
1	ſ		1705 1709 1716-1717 1722 1727
1	1		
			1730 1735 1739 1741 1743-1744
			1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765
		,	1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776
lymphocytes	ATCC	LPC001	1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776 1778-1779 1786
lymphocytes	ATCC	LPC001	1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51
lymphocytes	ATCC	LPC001	1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776 1778-1779 1786
lymphocytes	ATCC	LPC001	1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223
lymphocytes	ATCC	LPC001	1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264
lymphocytes	ATCC	LPC001	1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325-
lymphocytes	ATCC	LPC001	1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384
lymphocytes	ATCC	LPC001	1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426-
lymphocytes	ATCC	LPC001	1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454-
lymphocytes	AŤCC	LPC001	1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537-
lymphocytes	AŤCC	LPC001	1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589
lymphocytes	ATCC	LPC001	1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630
lymphocytes	ATCC	LPC001	1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697
lymphocytes	ATCC	LPC001	1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786
lymphocytes	ATCC	LPC001	1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786 789-790 793 800 802 822 838 849
lymphocytes	ATCC	LPC001	1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786
lymphocytes	ATCC	LPC001	1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786 789-790 793 800 802 822 838 849 866 869 876 881-883 892 898 906-
lymphocytes	AŤCC	LPC001	1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786 789-790 793 800 802 822 838 849 866 869 876 881-883 892 898 906- 907 911 921-923 928 975 990 992 996 1001 1004-1007 1033 1050 1054 1078 1107 1135 1140-1141
lymphocytes	ATCC	LPC001	1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786 789-790 793 800 802 822 838 849 866 869 876 881-883 892 898 906- 907 911 921-923 928 975 990 992 996 1001 1004-1007 1033 1050 1054 1078 1107 1135 1140-1141 1143 1148 1158 1163 1177 1199
lymphocytes	ATCC	LPC001	1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786 789-790 793 800 802 822 838 849 866 869 876 881-883 892 898 906- 907 911 921-923 928 975 990 992 996 1001 1004-1007 1033 1050 1054 1078 1107 1135 1140-1141 1143 1148 1158 1163 1177 1199 1205 1216 1226 1231 1236 1241
lymphocytes	ATCC	LPC001	1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786 789-790 793 800 802 822 838 849 866 869 876 881-883 892 898 906- 907 911 921-923 928 975 990 992 996 1001 1004-1007 1033 1050 1054 1078 1107 1135 1140-1141 1143 1148 1158 1163 1177 1199 1205 1216 1226 1231 1236 1241 1244 1250 1258 1260 1265 1269-
lymphocytes	ATCC	LPC001	1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786 789-790 793 800 802 822 838 849 866 869 876 881-883 892 898 906- 907 911 921-923 928 975 990 992 996 1001 1004-1007 1033 1050 1054 1078 1107 1135 1140-1141 1143 1148 1158 1163 1177 1199 1205 1216 1226 1231 1236 1241 1244 1250 1258 1260 1265 1269- 1271 1290-1293 1308 1312 1317
lymphocytes	ATCC	LPC001	1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786 789-790 793 800 802 822 838 849 866 869 876 881-883 892 898 906- 907 911 921-923 928 975 990 992 996 1001 1004-1007 1033 1050 1054 1078 1107 1135 1140-1141 1143 1148 1158 1163 1177 1199 1205 1216 1226 1231 1236 1241 1244 1250 1258 1260 1265 1269- 1271 1290-1293 1308 1312 1317
lymphocytes	ATCC	LPC001	1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786 789-790 793 800 802 822 838 849 866 869 876 881-883 892 898 906- 907 911 921-923 928 975 990 992 996 1001 1004-1007 1033 1050 1054 1078 1107 1135 1140-1141 1143 1148 1158 1163 1177 1199 1205 1216 1226 1231 1236 1241 1244 1250 1258 1260 1265 1269- 1271 1290-1293 1308 1312 1317 1319-1320 1339 1345-1346 1348 1350-1351 1357 1367 1369 1379
lymphocytes	ATCC	LPC001	1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786 789-790 793 800 802 822 838 849 866 869 876 881-883 892 898 906- 907 911 921-923 928 975 990 992 996 1001 1004-1007 1033 1050 1054 1078 1107 1135 1140-1141 1143 1148 1158 1163 1177 1199 1205 1216 1226 1231 1236 1241 1244 1250 1258 1260 1265 1269- 1271 1290-1293 1308 1312 1317 1319-1320 1339 1345-1346 1348 1350-1351 1357 1367 1369 1379 1381 1383-1384 1386-1387 1389
lymphocytes	ATCC	LPC001	1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786 789-790 793 800 802 822 838 849 866 869 876 881-883 892 898 906- 907 911 921-923 928 975 990 992 996 1001 1004-1007 1033 1050 1054 1078 1107 1135 1140-1141 1143 1148 1158 1163 1177 1199 1205 1216 1226 1231 1236 1241 1244 1250 1258 1260 1265 1269- 1271 1290-1293 1308 1312 1317 1319-1320 1339 1345-1346 1348 1350-1351 1357 1367 1369 1379 1381 1383-1384 1386-1387 1389 1394 1397 1405 1423 1425-1428
lymphocytes	ATCC	LPC001	1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786 789-790 793 800 802 822 838 849 866 869 876 881-883 892 898 906- 907 911 921-923 928 975 990 992 996 1001 1004-1007 1033 1050 1054 1078 1107 1135 1140-1141 1143 1148 1158 1163 1177 1199 1205 1216 1226 1231 1236 1241 1244 1250 1258 1260 1265 1269- 1271 1290-1293 1308 1312 1317 1319-1320 1339 1345-1346 1348 1350-1351 1357 1367 1369 1379 1381 1383-1384 1386-1387 1389 1394 1397 1405 1423 1425-1428 1431 1437 1446 1448 1461 1466
lymphocytes	ATCC	LPC001	1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786 789-790 793 800 802 822 838 849 866 869 876 881-883 892 898 906- 907 911 921-923 928 975 990 992 996 1001 1004-1007 1033 1050 1054 1078 1107 1135 1140-1141 1143 1148 1158 1163 1177 1199 1205 1216 1226 1231 1236 1241 1244 1250 1258 1260 1265 1269- 1271 1290-1293 1308 1312 1317 1319-1320 1339 1345-1346 1348 1350-1351 1357 1367 1369 1379 1381 1383-1384 1386-1387 1389 1394 1397 1405 1423 1425-1428 1431 1437 1446 1448 1461 1466 1470 1472 1474 1482 1492 1506
lymphocytes	ATCC	LPC001	1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776 1778-1779 1786 4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786 789-790 793 800 802 822 838 849 866 869 876 881-883 892 898 906- 907 911 921-923 928 975 990 992 996 1001 1004-1007 1033 1050 1054 1078 1107 1135 1140-1141 1143 1148 1158 1163 1177 1199 1205 1216 1226 1231 1236 1241 1244 1250 1258 1260 1265 1269- 1271 1290-1293 1308 1312 1317 1319-1320 1339 1345-1346 1348 1350-1351 1357 1367 1369 1379 1381 1383-1384 1386-1387 1389 1394 1397 1405 1423 1425-1428 1431 1437 1446 1448 1461 1466

Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
		Library Name	
			1638 1647-1649 1651 1658-1659
		•	1664 1676-1677 1680-1681 1687- 1688 1699 1711 1715-1716 1726
			1728 1737 1740 1746 1748 1752
			1756 1758 1777 1779
laukocyte	GIBCO	LUC001	3-4 10-11 13 15-18 20-21 24-25
leukocyte	01200]	30-31 35-36 40 43-45 48 50-51
			54-58 60-63 68-69 75 79-80 82-83
			85 88-91 93-96 98 100 103-104
			107-108 112 116 119 123 125-128
		Ì	134-140 142 147-149 151 153 155 157 162-163 167 169-172 174 177-
	ł		179 186 190 192-199 203-207 210
	1	Ţ	212-215 217-219 222-223 229 235-
	{		236 247 251 255-258 260 262 272
	l		274-277 280-281 285-286 297-301
	İ	Ì	307-310 313-314 316-317 321 325-
	ĺ		330 333-334 340-342 348-349 352
	1		354-358 370-371 380-385 387-388 400 405 408-410 412 414-416 421-
			425 430-431 434-435 437 439 441-
		ľ	412 445-451 453-454 456 459 461-
			464 468-472 474-479 481 483-485
			487-491 496 499-501 503-504 509-
}			513 516-519 522 526-527 529-531
	J)	534 536-540 542 547-549 553-559
•	İ		566-567 571 574-577 579 582 584- 586 589 593 595-597 601-602 604
	}	}	606-607 611-613 615-621 623 627-
			629 633 636-637 642 644-650 655
	İ		659-660 662-665 667 669 674-675
}	}		678 682-684 692-696 698 700 706
	1		708 710 716-720 725-726 729-736
	1	1	738-739 743-746 749 751 753 756 759 765-766 768 770-778 780 784-
		}	786 788-790 793 796 798 800 802-
	1.		803 810-811 814 817 819 826 828-
	}		830 832 834-836 838 843 845-860
	1	,	863-864 866-871 877-879 881-892
			894-896 898 902 904-914 916 919-
		1	925 927 930-932 935-936 941-942 945 948-949 953 955-956 958 960-
			962 964 967 970-971 973 975 977
	Į.		985-990 992-993 995-996 999-1002
j]		1004~1009 1011 1014 1017-1019
			1022-1023 1025 1027 1029-1031
1			1033-1036 1038 1041 1043 1047
1			1050 1053-1054 1058-1059 1061- 1062 1064 1068 1070 1072 1078
	1	1	1082 1084 1088 1070 1072 1070
1		1	1106-1107 1110-1113 1115-1117
}	1	ļ	1122-1123 1125 1129 1132-1133
1	\		1135-1137 1140-1145 1152 1158
1	1	1	1163 1168 1170-1174 1176-1178
1			1180 1182-1183 1186 1195 1198- 1200 1202 1205-1206 1211 1216
1		Ì	1200 1202 1205-1206 1211 1216
}			1238-1242 1247 1252 1254 1256
	Į.	1	1258 1261-1262 1264-1265 1269-
		1	1270 1272-1275 1277 1280-1284
1		1	1287-1293 1299-1300 1306 1308
			1312-1313 1317-1320 1322 1324-
}	1	1	1330 1333-1335 1339 1341 1343-
		j	1347 1349 1353-1357 1359-1361 1365-1367 1369-1370 1373-1374
		1	1377 1379-1381 1386-1387 1394
	1		1400 1403 1409 1419 1423 1425-
			1428 1430-1431 1433-1434 1437-
			1438 1440-1442 1446-1448 1450
L		<u> </u>	

Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
iissue origin	Allor Double	Library Name	
			1453 1458-1459 1463-1464 1468 1470-1471 1474 1477-1478 1482-
1			1488 1490-1493 1496-1501 1504
	}		1506 1509 1512-1513 1516 1519
			1521-1522 1524-1525 1527-1528
	ļ		1531 1534 1538 1541 1545-1547
			1549-1550 1553 1555-1556 1560
			1565 1567 1575 1580 1589 1591 1594 1596 1598 1600-1602 1606-
·			1608 1611 1614 1620-1621 1624
			1626-1629 1631-1632 1636 1638-
			1639 1641 1644-1645 1648-1650
			1653-1655 1658-1660 1662 1669-
			1670 1675-1679 1684-1688 1690- 1692 1696 1700 1702 1707-1709
			1711 1716-1717 1720 1723 1725-
1			1727 1733 1737-1738 1741 1743-
			1744 1748-1749 1752 1755 1760-
			1762 1765 1769 1771-1772 1781-
			1784 1786
leukocyte	Clontech	LUC003	4 35-36 44-45 61 68-69 75 82 102 119 139 154 179 197 244 280-281
			324 372 404 430-431 455 461 476-
}			477 481 503 537-540 554 575-576
[•	581 589 608-609 621-622 624 630
}			632 647 662-664 669 679 698 764
			773 775-777 802 848 851 856-857
			879 905-907 915 949 952 990 992 1002 1113 1119 1170 1183 1216
}			1236-1237 1241 1275 1346 1353
			1357 1359 1377 1506 1515 1534
	•		1553 1591 1600 1613-1614 1621
			1628 1670 1676-1677 1691-1692
		MEL004	1699 1733 1738 1772 25 35-36 43 80 104 126 128 150
melanoma from cell line ATCC	Clontech	MELOUA	163 166 188-189 197 210 215 220
#CRL 1424			271 277 280-281 310 317 336-338
,,	}	}	345 351 372 380-381 383 387 412
			415-416 430 445 448 454 456 467 481 490 499 503 526 528 546 548
	Į.		
		1	
			567 575-576 588 601 613 615 647 660 665 734-735 737 759 778 787
}			567 575-576 588 601 613 615 647 660 665 734-735 737 759 778 787 790 800 832 845 856 859 869 878
			567 575-576 588 601 613 615 647 660 665 734-735 737 759 778 787 790 800 832 845 856 859 869 878 883 887 905 914 932 934 958 976
			567 575-576 588 601 613 615 647 660 665 734-735 737 759 778 787 790 800 832 845 856 859 869 878 883 887 905 914 932 934 958 976 985 990 992 999-1000 1025 1031
			567 575-576 588 601 613 615 647 660 665 734-735 737 759 778 787 790 800 832 845 856 859 869 878 883 887 905 914 932 934 958 976 985 990 992 999-1000 1025 1031 1038 1050 1055 1068 1074 1088
			567 575-576 588 601 613 615 647 660 665 734-735 737 759 778 787 790 800 832 845 856 859 869 878 883 887 905 914 932 934 958 976 985 990 992 999-1000 1025 1031 1038 1050 1055 1068 1074 1088 1099-1102 1107 1136-1138 1149
			567 575-576 588 601 613 615 647 660 665 734-735 737 759 778 787 790 800 832 845 856 859 869 878 883 887 905 914 932 934 958 976 985 990 992 999-1000 1025 1031 1038 1050 1055 1068 1074 1088 1099-1102 1107 1136-1138 1149 1156 1163 1172 1190 1195 1200 1214-1215 1217 1226-1227 1235
			567 575-576 588 601 613 615 647 660 665 734-735 737 759 778 787 790 800 832 845 856 859 869 878 883 887 905 914 932 934 958 976 985 990 992 999-1000 1025 1031 1038 1050 1055 1068 1074 1088 1099-1102 1107 1136-1138 1149 1156 1163 1172 1190 1195 1200 1214-1215 1217 1226-1227 1235 1238-1239 1244 1253 1278 1280
			567 575-576 588 601 613 615 647 660 665 734-735 737 759 778 787 790 800 832 845 856 859 869 878 883 887 905 914 932 934 958 976 985 990 992 999-1000 1025 1031 1038 1050 1055 1068 1074 1088 1099-1102 1107 1136-1138 1149 1156 1163 1172 1190 1195 1200 1214-1215 1217 1226-1227 1235 1238-1239 1244 1253 1278 1280 1293 1311 1320 1330 1334-1335
			567 575-576 588 601 613 615 647 660 665 734-735 737 759 778 787 790 800 832 845 856 859 869 878 883 887 905 914 932 934 958 976 985 990 992 999-1000 1025 1031 1038 1050 1055 1068 1074 1088 1099-1102 1107 1136-1138 1149 1156 1163 1172 1190 1195 1200 1214-1215 1217 1226-1227 1235 1238-1239 1244 1253 1278 1230 1293 1311 1320 1330 1334-1335 1345 1355 1367 1386-1387 1394
			567 575-576 588 601 613 615 647 660 665 734-735 737 759 778 787 790 800 832 845 856 859 869 878 883 887 905 914 932 934 958 976 985 990 992 999-1000 1025 1031 1038 1050 1055 1068 1074 1088 1099-1102 1107 1136-1138 1149 1156 1163 1172 1190 1195 1200 1214-1215 1217 1226-1227 1235 1238-1239 1244 1253 1278 1230 1293 1311 1320 1330 1334-1335 1345 1355 1367 1386-1387 1394 1403 1406 1414 1423 1437 1442 1465 1521 1529 1536 1539 1541
			567 575-576 588 601 613 615 647 660 665 734-735 737 759 778 787 790 800 832 845 856 859 869 878 883 887 905 914 932 934 958 976 985 990 992 999-1000 1025 1031 1038 1050 1055 1068 1074 1088 1099-1102 1107 1136-1138 1149 1156 1163 1172 1190 1195 1200 1214-1215 1217 1226-1227 1235 1238-1239 1244 1253 1278 1280 1293 1311 1320 1330 1334-1335 1345 1355 1367 1386-1387 1394 1403 1406 1414 1423 1437 1442 1465 1521 1529 1536 1539 1541 1547-1548 1582 1620 1626 1631
			567 575-576 588 601 613 615 647 660 665 734-735 737 759 778 787 790 800 832 845 856 859 869 878 883 887 905 914 932 934 958 976 985 990 992 999-1000 1025 1031 1038 1050 1055 1068 1074 1088 1099-1102 1107 1136-1138 1149 1156 1163 1172 1190 1195 1200 1214-1215 1217 1226-1227 1235 1238-1239 1244 1253 1278 1280 1293 1311 1320 1330 1334-1335 1345 1355 1367 1386-1387 1394 1403 1406 1414 1423 1437 1442 1465 1521 1529 1536 1539 1541 1547-1548 1582 1620 1626 1631 1638 1647 1653 1660 1667 1669-
			567 575-576 588 601 613 615 647 660 665 734-735 737 759 778 787 790 800 832 845 856 859 869 878 883 887 905 914 932 934 958 976 985 990 992 999-1000 1025 1031 1038 1050 1055 1068 1074 1088 1099-1102 1107 1136-1138 1149 1156 1163 1172 1190 1195 1200 1214-1215 1217 1226-1227 1235 1238-1239 1244 1253 1278 1280 1293 1311 1320 1330 1334-1335 1345 1355 1367 1386-1387 1394 1403 1406 1414 1423 1437 1442 1465 1521 1529 1536 1539 1541 1547-1548 1582 1620 1626 1631 1638 1647 1653 1660 1667 1669- 1670 1680-1681 1696 1704 1715
			567 575-576 588 601 613 615 647 660 665 734-735 737 759 778 787 790 800 832 845 856 859 869 878 883 887 905 914 932 934 958 976 985 990 992 999-1000 1025 1031 1038 1050 1055 1068 1074 1088 1099-1102 1107 1136-1138 1149 1156 1163 1172 1190 1195 1200 1214-1215 1217 1226-1227 1235 1238-1239 1244 1253 1278 1280 1293 1311 1320 1330 1334-1335 1345 1355 1367 1386-1387 1394 1403 1406 1414 1423 1437 1442 1465 1521 1529 1536 1539 1541 1547-1548 1582 1620 1626 1631 1638 1647 1653 1660 1667 1669-1670 1680-1681 1696 1704 1715 1724-1725 1731-1732 1750 1760-
	Invitrocen	MMG001	567 575-576 588 601 613 615 647 660 665 734-735 737 759 778 787 790 800 832 845 856 859 869 878 883 887 905 914 932 934 958 976 985 990 992 999-1000 1025 1031 1038 1050 1055 1068 1074 1088 1099-1102 1107 1136-1138 1149 1156 1163 1172 1190 1195 1200 1214-1215 1217 1226-1227 1235 1238-1239 1244 1253 1278 1280 1293 1311 1320 1330 1334-1335 1345 1355 1367 1386-1387 1394 1403 1406 1414 1423 1437 1442 1465 1521 1529 1536 1539 1541 1547-1548 1582 1620 1626 1631 1638 1647 1653 1660 1667 1669- 1670 1680-1681 1696 1704 1715 1724-1725 1731-1732 1750 1760- 1761
mammary gland	Invitrogen	MMG001	567 575-576 588 601 613 615 647 660 665 734-735 737 759 778 787 790 800 832 845 856 859 869 878 883 887 905 914 932 934 958 976 985 990 992 999-1000 1025 1031 1038 1050 1055 1068 1074 1088 1099-1102 1107 1136-1138 1149 1156 1163 1172 1190 1195 1200 1214-1215 1217 1226-1227 1235 1238-1239 1244 1253 1278 1290 1293 1311 1320 1330 1334-1335 1345 1355 1367 1386-1387 1394 1403 1406 1414 1423 1437 1442 1465 1521 1529 1536 1539 1541 1547-1548 1582 1620 1626 1631 1638 1647 1653 1660 1667 1669- 1670 1680-1681 1696 1704 1715 1724-1725 1731-1732 1750 1760- 1761 5-8 10 12 14-18 20-21 24-25 29 33-39 42-43 52 55-58 60-64 68-69
mammary gland	Invitrogen	MMG001	567 575-576 588 601 613 615 647 660 665 734-735 737 759 778 787 790 800 832 845 856 859 869 878 883 887 905 914 932 934 958 976 985 990 992 999-1000 1025 1031 1038 1050 1055 1068 1074 1088 1099-1102 1107 1136-1138 1149 1156 1163 1172 1190 1195 1200 1214-1215 1217 1226-1227 1235 1238-1239 1244 1253 1278 1280 1293 1311 1320 1330 1334-1335 1345 1355 1367 1386-1387 1394 1403 1406 1414 1423 1437 1442 1465 1521 1529 1536 1539 1541 1547-1548 1582 1620 1626 1631 1638 1647 1653 1660 1667 1669- 1670 1680-1681 1696 1704 1715 1724-1725 1731-1732 1750 1760- 1761 5-8 10 12 14-18 20-21 24-25 29 33-39 42-43 52 55-58 60-64 68-69 71 73-74 79-80 82 89 98 100 103
mammary gland	Invitrogen	MMG001	567 575-576 588 601 613 615 647 660 665 734-735 737 759 778 787 790 800 832 845 856 859 869 878 883 887 905 914 932 934 958 976 985 990 992 999-1000 1025 1031 1038 1050 1055 1068 1074 1088 1099-1102 1107 1136-1138 1149 1156 1163 1172 1190 1195 1200 1214-1215 1217 1226-1227 1235 1238-1239 1244 1253 1278 1280 1293 1311 1320 1330 1334-1335 1345 1355 1367 1386-1387 1394 1403 1406 1414 1423 1437 1442 1465 1521 1529 1536 1539 1541 1547-1548 1582 1620 1626 1631 1638 1647 1653 1660 1667 1669- 1670 1680-1681 1696 1704 1715 1724-1725 1731-1732 1750 1760- 1761 5-8 10 12 14-18 20-21 24-25 29 33-39 42-43 52 55-58 60-64 68-69 71 73-74 79-80 82 89 98 100 103 106 108 112 123 128 133-137 144-
mammary gland	Invitrogen	MMG001	567 575-576 588 601 613 615 647 660 665 734-735 737 759 778 787 790 800 832 845 856 859 869 878 883 887 905 914 932 934 958 976 985 990 992 999-1000 1025 1031 1038 1050 1055 1068 1074 1088 1099-1102 1107 1136-1138 1149 1156 1163 1172 1190 1195 1200 1214-1215 1217 1226-1227 1235 1238-1239 1244 1253 1278 1230 1293 1311 1320 1330 1334-1335 1345 1355 1367 1386-1387 1394 1403 1406 1414 1423 1437 1442 1465 1521 1529 1536 1539 1541 1547-1548 1582 1620 1626 1631 1638 1647 1653 1660 1667 1669- 1670 1680-1681 1696 1704 1715 1724-1725 1731-1732 1750 1760- 1761 5-8 10 12 14-18 20-21 24-25 29 33-39 42-43 52 55-58 60-64 68-69 71 73-74 79-80 82 89 98 100 103 106 108 112 123 128 133-137 144- 146 148 150-152 154 158-159 165-
mammary gland	Invitrogen	MMG001	567 575-576 588 601 613 615 647 660 665 734-735 737 759 778 787 790 800 832 845 856 859 869 878 883 887 905 914 932 934 958 976 985 990 992 999-1000 1025 1031 1038 1050 1055 1068 1074 1088 1099-1102 1107 1136-1138 1149 1156 1163 1172 1190 1195 1200 1214-1215 1217 1226-1227 1235 1238-1239 1244 1253 1278 1280 1293 1311 1320 1330 1334-1335 1345 1355 1367 1386-1387 1394 1403 1406 1414 1423 1437 1442 1465 1521 1529 1536 1539 1541 1547-1548 1582 1620 1626 1631 1638 1647 1653 1660 1667 1669- 1670 1680-1681 1696 1704 1715 1724-1725 1731-1732 1750 1760- 1761 5-8 10 12 14-18 20-21 24-25 29 33-39 42-43 52 55-58 60-64 68-69 71 73-74 79-80 82 89 98 100 103 106 108 112 123 128 133-137 144- 146 148 150-152 154 158-159 165- 166 170-172 174 176 178 181-185
mammary gland	Invitrogen	MMG001	567 575-576 588 601 613 615 647 660 665 734-735 737 759 778 787 790 800 832 845 856 859 869 878 883 887 905 914 932 934 958 976 985 990 992 999-1000 1025 1031 1038 1050 1055 1068 1074 1088 1099-1102 1107 1136-1138 1149 1156 1163 1172 1190 1195 1200 1214-1215 1217 1226-1227 1235 1238-1239 1244 1253 1278 1280 1293 1311 1320 1330 1334-1335 1345 1355 1367 1386-1387 1394 1403 1406 1414 1423 1437 1442 1465 1521 1529 1536 1539 1541 1547-1548 1582 1620 1626 1631 1638 1647 1653 1660 1667 1669- 1670 1680-1681 1696 1704 1715 1724-1725 1731-1732 1750 1760- 1761 5-8 10 12 14-18 20-21 24-25 29 33-39 42-43 52 55-58 60-64 68-69 71 73-74 79-80 82 89 98 100 103 106 108 112 123 128 133-137 144- 146 148 150-152 154 158-159 165- 166 170-172 174 176 178 181-185 188-190 194-198 201-206 210 217-
mammary gland	Invitrogen	MMG001	567 575-576 588 601 613 615 647 660 665 734-735 737 759 778 787 790 800 832 845 856 859 869 878 883 887 905 914 932 934 958 976 985 990 992 999-1000 1025 1031 1038 1050 1055 1068 1074 1088 1099-1102 1107 1136-1138 1149 1156 1163 1172 1190 1195 1200 1214-1215 1217 1226-1227 1235 1238-1239 1244 1253 1278 1280 1293 1311 1320 1330 1334-1335 1345 1355 1367 1386-1387 1394 1403 1406 1414 1423 1437 1442 1465 1521 1529 1536 1539 1541 1547-1548 1582 1620 1626 1631 1638 1647 1653 1660 1667 1669- 1670 1680-1681 1696 1704 1715 1724-1725 1731-1732 1750 1760- 1761 5-8 10 12 14-18 20-21 24-25 29 33-39 42-43 52 55-58 60-64 68-69 71 73-74 79-80 82 89 98 100 103 106 108 112 123 128 133-137 144- 146 148 150-152 154 158-159 165- 166 170-172 174 176 178 181-185

Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
iissde Origin	KWA SOUTCE	Library Name	
			290 297 299 301 304 309-312 318
	1		320-321 323-325 327-329 331-332 334 339 341 344-345 348 350 356
ì			359-360 362-363 368 371 376 379-
	1		383 388 390 393-395 397-398 405
	}		408 412 414-415 423 430 434-437
	\		441-444 448 451-455 462-464 474
			476 479 482 485-486 488 490 494-
			495 498 503 506 509-512 516-517 519-520 522 527 529 534 537-541
			.547 549 554 557 562 572-574 587
			589-591 597 602 607 618 623 628-
(629 632 634-640 644 647-648 650-
	1		652 655 657-658 660 665 667 669-
			672 674-676 679 682 688 695-696
	Í		706-707 710 713 717 720 722-730
	,		732-734 736 738 743 747-748 750 755 759 761 766 770 780 784 786-
	· ·		789 794 803 806-807 809 814 817-
	ł		B22 827-829 837 842 854-858 863-
	1		864 866 869-870 872 878 881 889
	Ì		893-900 904 906-907 911 916 919
			921-923 926 935-937 946 948-949
			953-954 957 960-961 963 965-966 970 977-978 984-989 993-997
]			1000-1001 1005-1006 1008 1013-
			1014 1016-1017 1023 1025 1027
			1032-1033 1036 1039 1043 1045
			1055 1057-1058 1063 1068-1075
(1077-1078 1085 1087 1089-1091
	}		1095-1102 1107-1108 1112-1119 1121-1123 1131-1133 1136-1137
1			1139-1142 1144-1145 1148-1149
	}		1153 1159 1167 1170 1172-1173
			1183-1185 1190-1192 1196-1199
į	[1207-1208 1212 1216-1218 1222-
			1223 1225 1231 1234 1240-1241
			1247 1253-1254 1258-1259 1261- 1262 1270-1280 1283 1285-1286
}	1		1298 1307 1314 1316-1320 1323-
			1325 1330 1334-1335 1342-1345
			1349-1352 1354-1355 1359 1369-
		•	1370 1377 1379 1381 1383-1384
	Ì		1389 1405 1414 1419 1421-1423
			1425-1426 1428-1429 1431 1434- 1437 1439 1448-1449 1454 1457
			1437 1439 1448-1449 1434 1437
			1487 1489-1491 1493 1505 1507
			1512 1519 1526-1528 1532 1534
1			1536 1539 1542 1547 1549-1550
		1	1554 1561-1562 1564 1567 1572
			1576-1579 1581-1582 1587-1588 1592 1594 1596-1597 1601-1602
			1607-1608 1610 1612-1616 1618
			1621-1622 1625-1626 1631 1635-
1	1	ļ	1636 1641 1643-1644 1647 1650
1			1652 1654-1655 1657-1658 1660
		}	1662 1664-1666 1669-1671 1673-
1	1		1674 1676-1677 1680-1685 1689-
			1692 1701 1706 1713-1715 1719- 1720 1723-1728 1730-1732 1738
			1740 1742-1744 1746-1747 1749
			1751 1753 1760-1762 1765-1768
			1771 1774 1776-1777 1779 1783-
		-	1784 1786
induced neuron	Strategene	NTD001	29 35-36 80 116 123 156 163 181
cells			214 230 280-281 284-285 307 321
	}	1	330 340 358 371 375 377 380 382 422 424 492 497 532-533 542 546
L	J	L	146 464 476 437 336-333 346 340

	Tissue Origin	DAIN Course		
		RNA Source	Hyseq Library Name	SEQ ID NOS:
			1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	549 566 586 595 612 645-647 654
	}	1	}	734 775-778 780 792 799 821 826
				856 858 875 936 953 985 990 992
				1041-1043 1055 1072 1104 1193-
			ł	1194 1206 1223 1246 1253 1274 1288-1289 1291 1294 1311 1320
		j]	1349 1359 1412 1423 1485 1620
				1623 1645 1684 1705 1715 1751
	retinoid acid	Strategene	NTRO01	5-8 78 268-269 277 383 431 506
	induced neuronal cells		1	623 677 731 999-1000 1199 1425-
	neuronal cells	Strategene	NTU001	1426 1547
ì		Jeracegene	NIOUUI	29 65-66 80 82 110 119 146 152
				166 174 181-185 198 227-228 253 284 309 325 332 334 336-338 375
ļ		1		391 393 406 414-416 454 465-466
				470 488 503 506 510-512 519 537-
				540 572-574 597 602 607 623 647
		1		661 700 702 716 743 771 792 858
ĺ				904 948 954 977 1000 1005-1006
ĺ				1025 1064 1068 1122 1148 1185
-				1219 1226 1234 1246 1271 1283 1295-1296 1311 1317-1320 1329-
١				1330 1350 1355 1365-1366 1378
-				1383-1384 1400 1412 1445 1505
İ		1		1539 1547 1578 1647 1656 1683
-	pituitary	Clontech	D. marci	1690 1738 1749 1783-1784
1	gland	Croncecn	PITO04	311 314 379 408 419 430 454 1055
1	3			1095-1096 1272-1273 1312 1320 1378 1652 1671 1720 1725 1736
L		1		1741 1755
1	placenta	Clontech	PLA003	5-8 124 208 277 370 843 906-907
1	•		•	1280 1317-1319 1359 1609 1621
H	prostate	Clontech		1737
1	Probluce	Cloursey	PRT001	9 46 57 71 107 147 171 177 197
ı	•			201 229 231 242-243 274 280-281 307 310 317 330 358 373 382-383
ı				400 430 434-436 461-462 469 477
1				489 497 500 505-506 513 521 526
				531-533 547 618 649 657-658 662-
			•	664 710 729 767 771 789 820 861
ı			1	871 874 890-891 905 938 945 963-
L				964 988-989 1002 1025 1033 1045 1061 1095-1096 1112 1125 1142
1				1196 1198 1202 1232-1233 1241
1	(į	1258 1272-1273 1287 1295 1313
1	Ì		}	1333 1341 1344 1349 1360 1362-
		1		1363 1367 1437 1442 1447 1475
	ſ	1	ľ	1478-1479 1482 1489 1513 1517
		ł		1527 1531 1536 1598-1599 1628 1636 1657 1680-1681 1687-1688
L				1717 1738 1743-1744
1	rectum	Invitrogen	REC001	17-18 29 33 62-63 71 73-74 83 86
	1	į		113 126 146 153 158 167-169 195
l	l	}	1	200 206 261 309 312 341 344 368
1			l	373 388 395 408 414 420 430 441-
	[j	442 446 448 464 468 483 517 537- 540 547 567 585 589 602 623 628-
1	Ì	1	1	629 632 645-647 651 657-658 669
	j	j	j	717-719 721 725-726 738 748 750
				756 762-763 766 770 774 790 819
ĺ	1	1	1	825 843 849 851 881 903 909 948-
		}	J	949 960 986 996 1020 1023 1033-
1				1034 1064 1067 1070 1075 1086
				1108-1109 1113 1130 1139 1153
	1	ļ		1159 1172 1178 1185 1187-1189 1205 1220 1225 1240 1244 1271
l				1317-1320 1323 1334-1335 1350-
Ĺ				1351 1355 1369 1373 1375 1425-

Ticono Origina	RNA Source	Hyseq	SEC ID NOS:
Tissue Origin	KNA Source	Library Name	SEQ ID NOS:
		•	1426 1436 1439 1469 1474 1477
			1482 1546 1587-1588 1592 1596
			1610 1622 1627 1644 1658 1662
			1665-1666 1669 1675-1677 1749 1786
salivary gland	Clontech	SAL001	10 55 97 103 110 140 149 152 158
Salivary grand	Cloudecu	SABOUL	198 217-218 242-243 256 301 308
			312 321 333 351 354 360 410 437
1		•	448 473 487 494 496 501 535 555
,			569-570 572-573 590-591 624 636
			651 759 762 764 768 771 788 800
1			809 826 848 865 879 906-907 925 933 963 1016 1020 1025 1040 1046
			1055 1066 1103 1150 1172 1181
ļ			1234 1281-1282 1288-1289 1298
			1315 1320 1333 1336-1337 1346
]			1359 1373 1379 1424 1447 1449
			1474 1482 1492 1494 1498 1511
}			1523-1524 1537 1554 1596 1626-
			1627 1636 1652-1655 1658 1665
001 irrage: 010=3	Clontech	SALs03	1671-1672 1691-1692 158 326 1423 1463-1464
salivary gland skin	ATCC	SFB001	1320 1400
fibroblast	AICC	375001	1320 1400
skin	ATCC	SFB002	262 736 1025 1253
fibroblast			
skin	ATCC	SFB003	709 1119 1350 1631 1653
fibroblast	61	0711007	25 142 146-147 151 155 198 203
small intestine	Clontech	SIN001	25 142 146-147 151 155 198 203
Intestine			301-302 308 312 334 340 371 398
			408 412 414 416 423 425-427 430
		1	434-435 445 452 454 478 503 516
	i	}	519 521 523 543 547 549 555 559
			563 569-570 585 592 604 611 626 628-629 632 650 659 681 710 714
	ì	}	718 750 764 780 798 829 842 857
			859 866 887 892 894-895 901 904
			906-907 912 919 935 997-998 1000
			1007-1008 1026-1028 1044 1055
	ļ		1089 1097 1116-1117 1131 1148
1	1	1	1169 1199 1219 1234 1247 1264 1279 1316 1320 1326 1341 1343
	1		1349 1351 1374 1387 1398 1400
	<u> </u>		1403 1407 1423 1428 1468 1498
			1501 1521 1550 1556 1585 1597
			1636 1638-1639 1645 1653 1656
	1		1662 1671 1675 1684 1691-1692
	(1704 1711 1717 1719 1722 1725-
)	1	1726 1729 1733-1734 1743-1744 1762 1767 1780 1785
skeletal	Clontech	SKM001	18 20-21 82 84 101 118 134 148
muscle			151 153 166 225-226 258 274 277
			289 329 361 412 414 424 440 452
1		1	459 470 488 503-504 537-540 647
	}		660 673-675 715 773 780 786 830
	1	1	905 922 950 963 982 990 992 1020
1	[1047 1063 1115-1117 1121 1134
	ł	l	1336-1337 1343 1409 1413-1414
			1509 1599 1624 1644 1653 1712
skeletal	Clontech	SKM002	168 1683 1712
muscle	<u></u>		
skeletal	Clontech	SKMs03	235-236 1409
muscle	<u></u>		
skeletal	Clontech	SKMs04	235-236
muscle	Clontech	SPC001	4 9 11 17 30-31 35-36 43 46 60
spinal cord			

Tissue Origin	RNA Source	Hyseq	
		Library Name	SEQ ID NOS:
			82 85 92 94 108 110 116 139 157 167 198 204-205 210 215 229 256 259 277 280-281 300-302 304 315 317 372 379 387 392 419 426-427 430 433 448 467 473 487 489 506 509 513 519 524 526 537-540 543 547 549 551 559 567 569-570 593 607 616-617 623 625 637 649-650 652 657-658 670-671 673 679 681- 682 709 711 715 719 728-729 734 749-750 753 775-777 781 789 791 809 820 832 834-836 847-849 854- 855 858 861 864 871-872 875 884 898 906-908 917 919 924 934 942 944 970 985 990 992-993 998 1013 1039 1053 1059 1065 1072 1075 1077 1082 1085 1097 1103 1109 1116-1117 1128 1134 1151 1170 1174 1192-1194 1215 1225 1241 1243 1283 1294 1307 1312 1320 1323 1327 1330 1350 1353-1354
			1356 1359 1368 1375 1400 1406- 1407 1423 1429 1437 1443 1448
		·	1454 1470 1482 1492 1501 1508 1511 1529 1538 1548-1549 1565 1571 1578 1598 1600 1614 1625 1627 1630 1639 1646 1651-1652 1670 1686 1696 1740 1751 1755
adult spleen	Clontech	SPLc01	117 312 326 348 424 426-427 431
			845 866 1320 1330 1333 1344 1355-1357 1371 1387 1397 1446 1538 1579 1669 1686 1739 1767
stomach	Clontech	ST0001	10 15-16 61 68-69 100 117 149
			197 201 227-228 231 249 273 280- 281 287 291-292 302 312 358 362 426-427 430 446 462 475 479 535 597 620 630 651 662-664 722 739 780 782 785 846 919 960 964 966- 967 976 1008 1012 1032 1042 1063 1071 1135 1170 1208 1234-1235 1259 1277 1280-1281 1322 1349 1359 1369 1449 1468 1474 1478 1487 1493 1498 1557-1559 1622 1634 1651 1653 1729
thalamus	Clontech	THA002	9 11 25 85 87 112 137 146 180
			190 198 206 210 212-213 235-236 239 261 268-269 279 290 301 325 333-334 341 351 356 364-365 379 388 393 396 419-420 441-442 458 477 483 508 525 531 549 567 606 608-609 647 681 715 725-727 736 774 782 784 794 827 883 890-891 899-900 961 997 999-1001 1004 1034 1055 1097 1129 1144-1145 1150-1151 1157 1172-1173 1177
			1193-1194 1208 1220 1249 1280 1305 1345 1355 1369 1434-1435 1440-1441 1454 1496 1546 1549 1562 1572 1578 1590 1594 1613- 1614 1640 1651-1652 1671 1687- 1688 1703 1743-1744 1746-1747 1753
thymus	Clontech	THM001	44-45 54 57-58 62-64 79 104 123
			126 134 153 193 212-213 218 242- 243 258 274 277 279 297 301 307 327 330 333 342 351 358 371 410 430 445 465-466 468 471 483 487 493 503 506 509 517 526 535 537-

Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
		Library Name	
			540 546 548 554 567 584 586 590- 591 604 612 621 638-640 645-647 649 656 660 655 670 698 710 720 728 735 739 746 759 762 766-767 775-777 780 784-785 800 802 809 824 826 828 845 851 858-859 864 866 870-871 878 884 887 892 899-
			900 927 930-931 967 983 986 990 992 999 1014 1029-1030 1033 1059 1066 1073 1103 1107 1113 1116- 1117 1119 1140-1142 1158 1163 1172 1177 1195 1206 1209 1213 1216 1218-1219 1221-1222 1227 1271 1277 1282 1320 1329 1349
			1367 1369 1383-1384 1417 1419 1423 1425-1427 1448 1477 1488 1493 1536 1554 1620 1644 1646 1549 1654-1655 1661-1652 1669- 1670 1674 1676-1677 1685-1688 1707 1711 1731-1732 1737
thymus	Clontech	ТНМСО2	1707 1711 1731-1732 1737
			1658 1662-1663 1671 1673 1678- 1681 1686-1688 1693 1705 1707 1711 1717-1718 1726-1727 1731- 1733 1737-1738 1743-1745 1758- 1761 1771-1772 1779 1786

Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
h.h. = -/		Library Name	
thyroid gland	Clontech	THR001	4 9-10 20-21 37-39 48 50-51 54-
		1 '	57 60-61 65-66 71 83 94-96 98- 100 102 104 110 112 115-117 119
		}	123 127 133 136-137 140 149 152-
		1	153 155-158 163-164 168-169 171
		Į	186 190-192 197 201-203 219-220
		j	229 233-237 246-247 253 256 258 262 265-266 268-269 277 280-281
[[Ì	284-286 288-289 298-299 302 309-
			311 317 321 326 332 335 341-342
			344 348 350 354 358-359 363 368 371-373 382-383 385 394 398 400-
[. ·			401 411 414-415 421 424 430-431
1			433-436 443-446 450-452 454-455
			458 472-474 476-478 482 484-485
			487-488 490-494 496-497 500-501 503-504 506 509-513 516-517 519
			524 526-527 529 535-540 547 549
			562 564 569-570 575-576 588 594-
			595 601-602 604 606 610 612 615-
	=		617 619-623 628-630 634-635 642 647 649-651 660 662-665 668 670
			681 690-694 696 698 700 709 721
			727-729 732 734 738 740-741 743
		•	745 750 759 761 763 765 770 773 780 785 795-796 798 802 804 823-
			824 826 828 833 838 841-845 847
	İ		849 857-860 867 874-875 878 88C-
			881 887-888 890-892 894-895 898
1			908 910-911 913-914 922-923 926- 927 929 932-934 937 939 941-942
1 . 1			948 953 957 961 963-964 966 978-
			979 981-982 987 990 992 1001
(ļ		1004-1006 1010 1014 1020 1024 1033 1038-1039 1044 1047 1050
1	}		1052-1054 1056 1058 1068 1070-
			1071 1077-1079 1088 1094-1097
	ł		1105-1106 1112-1113 1116-1117 1124 1126 1128-1129 1131 1134
			1136-1137 1142-1143 1146-1147
	ľ		1149-1150 1156 1161-1164 1167
	ł	ĺ	1170-1173 1177-1181 1190 1192
	·	ļ	1197 1200 1204 1208-1209 1214 1217 1219 1222 1230 1232-1233
	ĺ	ĺ	1235 1241 1245 1247 1254 1257-
	1		1258 1260 1262 1271-1273 1283
}			1286-1289 1299 1306 1314 1320 1330-1332 1334-1335 1342 1345
			1349 1365-1367 1370-1372 1374
	1	ļ	1381 1394 1407 1419 1428 1436-
] .]	Ì]	1437 1440-1441 1443 1446-1449 1454 1459 1461-1462 1468 1470-
	ſ	l	1471 1475 1477 1479 1482 1491
	}	}	1497-1498 1504-1505 1507 1513
]	ł	1	1522 1524-1526 1528 1531 1534
1	. }	1	1536-1537 1548 1550 1553 1555- 1559 1562 1567 1578 1590-1591
	ł	j	1597 1599-1601 1612 1614 1616
	-		1619-1620 1622 1624-1626 1628
	1	į	1631-1632 1634 1636 1639 1644-
	į	Ţ	1645 1648 1651 1653-1656 1658 1660 1662-1663 1667 1669 1671
		1	1675 1678-1681 1683-1686 1689
	}	}	1691-1692 1703 1709-1711 1717
			1724-1726 1729 1734 1737-1738
			1740 1743-1744 1749 1753 1759- 1761 1770 1777 1786
trachea	Clontech	TRC001	9 29-31 46 48 87 104 107 110 135
	·		158 222 262 266 286 301 318 331

Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
		Library Name	DEG 15 NOO.
		Distry Name	352 372 377 384 414 424 445-446 454 472 474 491 496 560 579 588 593 597 607 612 626 681 702 719 810 859 866 878 894-895 912 916 922 932 935 1046 1075 1080 1099- 1102 1113 1208 1215 1232-1233
			1237 1281 1312 1385 1387 1405 1414 1424 1430 1437 1447 1505 1569 1579 1586 1600 1641 1653 1667 1671 1676-1677 1683 1691- 1692 1711 1717 1726 1772
uterus	Clontech	UTRO01	17 19 25 41 46 57-58 61 89 104 108 139 152 174 198 200-201 206 263-265 274 290 387 408 420 438 446 448 452 473 491 493 499 503 506 513 519 522 526 530 542-543 560 601 610 632 659 665 720 751 773 780 833 845 857 872 877 912 929 934 937 996 1009 1011 1018 1050 1075 1107 1124 1170 1219 1258 1279 1287 1310 1320 1323 1343-1344 1375 1437 1451-1452 1478 1481 1498 1519 1521 1536 1552 1579 1597 1602 1606 1620 1626-1627 1649 1652 1661 1670 1719 1722-1723

TRADOCS:1416191.1(%CQN01!.DOC)

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-	ą.
NO:	Y41736			WATERMAN SCORE	IDENTITY
	1	Homo sapiens	Human PRO1114 protein sequence.	1398	100
2	Y66656	Homo sapiens	Membrane-bound protein PRO943.	2389	99
3	AF113136	Homo sapiens	IL-1 receptor-associated- kinase-M; IRAK-M	3043	100
4	AF017806	Mus musculus	Zn-15 transcription factor	6351	77
5	X02761	Homo sapiens	fibronectir precursor	10535	98
6 B	X02761 X02761	Homo sapiens	fibronectin precursor	8990	89
9	AJ011679	Homo sapiens	fibronectin precursor	12564	99
	AUUIIU/	Homo sapiens	Rab6 GTPase activating protein, GAPCenA	5251	99
10	W88501	Homo sapiens	Human stomach carcinoma clone HP10415-encoded protein.	2381	100
11	AF117754	Homo sapiens	thyroid hormone receptor- associated protein complex component TRAP240	11336	98
12	297630	Homo sapiens	dJ466N1.4 (novel protein similar to ANK3 (ankyrin 3, node of Ranvier (ankyrin G)))	896	100
13	Y58620	Homo sapiens	Protein regulating gene expression PRGE-13.	1894	98
14	AF213457	Homo sapiens	triggering receptor expressed on myeloid cells 2	1238	100
16	AF233453	Homo sapiens	RACK-like protein PRKCBP1	3124	99
17	AF201303	Homo sapiens	dhfr oribeta-binding protein RIP60	3130	98
18	AF064205	Homo sapiens	dynactin 1 p150 isoform	6377	100
	U00059	s cerevisiae	Yhr121wp	174	26
20	AB032903	Homo sapiens	guanosine monophosphate reductase isolog	1801	99
21	AB032903	Homo sapiens	guanosine monophosphate reductase isolog	1485	99
	AF140507	Homo sapiens	Ca2+/calmodulin-dependent protein kinase kinase beta	3083	99
23	AF140507	Homo sapiens	Ca2+/calmodulin-dependent protein kinase kinase beta	2300	99
24	AJ289131	Homo sapiens	chondroitin 4-0- sulfotransferase	2211	99
25	U33460	Homo sapiens	DNA-directed RNA polymerase I, largest subunit	8777	98
26	Y44488	Homo sapiens	ACRP30R2 variant protein.	1387	100
27 28	U43701 U02032	Homo sapiens	ribosomal protein L23a	791	100
28	V02032 Y41324	Homo sapiens Homo sapiens	ribosomal protein L23a	767	97
	171324	AOMO Bapiens	Human secreted protein encoded by gene 17 clone HNFIY77.	1083	99
30	W71749	Homo sapiens	Human ubiquitin conjugation system protein 2.	715	90
31	W71749	Homo sapiens	Human ubiquitin conjugation system protein 2.	631	82
32	AF231917	Homo sapiens	long-chain 2-hydroxy acid oxidase HAOX2	1811	100
33	Z29481	Homo sapiens	3-hydroxyanthranilic acid dioxygenase	1507	99
34	AB001451	Homo sapiens	Sck	2869	100
35	Y00644	Homo sapiens	precursor polypeptide (AA -34 to 287)	1667	99
36	Y00644	Homo sapiens	precursor polypeptide (AA -34 to 287)	1104	98
37	¥78795	Homo sapiens	Human antizuai-2 (AZ-2) amino	3586	78
38		Homo sapiens	acid sequence.	• 1	ì

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	8
ID NO:	NUMBER			WATERMAN SCORE	IDENTITY
39	¥78795	Homo sapiens	Human antizuai-2 (AZ-2) amino	3556	77
40	U93121	Y70	acid sequence. M-phase phosphoprotein-1	3747	
41	Y42750	Homo sapiens	Human calcium binding protein	795	100
		<u> </u>	1 (CaBP-1).		
42	AF282626	Homo sapiens	latexin	1189	100
43	G02150	Homo sapiens	Human secreted protein, SEQ ID NO: 6231.	384	94
44	U19617	Mus musculus	Elf-1	2724	88
45	U19617	Mus musculus	Elf-1	2062	86
46	AF100758	Homo sapiens	osteoinductive factor OIF	1538	100
47	Y87591	Homo sapiens	Human SPROUTY-1 protein, SEQ ID NO:24.	1737	99
49	X04145	Homo sapiens	T3 gamma precursor (aa -22 to 160)	942	99
51	X63547	Homo sapiens	oncogene	5845	99
52	M94043	Rattus	rab-related GTP-binding	1089	96
	<u> </u>	norvegicus	protein		
53	L31783 X83973	Mus musculus	uridine kinase	917	71
54		Homo sapiens	transcription factor	4486	98
55 56	AF224741 W74805	Homo sapiens	chloride channel protein 7 Human secreted protein	4128	99
56	W/4803	Homo sapiens	encoded by gene 77 clone HOEAS24.	1491	100
57	250907	Homo sapiens	Human TBC-1 cDNA from second transcript.	4824	100
58	D79994	Homo sapiens	similar to ankyrin of Chromatium vinosum.	6089	99
59	D79994	Homo sapiens	similar to ankyrin of Chromatium vinosum.	4014	91
60	Y59738	Homo sapiens	Human normal ovarian tissue derived protein 15.	601	100
61	AB031069	Homo sapiens	protein containing CXXC	1390	100
62	X66660	Homo	domain 1 Membrane-bound protein	2492	99
63	Y66660	sapiens Homo	PRO783. Membrane-bound protein	1709	
	J	sapiens	PRO783.	1	99
64	S70011	Rattus sp.	tricarboxylate carrier	895	55
65	AF139518	Rattus	A-kinase anchor protein	178	24
66	W29666	norvegicus Homo sapiens	Homo sapiens DH1308_1 clone	157	30
			secreted protein.		
67	AJ245738	Homo sapiens	claudin-15	1206	100
68	AF099138	Rattus norvegicus	GLUT4 vesicle protein	4183	87
69	AF099138	Rattus norvegicus	GLUT4 vesicle protein	4906	86
70	282059	Caenorhabdit is elegans	Similarity to Drosophila ring canal protein comes from this gene	1285	44
71	AF224278	Homo sapiens	PMEPAl protein	1282	100
72	AF126426	Homo sapiens	neurotrimin	1809	100
73	Y41652	Homo sapiens	Human MEKZ protein sequence.	2065	99
74	Y41652	Homo sapiens	Human MEK2 protein sequence.	1207	100
75	AF188622	Mus musculus	selectively expressed in embryonic epithelia protein-1	1485	74
76	AE000406	Escherichia coli	putative DNA topoisomerase	950	100
77	X99302	Homo sapiens	Pop1	655	100
78	AL136538	Schizosaccha romyces	similarity to S. cerevisiae ktil2 protein	210	31
	1 200000	pombe		<u> </u>	
79	AF129756	Homo sapiens	G4	1554	99

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-	8
NO:	AL096768	7		WATERMAN SCORE	IDENTITY
80	AL096 768	Homo sapiens		2033	100
ĺ.	1		(phosphatidylserine decarboxylase (PSSC, EC		1
ļ	1	J	4.1.1.65))		Ì
81	AL096768	Homo sapiens		1220	96
}	1		(phosphatidylserine	1220	30
			decarboxylase (PSSC, EC		
82	X57351	 	4.1.1.65))	Ţ	
83	AC005594	Homo sapiens		677	98
84	X73113	Homo sapiens		2700	98
85	AF097330	Homo sapiens		5959	99
	1		CLIC4	1305	99
86	AB018423	Mus musculus	SH2 domain-containing protein	1360	78
87	AF272151	Homo sapiens	adaptor protein CIKS	3084	99
88	AF196329	Homo	triggering receptor expressed	1214	100
89	1	sapiens	on monocytes 1		1 - 3 - 3
89	AB016879	Arabidopsis	contains similarity to pre-	634	36
	1	thaliana	mRNA splicing		1
90	AJ133721	Mus musculus	factor~gene_id:MRB17.2 homeodomain protein		1_
91	AJ242864	Mus musculus	phtf protein	654	57
92	A61971	unidentified	MCSP	619	61
93	Y99365	Homo sapiens	Human PRO1250 (UNQ633) amino	11676 3890	100
	<u> </u>	• • • • • • • • • • • • • • • • • • • •	acid sequence SEQ ID NO:85.	3090	100
94	Y87231	Homo sapiens	Human signal peptide	1031	100
			containing protein HSPP-8	1	
95	AF227741	1	SEQ ID NO:8.		
95	AF22//41	Rattus norvegicus	protein kinase WNK1	2428	95
96	AF227741	Rattus	protein kinase WNK1		
	1	norvegicus	process kinase word	1961	94
97	Y92513	Homo sapiens	Human OXRE-10.	1626	100
98	AL021366	Homo sapiens	cICK0721Q.3 (Kinesin related	3423	100
			protein)	7.23	100
99 100	AC005783	Homo sapiens	R33083_1	1974	99
100	Y95293	Homo sapiens	Human GEF containing NEK-like	4092	99
101	AL118501	Homo sapiens	kinase substrate sGNK.		
		nomo saptens	dJ1191N16.1 (A novel protein (translation of the cDNA	1509	100
			DKFZp566A0946, Em:AL050069))		Ì
102	AJ006267	Homo sapiens	ClpX-like protein	3233	100
103	AF100753	Homo sapiens	ancient ubiquitous 46 kDa	2042	96
			protein AUP1		50
104	AB015982	Homo sapiens	serine/threonine kinase	4718	100
105	AF151074	Homo sapiens	HSPC240	831	64
100	M35522	Canis familiaris	GTP-binding protein (rab7)	354	50
107	R99800	Homo sapiens	NWITT .		
		nomo sapiena	NTII-1 nerve protein, facilitates regeneration of	2337	93
			nerve cells.		i
108	AF125533	Homo sapiens	NADH-cytochrome b5 reductase	1290	
		_	isoform	1290	93
109	AC005614	Homo sapiens	F23269_2	3369	99
110	AF064729	Homo sapiens	RAN binding protein 16	3285	100
111	X52425	Homo sapiens	interleukin 4 receptor	4496	100
112	Y41686	Homo	Human PRO274 protein	2285	100
113	W15506	sapiens	sequence.	}	J
	MIDDUE	Homo sapiens	Mitogen activating protein	1991	100
114	Y71071	Homo sapiens	kinase ERK1.		
		sapiens	Human membrane transport protein, MTRP-16.	1190	99
115	AL049548	Homo sapiens	protein, MTRP-16. dJ398G3.1 (ortholog of rat	-3469	
[CPG2)	3497	99
	AF189817	Mus musculus	evectin-2	1124	90
117	W30891	Homo	Human cytostatin III protein.	715	99
			P-OCCIII.		<u></u> -

-

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
		sapiens		1.66	100
118	AF116618	Homo sapiens	PRO1038	1469	100
119	Y08915 AF098070	Homo sapiens	alpha 4 protein	192	39
120		Drosophila melanogaster	Lisl homolog		
121	AF052432	Homo sapiens	katanin p80 subunit	181	37
122	Y70743	Homo sapiens	PSEQ-1 protein encoded by NSEQ gene associated with matrix remodelling.	2637	98
123	AF083246	Homo sapiens	HSPC028	2132	100
124	Y27096	Homo sapiens	Human viral receptor protein (ACVRP).	833	99
125	M63109	Leishmania major	glycoprotein 96-92	172	27
126	U75467	Drosophila melanogaster	Atu	935	36
127	Z68220	Caenorhabdit is elegans	Similarity to Human ADP/ATP carrier protein	438	43
128	AF095927	Rattus norvegicus	protein phosphatase 2C	1927	94
129	W92958	Homo sapiens	Human zsig44 protein.	463	100
130	AF115391	Lactobacillu s sakei	ribokinase RbsK	508	37
131	X93498	Homo sapiens	21-Glutamic Acid-Rich Protein	1250	100
132	X93498	Homo sapiens	21-Glutamic Acid-Rich Protein	916	87
133	W52B11	Homo sapiens	Human DBI/ACBP -like protein (DBIH).	705	97
134	Y84444	Homo sapiens	Amino acid sequence of a human RNA-associated protein.	3230	100
135	M69181	Homo sapiens	non-muscle myosin B	189	20
136	W74882	Homo sapiens	Human secreted protein encoded by gene 154 clone HE6FL83.	480	100
137	W78200	Homo sapiens	Human secreted protein encoded by gene 75 clone HHGAU81.	855	99
138	AL033520	Homo sapiens	dJ349A12.1 (similar to KIAA0701 protein)	424	39
139	AF020261	Santalum album	proline rich protein	119	30
140	X70394	Homo sapiens	zinc finger protein	1634	100
14).	Y06439	Homo sapiens	Human protease HUPM-8.	936	100
142	268493	Caenorhabdit is elegans	predicted using Genefinder	365	42
143	AB018107	Arabidopsis thaliana	ADP-ribosylation factor-like protein	596	65
144	AF161483	Homo sapiens	HSPC134	580	51
145	Y84902	Homo sapiens	A.human proliferation and apoptosis related protein.	480	100
146	AB004906	Ipomoea purpurea	transposase	146	20
147	AC007357	Arabidopsis thaliana	F3F19.18	647	31
148	W75155	Homo sapiens	Human secreted protein encoded by gene 41 clone HNTME13.	1494	98
149	AF056490	Homo sapiens	cAMP-specific phosphodiesterase 8A	3710	99
150	Y58171	Homo sapiens	Human hydrolase homologue	785	99
151	U10397	Saccharomyce s cerevisiae	Yhr148wp	515	53
152	X73478	Homo sapiens	phosphotyrosyl phosphatase activator	1719	99
153	AL049697	Homo sapiens	dJ382I10.5.1 (novel protein	2034	99

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
ID	NUMBER	1		WATERMAN	IDENTITY
NO:				SCORE	
	100000	<u> </u>	similar to arginyl-tRNA)		
154	AF169802	Homo sapiens	cytochrome b5 reductase b5R.2	1455	99
155	X94703	Homo sapiens	rab28	1126	99
156	Y25716	Homo sapiens	Human secreted protein	1471	100
158	W77404	77.2	encoded from gene 6.	<u></u>	
128	W//404	Homo sapiens	Secreted salivary polypeptide	937	100
159	¥17248	Homo sapiens	zsig32. Human protein kinase	ļ	
133	-1/240	HOMO Saptems	inhibitor-2 (PKI-2).	383	100
160	J04970	Homo sapiens	carboxypeptidase M precursor	2395	
161	W54040	Homo sapiens	Human interferon-inducible	484	100
	""	nome suprems	protein. HIFI.	404	98
162	AL022724	Homo sapiens	dJ413H6.1.1 (hamster	1357	100
			Androgen-dependent Expressed	1337	100
	l		Protein LIKE PUTATIVE		ì
			protein) (isoform 1)	j	
163	AF125535	Homo sapiens	pp21 homolog	193	45
164	G03632	Homo sapiens	Human secreted protein, SEQ	463	97
	L	_	ID NO: 7713.	-	
165	AJ250839	Homo sapiens	serine/threonine protein	1442	71
			kinase		
166	L09649	Zymomonas	zm2	173	37
		mobilis	<u> </u>]	j
167	¥73337	Homo sapiens	HTRM clone 1944530 protein	1204	100
			sequence.	<u> </u>	ľ
168	W88645	Homo sapiens	Secreted protein encoded by	1084	100
169	AF214731	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	gene 112 clone HUKFC71.		Adm) -
170	AF214731 AE000871	Homo sapiens	ATP-dependent RNA helicase	4402	100
1/0	AE0008/1	Methanobacte rium	conserved protein	166	27
	1	thermoautotr		ļ	ł
		ophicum			
171	¥27684	Homo sapiens	Human secreted protein	821	100
		Jacano Bupicas	encoded by gene No. 118.	821	100
172	AF226044	Homo sapiens	HSNFRK	2904	100
173	AJ245946	Homo sapiens	neuroglobin	779	100
174	D43949	Homo sapiens	This gene is novel.	3202	100
175	¥07923	Homo sapiens	GTP-binding protein	1205	100
176	W90338	Homo	Human DP1 homologue protein.	966	100
		sapiens			
177	Y41675	Homo sapiens	Human channel-related	1122	100
			molecule HCRM-3.		
178	Y41674	Homo sapiens	Human channel-related	936	99
179	20000		molecule HCRM-2.		
179	AF220492	Homo sapiens	krueppel-like zinc finger	4100	99
180	X03084	Wamp a	protein HZF2		
181	U57344	Homo sapiens	Clq B-chain precursor	1240	100
183	U57344	Mus musculus Mus musculus	Meis3	1813	89
184	U57344	Mus musculus	Meis3	1743	86
185	AF033120	Homo sapiens		1070	86
}		TOUG Sabrens	p53 regulated PA26-T2 nuclear protein	1389	58
186	AF200357	Mus musculus	pantothenate kinase 1 beta	1605	
187	W75058	Homo sapiens	Human secreted protein	1605	82
	",5050	nomo saptens	encoded by gene 2 clone	1188	99
ſ	(HLDBG33.		ı
188	AJ292529	Homo sapiens	suppressor of sterile four 1	2424	7.00
190	X54134	Homo sapiens	protein-tyrosine phosphatase	3705	100
191	Y22203	Homo sapiens	Human calcium-binding	1083	99
			phosphoprotein, CBPP-1,	1003	23
1	ľ		protein sequence.		
192	W63692	Homo	Human secreted protein 12.	1975	100
	ĺ	sapiens	Transfer process 12.	23,3	100
			Human serum glucocorticoid-	2605	
193	W87772	nomo sapiens i	numan serum grucocorricona-	2605 '	99 '
193	W87772	Homo sapiens	regulated kinase (H-SGK2)	2605	99

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	1 %
ID	NUMBER			WATERMAN	IDENTITY
NO:				SCORE	
194	AF084259	Mus musculus	bromodomain-containing protein BP75	693	54
195	Y00752	Rattus norvegicus	serine dehydratase (AA 1 - 327)	994	61
196	W95349	Homo sapiens	Human foetal brain secreted protein fh170 7.	2596	100
197	AB028859	Homo sapiens	hDj9	1890	100
198	W95633	Homo sapiens	Homo sapiens secreted protein gene clone hm236 1.	1614	100
199	Y44277	Homo sapiens	Human nucleic acid methylase-	2096	99
200	AB030039	Homo sapiens	hPACPL1	2258	100
201	X54162	Homo sapiens	64 Kd autoantigen	2918	99
202	G02061	Homo sapiens	Human secreted protein, SEQ	558	99
203	X13885	Nicotiana tabacum	extensin (AA 1-620)	185	33
204	J04204	Bos taurus	32 kd accessory protein	1837	100
205	J04204	Bos taurus	32 kd accessory protein	1101	100
207	Y87283	Homo sapiens	Human signal peptide	1318	100
			containing protein HSPP-60 SEQ ID NO:60.		
208	X05860	Homo sapiens	Fragment of human secreted protein encoded by gene 65.	936	98
209	AL121889	Homo sapiens	dJ1076E17.1 (KIAA0823 protein (continues in AL023803))	694	54
210	AF226732	Homo sapiens	NPD007	1345	76
211	X66295	Mus musculus	Clq C chair.	970	73
212	Z29328	Homo sapiens	Ubiquitin-conjugating enzyme UbcH2	966	100
213	229328	Homo sapiens	Ubiquitin-conjugating enzyme UbcH2	542	98
214	0E0200LA	Homo sapiens	progresterone binding protein	1163	100
215	X70649	Homo sapiens	member of DEAD box protein family	3933	100
216	AF250558	Homo sapiens	claudin-2	1169	99
217	AL021453	Homo sapiens	dJ821D11.1 (PUTATIVE protein)	259	100
218	Y08565	Homo sapiens	UDP-GalNAc:polypeptide N- acetylgalactosaminyltransfera se	3331	99
219	Y94452	Homo sapiens	Human inflammation associated protein	2067	100
220	AL035521	Arabidopsis	putative protein	315	42
221	AL031786	thaliana Schizosaccha	putative proline-trna	811	41
		romyces pombe	synthetase	011	41
222	AL109736	Schizosaccha romyces pombe	WD repeat protein	626	40
223	X52493	Glycine max	DNA-directed RNA polymerase	136	23
224	AL035659	Homo sapiens	dJ979N1.1 (dJ979N1.1)	5199	98
225	AB032401	Mus musculus	mmDj4	1761	92
226	AB032401	Mus musculus	mmDj4	1988	92
227	X83502	Saccharomyce s cerevisiae	J1007	112	26
228	X83502	Saccharomyce s cerevisiae	J1007	79	25
229	AF143723	Homo sapiens	heat shock protein HSP60	2557	99
230	Y66677	Homo sapiens	Membrane-bound protein PRO828.	982	100
231	AB027466	Homo sapiens	spondin 2	1756	99
232	W95634	Homo sapiens	Homo sapiens secreted protein.	1391	100
233	W00365	Homo sapiens	Human cyclin Bl.	2218	99
234	Y53762	Homo sapiens	A GTP-binding polypeptide	2210	1

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
235	250749	Homo sapiens	designated RAQ.	•	
236	250749	Homo sapiens		1800	100
237	AB026491	Homo sapiens	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1754	98
238	AJ270205	Entodinium		2137	100
220	12270203	caudatum	putative	114	37
ì	1	cadacam	phosphatidylinositol-4- phosphate 5-kinase		ì
239	AB030189	Mus musculus			
	1-000000	mascaras	region and ATP binding region	710	93
240	W56538	Homo sapiens	Human hedgehog interacting		
·		Julius Baptens	protein (HIP).	3785	99
241	W56538	Homo sapiens	Human hedgehog interacting	1 2 2 2	
		1	protein (HIP).	3436	99
242	AF155107	Homo sapiens	NY-REN-37 antigen	1996	
243	AF155107	Homo sapiens	NY-REN-37 antigen	1	99
244	AL031320	Homo sapiens	dJ20N2.1 (novel protein	1005	100
		January Suprems	similar to yeast and	763	99
	}	}	bacterial cytosine	!	1
			deaminase)		
245	U37026	Rattus	sodium channel beta 2 subunit		
	1	norvegicus	sodium channel beta 2 subunit	162	30
246	AL078599	Homo sapiens	dJ991C6.1 (novel protein	<u> </u>	
		January Supremp	similar to C. elegans	2391	98
			FSSA12.9 (Tr:P91086))		ļ
247	U32274	Saccharomyce	Ydr386wp; CAI: 0.12	 	
		s cerevisiae	101300WP, CAL: 0.12	191	37
248	Y41719	Homo	Human PRO864 protein	1879	
		sapiens	sequence.	1879	100 ,
249	AB029434	Homo sapiens	ghrelin precursor	 	
250	X97831	Rattus	carnitine/acylcarnitine	611 246	100
		norvegicus	carrier protein	246	38
251	W80993	Homo	Human RIP-interacting factor	1724	-
		sapiens	RIF.	1/24	100
252	Y94873	Homo	Human protein clone HP02632.	1876	100
		sapiens		1070	100
253	W59878	Homo sapiens	Amino acid sequence of the	765	100
	i	ļ	cDNA clone AIF-2 (HEBGM49)	1 703	1 200
254	AL354533	Leishmania	possible adenylate kinase	265	34
		major		1	33
255	AF233322	Mus musculus	zinc transporter like 2	1916	95
256	Y78113	Homo sapiens	Human cytokine signal	2247	99 -
			regulator CKSR-1 SEQ ID]	
			NO:1.	Í	
257	AL035539	Arabidopsis	putative amino acid transport	390	27
		thaliana	protein	1	- '
258	W74787	Homo sapiens	Human secreted protein	1171	100
			encoded by gene 58 clone		
			HHFHN61.		
259	AL035689	Homo sapiens	dJ187J11.1 (novel protein	974	100
			similar to protein kinase C		100
			inhibitors)		
260	AE000909	Methanobacte	serine/threonine protein	363	30
	}	rium	kinase related protein		
ļ		thermoautotr		1	1
262	310555	ophicum		1	l
261	AL050131	Homo sapiens	hypothetical protein	626	100
262	AF019661	Mus musculus	zeta proteasome chain; PSMA5	1214	100
263	AL035593	Homo sapiens	dJ310J6.1 (novel protein)	821	100
264	AL022318	Homo sapiens	bK150C2.3 (PUTATIVE novel	1072	100
لــــا			protein similar to APOBEC1)		
265	AF205940	Homo sapiens	endomucin	1289	100
266	AL023583	Homo sapiens	dJ500L14.1 (novel protein)	789	100
267	AL034548	Homo sapiens	dJ1103G7.3 (novel protein	1888	99
	i i	- ,	kinase domains containing		
- 1	1	í	kindse domains containing i	I	1
ĺ	(1	protein similar to phosphoprotein CBFW)	1	ł

SEQ	ACCESSION	SPECIES	DESCRIPTION		
ID NO:	NUMBER		DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
268	AF161470	Homo sapiens	HSPC121	1884	+
269	AF161470	Homo sapiens	HSPC121	1232	98
270	X90763	Ното	HHa5 hair keratin type I	2190	96
	1	sapiens	intermediate filament	2190	99
271	AF207600	Homo sapiens	ethanolamine kinase	1952	100
272	M32334	Homo sapiens	intercellular adhesion	1436	
}	Ì	1	molecule 2	1436	100
273	AF161483	Homo sapiens			
274	Y53052	Homo sapiens		663	61
			df202_3 protein sequence SEQ ID NO:110.	587	100
276	¥77576	Homo sapiens	(HCYT) (clone 2195418).	762	100
277	AF077042	Homo sapiens	30S ribosomal protein S7	1269	100
278	Y94907	Homo sapiens	Human secreted protein clone	1619	
		-	ca106_19x protein sequence SEQ ID NO:20.	1619	98
279	Y68788	Homo sapiens	Amino acid sequence of a	2801	99
1	j		human phosphorylation	2001	199
L			effector PHSP-20.		
280	275134	Canis familiaris	rod transducin	1816	100
281	275134	Canis familiaris	rod transducin	1718	96
282	AF249873	Homo sapiens	muscle-specific protein	1395	100
283	AL050007	Homo sapiens	hypothetical protein	405	98
284	AF201931	Homo sapiens	DC1	1859	1_
285	AF156102	Homo sapiens	ELL complex EAP30 subunit		99
286	Y35897	Homo sapiens	Extended human secreted	1318	99
			protein sequence, SEQ ID NO. 146.	1250	99
287	U88964	Homo sapiens	HEM45	923	100
288	AL050143	Homo sapiens	hypothetical protein	598	100
289	AJ011098	Homo sapiens	telethonin	574	100
290	Y65724	Homo	Membrane-bound protein	2321	100
	L	sapiens	PRO836.	====	100
291	AF034801	Homo sapiens	liprin-alpha4	2565	98
292	AF034801	Homo sapiens	liprin-alpha4	2590	100
293	AL049851	Homo sapiens	dJ889J22B.1 (novel protein	1738	
294	Y73348	Homo sapiens	(isoform 1)) HTRM clone 839651 protein	1245	100
295	L11672	Homo sapiens	sequence. zinc finger protein		99
296	AL035423	Homo sapiens	dJ2013.1 (brain mitochondrial	1694	44
297	AF198532	Homo sapiens	carrier protein-1 (BMCP1)) lymphoid enhancer binding	2173	79
	i	•	factor-1	Z1/3	100
298	AF161417	Homo sapiens	HSPC299		
299	AF159141	Homo sapiens	breast cancer metastasis-	1147	85 99
300	U26397	Rattus norvegicus	suppressor 1 inositol polyphosphate 4-	160	30
301	AF036145	Homo sapiens	phosphatase meningioma-expressed antigen	3458	100
302	Z82022	Homo	5	j	
303		Homo sapiens	GlcNac-1-P transferase	2067	99
	AF269232	Mus musculus	butyrophilin-like protein BUTR-1	271	50
304	AJ222644	Arabidopsis thaliana	asparaginyl-tRNA synthetase	659	50
305	AF054180	Homo sapiens	hematopoietic cell derived zinc finger protein	351	79
306	AJ272079	Homo sapiens	APOBEC-1 stimulating protein	3056	100
308	Y44486	Homo sapiens	Human GPRW receptor polypeptide.	1721	100
309	AJ131891	Homo sapiens	DNA polymerase mu	3500	
			F1	2598	100

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	
ID NO:	NUMBER			WATERMAN SCORE	IDENTITY
310	AF293335	Homo sapiens	p30 DBC	1248	92
311	AF176525	Mus musculus	F-box protein FBL12	1501	93
312	X57802	Homo sapiens	immunoglobulin lambda light	959 .	81
313	236715		chain Net		
314		Homo sapiens		2048	98
315	AF161532 AF208068	Homo sapiens	HSPC047	727	100
316	Y66666	Homo Sapiens	kelch-like protein KLHL3a Membrane-bound protein	3046	100
		sapiens	PRO1013.	1166	100
317	Y29666	Homo sapiens	Human Ras protein RAPR-1.	1253	98
318	AJ387747	Homo sapiens	sialin	2614	99
319	AF161362	Homo sapiens	HSPC099	224	40
320	¥68773	Homo sapiens	Amino acid sequence of a human phosphorylation effector PHSP-5.	2243	99
321	AJ238379	Homo sapiens	putative TH1 protein	3013	100
322	AB040812	Homo sapiens	protein kinase PAK5	3792	99
323	Y95013	Homo sapiens	Human secreted protein vc48 1, SEQ ID NO:66.	913	100
324	Y13381	Homo sapiens	Amino acid sequence of protein PRO271.	1976	100
325	¥94944	Homo sapiens	Human secreted protein clone	2305	98
			bf157_16 protein sequence SEQ ID NO:94.	2305	98
326	Y76884	Homo sapiens	Retinoblastoma binding protein-7sequence.	6728	99
327	AF198532	Homo sapiens	lymphoid enhancer binding factor-1	2173	100
328	278013	Caenorhabdit is elegans	Similarity to Drosophila Cadherin-related tumor suppressor	569	33
329	AF212921	Mus musculus	MMTV receptor variant 1	484	94
330	275330	Homo sapiens] >R65207 R65207 02- MAR-1995 27- AUG-1993 Human stromalin-1. [Homo sapiens	nuclear protein SA-1	6492	99
331	AL008583	Homo sapiens	dJ327J16.3 (supported by GENSCAN, FGENES and GENEWISE)	2133	99
332	Y36104	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 489.	310	41
333	AJ271669	Homo sapiens	putative sialoglycoprotease	1747	100
334	AF156598	Mus musculus	p53-regulated DDA3	997	64
335	M99058	Eimeria maxima	em100 gene is homologous the Eimeria tenella gene et100	154	26
336	Y85564	Homo sapiens	Human homologue of UNC-53 (Hs-UNC-53/1) sequence.	3386	97
337	Y85564	Homo sapiens	Human homologue of UNC-53 (Hs-UNC-53/1) sequence.	2602	94
338	¥85564	Homo sapiens	Human homologue of UNC-53 (Hs-UNC-53/1) sequence.	3447	98
339	266561	Caenorhabdit is elegans	Similarity to Human rab13 protein (PIR Acc. No. A49647).	716	34
340	AB021643	Homo sapiens	gonadotropin inducible transcription repressor-3	2761	99
341	G01946	Homo sapiens	Human secreted protein, SEQ ID NO: 6027.	465	98
342	AF020591	Homo sapiens	zinc finger protein	1091	48
343	L29154	Homo sapiens	immunoglobulin heavy chain	439 .	84

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	8
NO:	NUMBER			WATERMAN SCORE	IDENTITY
344	U10281		VDJ region		
345	AK000404	Sus scrofa	gastric mucin	279	24
346	L22557	Homo sapiens	unnamed protein product	1177	99
		norvegicus	calmodulin-binding protein	1949	84
347	L22557	Rattus norvegicus	calmodulin-binding protein	2363	91
348	AL049481	Arabidopsis thaliana	AIG1-like protein	316	30
350	AJ251516	Mus musculus	cysteine and histidine-rich protein	1460	99
351	AK024477	Homo sapiens	FLJ00070 protein	1773	100
352	U50133	Homo sapiens	ankyrin	502	33
353	AK000625	Homo sapiens	unnamed protein product	721	100
354	AF161420	Homo sapiens	HSPC302	2623	97
355	AJ010014	Homo sapiens	M96A protein	1269	47
356	AF151029	Homo sapiens	HSPC195	941	91
357	AL022327	Homo sapiens	dJ355C18.1 (KIAA0027)	1911	100
358	W78128	Homo sapiens	Human secreted protein encoded by gene 3 clone HOSB196.	1117	100
359	X03414	Drosophila melanogaster	Kr polypeptide	316	45
360	AF151079	Homo sapiens	HSPC245	643	100
361	Y53886	Homo sapiens	A suppressor of cytokine signalling protein designated HSCOP-6.	530	41
362	AF254741	Drosophila melanogaster	Centaurin Gamma 1A	681	46
363	AF213465	Homo sapiens	dual oxidase	2016	100
364	AF181562	Homo sapiens	proSAAS	1319	100
365	AF181562	Homo sapiens	proSAAS	1024	99
366	U73200	Mus musculus	pl16Rip	884	82
367	AF263744	Homo sapiens	erbb2-interacting protein ERBIN	4973	99
368	U37501	Mus musculus	laminin alpha 5 chain	5867	72
369	AF043695	Caenorhabdit is elegans	similar to the protein phosphates 2c family	549	36
370	¥73440	Homo sapiens	Human secreted protein clone yj23_1 protein sequence SEQ ID NO:102.	1484	99
371	AF272833	Homo sapiens	misato	2869	97
372	AF198454	Homo sapiens	epithelial protein lost in neoplasm beta	3927	100
373	¥73345	Homo sapiens	HTRM clone 438283 protein sequence.	273	83
374	AF169017	Homo sapiens	formiminotransferase cyclodeaminase	2717	98
375	A95106	unidentified	RED ALPHA	1202	99
376	W74828	Homo sapiens	Human secreted protein encoded by gene 100 clone HLQA952.	1012	99
377	Y32131	Homo sapiens	Human LYST-2 protein.	3556	99
378	M14912	Homo sapiens	pol	132	86
379	AF090934	Homo sapiens	PR00518	382	100
380	X66363	Homo sapiens	serine/threonine protein kinase	2499	100
381	Y41699	Homo sapiens	Human PRO703 protein sequence.	2362	100
382	AF174498	Homo sapiens	GR AF-1 specific protein phosphatase	7008	98
383	U64608	Caenorhabdit is elegans	coded for by C. elegans cDNA yk173c12.5	246	36
384	US0133	Homo sapiens	ankyrin	502	33
385	AJ238520	Homo sapiens	putative transcription	4123	97
			factor-like nuclear regulator	1	

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	9
ID NO:	NUMBER			WATERMAN SCORE	IDENTITY
387	AF208845	Homo sapiens	BM-003	1375	99
389	X57821	Homo sapiens	immunoglobulin lambda light	797	76
390	AF182404	Homo sapiens	chain mitochondrial uncoupling	1670	
391	Y85564	Homo sapiens	protein 1	_	99
393	AF178432		Human homologue of UNC-53 (Hs-UNC-53/1) sequence.	3386	97
394	AF178432 AF229928	Homo sapiens	SH3 protein	3700	100
		Drosophila melanogaster	cytoplasmic protein 89BC	1616	62
395 396	AF181721	Homo sapiens	RU2S	2254	100
	¥69197	Homo sapiens	Amino acid sequence of a human betaIV-spectrin protein.	1626	98
397	U48238	Mus musculus	zinc finger protein neuro-d4	749	60
398	AL390137	Homo sapiens	hypothetical protein	263	51
399	AF217525	Homo sapiens	Down syndrome cell adhesion molecule	5337	60
400	AL022599	Schizosaccha	WD repeat protein	447	27
		romyces pombe		11/	27
401	AC004B59	Homo sapiens	similar to 2-oxoglutarate	4176	78
			dehydrogenase; similar to Q02218 (PID:g1352618)	4176	/*
402	AB010266	Mus musculus	tenascin-X	10246	62
403	AL133288	Homo sapiens	dJ671D7.1 (similar to	761	100
		1	D.melanogaster CG5986 protein)	, , ,	
404	Z68753	Caenorhabdit is elegans	ZC518.3b	888	48
405	Z78013	Caenorhabdit	Similarity to Drosophila	569	33
-		is elegans	Cadherin-related tumor suppressor	363	33
406	AB031230	Homo sapiens	protein containing CXXC domain 2	1196	97
407	AF155106	Homo sapiens	NY-REN-36 antigen	1168	100
408	Y57945	Homo sapiens	Human transmembrane protein HTMPN-69.	1538	99
409	Z18361	Ovis aries	trichohyalin	184	30
410	AF249744	Homo sapiens	RhoGEF	2733	100
411	AF176529	Mus musculus	F-box protein FBX13	2072	94
412	AF210842	Homo sapiens	HARP	4880	100
413	AL031658	Homo sapiens	dJ310013.7 (novel protein similar to H. roretzi HRPET- 3)	776	98
414	X57398	Homo sapiens	pm5 protein	6131	99
415	AB029826	Homo sapiens	3-methylcrotonyl-CoA carboxylase biotin-containing	2961	99
416	U43503	Saccharomyce s cerevisiae	Eph1p	115	42
417	AL160493	Leishmania	possible t26f17.21	239	35
418	Y08100	major	Human DD022		
419	U15131	Homo sapiens	Human PRO331 protein.	330	29
420	AF117946		p126	2228	54
		Homo sapiens	Link guanine nucleotide exchange factor II	2363	100
421	AF190635	Drosophila melanogaster	ankyrin 2	755	30
422	AF302150	Homo sapiens	phosphoinositol 3-phosphate- binding protein-2	1962	100
123	AL137530	Homo sapiens	hypothetical protein	433	94
124	X63753	Homo sapiens	son-a	7269	100
125	AB027249	Homo sapiens	MAPKK like protein kinase	1693	100
126	AF279144	Homo sapiens	tumor endothelial marker 7 precursor	1084	55

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	}
ID NO:	NUMBER AF279144			WATERMAN SCORE	IDENTITY
[Homo sapiens	precursor	1259	56
428	AE003683	Drosophila melanogaster		149	29
429	Y07829	Homo sapiens	RING finger protein	2201	99
430	AF096897	Drosophila melanogaster	pushover	4442	47
431	U41387	Homo sapiens	Gu protein	4021	99
432	AF023674	Homo sapiens	nephrocystin	3783	100
433	AF146760	Homo sapiens	septin 2-like cell division control protein	2284	100
434	AB006697	Arabidopsis thaliana	cleft lip and palate associated transmembrane protein-like	886	42
437	Y94247	Homo sapiens	Human calcium binding protein hCBP.	1704	100
438	AB040672	Homo sapiens	UDP-GalNAc: polypeptide N- acetylgalactosaminyltransfera se	1075	63
439	AF105228	Bos taurus	tuftelin .	285	33
440	R06463	Homo sapiens	Derived protein of clone ICA13 (ATCC 40553).	3073	99
441	X14971	Mus musculus	alpha-adaptin (A) (AA 1-977)	4897	98
442	X53773	Rattus norvegicus	alpha-c large chain (AA 1- 938)	3979	81
443	Y66689	Homo sapiens	Membrane-bound protein PRO1136.	3299	99
444	AC067754	Arabidopsis thaliana	unknown protein; 20348-23707	114	33
445	AF229032	Mus musculus	piL	2077	93
446	AF056035	Rattus norvegicus	s-nexilin	2662	85
447	AF132484	Mus musculus	unknown	478	51
448	W89024	Homo sapiens	Polypeptide fragment encoded by gene 156.	528	45
449	AF161445	Homo sapiens	HSPC327	1606	100
450	268753	Caenorhabdit is elegans	ZC518.3b	951	49
451	W39160	Homo sapiens	Human partial complement factor H protein fragment 3.	155	32
452	W85727	Homo sapiens	Novel protein (Clone BM46_10).	2799	99
453	¥53629	Homo sapiens	A bone marrow secreted protein designated BMS115.	2810	100
454	D87438	Homo sapiens	Similar to a C.elegans protein in cosmid C14H10	4069	100
455	AF240468	Homo sapiens	nicastrin	3687	100
456	Z15005	Homo sapiens	CENP-E	13305	99
457	M59216	Homo sapiens	gamma-aminobutyric acid receptor beta-1 subunit	2477	100
458	¥73467	Homo sapiens	Human secreted protein clone yd61_1 protein sequence SEQ ID NO:156.	966	100
459	W67824	Homo sapiens	Human sccreted protein encoded by gene 18 clone HSLFM29.	535	100
460	AF163151	Homo sapiens	dentin sialophosphoprotein precursor	279	19
461	D87446	Homo sapiens	Similar to a C.elegans protein encoded in cosmid C27F2 (U40419)	9196	99
462	G04044	Homo sapiens	Human secreted protein, SEQ ID NO: 8125.	486	93
463	AC002398	Homo sapiens	F25965 1	1018	100
464	AF064856	Rattus sp.	7acomp protein	1845	84
465	AF223408	Homo sapiens	B99	3686	99

SEO	ACCESSION	SPECIES			
ID	NUMBER	SPECIES	DESCRIPTION	SMITH-	ક
NO:		{		WATERMAN	IDENTITY
466	AF223408	Homo sapiens	B99	SCORE	
467	AF104415	Mus musculus	1	2878	87
468	U53450	Rattus	Jun dimerization protein 1	6336	91
		norvegicus	JDP-1	196	49
469	AL031297	Homo sapiens			
470	AF257077	Homo sapiens		3564	99
		1.0000 Sabrens	eukaryotic translation initiation factor EIF2B	1274	95
			subunit 3		
471	L28125	Podospora			1
	1 20222	anserina	beta transducin-like protein	284	38
472	Y84903	Homo sapiens	A human		
	1	"TOMO SAPTEMS		2337	100
473	AF144237	Homo sapiens	apoptosis related protein.		ŀ
474	Y71213	Homo sapiens		252	44
	1	110 WO Saptems		838	100 .
475	Y95006	Homo sapiens	related polypeptide IMX39.		!
175	133000	HOME Sapiens		3411	100
476	D38549	Homo sapiens	ve13_1, SEQ ID NO:52.		
477	AF241230	Homo sapiens	hal025 is new	6533	99
478	AL031534	Schizosaccha	TAK1-binding protein 2	3656	100
170	ML031334		putative asparagine synthase	482	40
		romyces			
479	L28125	Podospora			
2/3	1120125	anserina	beta transducin-like protein	233	26
480	AF161544	Homo sapiens			1
481	AJ238248	Homo sapiens	HSPC059	434	77
482	Z38061		centaurin beta2	3986	99
402	230301	Saccharomyce s cerevisiae	mal5, sta1, len: 1367, CAI:	295	23
	į	a cerevisiae	0.3, AMYH_YEAST P08640		
483	AF161381	Homo sapiens	GLUCOAMYLASE S1 (EC 3.2.1.3)		
484	AF223468	Homo sapiens	HSPC263	1404	100
486	X57527	Homo sapiens	AD021 protein	1314	100
487	Y19062	Homo sapiens	alpha 1(VIII) collagen	4166	99
488	Y73373	Homo sapiens	39k3 protein	2475	100
	1,33,3	nomo sapiens	HTRM clone 921803 protein	555	56
489	AL021918	Homo	sequence.		
	1.2022320	sapiens	b3418.1 (Kruppel related Zinc	4184	100
490	X53773	Rattus	Finger protein 184) alpha-c large chain (AA 1-		<u></u>
		norvegicus	alpha-c large chain (AA 1-	4675	97
491	U52426	Homo sapiens	GOK		
492	AL359773	Leishmania		1459	59
		major	possible threonine synthase	702	45
493	AF226614	Homo sapiens	ferroportin1		
494	293241	Homo sapiens	dJ222E13.1 (novel protein	2929	100
		bapicins	with some similarity to	513	96
			Drosophila KRAKEN)		
495	AF036977	Homo sapiens	unknown		
496	U93564	Homo sapiens	p40	1812	100
197	Y91405	Homo sapiens	Human secreted protein	133	45
•		Cupicino	sequence encoded by gene 2	357	100
			SEQ ID NO:126.		
498	AF069781	Drosophila	Bem46-like protein		
ĺ		melanogaster	bem46-like protein	653	43
499	Y16601	Homo sapiens	Human cell-cycle		
,		oulo paptente	human cell-cycle	1658	98
500	X70944	Homo sapiens	phosphoprotein CECYP-2.		
1		paptens	PTB-associated splicing	3883	100
501	AF027503	Mus	factor		
		musculus	putative membrane-associated	205	36
502	AF282874		guanylate kinase 1		
503	AJ249732	Homo sapiens	nectin 3; PRR3	2856	99
504	AF208861	Homo sapiens	G8 protein	669	100
505		Homo sapiens	BM-019	1629	100
07		Homo sapiens	complement component C2	4022	100
08		Mus musculus	HC1 ORF		43
		Rattus	Na+,K+-ATPase alpha-subunit		99
		norvegicus		į	1

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	당
ID NO:	NUMBER			WATERMAN SCORE	IDENTITY
509	Y94971	Homo sapiens		2176	100
j]		fal71_1 protein sequence SEQ ID NO:148.	1	
510	AB019038	Homo sapiens	beta-1,4 mannosyltransferase	781	 77
511	AB019038	Homo sapiens	beta-1,4 mannosyltransferase	1347	100
512	AB019038	Homo sapiens	beta-1,4 mannosyltransferase	1520	99
513	X84908	Homo sapiens		5729	99
514 515	X52851 AF186084	Homo sapiens	1	650	76
		sapiens	epidermal growth factor repeat containing protein	3046	99
516	G03602	Homo sapiens	Human secreted protein, SEQ ID NO: 7683.	505	99
517	U04706	Bos taurus	50 kDa protein	1749	77
518	G00653	Homo sapiens	Human secreted protein, SEQ ID NO: 4734.	530	100
519	AF161475	Homo sapiens	HSPC126	1368	100
520	Y99366	Homo sapiens	Human PRO1475 (UNQ746) amino acid sequence SEQ ID NO:88.	3394	97
521	AF266852	Homo sapiens	PTPLA	1295	100
522	AE000995	Archaeoglobu	chromosome segregation	153	20
523	AF062249	s fulgidus	protein (smcl)]	
		Homo sapiens	immunoglobulin heavy chain variable region	605	97
524	AJ223830	Rattus norvegicus	ARE1	2950	98
525	W01535	Homo sapiens	Cellular homologue of the SV40 large T antigen.	1276	83
526	AF145658	Drosophila melanogaster	BcDNA.GH10229	320	33
527	AF112213	Homo sapiens	putative Rab5-interacting	524	79
528	D49387	Homo	protein NADP dependent leukotriene b4	1616	100
529	Y30819	sapiens Homo sapiens	12-hydroxydehydrogenase Human secreted protein		<u> </u>
		-	encoded from gene 9.	328	32
530	AL079335	Homo sapiens	dJ132F21.3 (72.1 KDa protein (DKFZP564A032, SBBI88) similar to mouse IFN-gamma induce MG11.)	1059	99
531	Y91506	Homo sapiens	Human secreted protein sequence encoded by gene 56	1159	98
532	X76116	Caenorhabdit	SEQ ID NO:179. carrier protein (c2)		
		is elegans	carrier process (62)	576	50
533	X76116	Caenorhabdit is elegans	carrier protein (c2)	506	50
534	X12966	Homo sapiens	3-oxoacyl-CoA thiolase propeptide (424 AA)	1972	100
535	Y09267	Homo sapiens	flavin-containing monooxygenase 2	2486	100
536	Z11773	Homo sapiens	SRE-ZBP	2201	99
537	D84224	Homo sapiens	methionyl tRNA synthetase	4741	99
538	D84224	Homo sapiens	methionyl tRNA synthetase	3887	99
539	D84224	Homo sapiens	methionyl tRNA synthetase	2933	96
540 541	D84224 J03244	Homo sapiens Bos taurus	methionyl tRNA synthetase	4529	99
			H+ ATPase 31kDa subunit (EC 3.6.1.3)	848	77
542 543	Y92514	Homo sapiens	Human OXRE-11.	2301	99
	AF221712	Homo sapiens	Smad- and Olf-interacting zinc finger protein	2151	61
544	AE000919	Methanobacte	conserved protein	207	38
		rium thermoautotr			}
545	A06669	ophicum synthetic	TO 1		
		construct	preTGF-betal	2070	99

No. NAMER No. Society	SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	<u> </u>
Section					WATERMAN	IDENTITY
100 100	546	102698	1 -	encoded by gene 49 clone	854	98
Section Sect			Homo sapiens	WSB-1 protein	2275	130
ACO1662					_	
Sapiens				putative GTPase		1 -
1952 197880 Homo sapiens Human trusmembrane protein 1112 95				protein-2.	429	68
1952 197880 Homo sapiens Human transmebrane protein 1112 95				NEDD4-like ubicuitin ligase 1	8290	99
100 100			_	HTMPN-4.	1112	95
Accompage Acco		.1			265	67
Section					1332	100
Section			thaliana	• "	540	40
100 100				similar to BAA77027 (PID:g4650844)	515	44
W74825 Homo sapiens Homo sapie					1623	98
### Secreted Potein 225 56		1			117	
AF003136 Caenorhabdit Some seak similarity to 2926 54 562 AL109839 Home sapiens Goldon APP-binding motif 100				encoded by gene 97 clone	225	56
1s elegans 1s elegans 1s elegans 20106972.3.1 (novel PABPC1 877 100 10		1			373	88
AF181640 Drosophila BcDNA.GH09817 289 42			is elegans	an AMP-binding motif	2926	
AF181640 Drosophila BeDNA.GH09817 289 42				dJ1069P2.3.1 (novel PABPC1 (poly(A)-binding protein)	877	100
Second S		AF181640	Drosophila melanogaster	BCDNA.GH09817	289	42
100 100			Feline leukemia	gag-pol precursor polyprotein gPr80	1547	43
100 100			Homo sapiens	HSPC123	439	44
109848				pt326_4 secreted protein.		
AF155113 Homo sapiens NY-REN-55 antigen 3603 93				zinc finger protein		
AL032821 Homo sapiens MT-KAT-55 antigen 3951 99					3603	
1821 98 187				NY-REN-55 antigen	3951	99
100 100				dJ55C23.1 (vanin 1)	1821	98
Y59678				non-muscle myosin B	7350	99
### Secretarian Potein 108-008-5-0- 772 100				non-muscle myosin B		98
thaliana 576 AL365234 Arabidopsis thaliana 577 X06745 Homo sapiens DNA polymerase alpha-subunit (AA 1 - 1462) 578 AB041642 Homo sapiens PAR-6 579 D86984 Homo sapiens similar to yeast adenylate cyclase (S56776) 580 AF165124 Homo sapiens gamma-aminobutyric acid A cyclase (S56776) 581 W88812 Homo sapiens Polypeptide fragment encoded by gene 58. 582 U82319 Homo sapiens novel ORF 583 P92219 Homo sapiens CR1 protein. 584 AJ223948 Homo sapiens RNA helicase 585 Y08612 Homo sapiens 88kDa nuclear pore complex protein 586 Y42384 Homo sapiens Amino acid sequence of sapiens sapiens sapiens lavator. 587 AF129756 Homo sapiens RNA helicase 588 AMINO acid sequence of sapiens sapiens sapiens lavator. 588 AMINO acid sequence of loor 37			•	E6-PL.		100
thaliana DNA polymerase alpha-subunit 7619 99			thaliana	_	788	40
AB041642			thaliana		788	40
1342 100 1342 100 1342 100 1342 100 1342 100 1342 100 1342 100 1342 100 1342 100 1342 100 1342 100 1342 100 1342				(AA 1 - 1462)	7619	99
D86984					1342	100
Second S				cyclase (S56776)	2446	100
by gene 58. 1082319	i		_		2499	99
100 100			Homo sapiens	Polypeptide fragment encoded	2339	99
P92219			Homo sapiens		342	100
1007 37 1007 10		P92219				_ '
708612 Homo sapiens 88kDa nuclear pore complex 3874 99 Fig. 1007 37 Fig. 1007 37 Fig. 1007 37 Fig. 1007 37			Homo sapiens	RNA helicase	6608	99
866 Y42384 Homo Amino acid sequence of 1007 37 sapiens 1v310 7.		Y08612		88kDa nuclear pore complex		
587 AF129756 Home conserved Barrier		Y42384	sapiens	Amino acid sequence of	1007	37
	587	AF129756	Homo sapiens		1873	98

ID	ACCESSION	SPECIES	DESCRIPTION	SMITH-	8
NO:	NUMBER			WATERMAN SCORE	IDENTITY
588	AF131775	Homo sapiens	Unknown	1929	99
589	AJ250865	Homo sapiens	TESS 2	2348	100
591	Z988B5	Homo sapiens	dJ522J7.2 (bromodomain-	4167	100
	1		containing 1 (similar to		
	J		peregrin, BR140))	}	j
592	L76571	Homo sapiens	nuclear hormone receptor	1355	100
593	AF091622	Homo sapiens	PHD finger protein 3	9054	100
594	X56807	Homo sapiens	desmocollin type 2a	4443	100
595	AL137802	Homo sapiens	dJ798A10.1 (novel protein)	212	55
596	AL022329	Homo	bK407F11.2 (adrenergic, beta,	3653	100
		sapiens	receptor kinase 2)		
597	AF226048	Homo sapiens	GL003	2009	99
598	AJ278112	Homo	putative cell cycle control	335	23
		sapiens)	protein]
		>Y49635		Ì	i
		Y49635 21-	}	1	ļ
		OCT-1999 15-		i	
	İ	APR-1998			
		Human sdp3.5			
		protein.	1	1	
	1	[Homo			
	1	sapiens			
599	¥59741	Homo sapiens	Human normal ovarian tissue	1574	99
	ļ	~	derived protein 18.		
600	L36531	Homo sapiens	integrin alpha 8 subunit	5386	99
601	Y38458	Homo sapiens	Human secreted protein	895	100
		_	encoded by gene No. 20.		
602	AF218584	Homo sapiens	GGA1	3265	100
603	Y13115	Homo sapiens	serine/threonine protein	5071	99
		_	kinase		
604	AL132776	Homo sapiens	dJ393D12.1 (KIAA0776)	2413	99
605	AL034452	Homo sapiens	dJ682J15.1 (novel Collagen	1979	100
	1	-	triple helix repeat	12.5	1 200
			containing protein)		
606	Y14494	Homo sapiens	aralar1	3465	99
607	AJ001981	Homo sapiens	OXA1L	2603	100
608	X86098	Homo	binds directly to adenovirus	3069	100
		sapiens	type 5 E1A protein		
610	AF163572				
010	ME 1035/2	Homo sapiens	Forssman glycolipid	1865	99
		Homo sapiens	synthetase	1865	99
611	AF163572 AF161503	Homo sapiens		1865	99
611 612	AF161503 L41834	Homo sapiens Ensis minor	synthetase HSPC154 nuclear protein		<u> </u>
611	AF161503	Fomo sapiens	synthetase HSPC154 nuclear protein Human cytoskeleton associated	1261	97
611 612 613	AF161503 L41834	Homo sapiens Ensis minor	synthetase HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9).	1261 345	97
611 612 613	AF161503 L41834	Homo sapiens Ensis minor	synthetase HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027)	1261 345	97
611 612 613 614 615	AF161503 L41834 Y91954 AL022327 X85786	Fomo sapiens Ensis minor Homo sapiens	synthetase HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027)	1261 345 3668	97 30 100
611 612 613	AF161503 L41834 Y91954 AL022327	Homo sapiens Ensis minor Homo sapiens Homo sapiens	synthetase HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9).	1261 345 3668	97 30 100 94
611 612 613 614 615	AF161503 L41834 Y91954 AL022327 X85786	Homo sapiens Ensis minor Homo sapiens Homo sapiens Homo sapiens	synthetase HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor	1261 345 3668 361 3203 3487	97 30 100 94 100 99
611 612 613 614 615 616	AF161503 L41834 Y91954 AL022327 X85786 Y08319	Homo sapiens Ensis minor Homo sapiens Homo sapiens Homo sapiens Homo sapiens	synthetase HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2	1261 345 3668 361 3203 3487 3609	97 30 100 94 100 99 97
611 612 613 614 615 616 617	AF161503 L41834 Y91954 AL022327 X85786 Y08319 D12644	Fomo sapiens Ensis minor Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus	synthetase HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT	1261 345 3668 361 3203 3487 3609 5936	97 30 100 94 100 99 97 89
611 612 613 614 615 616 617 618	AF161503 L41834 Y91954 AL022327 X85786 Y08319 D12644 U28789	Fomo sapiens Ensis minor Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus	synthetase HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dv355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted	1261 345 3668 361 3203 3487 3609	97 30 100 94 100 99 97
611 612 613 614 615 616 617 618	AF161503 L41834 Y91954 AL022327 X85786 Y08319 D12644 U28789	Fomo sapiens Ensis minor Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus	synthetase HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT	1261 345 3668 361 3203 3487 3609 5936	97 30 100 94 100 99 97 89
611 612 613 614 615 616 617 618	AF161503 L41834 Y91954 AL022327 X85786 Y08319 D12644 U28789	Fomo sapiens Ensis minor Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus	synthetase HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO. 163.	1261 345 3668 361 3203 3487 3609 5936 1684	97 30 100 94 100 99 97 89
611 612 613 614 615 616 617 618 619	AF161503 L41834 Y91954 AL022327 X85786 Y08319 D12644 U28789 Y35914	Homo sapiens Ensis minor Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus Homo sapiens	synthetase HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO. 163. testis-abundant finger	1261 345 3668 361 3203 3487 3609 5936	97 30 100 94 100 99 97 89
611 612 613 614 615 616 617 618 619	AF161503 L41834 Y91954 AL022327 X85786 Y08319 D12644 U28789 Y35914	Fomo sapiens Ensis minor Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus Homo sapiens	synthetase HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO. 163. testis-abundant finger protein	1261 345 3668 361 3203 3487 3609 5936 1684	97 30 100 94 100 99 97 89 99
611 612 613 614 615 616 617 618 619	AF161503 L41834 Y91954 AL022327 X85786 Y08319 D12644 U28789 Y35914 AB046382	Homo sapiens Ensis minor Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus Homo sapiens	synthetase HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO. 163. testis-abundant finger	1261 345 3668 361 3203 3487 3609 5936 1684	97 30 100 94 100 99 97 89
611 612 613 614 615 616 617 618 619	AF161503 L41834 Y91954 AL022327 X85786 Y08319 D12644 U28789 Y35914 AB046382	Fomo sapiens Ensis minor Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus Homo sapiens Mus musculus Homo sapiens	synthetase HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO. 163. testis-abundant finger protein precursor polypeptide (AA -23 to 1120)	1261 345 3668 361 3203 3487 3609 5936 1684	97 30 100 94 100 99 97 89 99
611 612 613 614 615 616 617 618 619	AF161503 L41834 Y91954 AL022327 X85786 Y08319 D12644 U28789 Y35914 AB046382	Fomo sapiens Ensis minor Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus Homo sapiens Mus musculus Homo sapiens Mus musculus Homo sapiens	synthetase HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO. 163. testis-abundant finger protein precursor polypeptide (AA -23 to 1120) HDCMD38P	1261 345 3668 361 3203 3487 3609 5936 1684	97 30 100 94 100 99 97 89 99
611 612 613 614 615 616 617 618 619 620 621	AF161503 L41834 Y91954 AL022327 X85786 Y08319 D12644 U28789 Y35914 AB046382 Y00062 AF068286 X98248	Fomo sapiens Ensis minor Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus Homo sapiens Mus musculus Homo sapiens Homo sapiens Homo sapiens	synthetase HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO. 163. testis-abundant finger protein precursor polypeptide (AA -23 to 1120) HDCMD38P sortilin	1261 345 3668 361 3203 3487 3609 5936 1684 199 3440	97 30 100 94 100 99 97 89 99 23 99
611 612 613 614 615 616 617 618 619 620	AF161503 L41834 Y91954 AL022327 X85786 Y08319 D12644 U28789 Y35914 AB046382 Y00062	Fomo sapiens Ensis minor Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus Homo sapiens Mus musculus Homo sapiens Mus musculus Homo sapiens	synthetase HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO. 163. testis-abundant finger protein precursor polypeptide (AA -23 to 1120) HDCMD38P sortilin 75 kDa subunit NADH	1261 345 3668 361 3203 3487 3609 5936 1684	97 30 100 94 100 99 97 89 99
611 612 613 614 615 616 617 618 619 620 621 622 623 624	AF161503 L41834 Y91954 AL022327 X85786 Y08319 D12644 U28789 Y35914 AB046382 Y00062 AF068286 X98248 X61100	Fomo sapiens Ensis minor Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus Homo sapiens Mus musculus Homo sapiens Homo sapiens Homo sapiens Homo sapiens	synthetase HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO. 163. testis-abundant finger protein precursor polypeptide (AA -23 to 1120) HDCMD38P sortilin 75 kDa subunit NADH dehydrogenase precursor	1261 345 3668 361 3203 3487 3609 5936 1684 199 3440 861 4436 3734	97 30 100 94 100 99 97 89 99 23 99
611 612 613 614 615 616 617 618 619 620 621	AF161503 L41834 Y91954 AL022327 X85786 Y08319 D12644 U28789 Y35914 AB046382 Y00062 AF068286 X98248	Fomo sapiens Ensis minor Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus Homo sapiens Mus musculus Homo sapiens Homo sapiens Homo sapiens	synthetase HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO. 163. testis-abundant finger protein precursor polypeptide (AA -23 to 1120) HDCMD38P sortilin 75 kDa subunit NADH dehydrogenase precursor 75 kda infertility-related	1261 345 3668 361 3203 3487 3609 5936 1684 199 3440	97 30 100 94 100 99 97 89 99 23 99
611 612 613 614 615 616 617 618 619 620 621 622 623 624	AF161503 L41834 Y91954 AL022327 X85786 Y08319 D12644 U28789 Y35914 AB046382 Y00062 AF068286 X98248 X61100 S58544	Homo sapiens Ensis minor Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus Homo sapiens Mus musculus Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	synthetase HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO. 163. testis-abundant finger protein precursor polypeptide (AA -23 to 1120) HDCMD38P sortilin 75 kDa subunit NADH dehydrogenase precursor 75 kda infertility-related sperm protein	1261 345 3668 361 3203 3487 3609 5936 1684 199 3440 861 4436 3734 2125	97 30 100 94 100 99 97 89 99 23 99 100 99
611 612 613 614 615 616 617 618 619 620 621 622 623 624 625	AF161503 L41834 Y91954 AL022327 X85786 Y08319 D12644 U28789 Y35914 AB046382 Y00062 AF068286 X98248 X61100 S58544 AF151027	Fomo sapiens Ensis minor Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus Homo sapiens Mus musculus Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	synthetase HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO. 163. testis-abundant finger protein precursor polypeptide (AA -23 to 1120) HDCMD38P sortilin 75 kDa subunit NADH dehydrogenase precursor 75 kda infertility-related sperm protein HSPC193	1261 345 3668 361 3203 3487 3609 5936 1684 199 3440 861 4436 3734 2125	97 30 100 94 100 99 97 89 99 23 99 100 99 99
611 612 613 614 615 616 617 618 619 620 621 622 623 624	AF161503 L41834 Y91954 AL022327 X85786 Y08319 D12644 U28789 Y35914 AB046382 Y00062 AF068286 X98248 X61100 S58544	Homo sapiens Ensis minor Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus Homo sapiens Mus musculus Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	synthetase HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO. 163. testis-abundant finger protein precursor polypeptide (AA -23 to 1120) HDCMD38P sortilin 75 kDa subunit NADH dehydrogenase precursor 75 kda infertility-related sperm protein	1261 345 3668 361 3203 3487 3609 5936 1684 199 3440 861 4436 3734 2125	97 30 100 94 100 99 97 89 99 23 99 100 99

TABLE 2

SEQ	ACCESSION	SPECIES	DESCRIPTION	Ch/Ymy	
ID NO:	NUMBER		·	SMITH- WATERMAN SCORE	IDENTITY
629	Y50911	Homo sapiens	Human fetal brain cDNA clone vb7_1 derived protein	1694	100
630	AF098786	Homo sapiens	17 beta-hydroxysteroid dehydrogenase type VII	1754	100
631	AL034555	Homo sapiens	dJ134019.3 (zinc finger protein 151 (pHZ-67))	4273	100
632	W74826	Homo sapiens	Human secreted protein encoded by gene 98 clone	794	96
633	AF288288	Homo sapiens	HAQBT94.	2236	.100
634	AF041429	Homo sapiens		823	99
635	X66357	Homo sapiens	serine/threonine protein kinase	1589	100
636	Y11284 AB004884	Homo sapiens	AFX1	2571	98
638	AJ002303	Homo sapiens Homo sapiens	PKU-alpha	3718	99
639	AJ002303	Homo sapiens	synaptogyrin 1c synaptogyrin 1b	1020	100
640	AJ002303	Homo sapiens	synaptogyrin ic	1002 933	100 94
641	D87682	Homo sapiens	similar to a C.elegans protein encoded in cosmid T26A5.	2676	100
642	M14660	Homo sapiens	ISG-K54	2473	99
643	X06661	Homo sapiens	calbindin (AA 1-261)	1358	100
644	AF119900	Homo sapiens	PRO2822	185	76
645	AB031048	Drosophila melanogaster	microtubule associated- protein orbit	738	27
646	AF250842	Drosophila melanogaster	multiple asters	834	29
647	X86691 U67934	Homo sapiens	Mi-2 protein	10110	99
649		Homo sapiens	44.9 kDa protein C18B11 homolog	827	96
	AF236061	Oryctolagus cuniculus	RING-finger binding protein	3830	91
650	AL034553	Homo sapiens	dJ914P20.2 (KIAA0784 protein similar to Mus musculus activity-dependent neuroprotective protein (Adnp))	5708	100
653	X14766	Homo sapiens	GABA-A receptor alpha 1 subunit	2388	99
654	AC004614	Homo sapiens	similar to f-spondin proteins AB006086 (PID:g2529225)	3026	99
655	Y57908	Homo sapiens	Human transmembrane protein HTMPN-32.	608	99
656 658	Z34975	Homo sapiens	ldlCp	3733	100
659	AL050306 W76734	Homo sapiens	dJ475B7.2 (novel protein) Human mDia Rho targeting	1942 781	99 34
		sapiens	protein.	.	24
660	AF202724	Homo sapiens	Sadl unc-84 domain protein 1	2172	100
661 662	Z21966 AJ242954	Homo sapiens	mPOU homeobox protein	1529	100
663	AF182316	Mus musculus Komo sapiens	dysferlin myoferlin	4752	59
665	AL161516	Arabidopsis thaliana	hypothetical protein	6232 209	99 30
667	X59303	Homo sapiens	valyl-tRNA synthetase	3393	0.0
668	Y13355	Homo sapiens	Amino acid sequence of protein PRO220.	3692	99 100
669	AB010692	Arabidopsis thaliana	contains similarity to endo- beta-N-acetylglucosaminidase gene	611	52
671	X56123	Mus musculus	talin	4474	76
672	AB039371	Homo sapiens	mitochondrial ABC transporter	2902	99
673	AF269223	Homo sapiens	TCP11	806	42
674 675	AF229633 L14463	Mus musculus	groucho-related protein 4	4053	99
<u> </u>	-71403	Rattus	transducin	3619	92

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
<u> </u>	7.0000000	norvegicus	220614	2779	100
676	AC005757	Homo sapiens	R32611_1 reverse transcriptase	252	65
677	861069	Homo sapiens	homolog=pol (retroviral element)	252	65
678	AF271388	Homo sapiens	CMP-N-acetylneuraminic acid synthase	2273	100
679	X79066	Homo sapiens	ERF-1	1783	100
680	AF118566	Mus musculus	hematopoietic zinc finger protein	769	50
681	Y51415	Homo sapiens	Human wild type pKe83 , protein.	2621	99
682	AL133545	Homo sapiens	bA386N14.1 (novel protein similar to a dual specificity phosphatase)	700	68
683	Y86214	Homo sapiens	Nuclear transport protein clone hfb341 protein sequence.	5888	99 .
684	Y94952	Homo sapiens	Human secreted protein clone fhl16_11 protein sequence SEQ ID NO:110.	354	98
685	AL021878	Homo sapiens	dJ257120.4 (transcription factor 20 (AR1) (KIAA0292) (isoform 2))	154	67
686	AE000198	Escherichia coli	orf, hypothetical protein	628	100
687	M58378	Homo sapiens	synapsin I	3730	99
688	AF039697	Homo sapiens	antigen NY-CO-31	508	98
689	U09355	Oryctolagus cuniculus	protein phosphatase 2A1 B gamma subunit	2356	99
690	AF155106	Homo sapiens	NY-REN-36 antigen	265	50
691	AC004774	Homo sapiens	Dlx-5	1542	100
692	X90530	Homo sapiens	ragB	1926	99
693	X90530	Homo sapiens	ragB	1405	99
694	X90530	Homo sapiens	ragB	1590	85
695	G01563	Homo sapiens	Human secreted protein, SEQ ID NO: 5644.	330	100
696	AC011810	Arabidopsis thaliana	Putative methionine aminopeptidase	669	52
697	AJ250425	Rattus norvegicus	Collybistin I	2455	98
698	AB037901	Homo sapiens	gene amplified in squamous cell carcinoma-1	5364	99
699	Y99401	Homo sapiens	Human PRO1327 (UNQ687) amino acid sequence SEQ ID NO:218.	1386	100
701	AF221712	Homo sapiens	Smad- and Olf-interacting zinc finger protein	6705	100
702	X83573	Homo sapiens	ARSE	3184 2078	99
703 704	AJ243274 Y71262	Homo sapiens Homo sapiens	AP-2rep protein Human chondromodulin-like protein, Zchm1.	1697	94
705	¥71262	Homo sapiens	Human chondromodulin-like protein, Zchml.	1736	99
706	¥41257	Homo sapiens	Amino acid sequence of long human FAIM.	1060	100
707	AL022237	Homo sapiens	bK1191B2.3 (PUTATIVE novel Acyl Transferase similar to C. elegans C50D2.7) (isoform 1))	2030	100
708	AJ006266	Homo sapiens	AND-1 protein	5942	100
709	G01571	Homo sapiens	Human secreted protein, SEQ ID NO: 5652.	777	99
710	Y08698	Homo sapiens	ranbp3	2849	98
711	Y68770	Homo sapiens	Amino acid sequence of a human phosphorylation effector PHSP-2.	754	99

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	7
ID	NUMBER			WATERMAN	IDENTITY
NO:				SCORE	
712	U93574	Homo sapiens	putative p150	799	59
713	AC004531	Homo sapiens	Gene with similaity to DEAD	2715	99
			box helicases		
714	D89016	Homo sapiens	Neuroblastoma	538	48
715	Y92175	Homo sapiens	Human cardiovascular system	734	98
			associated protein tyrosine		i
			phosphatase 2.		1
716	AL137013	Homo sapiens	bA311P8.3 (probable uracil	862	100
			phosphoribosyltranferase)		
717	AB035123	Mus musculus	GD1 alpha/GT1a alpha/GQ1b alpha synthase	1696	93
718	Y96290	Homo >P40254	Human IGFAM-2 immunoglobulin.	2345	85
1		P40254 25-	Manual Torray 2 Institutiog10Du1111.	2345	85
1		OCT-1984 09-		1	
ľ	Ì	APR-1983	İ		ì
		Human IqD.		1	
		[Homo			,
ļ		sapiens			
719	X07979	Homo sapiens	integrin beta 1 subunit	4347	99
		_	precursor		"
720	AJ224819	Homo sapiens	tumor suppressor	2149	99
721	Y07595	Homo sapiens	transcription factor TFIIH	2373	100
722	W41565	Homo	Human calpain.	1591	99
1		sapiens]	-		"
1		>W41564		1	
İ		W41564 08-	1)	J
i		OCT-1997 05-			1
		APR-1996			
i		Human	•		1
ĺ	ĺ	calpain.	Í	1	ĺ
1		[Homo		İ	
723	370-6-0	sapiens			
724	AF161341 AF187318	Homo sapiens	HSPC078	1097	98
725	AC006708	Homo sapiens Caenorhabdit	F-box protein Fbx2 contains simlarity to	1607	100
1.23	1.000700	is elegans	Saccharomyces cerevisiae pre-	1143	46
1	ŀ	15 Cicgans	mRNA splicing protein PRP31		
	}		(GB: 272876)	j]
726	AC006708	Caenorhabdit	contains simlarity to	988	46
		is elegans	Saccharomyces cerevisiae pre-	588	30
			mRNA splicing protein PRP31		
ĺ			(GB:Z72876)	ľ	
727	AC024818	Caenorhabdit	contains similarity to Pfam	950	44
		is elegans	family PF00400 (WD domain,		•
		_	G-beta repeat), score=81.8,		
		,	E=1.4e-20, N=3		
728	AJ005897	Homo sapiens	JMS	831	47
729	Y45377	Homo sapiens	Human secreted protein	908	97
			fragment encoded from gene	1	
			27.	1	i
730	G03931	Homo sapiens	Human secreted protein, SEQ	578	100
LI			ID NO: 8012.		
731	AB012720	Oncorhynchus	GTP-binding protein	3865	76
	AD012/20		orr binding process	3000	76
		masou	1	3865	/6
732	W73404		Human secreted protein	862	97
	W73404	masou Homo sapiens	Human secreted protein encoded by Gene No. 8.		
732		masou	Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ		
733	W73404 G02650	masou Homo sapiens Homo sapiens	Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731.	862	97
	W73404	masou Homo sapiens Homo sapiens Caenorhabdit	Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. Hypothetical protein	862	97
733	W73404 G02650 AC024813	masou Homo sapiens Homo sapiens Caenorhabdit is elegans	Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. Hypothetical protein Y54F10AL.a	862	97
733	W73404 G02650	masou Homo sapiens Homo sapiens Caenorhabdit	Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. Hypothetical protein Y54F10AL.a dJ967N21.6 (novel CDP-alcohol	862	97
733	W73404 G02650 AC024813	masou Homo sapiens Homo sapiens Caenorhabdit is elegans	Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. Hypothetical protein Y54F10AL.a dJ967N21.6 (novel CDP-alcohol phosphatidyltransferase	862 644 152	97
733 734 735	W73404 G02650 AC024813 AL035461	masou Homo sapiens Homo sapiens Caenorhabdit is elegans Homo sapiens	Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID No: 6731. Hypothetical protein Y54F10AL.a dJ967N21.6 (novel CDP-alcohol phosphatidyltransferase family member protein)	862 644 152 1562	97
733	W73404 G02650 AC024813	masou Homo sapiens Homo sapiens Caenorhabdit is elegans Homo sapiens Caenorhabdit	Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. Hypothetical protein Y54F10AL.a dJ967N21.6 (novel CDP-alcohol phosphatidyltransferase family member protein) similar to S. cerevisiae YJU2	862 644 152	97
733 734 735 736	W73404 G02650 AC024813 AL035461 U00033	masou Homo sapiens Homo sapiens Caenorhabdit is elegans Homo sapiens Caenorhabdit is elegans	Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. Hypothetical protein Y54F10AL.a dJ967N21.6 (novel CDP-alcohol phosphatidyltransferase family member protein) similar to S. cerevisiae YJU2 protein	862 644 152 1562	97 97 24 98
733 734 735	W73404 G02650 AC024813 AL035461	masou Homo sapiens Homo sapiens Caenorhabdit is elegans Homo sapiens Caenorhabdit	Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. Hypothetical protein Y54F10AL.a dJ967N21.6 (novel CDP-alcohol phosphatidyltransferase family member protein) similar to S. cerevisiae YJU2	862 644 152 1562	97 97 24 98

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	
ID	NUMBER	SPECIES	DESCRIPTION	WATERMAN	\$ - DDM
NO:				SCORE	IDENTITY
738	AJ131712	Homo sapiens	nucleolar RNA-helicase	2793	
739	AJ133115	Homo sapiens	TSC-22-like protein	1	100
740	X98258	Homo sapiens		2054	9 9
741	X98258	Homo sapiens	M-phase phosphoprotein 9	953	100
742	U97191	Caenorhabdit		564	74
/ 32	03/131		strong similarity to the YPT1	960	85
743	X76057	is elegans	sub-family of RAS proteins		
744	G03209	Homo sapiens	phosphomannose isomerase	2191	100
/***	603209	Homo sapiens	Human secreted protein, SEQ	496	98
745	X97064	 ,, 	ID NO: 7290.	<u> </u>	
746	W93946	Homo sapiens	Sec23 protein	4034	99
/46	W93946	Homo sapiens	Human regulatory molecule	994	100
747	7,000		HRM-2 protein.		
/4/	¥73388	Homo sapiens	HTRM clone 3376404 protein	1565	99
			sequence.	1	
748	M19529	Sus scrofa	follistatin A	1906	98
749	AJ249457	Trichomonas	centrin, putative	183	28
		vaginalis	[1	ľ
750	AC004410	Homo sapiens	fos39554_1	2094	100
751	AF074968	Homo sapiens	p47ING3 protein	2167	100
752	AF252284	Homo sapiens	transcription specificity	4005	100
	1		factor Spl		
753	AB049629	Homo sapiens	phospholysine	1375	99
i			phosphohistidine inorganic	1	1 33
ļ	1		pyrophosphate phosphatase		
754	D79205	Homo sapiens	ribosomal protein L39	160	77
755	AB008430	Homo sapiens	CDEP	142	29
758	L32162	Homo sapiens	transcription factor	574	80
759	AF037204	Homo sapiens	RING zinc finger protein	295	54
760	Y44250	Homo	Human cell signalling	625	100
1		sapiens	protein-13.	023	1 100
761	AF218586	Homo sapiens	Cide-b	1136	100
762	U38934	Gallus	histone H2A	625	97
1	*****	gallus	miscone nza	625	97
763	AF226053	Homo sapiens	HSKM-B	606	32
764	X13403	Homo sapiens	,	3626	100
765	D87446	Homo sapiens	Similar to a C.elegans	568	38
			protein encoded in cosmid C27F2 (U40419)	566	38
766	AL023828	Caenorhabdit	Y17G7B.14	200	27
		is elegans		200	- '
767	Y82777	Homo sapiens	Human chordin related protein	2551	99
			(Clone dw665_4).	2223	1 99
768	X92475	Homo sapiens	ITBA1	1429	100
769	Y42752	Homo sapiens	Human calcium binding protein	1426	100
		Japan Sapaons	3 (CaBP-3).	1420	100
770	X51416	Homo sapiens	hormone receptor hERR1 (AA 1-	2641	97
İ			521)	2071	
771	AJ006591	Homo sapiens	cysteine-rich protein	1793	100
772	A08695	Homo sapiens	rap2		100
773	Z12173	Homo sapiens	N-acetylglucosamine-6-	935	100
'		sapiens	n-acetylgiucosamine-6- sulphatase	2970	100
774	Y91950	Homo sapiens	Human cytoskeleton associated		
· · · -		sapicits		565	43
776	AL023799	Homo sapiens	protein 5 (CYSKP-5).		
777	AL023799		dJ322P7.1 (zinc finger)	855	56
778		Homo sapiens	dJ322P7.1 (zinc finger)	855	56
//8	G01880	Homo sapiens	Human secreted protein, SEQ	849	98
222	3.70.7.7.7.		ID NO: 5961.		
779	AJ012590	Homo sapiens	glucose 1-dehydrogenase	4155	99
780	AL078582	Homo sapiens	dJ130E4.2 (KIAAD796)	1321	68
781	275955	Caenorhabdit	similar to mitochondrial	384	34
		is elegans	carrier protein]
782	AL109965	Homo	dJ1121G12.2 (SCAN domain-	900	100
		sapiens	containing 1 protein)	-	
783	AF061262	Mus	semaF cytoplasmic domain	1316	83
		musculus	associated protein 2		
784	G03873	Homo sapiens	Human secreted protein, SEQ	649	95
				V-2-2	

ID NUMBER 785 Y84441 786 Y00918 787 Z97029 788 AB035384 789 AF024631 790 AJ006710 792 V00638 793 AF049103 795 Z26317 796 Y76884 797 U15155 798 U97189 799 AF112201 800 AF234765 801 AF267852 802 AF208851 803 Z81097 804 G02113 805 AL121673 806 AC013483 807 AC013483 808 AB013885 809 AF078842 810 AF161421 811 AF261689 812 Z74029 813 Z73497 814 W87689 815 X16282 816 Z92539	Homo sapiens Homo sapiens	ID NO: 7954. Amino acid sequence of a human RNA-associated	WATERMAN SCORE	IDENTITY
785 Y84441 786 Y00918 787 Z97029 788 AB035384 789 AF024631 790 AJ006710 792 V00638 793 AF049103 795 Z26317 796 Y76884 797 U15155 798 U97189 799 AF112201 800 AF234765 801 AF267852 802 AF208851 803 Z81097 804 G02113 805 AL121673 806 AC013483 807 AC013483 808 AB013885 809 AF078842 810 AF161421 811 AF261689 812 Z74029 813 Z73497 814 W87689 815 X16282 816 Z92539 818 AB030483 819 AL117555	Homo sapiens	Amino acid sequence of a	SCORE	
786 Y00918 787 Z97029 788 AB035384 789 AF024631 790 AJ006710 792 V00638 793 AF049103 795 Z26317 796 Y76884	Homo sapiens	Amino acid sequence of a		
786 Y00918 787 Z97029 788 AB035384 789 AF024631 790 AJ006710 792 V00638 793 AF049103 795 Z26317 796 Y76884 797 U15155 798 U97189 799 AF112201 800 AF234765 801 AF267852 802 AF208851 803 Z81097 804 G02113 805 AL121673 806 AC013483 807 AC013483 808 AB013885 809 AF078842 810 AF161421 811 AF261689 812 Z74029 813 Z73497 814 W87689 815 X16282 816 Z92539 818 AB030483 819 AL17555	Homo sapiens			
787 Z97029 788 AB035384 789 AF024631 790 AJ006710 792 V00638 793 AF049103 795 Z26317 796 Y76884 . 797 U15155 798 U97189 799 AF112201 800 AF234765 801 AF267852 802 AF208851 803 Z81097 804 G02113 805 AL121673 806 AC013483 807 AC013483 808 AB013885 809 AF078842 810 AF161421 811 AF261689 812 Z74029 813 Z73497 814 W87689 815 X16282 816 Z92539		inuman kwa-associared	2074	100
787 Z97029 788 AB035384 789 AF024631 790 AJ006710 792 V00638 793 AF049103 795 Z26317 796 Y76884 . 797 U15155 798 U97189 799 AF112201 800 AF234765 801 AF267852 802 AF208851 803 Z81097 804 G02113 805 AL121673 806 AC013483 807 AC013483 808 AB013885 809 AF078842 810 AF161421 811 AF261689 812 Z74029 813 Z73497 814 W87689 815 X16282 816 Z92539		protein.		
788 AB035384 789 AF024631 790 AJ006710 792 V00638 793 AF049103 795 Z26317 796 Y76884 797 U15155 798 U97189 799 AF112201 800 AF234765 801 AF267852 802 AF208851 803 Z81097 804 G02113 805 AL121673 806 AC013483 807 AC013483 808 AB013885 809 AF078842 810 AF161421 811 AF261689 812 Z74029 813 Z73497 814 W87689 815 X16282 816 Z92539 818 AB030483 819 AL117555			1048	99
788 AB035384 789 AF024631 790 AJ006710 792 V00638 793 AF049103 795 Z26317 796 Y76884 797 U15155 798 U97189 799 AF112201 800 AF234765 801 AF267852 802 AF208851 803 Z81097 804 G02113 805 AL121673 806 AC013483 807 AC013483 808 AB013885 809 AF078842 810 AF161421 811 AF261689 812 Z74029 813 Z73497 814 W87689 815 X16282 816 Z92539 818 AB030483 819 AL117555	Homo sanieno	protein sequence.	1040	99
789 AF024631 790 AJ006710 792 V00638 793 AF049103 795 Z26317 796 Y76884 797 U15155 798 U97189 799 AF112201 800 AF234765 801 AF267852 802 AF208851 803 Z81097 804 G02113 805 AL121673 806 AC013483 807 AC013483 808 AB013885 809 AF078842 810 AF161421 811 AF261689 812 Z74029 813 Z73497 814 W87689 815 X16282 816 Z92539 818 AB030483 819 AL117555			1548	99 .
790 AJ006710 792 V00638 793 AF049103 795 Z26317 796 Y76884 797 U15155 798 U97189 799 AF112201 800 AF234765 801 AF267852 802 AF208851 803 Z81097 804 G02113 805 AL121673 806 AC013483 807 AC013483 808 AB013885 809 AF078842 810 AF161421 811 AF261689 812 Z74029 813 Z73497 814 W87689 815 X16282 816 Z92539	Homo sapiens	SRp25 nuclear protein	962	94
792 V00638 793 AF049103 795 Z26317 796 Y76884 797 U15155 798 U97189 799 AF112201 800 AF234765 801 AF267852 802 AF208851 803 Z81097 804 G02113 805 AL121673 806 AC013483 807 AC013483 808 AB013885 809 AF7078842 810 AF161421 811 AF261689 812 Z74029 813 Z73497 814 W87689 815 X16282 816 Z92539 818 AB030483 819 AL117555	Homo sapiens	ANG2	2644	100
793 AF049103 795 Z26317 796 Y76884 797 U15155 798 U97189 799 AF112201 800 AF234765 801 AF267852 802 AF208851 803 Z81097 804 G02113 805 AL121673 806 AC013483 807 AC013483 808 AB013885 809 AF078842 810 AF161421 811 AF261689 812 Z74029 813 Z73497 814 W87689 815 X16282 816 Z92539	Rattus norvegicus	phosphatidylinositol 3-kinase	4508	97
795 Z26317 796 Y76884 . 797 U15155 798 U97189 799 AF112201 800 AF234765 801 AF267852 802 AF208851 803 Z81097 804 G02113 805 AL121673 806 AC013483 807 AC013483 808 AB013885 809 AF078842 810 AF161421 811 AF261689 812 Z74029 813 Z73497 814 W87689 815 X16282 816 Z92539	bacteriophag e lambda	reading frame eal0	600	100
796 Y76884 797 U15155 798 U97189 799 AF112201 800 AF234765 801 AF267852 802 AF208851 803 Z81097 804 G02113 805 AL121673 806 AC013483 807 AC013483 808 AB013885 809 AF078842 810 AF161421 811 AF261689 812 Z74029 813 Z73497 814 W87689 815 X16282 816 Z92539 818 AB030483 819 AL117555	Homo sapiens	Huntingtin interacting protein	819	100
797 U15155 798 U97189 799 AF112201 800 AF234765 801 AF267852 802 AF208851 803 Z81097 804 G02113 805 AL121673 806 AC013483 807 AC013483 808 AB013885 809 AF7078842 810 AF161421 811 AF261689 812 Z74029 813 Z73497 814 W87689 815 X16282 816 Z92539 818 AB030483 819 AL117555	Homo sapiens	desmoglein 2	4810	99
798 U97189 799 AF112201 800 AF234765 801 AF267852 802 AF208851 803 Z81097 804 G02113 805 AL121673 806 AC013483 807 AC013483 808 AB013885 809 AF078842 810 AF161421 811 AF261689 812 Z74029 813 Z73497 814 W87689 815 X16282 816 Z92539 818 AB030483 819 AL117555	Homo sapiens	Retinoblastoma binding protein-7sequence.	5080	99
799 AF112201 800 AF234765 801 AF267852 802 AF208851 803 Z81097 804 G02113 805 AL121673 806 AC013483 807 AC013483 808 AB013885 809 AF078842 810 AF161421 811 AF261689 812 Z74029 813 Z73497 814 W87689 815 X16282 816 Z92539 818 AB030483 819 AL117555	Gallus	trypsinogen	372	37
799 AF112201 800 AF234765 801 AF267852 802 AF208851 803 Z81097 804 G02113 805 AL121673 806 AC013483 807 AC013483 808 AB013885 809 AF078842 810 AF161421 811 AF261689 812 Z74029 813 Z73497 814 W87689 815 X16282 816 Z92539 818 AB030483 819 AL117555	gallus		1	1
800 AF234765 801 AF267852 802 AF208851 803 Z81097 804 G02113 805 AL121673 806 AC013483 807 AC013483 809 AF078842 810 AF161421 811 AF261689 812 Z74029 813 Z73497 814 W87689 815 X16282 816 Z92539 818 AB030483 819 AL117555	Caenorhabdit		227	28
800 AF234765 801 AF267852 802 AF208851 803 Z81097 804 G02113 805 AL121673 806 AC013483 807 AC013483 809 AF078842 810 AF161421 811 AF261689 812 Z74029 813 Z73497 814 W87689 815 X16282 816 Z92539 818 AB030483 819 AL117555	is elegans	P13/P14 family of kinases		
801 AF267852 802 AF208851 803 Z81097 804 G02113 805 AL121673 806 AC013483 807 AC013483 808 AB013885 809 AF7078842 810 AF161421 811 AF261689 812 Z74029 813 Z73497 814 W87689 815 X16282 816 Z92539 818 AB030483 819 AL117555	Homo sapiens	neuronal protein NP25	1053	100
802 AF208851 803 Z81097 804 G02113 805 AL121673 806 AC013483 807 AC013483 808 AB013885 809 AF078842 810 AF161421 811 AF261689 812 Z74029 813 Z73497 814 W87689 815 X16282 816 Z92539 818 AB030483 819 AL117555	norvegicus	serine-arginine-rich splicing regulatory protein SRRP86	958	63
803 Z81097 804 G02113 805 AL121673 806 AC013483 807 AC013483 808 AB013885 809 AF078842 810 AF161421 811 AF261689 812 Z74029 813 Z73497 814 W87689 815 X16282 816 Z92539 818 AB030483 819 AL117555	Homo sapiens	placental protein 13-like	743	99
803 Z81097 804 G02113 805 AL121673 806 AC013483 807 AC013483 808 AB013885 809 AF078842 810 AF161421 811 AF261689 812 Z74029 813 Z73497 814 W87689 815 X16282 816 Z92539 818 AB030483 819 AL117555	• • • • • • • • • • • • • • • • • • • •	protein	'33	33
804 G02113 805 AL121673 806 AC013483 807 AC013483 808 AB013885 809 AF078842 810 AF161421 811 AF261689 812 Z74029 813 Z73497 814 W87689 815 X16282 816 Z92539 818 AB030483 819 AL117555	Homo sapiens	BM-009	766	80
805 AL121673 806 AC013483 807 AC013483 808 AB013885 809 AF078842 810 AF161421 811 AF261689 812 Z74029 813 Z73497 814 W87689 815 X16282 816 Z92539 818 AB030483 819 AL117555	Caenorhabdit		152	27
805 AL121673 806 AC013483 807 AC013483 808 AB013885 809 AF078842 810 AF161421 811 AF261689 812 Z74029 813 Z73497 814 W87689 815 X16282 816 Z92539 818 AB030483 819 AL117555	is elegans	retinoblastoma-binding protein RBAP46 yk662d12.5 comes from this gene		
806 AC013483 807 AC013483 808 AB013885 809 AF078842 810 AF161421 811 AF261689 812 Z74029 813 Z73497 814 W87689 815 X16282 816 Z92539 818 AB030483 819 AL117555	Homo sapiens	Human secreted protein, SEQ ID NO: 6194.	496	98
807 AC013483 808 AB013885 809 AF078842 810 AF161421 811 AF261689 812 Z74029 813 Z73497 814 W87689 815 X16282 816 Z92539 818 AB030483 819 AL117555	Homo sapiens	bA305P22.1 (novel protein)	1160	100
808 AB013885 809 AF078842 810 AF161421 811 AF261689 812 Z74029 813 Z73497 814 W87689 815 X16282 816 Z92539 818 AB030483 819 AL117555	Arabidopsis thaliana	putative GTPase activator protein	264	30
809 AF078842 810 AF161421 811 AF261689 812 Z74029 813 Z73497 814 W87689 815 X16282 816 Z92539 818 AB030483 819 AL117555	Arabidopsis thaliana	putative GTPase activator protein	264	3C
810 AF161421 811 AF261689 812 Z74029 813 Z73497 814 W87689 815 X16282 816 Z92539 818 AB030483 819 AL117555	Homo sapiens	beta-ureidopropionase	1494	100
811 AF261689 812 Z74029 813 Z73497 814 W87689 815 X16282 816 Z92539 818 AB030483 819 AL117555	Homo sapiens	HOTTL protein	1581	99
812 Z74029 813 Z73497 814 W87689 815 X16282 816 Z92539 818 AB030483 819 AL117555	Homo sapiens	HSPC303	2134	96
813 Z73497 814 W87689 815 X16282 816 Z92539 818 AB030483 819 AL117555	Homo sapiens	DNA polymerase epsilon p17 subunit	734	100
814 W87689 815 X16282 816 Z92539 818 AB030483 819 AL117555	Caenorhabdit is elegans	Similarity to C.elegans alcohol dehydrogenase comes	610	71
814 W87689 815 X16282 816 Z92539 818 AB030483 819 AL117555		from this gene		_
815 X16282 816 Z92539 818 AB030483 819 AL117555	Homo sapiens	cU240C2.2 (Core histone H2A/H2B/H3/H4)	324	100
816 Z92539 818 AB030483 819 AL117555	Homo sapiens	Human HTXFT19 polypeptide.	1484	99
818 AB030483 819 AL117555	Homo sapiens	zinc finger protein (217 AA) (1 is 2nd base in codon)	1109	99
819 AL117555	Mycobacteriu	pth	300	36
819 AL117555	m tuberculosis			30
819 AL117555	Mus musculus	B9	197	27
	Homo sapiens	hypothetical protein	321	94
820 AC005328	Homo sapiens	R26660_2, partial CDS	865	97
821 G03951	Homo sapiens	Human secreted protein, SEQ ID NO: 8032.	700	99
822 L34807	Musca domestica	transposase	174	20
823 G02928	L MOUICHLICS I	Human secreted protein, SEQ ID NO: 7009.	558	78
824 Z99531	Homo sapiens	1	184	29

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	
ID NO:	NUMBER			WATERMAN SCORE	IDENTITY
		romyces	protein 1		
825	AJ006692	Homo sapiens	ultra high sulfer keratin	693	68
826	U23037	Oryctolagus cuniculus	eIF-2Bepsilon	3406	90
827	G03412	Homo sapiens	Human secreted protein, SEQ ID NO: 7493.	464	100
828	Y30327	Homo sapiens	Human secreted protein encoded from gene 17.	113	44
829	Y32199	Homo sapiens	Human receptor molecule (REC) encoded by Incyte clone 2022379.	1012	100
830	W78279	Homo sapiens	Fragment of human secreted protein encoded by gene 33.	1264	99
832	AB011542	Homo sapiens	MEGF9	2097	100
833	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	223	70
834	AF119664	Homo sapiens	transcriptional regulator protein HCNGP	1574	100
835	AF119664	Homo sapiens	transcriptional regulator protein HCNGP	1144	89
836	AF119664	Homo sapiens	transcriptional regulator protein HCNGP	1448	94
837	X12517	Homo sapiens	C protein (AA 1-159)	918	100
838	U32865	Drosophila melanogaster	linotte protein	164	24
839	AF067730	Homo sapiens	TLS-associated protein TASR-2	631	56
840	U27831 AF286366	Homo sapiens	striatum-enriched phosphatase	2840	98
842	G02309	Homo sapiens	CamKI-like protein kinase	1796	100
843	AE003615	Homo sapiens	Human secreted protein, SEQ ID NO: 6390.	278	98
844	G01350	Drosophila melanogaster	ade3 gene product	113	48
845		Homo sapiens	Human secreted protein, SEQ ID NO: 5431.	629	100
	U27838	Mus musculus	glycosyl-phosphatidyl- inositol-anchored protein homolog	3305	96
847	Y87788	Homo sapiens	Human RBP-26 protein.	2026	100
848	AF164794	Homo sapiens	Diff33 protein homolog	2398	100
849	U41315	Homo sapiens	ZNF127-Xp	2458	93
850	AF192784	Homo sapiens	makorin 1	2062	97
851	Y58628	Homo sapiens	Protein regulating gene expression PRGE-21.	1548	100 .
852	222968	Homo sapiens	M130 antigen	6205	100
853	Z22971	Homo sapiens	M130 antigen extracellular variant	6380	100
854	G03362	Homo sapiens	Human secreted protein, SEQ ID NO: 7443.	330	96
855	G03362	Homo sapiens	Human secreted protein, SEQ ID NO: 7443.	203	100
856	AF285118	Homo sapiens	CGI-203	452	100
857	AC006069	Arabidopsis thaliana	putative cleavage and polyadenylation specifity factor	1383	55
858	AL021546	Homo sapiens	Cytochrome C Oxidase Polypeptide VIa-liver precursor (EC 1.9.3.1)	593	100
859	L02956	Xenopus laevis	ribonucleoprotein	1664	85
860	AF201947	Homo sapiens	MEK binding partner 1	616	100
861	L31783	Mus musculus	uridine kinase	1266	92
862	AF161472	Homo sapiens	HSPC123	602	73
863	Z49068	Caenorhabdit is elegans	mitochondrial carrier protein	370	43
864	AF154108	Homo sapiens	tumor necrosis factor type 1	3559	99

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	\$ IDENTITY
865	AE001530	Helicobacter	receptor associated protein		
866	X57807	pylori J99		230	32
867		Homo sapiens	chain	699	91
	AL031673	Homo sapiens	KRAB box protein with 18 C2H2 type Zinc finger domains)	4066	99
868	Y11652	Homo sapiens		238	3.00
869	AF192968	Homo sapiens	protein 8	3041	99
870	AB020648	Homo sapiens		3237	59
871	AL031427	Homo sapiens		1608	100
872 873	AF151534	Homo sapiens		1866	100
874	AL021331 X14608	Homo sapiens	elegans UNC-93 (protein 1, C46F11.1) LIKE protein)	1129	100
875	AL117334	Homo sapiens	propionyl-CoA carboxylase	3579	100
_		Homo sapiens	dJ687F11.1 (novel protein (part of translation of cDNA DKFZp434N061, Em:AL110249))	306	100
876	X79489	Saccharomyce s cerevisiae	E-925 protein	446	35
877	Y53001	Homo sapiens	Human secreted protein clone dn834 1 protein sequence SEQ ID NO:8.	811	100
878	AF281064	Homo sapiens	CHMP1.5	957	100
879	X79417	Sus scrofa	40S ribosomal protein S12	687	100
880	AF001317	Saccharomyce s cerevisiae	Soilp	478	28
881	Y87275	Homo sapiens	Human signal peptide containing protein HSPP-52 SEQ ID NO:52.	2547	100
882	M14036	Homo sapiens	C1-inhibitor	598	77
883	AB041261	Homo sapiens	calcium-independent phospholipase A2	2903	100
884	AF020313	Mus musculus	proline-rich protein 48	999	84
885 886	Y10936	Homo sapiens	hypothetical protein	1104	99
	AF073997	Mus musculus	myotubularin related protein	866	36
887	Y57893	Homo sapiens	Human transmembrane protein HTMPN-17.	1099	94
888	AL117635	Homo sapiens	hypothetical protein	929	99
889	AF210317	Homo sapiens	facilitative glucose transporter family member GLUT9	2046	99
890	¥36031	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 416.	583	100
891	¥36031	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 416.	192	57
892	AF237631	Homo sapiens	ubiquitous tropomodulin U-	1798	100
893	AF090929	Homo sapiens	PRO0477p	653	99
894	AL031228	Homo sapiens	dJ1033B10.2 (WD40 protein BING4 (similar to S. cerevisiae YER082C, M. sexta MNG10 and C. elegans F28D1.1)	3196	100
895	AL031228	Homo sapiens	dJ1033B10.2 (WD40 protein BING4 (similar to S. cerevisiae YER082C, M. sexta MNG10 and C. elegans F28D1.1)	2825	96
			- and C. elegans F28D1.1)		
		Homo sapiens Drosophila	retinal degeneration B beta CG18176 gene product	1302	95

1998 297184 Homo sapiens EKE2 429		SMITH- WATERMAN SCORE	DESCRIPTION	SPECIES	ACCESSION NUMBER	SEQ ID NO:
901 AJ245587 Homo sapiens KEE2 A09	100	2443	DEAD Box Protein 5	Homo sapiens	AJ237946	898
No. 1245587 Nome Sapiens Kruppel-type zinc finger 1942	100			-		
100	98	,				
103 R95953 Homo sapiens Eukaryotic cell growth inhibiting factor. 1936 1935 193	100			l		
1904	100					
1904 1.04733 Homo sapiens Kinesin light chain 1936	96	414		Homo sapiens	R95953	903
MS5542 Homo sapiens Gilogal gene product 446 melanogaster		1026		11	7.04573	004
MS5542 Homo sapiens guanylate binding protein 2993	72	L		l		
	33		-	melanogaster		
150fcm I	98		isoform I			
WDProl. Sapiens TNF intracellular domain-	96	2901		Homo sapiens	M55542	907
Sapiens Interacting protein 2196	100	1889		Homo sapiens	W84085	908
910 AB029150 Homo saplens KRAB zinc finger protein HFB10L 911 G02871 Homo saplens Human secreted protein, SEQ 521 912 G03162 Homo saplens Human secreted protein, SEQ 1D NO: 6952. 913 AJ243721 Homo Saplens Human secreted protein, SEQ 1D NO: 7243. 913 AJ243721 Homo Saplens APR-2000 06 OCT-1998 Human OXRE-	100	647	TNF intracellular domain-	Homo	AF168676	909
HFB101L Human secreted protein, SEQ 521 1D NO: 6952. 1D NO: 6952. 1D NO: 6952. 1D NO: 7243. 1D		{		L	ł	
1D NO: 6952. Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens AJ243721 Homo sapiens Y92508 Y9250	100	2196	~ <u>-</u>	Homo sapiens	AB029150	910
912 G03162 Homo sapiens Human secreted protein, SEQ 1D NO: 7243. 913 AJ243721 Homo Sapiens AJPA-248EC-6-deoxy-D-glucose 4-reductase	100	521	• • • • • • • • • • • • • • • • • • • •	Homo sapiens	G02871	911
AJ243721 Homo Sapiens Sy92508 Y92508 APR-2000 06-OCT-1998 Human OXRE-5. [Homo sapiens Human OXRE-5. [Homo sapiens Human OXRE-5. [Homo sapiens Human OXRE-5. [Homo sapiens Human OXRE-5. [Homo sapiens Human OXRE-5. [Homo sapiens Human oxpelied by authors A human progesterone receptor complex p23-like protein. Substituting glycohydrolase (drag) Homo sapiens DHFR-coamplified protein 163	87	387	Human secreted protein, SEQ	Homo sapiens	G03162	912
Sapiens x192508 13- APR-2000 06- OCT-1998 Human OXRE- 5. [Homo sapiens	100	1710		Homo	AJ243721	913
14			4-reductase	>Y92508 Y92508 13- APR-2000 06- OCT-1998 Human OXRE- 5. [Homo		
is elegans Method: conceptual translation supplied by authors P15 Y02591 Homo sapiens A human progesterone receptor complex p23-like protein. P16 AE000984 Archaeoglobu dinitrogenase reductase activating glycohydrolase (draG) P18 M23159 Cricetus cricetus P19 L12018 Caenorhabdit is elegans P20 AF102177 Homo sapiens tumor antigen SLP-8p 1260 P21 AL096712 Homo sapiens dJ744124.2 (similar to a novel human gene mapping to Activator) P22 AL161495 Arabidopsis thaliana P23 AL161495 Arabidopsis putative WD-repeat protein 442 P24 U97001 Caenorhabdit similar to schizosaccharomyces pombe P25 X71978 Mus musculus Fif 1503 P06 M92288 Drosophila melanogaster	41	244	hymothetical protein 1207-1.	1 -	1124189	914
915 Y02591 Homo sapiens Complex p23-like protein. 916 AE000984 Archaeoglobu s fulgidus (drag) 918 M23159 Cricetus (drag) 919 L12018 Caenorhabdit is elegans 920 AF102177 Homo sapiens tumor antigen SLP-8p 1260 921 AL096712 Homo sapiens dJ744124.2 (similar to a novel human gene mapping to Activator) 922 AL161495 Arabidopsis thaliana 923 AL161495 Arabidopsis putative WD-repeat protein 442 924 U97001 Caenorhabdit is elegans Schizosaccharomyces pombe 925 X71978 Mus musculus Fif 1503 926 M92288 Drosophila melanogaster		244	Method: conceptual translation supplied by		024103	711
AE000984 Archaeoglobu s fulgidus dinitrogenase reductase activating glycohydrolase (draG) 918 M23159 Cricetus DHFR-coamplified protein 163 cricetus 919 L12018 Caenorhabdit putative 1232 is elegans 920 AF102177 Homo sapiens tumor antigen SLP-8p 1260 1260 921 AL096712 Homo sapiens dJ744124.2 (similar to a novel human gene mapping to Activator) 922 AL161495 Arabidopsis putative WD-repeat protein 866 123 AL161495 Arabidopsis thaliana 123 putative WD-repeat protein 13 elegans 142 Schizosaccharomyces pombe 15 elegans Schizosaccharomyces pombe 1503 1503 1503 1503 1503 1503 1503 1503	99	843	A human progesterone receptor	Homo sapiens	Y02591	915
s fulgidus activating glycohydrolase (draG) 918 M23159 Cricetus DHFR-coamplified protein 163 919 L12018 Caenorhabdit putative 1232 920 AF102177 Homo sapiens tumor antigen SLP-8p 1260 921 AL096712 Homo sapiens dJ744124.2 (similar to a novel human gene mapping to Activator) 922 AL161495 Arabidopsis putative WD-repeat protein 866 923 AL161495 Arabidopsis putative WD-repeat protein 442 924 U97001 Caenorhabdit similar to 3chizosaccharomyces pombe 925 X71978 Mus musculus Fif 1503 926 M92288 Drosophila melanogaster	26	171		Archaeoglobu	AE000984	916
918 M23159 Cricetus cricetus 919 L12018 Caenorhabdit is elegans 920 AF102177 Homo sapiens tumor antigen SLP-8p 1260 921 AL096712 Homo sapiens dJ744124.2 (similar to a novel human gene mapping to Activator) 922 AL161495 Arabidopsis thaliana 923 AL161495 Arabidopsis putative WD-repeat protein 442 924 U97001 Caenorhabdit similar to is elegans Schizosaccharomyces pombe 925 X71978 Mus musculus Fif 1503 926 M92288 Drosophila melanogaster			activating glycohydrolase			
	30	163		Cricetus	M23159	918
18 elegans 1260 1	1	}	-	cricetus		
920 AF102177 Homo sapiens tumor antigen SLP-8p 1260 921 AL096712 Homo sapiens dJ744124.2 (similar to a novel human gene mapping to Activator) 1017 922 AL161495 Arabidopsis thaliana putative WD-repeat protein 866 923 AL161495 Arabidopsis thaliana putative WD-repeat protein 442 924 U97001 Caenorhabdit is elegans similar to Schizosaccharomyces pombe 605 925 X71978 Mus musculus Fif 1503 926 M92288 Drosophila melanogaster beta-spectrin 290	41	1232	putative	1	L12018	919
921 AL096712 Homo sapiens dJ744124.2 (similar to a novel human gene mapping to Activator) 922 AL161495 Arabidopsis putative WD-repeat protein thaliana 923 AL161495 Arabidopsis putative WD-repeat protein thaliana 924 U97001 Caenorhabdit similar to schizosaccharomyces pombe 925 X71978 Mus musculus Fif 1503 926 M92288 Drosophila melanogaster	97	1260	tumor antigen SLP-8p		AF102177	920
922 AL161495 Arabidopsis putative WD-repeat protein 866 923 AL161495 Arabidopsis putative WD-repeat protein 442 924 U97001 Caenorhabdit similar to 15 elegans Schizosaccharomyces pombe 925 X71978 Mus musculus Fif 1503 926 M92288 Drosophila melanogaster 9290	78		dJ744124.2 (similar to a novel human gene mapping to		AL096712	921
923 AL161495 Arabidopsis thaliana putative WD-repeat protein 442 924 U97001 Caenorhabdit similar to schizosaccharomyces pombe 605 925 X71978 Mus musculus Fif 1503 926 M92288 Drosophila melanogaster beta-spectrin 290	42	866			AL161495	922
924 U97001 Caenorhabdit is imilar to schizosaccharomyces pombe 605 925 X71978 Mus musculus Fif 1503 926 M92288 Drosophila melanogaster beta-spectrin 290	36	442	putative WD-repeat protein	Arabidopsis	AL161495	923
925 X71978 Mus musculus Fif 1503 926 M92288 Drosophila beta-spectrin 290 melanogaster 1503 290	51	605	-	Caenorhabdit	U97001	924
926 M92288 Drosophila beta-spectrin 290 melanogaster		1503			V21020	025
melanogaster	95	<u> </u>				
000 1 1000000 1 17-4	51		-	melanogaster		
encoded by gene No. 9.	100	1392		Homo sapiens	Y27575	927
928 Y22499 Homo sapiens Human secreted protein 2249 sequence clone mh703_1.	100	2249	Human secreted protein	Homo sapiens	Y22499	928
930 AJ224326 Homo sapiens ribulose-5-phosphate- 912 epimerase	100	912		Homo sapiens	AJ224326	930
931 U28991 Caenorhabdit coded for by C. elegans cDNA 660	55	660 .		Caenorhabdit	U28991	931

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
		is elegans	cm21c7	JCORE	
932	AL080065	Homo sapiens		210	25
933	G01884	Homo sapiens	Human secreted protein, SEQ ID NO: 5965.	767	98
934	AJ276485	Homo sapiens	protein	1200	100
935	AL035681	Homo sapiens	dJ756G23.3 (novel protein similar to drosophila transcriptional repressor)	1142	80
936	AB026808	Mus musculus	synaptotagmin XI	2142	95
937	AB015345	Homo sapiens	HRIHFB2216	2601	99
938	X65724	Homo sapiens	ORF2	498	100
939	W89024	Homo sapiens	Polypeptide fragment encoded by gene 156.	1487	100
940	G04047	Homo sapiens	Human secreted protein, SEQ ID NO: 8128.	117	100
941	AF094583	Homo sapiens	putative HIV-1 infection related protein	452	100
942	AC024200	Caenorhabdit is elegans	contains similarity to several zinc finger proteins but not to the zinc finger domains	350	69
943	AF129756	Homo sapiens	G5c	273	1
944	M23765	Rattus norvegicus	alpha-tropomyosin	133	96
945	AC009917	Arabidopsis thaliana	Contains similarity to	583	47
946	AF223468	Homo sapiens	AD021 protein	551	44
947	AF055473	Homo sapiens	GAGE-8	273	51
948	X75756	Homo sapiens	protein kinase C mu	2019	68
949	AF143956	Mus musculus	coronin-2	2300	93
950	¥36729	Homo sapiens	Human PG1 protein sequence.	1861	99
951	W49041	Homo sapiens	Human low density lipoprotein binding protein LBP-2.	282	67
952	AB016881	Arabidopsis thaliana	gene_id:MXC17.7~	203	46
953	Y01785	Homo sapiens	Human ubiquitin-conjugating enzyme >Y25341 Y25341 01-JUL- 1999 12-AUG-1998 Human NCE-2 protein.	365	100
954	AF145615	Drosophila melanogaster	BcDNA.GH03377	823	46
955	U09410	Homo sapiens	zinc finger protein ZNF131	2483	99
956	U09410	Homo sapiens	zinc finger protein ZNF131	1853	99
957	AF195623	Homo sapiens	cholinephosphotransferase 1 alpha	2126	99
958	X94917	Drosophila melanogaster	head-elevated expression in 0.9 kb	155	32
959	U54807	Rattus norvegicus	GTP-binding protein	1167	97
960	AF058807	Bos taurus	GTP-binding protein rah	606	97
961	G03244	Homo sapiens	Human secreted protein, SEQ ID NO: 7325.	471	100
	AF078850	Homo sapiens	steroid dehydrogenase homolog	583	40
	AP001754	Homo sapiens	transient receptor potential- related channel 7, a novel putative Ca2+ channel protein	317	30
	AL035419	Homo sapiens	dJ1100H13.1 (putative novel protein)	1129	100
	X61381	Rattus rattus	interferon-induced protein	202	46
	D38169	Homo sapiens	inositol 1,4,5-trisphosphate 3-kinase isoenzyme	3278	100
967	AL031432	Homo sapiens	dJ465N24.2.1 (PUTATIVE novel protein) (isoform 1)	893	100

SEO	ACCESSION	SPECIES	DESCRIPTION	Charmy	
ID NO:	NUMBER		DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
968	U79275	Homo sapiens	unknown	611	100
969	AJ011306	Homo sapiens	guanine nucleotide exchange factor (long isoform)	2752	99
970	AF281134	Homo sapiens	exosome component Rrp46	1186	100
971	U53336	Caenorhabdit is elegans	weak similarity over a short region to myosin heavy chain	536	23
972	AC018749	Leishmania major	L8840.12	589	53
973	AP188504	Mus musculus	LNV	544	85
974	U25801	Homo sapiens	Taxl binding protein	852	98
975	AF049523	Homo sapiens	huntingtin-interacting protein HYPA/FBP11	1390	97
976	AF161530	Homo sapiens	HSPC182	1040	100
977	G04020	Homo sapiens	Human secreted protein, SEQ	626	100
978	AF164797	Homo sapiens	ribosomal protein L17 isolog	908	100
979	U94991	Xenopus laevis	transcription factor XLMO1	795	97
980	S73775	Homo sapiens	calmitine; calsequestrine	2029	100
981	Y94888	Homo sapiens	Human protein clone HP01462.	2501	100
982	AJ243191	Homo sapiens	heat shock protein	827	96
983	X65020	Bos taurus	PSST subunit of the NADH:	964	85
			ubiquinone oxidoreductase complex		
984	AJ249207	Rhodococcus sp. AD45	putative racemase	351	43
985	Z30093	Homo sapiens	basic transcription factor 2,	1576	99
986	AB030835	Homo sapiens	contains two glutamine rich domains, three zinc-finger domains, and matrin 3 homologous domain 3 (MH3)	4697	99
987	AF227258	Bos taurus	RPGR-interacting protein-1	1262	38
988	AL022238	Homo sapiens	dJ1042K10.2 (supported by GENSCAN, FGENES and GENEWISE)	4048	99
989	AL022238	Homo sapiens	dJ1042K10.2 (supported by GENSCAN, FGENES and GENEWISE)	2321	99
990	AF161426	Homo sapiens	HSPC308	448	92
991	AF161426	Homo sapiens	HSPC308	448	92
992	AF161426	Homo sapiens	HSPC308	453	92
993	AL023859	Schizosaccha romyces pombe	trna-splicing endonuclease subunit	172	42
994	AL049631	Homo sapiens	dJ513M9.1 (novel Homeobox domain protein)	241	47
995	AC005253	Homo sapiens	R26445_1	902	100
996	AF265206	Homo sapiens	MOG1 isoform A .	974	100
997	AJ248285	Pyrococcus abyssi	sarcosine oxidase, subunit beta (soxB)	195	28
998	AE003641	Drosophila melanogaster	BG:DS00941.3 gene product	218	58
999	W69343	Homo sapiens	Secreted protein of clone CR930 1.	1340	98
1000	AY007135	Homo sapiens	similar to bovine ADP/ATP translocase T1 mRNA with GenBank Accession Number M24102.1	1543	100
1001	Y73381	Homo sapiens	HTRM clone 1877278 protein sequence.	1668	100
1002	AF208844	Homo sapiens	BM-002	428	100
1003	AE004944	Pseudomonas aeruginosa	hypothetical protein	134	35
1004	AL031431	Homo sapiens	dJ462023.2 (novel protein)	2058	100
1005	S45367	Canis	centractin	1949	100
		familiaris			

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	T
NO:	NUMBER			WATERMAN SCORE	IDENTITY
1006	S45367 	Canis familiaris	centractin	1315	98
1007	AB022158	Mus musculus	chaperonin containing TCP-1 epsilon subunit	2649	96
1008	Y76332	Homo sapiens	protein encoded by gene 38.	1282	97
1009	AB011414	Homo sapiens	protein	1671	58
1010	Z68218	Caenorhabdit is elegans	K01H12.1	269	67
1011	AB011414	Homo sapiens	Kruppel-type zinc finger protein	1671	58
1012	Z14000	Homo sapiens	RING1	2017	100
1013	G02841	Homo sapiens	Human secreted protein, SEQ ID NO: 6922.	332	93
1014	AF145659	Drosophila melanogaster	BcDNA.GH10333	1244	52
1015	Y02860	Homo sapiens	Fragment of human secreted protein encoded by gene 65.	664	67
1016	Y02591	Homo sapiens	A human progesterone receptor complex p23-like protein.	772	97
1017	Y99448	Homo sapiens	Human PRO1759 (UNQ832) amino acid sequence SEQ ID NO:374.	2323	100
1018	X67250	Rattus norvegicus	n-chimaerin	1710	97
1019	AF183417	Homo sapiens	microtubule-associated proteins 1A/1B light chain 3	631	100
1020	AF164795	Homo sapiens	sex-regulated protein janus-a	674	100
1021	AF190625	Coturnix	qdg1-1	638	96
1022	AL133363	Arabidopsis thaliana	putative protein	155	37
1023	AB034912	Homo sapiens	WD-repeat like sequence	2483	100
1024	AY007091	Homo sapiens	similar to Homo sapiens mammalian inositol hexakisphosphate kinase 2 (IP6K2) mRNA with Ge	2243	100
1025	X69910	Homo sapiens	P63 protein	2958	99
1026	U80736	Homo sapiens	CAGF9	1657	100
1027	AB029333	Halocynthia roretzi	HrPET-1	1048	54
1028	AB032931	Homo sapiens	ubiquitin-conjugating enzyme isolog	1045	100
1029	G01797	Homo sapiens	Human secreted protein, SEQ ID NO: 5878.	749	98
1030	G01797	Homo sapiens	Human secreted protein, SEQ ID NO: 5878.	749	98 .
1031	AF193795	Homo sapiens	Vacuolar sorting protein VPS29/PEP11	960	100
1032	AJ222968	Mus musculus	L-periaxin	120	30
1033	281317	Schizosaccha romyces pombe	DNA2-NAM7 helicase family protein	685	31
1034	¥41519	Homo sapiens	Fragment of human secreted protein encoded by gene 75.	1321	99
1035	AJ276004	Mus musculus	Paxneb protein	1709	77
1036	AF025459	Caenorhabdit is elegans	H14A12.3 gene product	190	30
1037	Ŭ37251	Homo sapiens	Description: KRAB zinc finger protein; this is a splicing supplied by author	196	43
1038	W74580	Homo sapiens	Human membrane protein BA0306.	1921	97
1039	U88173	Caenorhabdit is elegans	weak similarity to Arabidopsis thaliana ubiquitin-like protein 8	331	80

TABLE 2

SEQ ACCESSION SPECIES DESCRIPTION NO: 1040 AF290204 Homo sapiens blood group carrier medical pooks 1041 Y96730 Homo PRO539, a Costal-2 homo sapiens 1042 AF140683 Mus musculus F-box protein FWD2 1043 AF151023 Homo sapiens HSPC189 1044 AF181631 Drosophila BcDNA.GH04929 melanogaster 1045 Y77985 Homo sapiens Human collectin amino sequence.	2397 1104 204 Dacid 1940	99 22 98 100
DOK1	2397 1104 204 Dacid 1940	98 100
sapiens 1042 AF140683 Mus musculus F-box protein FWD2 1043 AF151023 Homo sapiens HSPC189 1044 AF181631 Drosophila BcDNA.GH04929 melanogaster 1045 Y77985 Homo sapiens Human collectin amino sequence.	2397 1104 204 Dacid 1940	98
1043 AF151023 Homo sapiens HSPC189 1044 AF181631 Drosophila BcDNA.GH04929 melanogaster 1045 Y77985 Homo sapiens Human collectin amino sequence.	1104 204 pacid 1940	100
1044 AF181631 Drosophila BcDNA.GH04929 melanogaster 1045 Y77985 Homo sapiens Human collectin amino sequence.	204 p acid 1940	
melanogaster 1045 Y77985 Homo sapiens Human collectin amino sequence.	acid 1940	
sequence.		37
		100
1046 AJ243972 Homo sapiens 6-phosphogluconolactor		100
1047 AB035863 Homo sapiens ATP specific succinyl synthetase beta subuni precursor	iit	99
1048 AL034550 Homo sapiens dJ1184F4.2 (novel prosimilar to nucleolar part (NOLA) (NOLP))	protein	92
1049 AF163825 Homo sapiens pre-B lymphocyte prote		100
1050 AF201949 Homo sapiens 60S ribosomal protein isolog		100
1051 AF190624 Mus musculus mdgl-1	236	85
1052 AE003529 Drosophila CG6151 gene product melanogaster	160	44
1053 G01191 Homo sapiens Human secreted protein ID NO: 5272.		98 -
1054 AL162756 Neisseria Glu-tRNA(Gln) meningitidis amidotransferase subur		44
1055 AF191856 Rattus tRNA selenocysteine norvegicus associated protein	1525	99
s light chain reinhardtii		34
1057 AF159141 Homo sapiens breast cancer metasta: suppressor 1	1	53
1058 AF230929 Homo keratinocyte annexin- sapiens protein pemphaxin		99
1059 AJ270952 Homo sapiens putative membrane pro	i_	100
1050 AF224263 Heterodontus HoxD8 francisci	742	83
1061 X63417 Homo sapiens IRLB	1037	100
1062 AL079345 Streptomyces hypothetical protein coelicolor A3(2)	143	27
1063 Y71112 Homo sapiens Human Hydrolase prote: (HYDRL-10).	in-10 2547	100
1064 AF263614 Homo sapiens acetyl-CoA synthetase		99
1065 Y13356 Homo sapiens Amino acid sequence of protein PRO221.	İ	100
1066 AC006153 Homo sapiens similar to Aquifex aed GTP-binding protein; to AE000771 (PID:g2984	similar	98
1067 Y18930 Sulfolobus hypothetical protein solfataricus	162	29
1068 R65969 Homo Glioblastoma-derived sapiens T98G polypeptide.	887	100
1069 Y07964 Homo sapiens Human secreted protein fragment	1	96
1070 AF177476 Rattus CDK5 activator-binding norvegicus protein	g 1995	86
1071 AF245505 Homo sapiens adlican	3109	99
1072 U92794 Mus musculus alpha glucosidase II, subunit	•	36
1073 G03889 Homo sapiens Human secreted protein ID NO: 7970.	n, SEQ 698	98
1074 U15779 Homo sapiens p70	380	28
1075 Y13392 Homo sapiens Amino acid sequence of	f 1271	91

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	<u> </u>
ID	NUMBER			WATERMAN	IDENTITY
NO:	1	1		SCORE	IDENTITI
			protein PRO328.		-
1076	AF161457	Homo sapiens		571	100
1077	¥79509	Homo sapiens	Human carbohydrate-associated	2151	98
		<u> </u>	protein CRBAP-5.	1	
1078	AF223466	Homo sapiens		831	66
1079	AL132965	Arabidopsis	putative WD-40 repeat-protein	286	29
	-	thaliana			•
1080	AB024937	Homo sapiens	LUNX	1284	100
1081	Y14768	Homo sapiens	V-ATPase G-subunit like	579	100
1082	AF016416	000000000000000000000000000000000000000	protein		<u>1 </u>
1052	Ar 016416	Caenorhabdit is elegans	F29A7.4 gene product	141	31
1083	L13291	Homo sapiens	ADP-ribosylarginine hydrolase	-	
1084	AB041541	Mus musculus	unnamed protein product	802	45
1085	G01922	Homo sapiens	Human secreted protein, SEO	151	44
	001322		ID NO: 6003.	202	97
1086	AB030814	Homo sapiens	H-REV107 protein homolog	833	100
1087	AF151638	Homo sapiens	phosphatidylcholine transfer	1142	
		Suprems	protein	1146	100
1088	Y84432	Homo sapiens	Amino acid sequence of a	2783	100
			human RNA-associated	2703	100
		1	protein.	1	Ì
1089	Y94867	Ното	Human protein clone HP10563.	613	100
		sapiens	}		
1090	AK023982	Homo sapiens	unnamed protein product	130	49
1091	AB041586	Mus musculus	unnamed protein product	1103	81
1092	¥71277	Homo sapiens	Human Zlipo3 protein.	606	100 -
1093	U34973	Mus musculus	protein tyrosine phosphatase-	1131	95
1094	Y66677		like		
1094	1000//	Homo sapiens	Membrane-bound protein	522	56
1095	Y87276	Homo sapiens	PRO828. Human signal peptide		
	10,2,0	nomo saprens	containing protein HSPP-53	1029	99
			SEQ ID NO:53.		
1096	Y87276	Homo sapiens	Human signal peptide	863	98
		_	containing protein HSPP-53	1 005	30
			SEQ ID NO:53.	1	İ
1097	AF161455	Homo sapiens	HSPC337	742	98
1098	U80029	Caenorhabdit	similar to thioredoxin	242	39
		is elegans		}	,
1099	AJ005866	Homo sapiens	Sqv-7-like protein	1321	99
1100	AJ005865	Homo sapiens	Sqv-7-like protein	1118	99
1101	AJ005866 AJ005866	Homo sapiens	Sqv-7-like protein	891	99
1102	AL110244	Homo sapiens	Sqv-7-like protein	1016	99
1103	AL110244 AF242194	Homo sapiens	hypothetical protein	299	31
1104	AF 242194	Drosophila	brakeless-B	147	52
1105	AL031010	melanogaster			
1103	ALOSTOTO	Homo sapiens	dJ422F24.1 (PUTATIVE novel	968	100
			protein similar to C. elegans C02C2.5)		
1106	U28016	Mus musculus	parathion hydrolase	3634	
]	abourub	(phosphotriesterase) - related	1624	. 87
			protein		
1107	AJ278150	Homo sapiens	putative lipid kinase	2207	99
1108	G03733	Homo sapiens	Human secreted protein, SEQ	495	98
	}	•	ID NO: 7814.	177	
1109	AF217287	Drosophila	G protein RhoBTB	834	54
		melanogaster			_ -
1110	Y28921	Homo	Human regulatory protein	941	48
		sapiens	HRGP-7.	=	-
1111	Y28921	Homo	Human regulatory protein	1331	51
الحجين		sapiens	HRGP-7.	1	ļ
1112	AF176704	Homo sapiens	F-box protein FBX9	2027	99
1113	AF182076	Ното	glioma tumor suppressor	2418	100
1114	C04030	sapiens	candidate region protein 2		
	G04039	Homo sapiens	Human secreted protein, SEQ	475	96

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	<u> </u>
ID	NUMBER			WATERMAN	IDENTITY
NO:	ļ			SCORE	
4446	3 7000400		ID NO: 8120.		
1115	AF229439 L40357	Mus musculus	zinc finger protein 289	1697	91
1117	L40357	Homo sapiens	thyroid receptor interactor	509	100
1118	A12155	Homo sapiens	thyroid receptor interactor	404	85
1118	AL161542	Homo sapiens Arabidopsis	Human X5L cDNA.	1673	100
		thaliana	isomerase like protein	607	53
1120	AL023754	Homo sapiens	dJ272L16.1 (Rat Ca2+/Calmodulin dependent Protein Kinase LIKE protein)	2341	98
1121	Y57901	Homo sapiens	Human transmembrane protein HTMPN-25.	321	36
1122	Z14122	Xenopus laevis	XPGP5	455	77
1123	AF225418	Homo sapiens	lipase	1531	97
1124	Y06518	Homo sapiens	Zen GTPase interacting protein ZIP.	3227	100
1125	AL035690	Homo sapiens	dJ202I21.1 (novel protein)	952	100
1126	AJ000217	Homo sapiens	CLIC2	1286	99
1127	AB030505	Mus musculus	UBE-1c2	1069	79
1128	¥73375	Homo sapiens	HTRM clone 1427838 protein sequence.	874	100
1129	Y78941	Homo sapiens	Cyclophilin-type peptidyl prolyl cis/trans isomerase amino acid sequence.	877	100
1130	AL023553	Homo sapiens	dJ347H13.4 (novel protein)	557	100
1131	Y91945	Homo sapiens	Human chaperone protein 6 (HCHP-6).	1408	100
1132	Z68197	Schizosaccha romyces pombe	putative nuclear pore protein	596	39
1133	Z68197	Schizosaccha romyces pombe	putative nuclear pore protein	389	35
1134	AF180681	Homo sapiens	guanine nucleotide exchange factor	3597	100
1135	AF079765	Mus musculus	enhancer of polycomb	264	41
1136	M62419	Mus musculus	clathrin-associated protein	2189	99
1137	AJ006219	Drosophila melanogaster	clathrin-associated protein	1254	78
1138	Y76218	Homo sapiens	Human secreted protein encoded by gene 95.	440	98
1139	W88104	Homo sapiens	A Rab protein designated HRABS-2.	1065	99
1140	Y13401	Homo sapiens	Amino acid sequence of protein PRO339.	3979	98
1141	W85026	Chimeric - Homo sapiens	Green fluorescent protein- Zap70 fusion product.	3309	100
1142	Y13402	Homo sapiens	Amino acid sequence of protein PRO310.	1694	99
1143	G03875	Homo sapiens	Human secreted protein, SEQ ID NO: 7956.	660	99
1144	Y12917	Homo sapiens	Amino acid sequence of a	750	98
1145	Y12917	Homo sapiens	human secreted peptide. Amino acid sequence of a	1096	100
1146	AL022157	Homo sapiens	human secreted peptide. SPIN (SPINDLIN HOMOLOG	1233	100
1147	AL022157	Homo sapiens	(PROTEIN DXF34)) SPIN (SPINDLIN HOMOLOG	1233	100
1148	G02548	Homo sapiens	(PROTEIN DXF34)) Human secreted protein, SEQ	370	99
1149	Y73338	Homo sapiens	ID NO: 6629. HTRM clone 2019742 protein	1492	100
1150	W74841	Homo sapiens	sequence. Human secreted protein	228	55
	1	1	encoded by gene 113 clone		L

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	
ID	NUMBER			WATERMAN	IDENTITY
NO:				SCORE	122001111
1151	75044203	-	HEAAR60.		
1151	AF044201	Rattus norvegicus	neural membrane protein 35; NMP35	1570	92
1152	AF156774	Homo	lysophosphatidic acid	1855	99
ļ		sapiens	acyltransferase-gammal	1033	33
1153	AL118501	Homo sapiens	dJ1191N16.1 (A novel protein	872	64
			(translation of the cDNA		
1154	AF131852	Vome comican	DKFZp566A0946, Em:AL050069)) Unknown		
1155	Y41705	Homo sapiens	Human PRO352 protein	473 1381	100
		sapiens	sequence.	1381	97
1156	G04036	Homo sapiens	Human secreted protein, SEQ	607	99
	<u> </u>		ID NO: B117.		
1157	AF112444	Lupinus	L-asparaginase	287	43
1158	AF151848	luteus Homo sapiens	CGI-90 protein		
1159	AJ272267	Homo sapiens	choline dehydrogenase	232 2449	32
1160	AB001773	Ciona	PEM-6	196	33
]	savignyi		1	, ,
1161	Y87330	Homo sapiens	Human signal peptide	746	83
	ľ		containing protein HSPP-107		1
1162	Y87330	Homo sapiens	SEQ ID NO:107. Human signal peptide		ļ
	10,330	nomo saprens	containing protein HSPP-107	746	83
			SEQ ID NO:107.		Ì
1163	AF113534	Homo sapiens	HP1-BP74 protein	2723	96
1164	AF232226	Danio rerio	Dedd1	191	41
1165	AL118501	Homo sapiens	dJ1191N16.1 (A novel protein	1051	71
	ŀ		(translation of the cDNA DKFZp566A0946, Em:AL050069))		
1166	AL118501	Homo sapiens	dJ1191N16.1 (A novel protein	945	75
		<u>"</u>	(translation of the cDNA		' '
			DKFZp566A0946, Em:AL050069))		
1167	AF187733 AB019435	Homo sapiens	syntaphilin	831	42
1169	AF064604	Homo sapiens	phospholipase KEO3 protein	951	55
1170	Y01164	Homo sapiens	Polypeptide fragment encoded	324	33 100
			by gene 6.	1 1 2 1	100
1171	L03188	Saccharomyce	putative	180	22
1172	AF113751	s cerevisiae			-
11/2	AF113/51	Mus musculus	nuclear pore membrane glycoprotein POM210	3941	81
1173	AJ245417	Homo sapiens	G5b protein	794	100
1174	AL022238	Homo sapiens	dJ1042K10.3 (novel protein)	1285	100
1175	U41278	Caenorhabdit	F33G12.3 gene product	332	28
1176	Marca	is elegans		<u> </u>	
11,0	M35617	Homo sapiens	T-cell receptor V-alpha-J- alpha region	284	83
1177	AC012680	Arabidopsis	putative protein phosphatase	209	37
		thaliana	2C; 55455-56414	""	٠, د
1178	G01345	Homo sapiens	Human secreted protein, SEQ	692	99
1179	AT 006767	Trans.	ID NO: 5426.	<u> </u>	
44/3	AL096767	Homo sapiens	dJ579N16.3 (novel protein	1342	100
			similar to worm, Arabidopsis and pine proteins)		I
1180	AF039716	Caenorhabdit	similar to ATP synthase B	496	55
		is elegans	chain		
1181	Y11710	Homo sapiens	collagen type XIV	1048	97
1182	X82240	Homo	T cell leukemia/lymphoma 1	617	100
1	į	sapiens] >R94974]	1
i	I	R94974 09-			
1		MAY-1996 27-			.
]	OCT-1994			
	Ì	Human TCL-1			į
		polypeptide.		<u> </u>	

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	\$ IDENTITY
NO:		[Homo		SCORE	IDENTITI
		sapiens			
1183	U42841	Caenorhabdit is elegans	short region of weak similarity to collagen	161	33
1185	AJ131613	Homo sapiens	dicarboxylate carrier protein	1470	99
1186	L27645	Danio rerio	growth-associated protein	130	36
1187	Y02738	Homo sapiens	Human secreted protein encoded by gene 89 clone HLHFP03.	636	100
1188	AF217544	Xenopus laevis	ornithine decarboxylase-2	1459	60
1189	AL136307	Homo sapiens	dJ380B8.2 (Neuritin, a protein which promotes neurite outgrowth)	182 .	33 .
1190	X89602	Homo sapiens	rTSbeta	197	100
1191	U32828	Haemophilus influenzae Rd	ribosomal protein S6 modification protein (rimK)	268	31
1192	AF154831	Rattus norvegicus	PV-1	1403	60
1193	Y50926	Homo sapiens	Human fetal brain cDNA clone vc16_1 derived protein.	918	100
1194	AF026530	Rattus norvegicus	stathmin-like-protein splice variant RB3''	1093	97
1195	U35244	Rattus norvegicus	vacuolar protein sorting homolog r-vps33a	2981	96
1196	¥70470	Homo sapiens	Human p53 target molecule, PRG3 protein.	1680	100
1197	AF157318	Homo sapiens	AD-017 protein	912	47
1198	AF125443	Caenorhabdit is elegans	contains similarity to S. pombe phosphatidyl synthase (GB:Z28295)	460	39
1199	AF201934	Homo sapiens	DC12	1649	88
1200	AL031775	Homo sapiens	dJ30M3.3 (novel protein similar to C. elegans Y63D3A.4)	1902	100
1201	M21103	Ovis aries	BIIIB4 high-sulfur keratin	484	82
1202	285986	Homo sapiens	dJ108K11.3 (similar to yeast suppressor protein SRP40)	1143	75
1203	U18762	Rattus norvegicus	retinol dehydrogenase type I	890	52
1204	U35730	Mus musculus	jerky	2235	76
1205	AB002327	Homo sapiens	KIAA0329	151	24
1206	AB019233	Arabidopsis thaliana	ubiquinone/menaquinone biosynthesis methyltransferase-like	762	56
1207	AL136307	Homo sapiens	dJ380B8.2 (Neuritin, a protein which promotes neurite outgrowth)	742	100
1208	AF207989	Homo sapiens	orphan G-protein coupled receptor	2326	100
1209	Z97630	Homo sapiens	dJ466N1.4 (novel protein similar to ANK3 (ankyrin 3, node of Ranvier (ankyrin G)))	181	44
1210	U21549	Mus musculus	Ac39/physophilin	1280	68
1211	¥27700	Homo sapiens	Human secreted protein encoded by gene No. 12.	1267	100
1212	AF117814	Mus musculus	odd-skipped related 1 protein	945	66
1213	AF277233	Naegleria fowleri	calcineurin B	222	39
1214	D14849	Mus musculus	meiosis-specific nuclear structural protein 1	1950	77
1215	G03022	Homo sapiens	Human secreted protein, SEQ ID NO: 7103.	590	100
1216	Z72510	Caenorhabdit	similarity to yeast UTR3	634	49

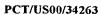
SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
		is elegans	protein (Swiss Prot accession yk677h11.5 comes from this gene		
1217	Z49703	Saccharomyce s cerevisiae	unknown	134	22
1218	AC013430	Arabidopsis thaliana	F3F9.18	199	29
1219	L10910	Homo sapiens	splicing factor	1026	71
1220	270750	Caenorhabdit	similar to vanadate	965	58
		is elegans	resistance protein transmembranous comes from this gene	765	56
1221	AL163815	Arabidopsis thaliana	putative protein	653	61
1222	AF155100	Homo sapiens	zinc finger protein NY-REN-21 antigen	2261	100
1223	J05071	Bos taurus	GTP-binding regulatory protein gamma-6 subunit	356	100
1224	Y73364	Homo sapiens	HTRM clone 2765991 protein sequence.	1169	99
1225	AL050170	Homo sapiens	hypothetical protein	714	100
1226	X64002	Homo sapiens	RAP74	2661	99
1227	X04085	Homo sapiens	catalase	2846	100
1228	AJ005620	Mus musculus	skeletal muscle-specific gene	1416	90
1229	AF045564	Rattus norvegicus	development-related protein	1715	93
1230	X97571	Mus musculus	HCMV-interacting protein	479	96
1231	L08239	Homo sapiens	located at OATL1	2274	100
1232	AF121863 AF121863	Homo sapiens	sorting nexin 14	1964	100
1233	AC024805	Homo sapiens	sorting nexin 14	1203	84
_		Caenorhabdit is elegans	contains similarity to TR:004595	744	31
1235	AC006634	Caenorhabdit is elegans	contains similarity to Saccharomyces cerevisiae probable membrane protein YLR418c (GB:U20162)	357	33
1236	Y18101	Mus musculus	macrophage actin-associated- tyrosine-phosphorylated protein	1559	87
1237	AB042646	Homo sapiens	TGIF2	1224	100
1238	AB026264	Homo sapiens	IMPACT	1694	100
1239	AB026264	Homo sapiens	IMPACT	1123	100
1240	G00429	Homo sapiens	Human secreted protein, SEQ ID NO: 4510.	324	100
1241	Y76144	Homo sapiens	Human secreted protein encoded by gene 21.	1363	53
1242	AL035602	Arabidopsis thaliana	putative protein	499	28
1243	X76483	Gallus gallus	Yes-associated protein (65kDa)	574	48
1244	AF220186	Homo sapiens	uncharacterized hypothalamus protein HT012	503	100
1245	AL021453	Homo sapiens	dJ821D11.3 (PUTATIVE protein)	856	100
1246	AJ276003	Homo sapiens	GAR1 protein	1216	100
1247	Y57910	Homo sapiens	Human transmembrane protein HTMPN-34.	1369	98
1248	AC004874	Homo sapiens	similar to N- acetylgalactosaminyltransfera se; similar to Q07537 (PID:g1171989)	957	100
1249	AF199597	Homo sapiens	A-type potassium channel modulatory protein 1	1139	100
1250	Y13148	Rattus norvegicus	PAG608	1350	88
1251	M24852	Rattus norvegicus	neuron-specific protein PEP-	124	46

SEQ	ACCESSION	SPECIES	DESCRIPTION	T over	
ID	NUMBER		DESCRIPTION	SMITH- WATERMAN	IDENTITY
NO:	AF146738	_		SCORE	122
	AF146/38	Rattus norvegicus	testis specific protein	771	83
1253	G02725	Homo sapiens	Human secreted protein, SEQ	419	97
1254	W44375	1,,	ID NO: 6806.		1
1234	1144373	Homo sapiens	Human ubiquitin-conjugating enzyme polypeptide.	1045	99
1255	AC006538	Homo sapiens	BC41195 1	831	78
1256	AB004316	Bos taurus	mitochondrial methionyl-tRNA	1556	88
1257	Z35094		transformylase	1	1
1258	Y13362	Homo sapiens		1354	97
		nome suprems	protein PRO214.	2383	100
1259	AC006014	Homo sapiens	similar to RFP transforming	1299	100
1			protein; similar to P14373		
1260	AC005099	Homo sapiens	(PID:g132517) match to AI222572		
İ		_	(NID:g3804775)	469	100
1261	V00507	Homo sapiens	coding sequence of DHFR (1 is	984	100
1			1st base in codon) (561 is	ļ	
1262	X15443	Rattus sp.	3rd base in codon) gamma-glutamyltranspeptidase		
			(AA 1-568)	697	32
1263	AF173871	Mus musculus	neuronal PAS3	977	94
1264	AF178983 X70473	Homo sapiens	Ras-associated protein Rapi	433	97
1203	170473	Homo sapiens	Human cyclic nucleotide- associated protein-1 (CNAP-	2785	99
			1).		
1266	Y41738	Homo	Human PRO541 protein	1622	100
1267	AF061346	sapiens Mus musculus	sequence.		
1268	U97006	Caenorhabdit	Edpl protein Cl3F10.4 gene product	1077	64
		is elegans	CISTIO.4 Gene product	154	23
1269	AF233582	Mus musculus	GTPase Rabi7	942	95
1270	AF195951	Homo sapiens	signal recognition particle	3127	98
1271	AL031177	Homo sapiens	dJ889M15.3 (novel protein)		
1272	AF201933	Homo sapiens	DC11	1150	55 100
1273	AF201933	Homo sapiens	DC11	346	98
1274	AL021710	Arabidopsis	putative protein	348	49
1275	AC004449	thaliana Homo sapiens	R33683 3		
1276	Y86295	Homo sapiens	Human secreted protein	556 1920	100
			HL2AG87, SEQ ID NO:210.	1920	100
1277	Y71111	Homo sapiens	Human Hydrolase protein-9	1576	99
1278	S94421	Homo sapiens	(HYDRL-9). T cell receptor eta-exon		
1279	Y66695	Homo	Membrane-bound protein	478 1909	100
		sapiens	PRO1344.	1909	100
1280 1281	AF161380	Homo sapiens	HSPC262	772	100
1201	Y48610	Homo sapiens	Human breast tumour-	779	100
1282	AC015446	Arabidopsis	associated protein 71. Similar to AIG1 protein	405	
		thaliana	processing and proces	408	35
1283	AK024432	Homo sapiens	FLJ00022 protein	403	35
1204	W96153	Homo sapiens	Human FADD-interacting	1825	81
1285	AJ001019	Homo sapiens	protein (FIP). ring finger protein	1202	
1286	AE003823	Drosophila	CG13178 gene product	1301	29
1205	250	melanogaster	•		23
1287	AF178632	Homo sapiens	FEM-1-like death receptor	3261	100
1288	AC006033	Homo	binding protein similar to MLN 64; similar to		
		sapiens	138027 (PID:g2135214)	1195	100
1289	AC006033	Homo	similar to MLN 64; similar to	668	93
1290	AB023811	Homo sapiens	I38027 (PID:g2135214)		
		nomo sapiens	TU3A	351	54

NO:	NUMBER		DESCRIPTION	SMITH- WATERMAN	\$ IDENTITY
1291	Z73424	Caenorhabdit	C44B9.1	SCORE 235	36
1292	Y94871	is elegans	Human protein clone HP02551.	1222	100
1293	AF180425	Homo sapiens	abbotiaced	489	29
1294	G03856	Homo sapiens	protein RAP140 Human secreted protein, SEQ ID NO: 7937.	538	99
1295	AF133670	Mus musculus		367	
1296	AJ249735	Homo sapiens	claudin-6	1142	100
1297	X57560	Escherichia coli	pspE protein	535	100
1298	AF169284	Homo sapiens	protein 1	1997	100
1299	U41023	Caenorhabdit is elegans	yk61f1.3; coded for by C. yk109h8.5	324	29
1300	AB024523	Homo sapiens		1206	100
1301	X55989	Homo sapiens	eosinophil cationic-related protein	737	99
1302	AF007151	Homo sapiens	unknown	1481	100
1304	X52904 U19577	Escherichia coli	open reading frame (AA 1-65)	359	100
1305	AF266508	Escherichia coli	galactonate dehydratase	242	93
1305	Y57901	Mus musculus	, was process	1409	97
1307	U58750	Homo sapiens Caenorhabdit	HTMPN-25.	932	100 -
1308	AF044774	is elegans Homo sapiens	similar to the mitochondrial carrier family	365	54
1309	AL078593		breakpoint cluster region protein 2	2681	99
1310	X82693	Homo sapiens	dJ210B1.1 (KIAA0680)	267	34
1311	282263	Caenorhabdit	E48 antigen C47A4.1	620	96
1312	AF131218	is elegans Homo sapiens	chromosome 16 open reading	283	35
1313	Y41763	Homo	frame 5 Human PRO938 protein	1493	100
1314	AF196972	sapiens	sequence.	1636	100
	AF053356	Homo sapiens	JM24 protein	2239	100
1316	Y66695	Homo	insulin receptor substrate like protein	228	97
1317	AF153127	sapiens Gallus	Membrane-bound protein PR01344.	1909	100
	AF153127	gallus Gallus	SAPK interacting protein	2442	89
	AF153127	gallus Gallus	SAPK interacting protein	1477	83
	X56932	gallus	SAPK interacting protein	1651	86
	AF174605	Homo sapiens	23 kD highly basic protein	1044	100
	AP174605	NOMO Sapiens] >Y83086 Y83086 09- MAR-2000 28- AUG-1998 F- box protein FBP-18. [Homo sapiens	F-box protein Fbx25	467	70
	M61732	Trypanosoma cruzi	neuraminidase	214	24
1323	Y17013	porcine endogenous	pol	304	64

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	1 8
ID	NUMBER	SFECIES	DESCRIPTION	WATERMAN	IDENTITY
NO:	I I I I I I I I I I I I I I I I I I I			SCORE	IDENTITI
		retrovirus		000.00	
1324	AL138655	Arabidopsis	putative protein	1174	37
		thaliana	Passassas Passassas		- '
1325	AL138655	Arabidopsis	putative protein	946	35
		thaliana			
1326	AL133215	Homo sapiens	bA108L7.2 (novel protein	1322	99 3
		_	similar to rat tricarboxylate		
			carrier)		
1327	AF161541	Homo sapiens	HSPC056	1357	99
1328	Y73346	Homo sapiens	HTRM clone 619699 protein	785	96
		İ	sequence.		İ
1329	L10910	Homo sapiens	splicing factor	912	82
1330	AF146568	Homo sapiens	MIL1 protein	1936	100
1331	W87772	Homo sapiens	Human serum glucocorticoid-	232	39
			regulated kinase (H-SGK2)		
			polypeptide.		
1332	Y41741	Homo	Human PRO704 protein	1860	100
		sapiens	sequence.		
1333	AF295096	Homo sapiens	zinc-finger protein ZBRK1	411	91
1334	Z82271	Caenorhabdit	Similarity to Mouse kinensin-	578	44
		is elegans	like protein KIF4 comes from		
			this gene		
1335	AE000810	Methanobacte	conserved protein	290	43
		rium			
		thermoautotr			
		ophicum			
1336	Y68779	Homo sapiens	Amino acid sequence of a	1019	91
			human phosphorylation		
			effector PHSP-11.		
1337	AB027003	Mus musculus	protein phosphatase	378	84
1338	U64856	Caenorhabdit	weak similarity to TPR	215	40
1339	AE001394	is elegans	domains		
1339	AE001394	Plasmodium falciparum	protein of the YMR7 family	170	29
1340	X76717	Homo sapiens	MT-11 protein	204	-
1341	AC011914	Arabidopsis	putative mutT protein; 68398-	204	89
1341	ACULTALA	thaliana	67881	289	45
1342	AJ276171	Homo sapiens	ASPIC	2122	100
1343	AF187016	Homo sapiens	myosin regulatory light chain	2303	99
23.13	1 20,020	nome suprems	interacting protein MIR	2303	39
1344	AC006963	Homo sapiens	similar to Kelch proteins;	894	35
			similar to BAA77027	1001	
		ļ	(PID:q4650844)	1	
1345	AF257466	Homo sapiens	N-acetylneuraminic acid	1880	99
		_	phosphate synthase		
1346	Y25896	Homo sapiens	Human secreted protein	1148	100
		_	fragment encoded from gene		
	1		64.	1	1
1347	AJ272073	Torpedo	male sterility protein 2-like	1664	58
		marmorata	protein	1	1
1348	AF161548	Homo sapiens	HSPC063	1018	98
1349	W78128	Homo sapiens	Human secreted protein	1117	100
	1	_	encoded by gene 3 clone	;	1
	<u></u>	L	HOSBI96.	1	1
1351	G02144	Homo sapiens	Human secreted protein, SEQ	418	100
	L		ID NO: 6225.	1	1
1352	D90869	Escherichia	similar to	2047	100
		coli		1	1
1353	A12029	Homo sapiens	MRP-14	613	100
1353			R26660 1, partial CDS	870	74
1354	AC005328	Homo sapiens		1 0.0	
	AC005328 AC024876	Caenorhabdit	contains similarity to	829	61
1354	AC024876	Caenorhabdit is elegans			61
1354 1355 1356	AC024876 AF077226	Caenorhabdit is elegans Homo sapiens	contains similarity to		61
1354 1355 1356 1359	AC024876 AF077226 AF217188	Caenorhabdit is elegans	CONTAINS SIMILARITY TO SW:RPB1_CRIGR	829	
1354 1355 1356	AC024876 AF077226	Caenorhabdit is elegans Homo sapiens	contains similarity to SW:RPB1_CRIGR copine III	829 1876	64

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	- 8
ID NO:	NUMBER			WATERMAN	IDENTITY
NO:	 		element binding and beta	SCORE	
			transducin family proteins		ĺ
1362	Z48475	Homo sapiens	glucokinase regulator	3160	99
1363	248475	Homo sapiens	glucokinase regulator	2682	97
1364	AF195764	Homo sapiens	megakaryocyte-enhanced gene	2055	99 ,
			transcript 1 protein; MEGT1 protein		
1365	AF116609	Homo sapiens	PRO0915	581	100
1366	AF116609	Homo sapiens	PRO0915	581	100
1367	AL117352	Homo sapiens	dJ876B10.3 (novel protein	2581	99
			similar to C. elegans T19B10.6 (Tr:Q22557))		
1368	Y34124	Homo	Human potassium channel	1342	100
		sapiens	K+Hnov15.		100
1369	AJ245621	Homo sapiens	CTL2 protein	3728	99
1370	AF008220	Bacillus	YtaG	429	45
		subtilis			1
1371	X05562	Homo sapiens	alpha-2 chain precursor (AA - 25 to 1018) (3416 is 2nd base in codon)	5908	99
1372	Z98048	Homo sapiens	dJ408N23.4 (novel DnaJ domain	1296	99
		1.5	protein)	1230	99
1373	AF154415	Homo sapiens	FLASH	10253	100
1374	U20286	Rattus	lamina associated polypeptide	1567	69
		norvegicus	1C		
1375	U53445	Homo sapiens	DOCI	1645	46
1376	AL117337	Homo	bA393J16.1 (zinc finger	250	60
1377	AC005328	sapiens	protein 33a (KOX 31))		
1378	U35113	Homo sapiens	R26660_1, partial CDS	1126	100
1379	L15313	Caenorhabdit	metastasis-associated gene	1823	69
		is elegans	_	858	58
1380	Y25756	Homo sapiens	Human secreted protein encoded from gene 46.	1508	100
1381	AB037360	Homo sapiens	ANKHZN	5734	95
1382	AB037360	Homo sapiens	ANKHZN	959	97
1383 1384	AF237676	Mus musculus	G beta-like protein GBL	1721	96
1384	AF237676 Y58793	Mus musculus	G beta-like protein GBL	1043	70
1386		Homo sapiens	Human calcium regulatory protein CaREG-1.	715	100
1386	AF212162	Homo sapiens	ninein	10369	99
1388	AL031685 AC004890	Homo sapiens	dJ963K23.2 (novel protein)	337	33
1300	AC004890	Homo sapiens	similar to zinc finger proteins; similar to BAA24380 >W06316 W06316 03-OCT-1996 27-APR-1995 TRP-1 protein.	542	86
1389	AF187989	Homo sapiens	zinc finger protein ZNF223	2665	99
1390·	AC035150	Homo sapiens	Zinc finger protein ZNF221	3459	100
1391	AF287894	Homo sapiens	PIST	1410	97
1392	AF282265	Homo sapiens	inner centromere protein INCENP	1794	99
1393	X90840	Homo sapiens	axonal transporter of synaptic vesicles	4584	99
1394	AF076249	Homo sapiens	zinc finger protein SBBIZ1	3208	99
1395	G02224	Homo sapiens	Human secreted protein, SEQ ID NO: 6305.	299	75
1396	AC004809	Arabidopsis thaliana	Similar to	130	34
1398	AF242519	Homo sapiens	zinc finger protein SBZF3	181	65
1399	AL133396	Homo sapiens	dJ1068H6.4 (prion protein like protein doppel)	962	100
1400	Y48611	Homo sapiens	Human breast tumour- associated protein 72.	817	99
1401	AC004472	Homo sapiens	P1.11659 5	280	54
1402	X91489	Saccharomyce	putative HMG box	164	27
		s cerevisiae			



SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	
ID NO:	NUMBER		BESCRIFTION	WATERMAN SCORE	IDENTITY
1403	Y79222	Homo sapiens	Human transferase TRNSFS-14.	2842	100
1404	X81058	Mus musculus	tex261	1010	99
1405	AB012084	Mus musculus	ITM	194	29
1406	AB030251	Homo sapiens	GTPase activating protein	3233	99
1407	AJ010585	Rattus	PTB-like protein	2684	99
1408	X75760	Drosophila melanogaster	LRR47	364	29
1409	U76618	Mus musculus	N-RAP	804	48
1410	AC005578	Homo sapiens	P20887 1, partial CDS	835	63
1411	AE000284	Escherichia coli	orf, hypothetical protein.	360	100
1412	X01563	Escherichia coli	L5 (rplE) (aa 1-179)	911	100
1413	W78279	Homo sapiens	Pragment of human secreted protein encoded by gene 33.	1264	99
1414	AB031051	Homo sapiens	Organic anion transporter	3832	100
1415	M17466	Homo sapiens	coagulation factor XII	3455	100
1416	AF097994	Homo sapiens	L-kynurenine/alpha- aminoadipate aminotransferase	2202	99
1417	AF151077	Homo sapiens	HSPC243	1262	99
1418	Y09945	Rattus norvegicus	putative integral membrane transport protein	1098	61
1419	U13152	Mesocricetus auratus	guanine nucleotide-binding protein beta 5	2179	76
1420	AL162458	Homo sapiens	bA465L10.5 (KIAA1176 (novel	5696	100
			protein, presumed ortholog of mouse K-Cl cotransporter KCC2))		
1421	Y99426	Homo sapiens	Human PRO1604 (UNQ785) amino acid sequence SEQ ID NO:308.	152	29
1422	Y94923	Homo sapiens	Human secreted protein clone qs14_3 protein sequence SEQ ID NO:52.	4039	99
1423	AF177388	Homo sapiens	cancer-amplified transcriptional coactivator ASC-2	10748	99
1424	Y48517	Homo sapiens	Human breast tumour- associated protein 62.	1851	99
1425	AF208848	Homo sapiens	BM-006	1454	89
1426	AF208848	Homo sapiens	BM-006	853	79
1427	AF112886	Bos taurus	differentiation enhancing factor 1	4693	95
1428	U41387	Homo sapiens	Gu protein	1372	63
1429	AF161534	Homo sapiens		2853	78
1430	AF125043	Mus musculus	bisphosphate 3'-nucleotidase	275	30
1431	Y66718	Homo sapiens	Membrane-bound protein PRO1106.	1886	100
1432	AF193613	Homo sapiens	cell recognition molecule Caspr2	568	100
1433	AB044560	Mus musculus	Gliacolin	192	34
1434	R99900	Homo sapiens	NTII-1 nerve protein, facilitates regeneration of	707	51
1435	AF220530	Homo sapiens	myo-inositol 1-phosphate synthase Al	2904	100
1436	X70944	Homo sapiens	PTB-associated splicing factor	1261	72
1437	AF271732	Homo sapiens	bridging integrator-3	1202	100
1438	Y30811	Homo sapiens	Human secreted protein encoded from gene 1.	1282 595	98
1439	AJ293659	Homo sapiens	mucolipidin	628	97
1440	AF219138	Homo sapiens	GGA3 long isoform	3083	100
1441	AF219138	Homo sapiens	GGA3 long isoform	3346	
	<u></u>		Torid TROTOTIII	2240	100

NUMBER No. NUMBER No.	SEQ	ACCESSION	SPECIES	DECOR TRATON		
No. No.	_		SPECIES	DESCRIPTION	SMITH-	8
1442 AB039669 Homo sapiens ALEXX 1944 100	1	None	İ			IDENTITY
1444		AB039669	Homo caniene	71.522		
Methods Meth					. [
1444	1	1 23//11	1 -	DIADIO,	191	27
1445 X73874 Homo Sapiens DisphoryLase Kinase 1539 38 38 38 38 38 38 38	1444	AJ011896	-1	No. 61 hoto nambai		
1446			_1		_1	_1
1447 AF003924 Homo sapiens NNC 2H01 2645 99						_{
1449	7440	WL 2141-4	Homo sapiens		3999	99
1448	1447	35003034		1		_
1449						99
1449 API55112 Homo sapiens N-REN-50 antigen 1184 89	1448	AF003136	1		2843	52
1450 Y95004	1440	37755110			_	J
1451 API07203 Homo sapiens ataxin 2-binding protein 688 57 1452 API07203 Homo sapiens ataxin 2-binding protein 456 78 1453 Z38011 Mus musculus DBR-NS 882 56 1454 X90568 Homo sapiens Frotein sequence and annotation available soon via LABBITEMBH-Heidelberg_DE 1455 AL035409 Homo sapiens dJ564Mil.3 (similar to sialyltranferase) 1456 D44480 Mus musculus MRH-12 protein 272 100 1456 AF141326 Homo sapiens RBA helicase HDB/D_CE1 478 45 1459 AF242552 Gallus retinovin 945 34 1460 U1036 Homo sapiens RBA helicase HDB/D_CE1 478 45 1461 ADS2528 Mus musculus granuphilin-a 545 39 1462 Y08134 Homo sapiens Ibd1 774 84 1461 ADS2528 Mus musculus granuphilin-a 545 39 1462 Y08134 Homo sapiens Monosapiens Miling/370977, R19699 (NID:g774333) 1464 AC004997 Homo sapiens match to ESTS Z43979 (NID:g774333) Match to ESTS Z43979 (NID:g774333) Match to ESTS Z43979 (NID:g774333) Match to ESTS Z43979 (NID:g774333) Match to ESTS Z43979 (NID:g774333) Match to ESTS Z43979 (NID:g774333) Match to ESTS Z43979 (NID:g774333) Match to ESTS Z43979 (NID:g774333) Match to ESTS Z43979 (NID:g774333) Match to ESTS Z43979 (NID:g774333) Match to ESTS Z43979 (NID:g774333) Match to ESTS Z43979 (NID:g73097), R19699 (NID:g774333) Match to ESTS Z43979 (NID:g73097), R19699 (NID:g774333) Match to ESTS Z43979 (NID:g774333) Match to ESTS Z43979 (NID:g774333) Match to ESTS Z43979 (NID:g774333) Match to ESTS Z43979 (NID:g774333) Match to ESTS Z43979 (NID:g774333) Match to ESTS Z43979 (NID:g774333) Match to ESTS Z43979 (NID:g774333) Match to ESTS Z43979 (NID:g774333) Match to ESTS Z43979 (NID:g774333) Match to ESTS Z43979 (NID:g774333) Match to ESTS Z43979 (NID:g774333) Match to ESTS Z43979 (NID:g774333) Match to ESTS Z43979 (NID:g774333) Match to Match to ESTS Z43979 (NID:g774333) Ma					(89
1451	1450	195004	Homo sapiens		985	100
1452 AF107203 Homo sapiens Stakin 2-binding protein 456 78 1453 Z38011 Mus musculus DMR-N9 882 56 1454 X99568 Homo sapiens Frotein sequence and annotation available soon via LABELTERMENL-Heidelberg_DE 1455 AL035409 Homo sapiens Silvanilar to sialyltranferase) 1456 D44480 Mus musculus Silvanilar to sialyltranferase) 1456 AF41326 Homo sapiens RNATH-2 protein 272 100 1458 AF141326 Homo sapiens RNATH-2 protein 272 100 1459 AF242525 Gallus gallus retinovin 945 34 1450 U11036 Homo sapiens Bodi 1724 84 1461 AR0325258 Mus musculus Syanuphilin-a 2428 99 1462 Y08134 Homo sapiens match to ESTS Z433979 869 98 1463 AC004997 Homo sapiens match to ESTS Z433979 869 98 1464 AC004997 Homo sapiens match to ESTS Z433979 869 98 1465 U32743 Haemophilus influenzae Rd Not56-like protein 2342 100 1466 Y09022 Homo sapiens Homolog of rat kidney-specific (KS) gene 1072 99 1468 AF071544 Spinacia Spina	1451	1220000				ļ
1453 Z38011				ataxin 2-binding protein	1	57
1454 X90568			<u> </u>			78
ALOUSTON Homo sapiens ALOUSTON ALOuston Alous				1	882	56
LABEITGEMBL-Heidelberg.DE	1454	X90568	Homo sapiens		510	28
1455				annotation available soon via		
1456 D44480 Mus musculus MATH-2 protein 272 100 1458 AF141326 Homo sapiens RATH-2 protein 272 100 1459 AF242552 Gallus gallus retinovin 945 34 1460 U11036 Homo sapiens Ibd1 724 86 1461 AB025258 Mus musculus granuphilin-a 545 39 1462 Y08134 Homo sapiens acid sphingomyelinase-like phosphodiesterase phosphodiesterase 1463 AC004997 Homo sapiens match to ESTS 243979 869 98 1464 AC004997 Homo sapiens match to ESTS 243979 (NID:9774333) 1465 U32743 Haemophilus influenzae Rd Rd Rd Rd Rd Rd Rd R				LABEIT@EMBL-Heidelberg.DE		
1456 D44480 Mus musculus MATH-2 protein 272 100 1459 AF141326 Homo sapiens RNA helicase HDE/DICE1 478 45 1459 AF242552 Gallus gallus retinovin 945 34 1460 Ul1036 Homo sapiens Ibdl 724 84 1461 AB025258 Mus musculus granuphilin-a 545 39 1462 Y08134 Homo sapiens acid sphingomyelinase-like 2428 99 1463 AC004997 Homo sapiens match to ESTS 243379 869 98 1464 AC004997 Homo sapiens match to ESTS 243379 869 98 1465 U32743 Haemophilus influenzae Rd Homo sapiens Mother of the first protein 2342 100 1466 Y09022 Homo sapiens Homolog of rat kidney- specific (KS) gene 1072 99 1467 AC003034 Homo sapiens Homolog of rat kidney- specific (KS) gene 1072 99 1468 AF071544 Spinacia carboxylase/oxygenase small subunit N-methyltransferase I 469 Y57930 Homo sapiens Homolog of rat kidney- specific (KS) gene 1072 99 1470 AF032666 Rattus rsec5 A504 93 1471 Y70467 Homo sapiens Human membrane protein 1053 100 1470 AF032666 Rattus rsec5 A504 93 1471 Y70467 Homo sapiens Human membrane channel protein-17 (MECHP-17). G221D2.1 (Ribosomal Large 1694 100 1	1455	AL035409	Homo sapiens		1356	100
1458 AF141326 Homo sapiens RNA helicase HDB/DCE1 478 45 1459 AF242552 Gallus retinovin 945 34 1460 U11036 Homo sapiens Ibd1 724 86 1461 AB025258 Mus musculus granuphilin-a 545 39 1462 Y08134 Homo sapiens acid sphingomyelinase-like 2428 99 1463 AC004997 Homo sapiens match to ESTS 243979 869 98 1464 AC004997 Homo sapiens match to ESTS 243979 869 98 1465 U32743 Haemophilus influenzae Rd Rd 1466 Y09022 Homo sapiens Mcmosapiens Homolog of rat kidney- 1072 99 1467 AC003034 Homo sapiens Homolog of rat kidney- 1072 99 1468 AF071544 Spinacia clerace carboxylase/oxygenase small carboxylase/oxygenase small carboxylase/oxygenase small HmMPN-54 Resconding to the more protein 1053 100 1470 AF032666 Rattus resc5 AE04 93 1471 Y70467 Homo sapiens Human membrane charnel protein-17 (MECHP-17) McCHP-17		1				1
1459 AF242552 Gallus retinovin 945 34 1460 Ul1036 Homo sapiens Ibdi 724 84 1461 AB025258 Mus musculus granuphilin-a 545 39 1462 Y08134 Homo sapiens acid sphingomyelinase-like 2428 99 1463 AC004997 Homo sapiens match to ESTS 24379 869 98 1464 AC004997 Homo sapiens match to ESTS 243979 869 98 1465 U32743 Haemophilus influenzae Rd Rd 1466 Y09022 Homo sapiens Not56-like protein 1072 99 1467 AC003034 Homo sapiens Not56-like protein 2342 100 1468 AF071544 Spinacia oleracea carboxylase/oxygenase small subunit N-methyltransferase 1470 AF032666 Rattus norvegicus Ruman transmembrane protein 1053 100 1470 AF032666 Rattus resc5 4504 93 1471 Y70467 Homo sapiens Ruman membrane Charnel AF07159 Homo sapiens Ruman membrane Ruman Ru			L		272	100
1460 Ulilo36 Homo sapiens Total Tota				RNA helicase HDB/DTCE1	478	45
1460	1459	AF242552		retinovin	945	34
1461 AB025258 Mus musculus granuphilin-a 545 39 1462 Y08134 Homo sapiens Racid sphingomyelinase-like 2428 99 1463 AC004997 Homo sapiens match to ESTs 243979 (NID:g573097), R19699 (NI						1
1462 Y08134 Homo sapiens Acid sphingomyelinase-like phosphodiesterase phos			Homo sapiens	Ibd1	724	84
1462 Y08134					545	39
Phosphodiesterase Phos	1462	Y08134	Homo sapiens	acid sphingomyelinase-like	2428	<u>L</u>
1464 AC004997 Homo sapiens match to ESTs Z43979 NID:g774333 match to ESTs Z43979 NID:g573097), R19699 NID:g573097, R19699 NID:g573097			<u></u>			
Note	1463	AC004997	Homo sapiens	match to ESTs Z43979	869	98
1464 AC004997 Homo sapiens				(NID:g573097), R19699		1
(NID:g573097), R19699			1	(NID:g774333)	1	
1465 U32743	1464	AC004997	Homo sapiens	match to ESTs 243979	869	98
1465 U32743				(NID:g573097), R19699		
1466 Y09022 Homo sapiens Not56-like protein 2342 100 1467 AC003034 Homo sapiens Homolog of rat kidney-specific (KS) gene 1072 99 1468 AF071544 Spinacia ribulose-1,5-bisphosphate oleracea carboxylase/oxygenase small subunit N-methyltransferase 1 1469 Y57930 Homo sapiens Human transmembrane protein HTMPN-54 Homo sapiens Human transmembrane protein 1053 100 1470 AF032666 Rattus resec5 4504 93 1471 Y70467 Homo sapiens Human membrane channel protein-17 (MECHP-17) 452 74 1472 AL031033 Homo sapiens C321D2.1 (Ribosomal Large 1694 100 Subunit Pseudouridine Synthase protein 137 4026 98 1474 S45936 Homo sapiens HTS1 1101 50 1475 Y86241 Homo sapiens Human secreted protein HoABR60, SEQ ID NO:156 1278 68 1476 AJ010317 Fugu Sand 1278 68 1477 U42831 Caenorhabdit coded for by C. elegans cDNA 248 44 1478 X62447 Homo sapiens FR 264 543 61						ļ
Rd	1465	U32743		fucose operon protein (fucU)	315	50
1466 Y09022						
1467 AC003034 Homo sapiens Homolog of rat kidney-specific (KS) gene 1072 99					1	
Specific (KS) gene				Not56-like protein	2342	100
1468	1467	AC003034	Homo sapiens		1072	99
Oleracea						
Subunit N-methyltransferase I	1468	AF071544		ribulose-1,5-bisphosphate	333	26
1469 Y57930 Homo sapiens Human transmembrane protein 100 1470 AF032666 Rattus norvegicus rsec5 4504 93 1471 Y70467 Homo sapiens Human membrane charnel protein-17 (MECHP-17). 452 74 1472 AL031033 Homo sapiens C321D2.1 (Ribosomal Large Subunit Pseudouridine Synthase protein) 1694 100 1473 AF177292 Homo sapiens HTS1 1101 50 1474 S45936 Homo sapiens HTS1 1101 50 1475 Y86241 Homo sapiens Human secreted protein HOABR60, SEQ ID NO:156. 1879 98 1476 AJ010317 Fugu rubripes Sand 1278 58 1477 U42831 Caenorhabdit is elegans coded for by C. elegans cDNA yk99b4.3; similar to human transforming protein (PIR:S22157) 846 44 1478 X62447 Homo sapiens PR 264 543 61		į	oleracea		ŀ	
HTMPN-54. HTMPN-54. HTMPN-54. HTMPN-54. HTMPN-54. HTMPN-54. HT			(
1470 AF032666 Rattus norvegicus rsec5 4504 93 1471 Y70467 Homo sapiens Human membrane charnel protein-17 (MECHP-17). 452 74 1472 AL031033 Homo sapiens C321D2.1 (Ribosomal Large Subunit Pseudouridine Synthase protein) 1694 100 1473 AF177292 Homo sapiens Genethonin 3 4026 98 1474 S45936 Homo sapiens HTS1 1101 50 1475 Y86241 Homo sapiens Human secreted protein HOABR60, SEQ ID NO:156. 1879 98 1476 AJ010317 Fugu rubripes Sand 1278 58 1477 U42831 Caenorhabdit is elegans coded for by C. elegans cDNA yk99b4.3; similar to human transforming protein (PIR:S22157) 846 44 1478 X62447 Homo sapiens PR 264 543 61	1469	Y57930	Homo sapiens		1053	100
1471 Y70467 Homo sapiens Human membrane channel protein-17 (MECHP-17). 1472 AL031033 Homo sapiens C321D2.1 (Ribosomal Large Subunit Pseudouridine Synthase protein) 1473 AF177292 Homo sapiens HTS1 1101 50 1474 S45936 Homo sapiens HTS1 1101 50 1475 Y86241 Homo sapiens Human secreted protein HOABR60, SEQ ID NO:156. 1476 AJ010317 Fugu rubripes Sand 1278 58 1477 U42831 Caenorhabdit coded for by C. elegans cDNA yk99b4.3; similar to human transforming protein (PIR:S22157) 1478 X62447 Homo sapiens PR 264 543 61 1478 S43 61				HTMPN-54.		
1471 Y70467 Homo sapiens Human membrane charnel Protein-17 (MECHP-17). 1472 AL031033 Homo sapiens C321D2.1 (Ribosomal Large Subunit Pseudouridine Synthase protein) 1473 AF177292 Homo sapiens Genethonin 3 4026 98 1474 S45936 Homo sapiens HTS1 1101 50 1475 Y86241 Homo sapiens Human secreted protein 1879 98 1476 AJ010317 Fugu Sand 1278 58 1477 U42831 Caenorhabdit coded for by C. elegans cDNA 1278 58 1478 X62447 Homo sapiens PR 264 543 61 1478 X62447 Homo sapiens PR 264 543 61 1478 1478 X62447 Homo sapiens PR 264 543 61 1478 1478 X62447 Homo sapiens PR 264 543 61 1478 1478 X62447 Homo sapiens PR 264 543 61 1478 1478 X62447 Homo sapiens PR 264 543 61 1478 1478 X62447 Homo sapiens PR 264 543 61 1478 X62447 Homo sapiens PR 264 1488	1470	AF032666		rsec5	4504	93
Protein-17 (MECHP-17). 1432 74 1472 AL031033 Homo sapiens C321D2.1 (Ribosomal Large Subunit Pseudouridine Synthase protein) Synthase protein Synthase protein 4026 98 1474 S45936 Homo sapiens HTS1 1101 50 1475 Y86241 Homo sapiens Human secreted protein HOABR60, SEQ ID NO:156. 1476 AJ010317 Fugu rubripes Sand 1278 58 1477 U42831 Caenorhabdit is elegans Coded for by C. elegans cDNA yk99b4.3; similar to human transforming protein (PIR:S22157) 1478 X62447 Homo sapiens PR 264 543 61 61 100		<u> </u>				ľ
Protein-17 (MECHP-17).	1471	Y70467	Homo sapiens	Human membrane charnel	452	74
1472 AL031033 Homo sapiens C321D2.1 (Ribosomal Large Subunit Pseudouridine Synthase protein) 1694 100 1473 AF177292 Homo sapiens genethonin 3 4026 98 1474 S45936 Homo sapiens HTS1 1101 50 1475 Y86241 Homo sapiens Human secreted protein HOABR60, SEQ ID NO:156. 1879 98 1476 AJ010317 Fugu rubripes Sand 1278 68 1477 U42831 Caenorhabdit is elegans yk99b4.3; similar to human transforming protein (PIR:S22157) 846 44 1478 X62447 Homo sapiens PR 264 543 61						
Subunit Pseudouridine Synthase protein Synthase protein Synthase protein Synthase protein Synthase protein Synthase protein 4026 98	1472	AL031033	Homo sapiens	C321D2.1 (Ribosomal Large	1694	100
Synthase protein]				
1473 AF177292 Homo sapiens genethonin 3 4026 98 1474 S45936 Homo sapiens HTS1 1101 50 1475 Y86241 Homo sapiens Human secreted protein HOABR60, SEQ ID NO:156. 1879 98 1476 AJ010317 Fugu rubripes Sand 1278 68 1477 U42831 Caenorhabdit is elegans yk99b4.3; similar to human transforming protein (PIR:S22157) 846 44 1478 X62447 Homo sapiens PR 264 543 61				Synthase protein)	1	
1474 \$45936 Homo sapiens HTS1 1101 50 1475 \$86241 Homo sapiens Human secreted protein HOABR60, SEQ ID NO:156. 1879 98 1476 AJ010317 Fugu rubripes Sand 1278 58 1477 U42831 Caenorhabdit is elegans coded for by C. elegans cDNA yk99b4.3; similar to human transforming protein (PIR:S22157) 846 44 1478 X62447 Homo sapiens PR 264 543 61			Homo sapiens		4026	98
1475 Y86241 Homo sapiens Human secreted protein HOABR60, SEQ ID NO:156. 1879 98 1476 AJ010317 Fugu rubripes Sand 1278 58 1477 U42831 Caenorhabdit is elegans yk99b4.3; similar to human transforming protein (PIR:S22157) 846 44 1478 X62447 Homo sapiens PR 264 543 61			Homo sapiens	HTS1		
HOABR60, SEQ ID NO:156.	1475	Y86241	Homo sapiens	Human secreted protein		
1476 AJ010317 Fugu rubripes Sand 1278 58 1477 U42831 Caenorhabdit coded for by C. elegans cDNA yk99b4.3; similar to human transforming protein (PIR:S22157) 1478 X62447 Homo sapiens PR 264 543 61		<u> </u>	-			
rubripes 1477 U42831 Caenorhabdit coded for by C. elegans cDNA yk99b4.3; similar to human transforming protein (PIR:S22157) 1478 X62447 Homo sapiens PR 264 543 61	1476	AJ010317	Fugu		1278	- 68
1477 U42831 Caenorhabdit coded for by C. elegans cDNA yk99b4.3; similar to human transforming protein (PIR:S22157) 1478 X62447 Homo sapiens PR 264 543 61			rubripes			"
is elegans yk99b4.3; similar to human transforming protein (PIR:S22157) 1478 X62447 Homo sapiens PR 264 543 61	1477	U42831		coded for by C. elegans cDNA	846	44
transforming protein (PIR:S22157) 1478 X62447 Homo sapiens PR 264 543 61						**
(PIR:S22157) 1478 X62447 Homo sapiens PR 264 543 61		(- i			ł
1478 X62447 Homo sapiens PR 264 543 61		[ļ	İ
	1478	X62447	Homo sapiens		543	61
1479 X82209 Homo sapiens MN1 7116 100	1479	X82209				
1480 U10536 Pan paniscus MHC.class I A 675 84	1480	U10536				

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	IDENTITY
1481	AL078599	Homo sapiens	dJ991C6.1 (novel protein similar to C. elegans	SCORE 1274	65
1400	900-		F55A12.9 (Tr:P91086))		
1482	298977	Schizosaccha romyces pombe	putative vacuolar protein	256	29
1483	AB005662	Mus musculus	JNK/SAPK-associated protein-1	4968	92
1484	AL050120	Homo sapiens	hypothetical protein	716	100
1485	M27878	Homo sapiens	DNA binding protein	1006	53
1486	Y69161	Homo sapiens	Amino acid sequence of a partial protein kinase.	575	99
1487	X84156	Saccharomyce s cerevisiae	ATH1.	341	29
1488	AF038963	Homo sapiens		446	34
1489	U56966	Caenorhabdit is elegans	coded for by C. elegans cDNA yk30b3.5; coded for by C. elegans cDNA yk30b3.3	620	42
1490	AE000989	Archaeoglobu s fulgidus	enoyl-CoA hydratase (fad-4)	533	46
1491	M80633	Rattus norvegicus	adenylyl cyclase type IV	707	95
1492	Y73342	Homo sapiens	HTRM clone 2709055 protein sequence.	3513	99
1493	Y17220	Homo sapiens	Human secreted protein (clone fj283-11).	452	37
1494	AF133670 Y94897	Mus musculus	ARL-6 interacting protein-2	701	97
1496	AL049699	Homo sapiens	Human protein clone HP10574.	1371	100
1497	AF037447	Homo sapiens	dJ747H23.2 (novel protein)	1550	100
1498	AL445067	Thermoplasma	ribosomal S6 protein kinase putative target YPL207w of	2427	100
		acidophilum	the HAP2 transcriptional complex related protein	269	35
1499	AB039947	Homo sapiens	X11L-binding protein 51	227	36
1501	AJ277750 AL050333	Homo sapiens	UBASH3A protein	3509	100
1502	AF179896	sapiens Homo sapiens	dJ93K22.1 (novel protein (contains DKFZP564B116))	2439	100
1503	AF178948	Homo sapiens	TALE homeobox protein Meis2b TALE homeobox protein Meis2a	1140	100
1504	¥53005	Homo sapiens	Human secreted protein clone pm749_8 protein sequence SEQ ID NO:16.	1177	99
1505	X82494	Homo sapiens	fibulin-2	3580	99
1506	X98296	Homo sapiens	ubiquitin hydrolase	783	42
1507	AL034548	Homo sapiens	dJ1103G7.6 (novel protein)	1098	100
1508	Y76144	Homo sapiens	Human secreted protein encoded by gene 21.	1736	100
1510	AF220182 U64601	Homo sapiens	uncharacterized hypothalamus protein HT008	1181	98
1511	AL356192	is elegans Neurospora	Gene probably begins in the next cosmid	415	58
1512	D17629	crassa	related to MDM1 protein	196	29
1513	AF168717	Homo sapiens	N-acetylgalactosamine 6- sulfate sulfatase (GALNS)	1829	100
1514	AJ243531	Homo sapiens	x 009 protein	694	99
1515	AC003672	Arabidopsis thaliana	nM15 protein putative C3HC4-type RING zinc	735	30
1516	AF115435	Rattus norvegicus	finger protein syntaxin 17	1374	90
1517	AF003140	Caenorhabdit is elegans	C44E4.5 gene product	274	31
1518	AB002584	Rattus norvegicus	beta-alanine-pyruvate aminotransferase	2238	82
1519	AL121764	Schizosaccha	yeast atp12 protein precursor	270	30

1520 1521 1522 1523 1524 1525 1526 1527 1528 1529 1530 1531 1532	AF255910 D31764 Y66634 Y94450 AC000107 AF109377 AL031427 Y08135 AK024423 AF154502 AF205598 AF251039 W74805 AF039023	romyces pombe Homo sapiens Homo sapiens Homo sapiens Homo sapiens Arabidopsis thaliana Mus musculus Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	vascular endothelial junction-associated molecule KIAA0064 Membrane-bound protein PRO190. Human inflammation associated protein F17F8.22 IdlEp dJ167A19.4 (novel protein) acid sphingomyelinase-like phosphodiesterase FLJ00012 protein quiescent cell proline dipeptidase transposase-like protein putative zinc finger protein Human secreted protein encoded by gene 77 clone	547 170 985 250 277 1277 1432 1496 611 679 1368 1420 493	100 27 100 43 37 83 99 79 100 100
1521 1522 1523 1524 1525 1526 1527 1528 1529 1530 1531 1532	D31764 Y66634 Y94450 AC000107 AF109377 AL031427 Y08135 AK024423 AF154502 AF205598 AF251039 W74805	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Arabidopsis thaliana Mus musculus Homo sapiens Mus musculus Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	junction-associated molecule KIAA0064 Membrane-bound protein PRO190. Human inflammation associated protein F17F8.22 IdlEp dJ167A19.4 (novel protein) acid sphingomyelinase-like phosphodiesterase FLJ00012 protein quiescent cell proline dipeptidase transposase-like protein putative zinc finger protein Human secreted protein	170 985 250 277 1277 1432 1496 611 679 1368 1420	27 100 43 37 83 99 79 100 100
1522 1523 1524 1525 1526 1527 1528 1529 1530 1531 1532	Y66634 Y94450 AC000107 AF109377 AL031427 Y08135 AK024423 AF154502 AF205598 AF251039 W74805 AF039023	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Arabidopsis thaliana Mus musculus Homo sapiens Mus musculus Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	KIAA0064 Membrane-bound protein PRO190. Human inflammation associated protein F17F8.22 IdlEp dJ167A19.4 (novel protein) acid sphingomyelinase-like phosphodiesterase FLJ00012 protein quiescent cell proline dipeptidase transposase-like protein putative zinc finger protein Human secreted protein	985 250 277 1277 1432 1496 611 679 1368 1420	100 43 37 83 99 79 100 100
1523 1524 1525 1526 1527 1528 1529 1530 1531 1532	Y94450 AC000107 AF109377 AL031427 Y08135 AK024423 AF154502 AF205598 AF251039 W74805 AF039023	Homo sapiens Homo sapiens Arabidopsis thaliana Mus musculus Homo sapiens Mus musculus Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	PRO190. Human inflammation associated protein F17F8.22 IdlEp dJ167A19.4 (novel protein) acid sphingomyelinase-like phosphodiesterase FLJ00012 protein quiescent cell proline dipeptidase transposase-like protein putative zinc finger protein Human secreted protein	985 250 277 1277 1432 1496 611 679 1368 1420	100 43 37 83 99 79 100 100
1524 1525 1526 1527 1528 1529 1530 1531 1532	AC000107 AF109377 AL031427 Y08135 AK024423 AF154502 AF205598 AF251039 W74805 AF039023	Homo sapiens Arabidopsis thaliana Mus musculus Homo sapiens Mus musculus Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	Human inflammation associated protein F17F8.22 IdlEp dJ167A19.4 (novel protein) acid sphingomyelinase-like phosphodiesterase FLJ00012 protein quiescent cell proline dipeptidase transposase-like protein putative zinc finger protein Human secreted protein	277 1277 1432 1496 611 679 1368 1420	37 83 99 79 100 100
1525 1526 1527 1528 1529 1530 1531 1532	AF109377 AL031427 Y08135 AK024423 AF154502 AF205598 AF251039 W74805	thaliana Mus musculus Homo sapiens Mus musculus Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	protein F17F8.22 IdlEp dJ167A19.4 (novel protein) acid sphingomyelinase-like phosphodiesterase FLJ00012 protein quiescent cell proline dipeptidase transposase-like protein putative zinc finger protein Human secreted protein	277 1277 1432 1496 611 679 1368 1420	37 83 99 79 100 100
1526 1527 1528 1529 1530 1531 1532	AL031427 Y08135 AK024423 AF154502 AF205598 AF251039 W74805 AF039023	thaliana Mus musculus Homo sapiens Mus musculus Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	ldlEp dJ167A19.4 (novel protein) acid sphingomyelinase-like phosphodiesterase FLJ00012 protein quiescent cell proline dipeptidase transposase-like protein putative zinc finger protein Human secreted protein	1277 1432 1496 611 679 1368 1420	83 99 79 100 100
1526 1527 1528 1529 1530 1531 1532	AL031427 Y08135 AK024423 AF154502 AF205598 AF251039 W74805 AF039023	Homo sapiens Mus musculus Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	dJ167A19.4 (novel protein) acid sphingomyelinase-like phosphodiesterase FLJ00012 protein quiescent cell proline dipeptidase transposase-like protein putative zinc finger protein Human secreted protein	1432 1496 611 679 1368 1420	99 79 100 100
1527 1528 1529 1530 1531 1532	Y08135 AK024423 AF154502 AF205598 AF251039 W74805 AF039023	Mus musculus Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	acid sphingomyelinase-like phosphodiesterase FLJ00012 protein quiescent cell proline dipeptidase transposase-like protein putative zinc finger protein Human secreted protein	1496 611 679 1368 1420	79 100 100
1528 1529 1530 1531 1532	AK024423 AF154502 AF205598 AF251039 W74805	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	phosphodiesterase FLJ00012 protein quiescent cell proline dipeptidase transposase-like protein putative zinc finger protein Human secreted protein	611 679 1368 1420	100
1529 1530 1531 1532	AF154502 AF205598 AF251039 W74805 AF039023	Homo sapiens Homo sapiens Homo sapiens Homo sapiens	FLJ00012 protein quiescent cell proline dipeptidase transposase-like protein putative zinc finger protein Human secreted protein	1368 1420	100
1530 1531 1532	AF205598 AF251039 W74805	Homo sapiens Homo sapiens Homo sapiens	quiescent cell proline dipeptidase transposase-like protein putative zinc finger protein Human secreted protein	1368 1420	100
1531 1532 1533	AF251039 W74805 AF039023	Homo sapiens Homo sapiens	dipeptidase transposase-like protein putative zinc finger protein Human secreted protein	1368	100
1531 1532 1533	AF251039 W74805 AF039023	Homo sapiens Homo sapiens	putative zinc finger protein Human secreted protein	1420	
1532	W74805 AF039023	Homo sapiens	Human secreted protein	I	50
1533	AF039023		Human secreted protein encoded by gene 77 clone	102	1 20
			HOEAS24.	4.53	57
		Homo sapiens	Ran-GTP binding protein; RanBP6	5707	99
1534	AC007190	Arabidopsis thaliana	F23N19.9	374	37
1535	AB027564	Homo sapiens	DINB1	4482	100
1536	Y36178	Homo sapiens	Human secreted protein	377	87
1537	Y50907	Homo sapiens	Human fetal brain cDNA clone vb3_1 derived protein.	3693	99
1538	AF017368	Mus musculus	faciogenital dysplasia protein 2	177	47
1539	AF266756	Homo sapiens	sphingosine kinase	2011	
1540	Z48804	Homo sapiens	OA1	2238	99 100
1541	AF000195	Caenorhabdit is elegans	Contains similarity to Pfam domain: PF30169 (PH), Score=20.6, E-value=1.9e-05, N=1	379	42
1542	Y71159	Homo sapiens	Human phosphodiesterase interacting protein, myomegalin.	9415	99
1543	X76092	Homo sapiens	DNA binding protein RFX3	3327	100
1544	AB015330	Homo sapiens	HRIHFB2007	631	50
	AF198487	Homo sapiens	transcription factor LBP-1b	2822	100
	AF016417	Caenorhabdit is elegans	Similar to BZIP transcription factor	518	42
	X55885	Homo sapiens	KDEL receptor	1106	100
1548	AB035495	Carassius auratus	ubiquitin-activating enzyme	836	42
1549	AL021707	Homo sapiens	dJ508115.4 (KIAA0668)	13600	100
1550	AJ223978	Bacillus subtilis	YvqK protein	3688 292	100
1551	AF145615	Drosophila	BcDNA.GH03377	822	44
	AL157734	melanogaster Schizosaccha romyces pombe	putative mannosyltransferase involved in N-glycosylation	435	37
	AF079527	Mus musculus	IERS	691	63
1554	AB026291		acetoacetyl-CoA synthetase	1099	88
		Homo sapiens	Human immune system molecule, ISMO-3.	1780	99
	j.	melanogaster	antennal-specific short-chain dehydrogenase/reductase	277	32
1557	Y71056	Homo sapiens	Human membrane transport	1975	99

SEQ	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	IDENTITY
NO:				SCORE	
	1.51055		protein, MTRP-1.	1975	
1558	Y71056	Homo sapiens	Human membrane transport protein, MTRP-1.		99
1559	Y71056	Homo sapiens	Human membrane transport protein, MTRP-1.	1894	97
1560	AF092050	Mus musculus	beta-1,3-N- acetylglucosaminyltransferase	262	44
1561	AL109827	Homo sapiens	dJ309K20.2 (acrosomal protein ACR55 (similar to rat sperm antigen 4 (SPAG4)))	1607	97
1562	AJ131890	Homo sapiens	DNA polymerase lambda	3002	100
1563	AL035424	Homo sapiens	dA22D12.1 (novel protein similar to Drosophila Kelch proteins)	3015	100
1564	AC002400	Homo sapiens	Gene product with similarity to Ubiquitin binding enzyme	2790	100
1565	AC005306	Homo sapiens	R27216_1	919	82
1566	AF000195	Caenorhabdit is elegans	Contains similarity to Pfam domain: PF00169 (PH), Score=20.6, E-value=1.9e-05, N=1	550	45
1567	AB033281	Homo sapiens	F-box and WD-repeats protein beta-TRCP2 isoform C	2879	100
1568	D49473	Mus musculus	truncated form of Sox17	1047	78
1569	AK025270	Homo sapiens	unnamed protein product	210	91
1570	X75756	Homo sapiens	protein kinase C mu	4797	99
1571	AF145713	Homo sapiens	SCHIP-1	2388 .	100
1572	AE003831	Drosophila melanogaster	CG18445 gene product	180	31
1573	AF074603	Streptomyces griseus subsp. griseus	NonF	205	38
1574	U28993	Caenorhabdit is elegans	F22D3.3 gene product	144	27
1575	AF129507	Homo sapiens	transcription factor ICBP90	287	68
1576	X64878	Homo sapiens	oxytocin receptor	2002	100
1577	AF237711	Drosophila melanogaster	Diablo	421	54
1578	G00975	Homo sapiens	Human secreted protein, SEQ ID NO: 5056.	480	100
1579	AF248744	Cryptosporid ium parvum	thrombospondin-related adhesive protein	123	33
1580	AL121782	Homo sapiens	dJ585I14.2 (novel protein (translation of cDNA Em:AK000219))	663	100
1581	AF041853	Homo sapiens	kinesin family member protein KIF3A	345	33
1582	AF025441	Homo sapiens	Opa-interacting protein OIP5	1198	100
1583	AE001803	Thermotoga maritima	glycerate kinase, putative	349	34
1584	AF252283	Homo sapiens	Kelch-like 1 protein	3973	100
1585	AF169675	Homo sapiens	leucine-rich repeat transmembrane protein FLRT1	3494	99
1586	AF118274	Homo sapiens	DNb-5	2628	97
1587	X79440	Homo sapiens	NADP+-dependent malic enzyme	3167	99
1588	X99802	Homo sapiens	ZYG homologue	3966	99
1589	AF169803	Homo sapiens	flavohemoprotein b5+b5R	2563	100
1590	Y29861	Homo sapiens	Human secreted protein clone cb98_4.	181	47
1591	225535	Homo sapiens	nuclear pore complex protein hnup153	7567	99
1592	X13293	Homo sapiens	B-myb protein (AA 1-700)	3678	99
1593	M74027	Homo sapiens	mucin	242	27
1594	AL139314	Schizosaccha	hypothetical protein	235	54

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	T &
ID	NUMBER		2.55.55.55.55.55.55.55.55.55.55.55.55.55	WATERMAN	IDENTITY
NO:				SCORE	TDEMILITY
		pombe		SCORE	
1595	W78324	Homo sapiens	Fragment of human secreted	1318	98
	}	_	protein encoded by gene 81.	1310	30
1596	Y94906	Homo sapiens	Human secreted protein clone	2236	98
	İ	_	rb649_3 protein sequence SEQ		""
	1		ID NO:18.		
1597	AF174605	Homo sapiens	F-box protein Fbx25	1408	99
1598	AB032254	Homo	bromodomain adjacent to zinc	9676	98
		sapiens	finger domain 2A		50
1599	X73114	Homo sapiens	slow MyBP-C	5568	95
1600	X82200	Homo sapiens	gpStaf50	2305	100
1601	Y00876	Homo	Human LAPH-1 protein	1149	98
		sapiens	sequence.		
1602	AJ223351	Homo sapiens	HIRA-interacting protein 3	2821	99
1603	AJ222801	Homo sapiens	neutral sphingomyelinase	2268	99
1604	AJ222801	Homo sapiens	neutral sphingomyelinase	1601	99
1605	AF185576	Mus musculus	POZ/zinc finger transcription	3435	97
			factor ODA-8		1
1606	AF093744	Homo sapiens	unknown	131	100
1607	A12142	synthetic	IFN-pseudo-omega 2	800	98
		construct			
1608	Y57949	Homo sapiens	Human transmembrane protein	1868	100
			HTMPN-73.		
1609	AF151044	Homo sapiens	HSPC210	681	97
1610	X15218	Homo sapiens	ski protein (AA 1 - 728)	3765	100
1611	Y08200	Homo sapiens	rab geranylgeranyl	2976	100
1610	1 2000		transferase		-
1612	AF220560	Homo sapiens	B/K protein	2486	99
1013	AC004481	Arabidopsis thaliana	nodulin-like protein	371	26
1614	Y09501	Homo sapiens	MARKE		
1615	Y15521	Homo sapiens	NADH-cytochrome-b5 reductase start position 1	1607	100
1616	AJ010750	Rattus	Castration induced prostatic	3150	97
	130010750	norvegicus	apoptosis related protein-1,	890	62
	ł		(CIPAR-1)		İ
1617	X58079	Homo sapiens	S100 alpha protein	481	100
1618	Y66678	Homo	Membrane-bound protein	967	100
	ľ	sapiens	PRO1009.	507	100
1619	AJ242973	Homo sapiens	peptide methionine sulfoxide	929	100
			reductase	1	100
1620	AF150733	Homo sapiens	AD-014 protein	288	100
1621	AJ007509	Homo sapiens	E1B-55kDa-associated protein	4646	98
1622	X64177	Homo sapiens	metallothionein	380	100
1623	AE001045	Archaeoglobu	A. fulgidus predicted coding	240	36
		s fulgidus	region AF0859		
1624	AL355013	Schizosaccha	mitochondrial carrier protein	403	34
		romyces		1	
1625	Y66746	pombe			
1023	100/40	Homo	Membrane-bound protein	1184	100
1626	D90053	sapiens Sus scrofa	PRO1198.		
1627	Y35954	Homo sapiens	destrin	863	100
1027	133334	HOMO Saptens	Extended human secreted	756	100
			protein sequence, SEQ ID NO. 203.	ļ	
1628	AL031775	Homo sapiens	dJ30M3.2 (novel protein)	470	100
1629	AF132484	Mus musculus	unknown	286	68
1630	AF017096	Drosophila	similar to C. elegans	493	61
		melanogaster	R10H10.6 and S. cerevisiae YD8419.03c	1,3	J.
1631	X03077	Homo sapiens	lactate dehydrogenase-A	1704	100
1632	AF151084	Homo sapiens	HSPC250	763	100
	AJ001874	Homo sapiens	orf	255	97
1633	AUDOTR/4 1				
	AC012187	Arabidopsis	Contains weak similarity to		
1633			Contains weak similarity to GATA-6 DNA-binding protein	143	38
1633		Arabidopsis			

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
1635	AF026246	Homo sapiens	HERV-E integrase	411	90
1636	Y50943	Homo sapiens	Human adult brain cDNA clone	1126	95
		<u> </u>	ve8_1 derived protein.		
1637	AF134593	Homo sapiens	L-pipecolic acid oxidase	2068	99
1638	AJ238247	Mus musculus	putative phosphatase subunit	1948	96
1639	Y94942	Homo sapiens	Human secreted protein clone yk251_1 protein sequence SEQ ID NO:90.	1320	100
1640	AF235030	Homo sapiens	BM88 antigen	766	99
1641	AF233288	Drosophila melanogaster	WDS	358	26
1642	M19351	Mus musculus	immunoglobulin heavy chain binding protein	145	34
1643	Y70452	Homo sapiens	Human membrane channel protein-2 (MECHP-2).	1352	100
1644	AF176520	Mus musculus	WD repeat-containing F-box	2676	88
1645	W67816	Homo sapiens	Human secreted protein encoded by gene 10 clone HCEMU42.	1156	100
1646	X67155	Homo sapiens	mitotic kinase-like protein-l	4456	99
1647	M63180	Homo sapiens	threonyl-tRNA synthetase	1040	61
1648	Y87342	Homo sapiens	Human signal peptide containing protein HSPP-119 SEQ ID NO:119.	1566	93
1649	R95332	Homo sapiens	Tumor necrosis factor receptor 1 death domain ligand (clone 3TW).	4137	100
1650	AC007136	Homo sapiens	Putative map kinase interacting kinase	856	99
1651	AB015346	Homo sapiens	Eps15R	4464	99
1652	AL161576	Arabidopsis thaliana	putative protein	1341	48
1653	AC005313	Arabidopsis thaliana	putative calmodulin	288	28
1654	AL031428	Homo sapiens	dJ184J9.1 (KIAA0601 protein)	3526	100
1655	AL031428	Homo sapiens	dJ184J9.1 (KIAA0601 protein)	3526	100
1656	AB017910	Dictyosteliu m discoideum	тусм	297	32
1657	Y28919	Homo sapiens	Human regulatory protein HRGP-5.	2251	99
1658	AF056191	Homo sapiens	TPA inducible protein	2744	98
1659	U76846	Arabidopsis thaliana	ubiquitin-specific protease	137	35
1660	AL078627	Schizosaccha romyces pombe	actin-like protein; (2 actin domains)	320	34
1662	X52022	Homo sapiens	collagen type VI, alpha 3 chain	16274	99
1663	AF300648	Homo sapiens	guanine nucleotide binding protein beta subunit 4	1811	100
1664	AF214736	Homo sapiens	EH domain containing protein 2	2774	100
1665	Z48613	Saccharomyce s cerevisiae	unknown	138	26
1666	AF177385	Homo sapiens	cytochrome c oxidase assembly protein isoform 2	1395	99
1667	AC007842	Homo sapiens	BC331191_1	1581	47
1668	S67513	Borna disease virus BDV, WT-1, Halle B1/91, horse brain, field isolate,	p40	397	43

1669 Z9975 1670 G0313 1671 M9662 1672 AF174 1673 Y5194 1674 AF255 1675 Y9486 1676 Y2571 1677 Y2571 1678 AF163 1680 AK024 1681 AF019 1682 AJ243 1683 Z6936 1684 X9491 1685 AF286 1686 AF191 1687 AJ275 1688 AJ275 1688 AJ275 1688 AJ275 1689 X07313 1690 AF2404 1691 AJ2720 1691 AJ2720 1692 AJ2720 1693 AF1779 1694 AF2635 1695 AF2226 1696 AK0001 1697 AB0410 1698 AB0410 1699 AF0257 1700 Y44676 1701 AK0224 1702 AB0245 1704 AF1980 1705 AE0035	ESSION JMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
1671 M9662 1672 AF174 1673 Y5194 1674 AF255 1675 Y9486 1676 Y2571 1677 Y2571 1678 AF163 1679 AF163 1680 AK024 1681 AF019 1692 AJ243 1683 Z6936 1684 X9491 1685 AF286 1686 AF191 1687 AJ275 1688 AJ275 1688 AJ275 1689 X07311 1690 AF2406 1691 AJ2720 1693 AF1773 1694 AF2635 1695 AF226 1696 AK0001 1697 AB0410 1698 AB0410 1699 AF0257 1700 Y44676 1701 AK0224 1702 AB0245 1703 AF1950 1704 AF1950 1705 AE0035	753	Schizosaccha	putative NOL1-NOP2-sun family		
1671 M9662 1672 AF174 1673 Y5194 1674 AF255 1675 Y9486 1676 Y2571 1677 Y2571 1678 AF163 1679 AF163 1680 AK024 1681 AF019 1692 AJ243 1683 Z6936 1684 X9491 1685 AF286 1686 AF191 1687 AJ275 1688 AJ275 1688 AJ275 1689 X07311 1690 AF2406 1691 AJ2720 1692 AJ2720 1693 AF1773 1694 AF2635 1695 AF226 1696 AK0001 1697 AB0410 1698 AB0410 1699 AF0257 1700 Y44676 1701 AK0224 1702 AB0245 1703 AF1590 1704 AF1590 1705 AE0035		romyces pombe	nucleolar protein	569	47
1672 AF174 1673 Y5194 1674 AF255 1675 Y9496 1676 Y2571 1677 Y2571 1678 AF163 1679 AF163 1680 AK024 1681 AF019 1682 AJ243 1683 Z6936 1684 X9491 1685 AF286 1686 AF191 1687 AJ275 1688 AJ275 1688 AJ275 1689 X07311 1690 AF2406 1691 AJ2720 1693 AF1775 1694 AF2635 1695 AF2226 1696 AK0001 1697 AB0410 1698 AB0410 1699 AF0257 1700 Y44676 1701 AK0224 1702 AB0245 1703 AF0550 1704 AF1980 1705 AE0035		Homo sapiens	ID NO: 7211.	427	97
1673 Y5184 1674 AF255 1675 Y9486 1676 Y2571 1677 Y2571 1678 AF163 1679 AF163 1680 AK024 1681 AF019 1682 AJ243 1683 Z6936 1684 X9491 1685 AF286 1686 AF191 1687 AJ275 1688 AJ275 1689 X07311 1690 AF2404 1691 AJ2720 1692 AJ2720 1693 AF1779 1694 AF2635 1695 AF2226 1696 AK0001 1697 AB0410 1698 AB0410 1699 AF0257 1700 Y44676 1701 AK0224 1702 AB0245 1703 AF1980 1705 AE0035		Gallus gallus	cardiac muscle tensin	1185	54
1674 AF255 1675 Y9496 1676 Y2571 1677 Y2571 1677 AF163 1679 AF163 1680 AK024 1681 AF019 1682 AJ243 1683 Z6936 1684 X9491 1685 AF286 1686 AF191 1687 AJ275 1688 AJ275 1689 X0731 1690 AF2406 1691 AJ2720 1693 AF177 1694 AF2635 1695 AF2226 1696 AK0001 1697 AB0410 1698 AB0410 1699 AF0257 1700 Y44676 1701 AK0224 1702 AB0245 1703 AF1980 1705 AE0035		Homo sapiens		2005	99
1675 Y9486 1676 Y2571 1677 Y2571 1678 AF163 1679 AF163 1680 AK024 1681 AF019 1682 AJ243 1683 Z6936 1684 X9491 1685 AF286 1686 AF191 1687 AJ275 1688 AJ275 1689 X07311 1690 AF2406 1691 AJ2720 1693 AF1773 1694 AF2635 1695 AF226 1696 AK0001 1697 AB0410 1698 AB0410 1699 AF0257 1700 Y44676 1701 AK0224 1702 AB0245 1703 AF1980 1704 AF1980 1705 AE0035	•	Homo sapiens	Human 18.1 homolog protein fragment.	233	29
1676 Y2571 1677 Y2571 1678 AF163 1679 AF163 1680 AK024 1681 AF019 1682 AJ243 1683 Z6936 1684 X9491 1685 AF286 1686 AF191 1687 AJ275 1688 AJ275 1689 X07311 1690 AF2406 1691 AJ2720 1692 AJ2720 1693 AF1775 1694 AF2635 1695 AF2226 1696 AK0001 1697 AB0410 1698 AB0410 1699 AF0257 1700 Y44676 1701 AK0224 1702 AB0245 1703 AF0550 1704 AF1980 1705 AE0035		Homo sapiens	EXP35	152	29
1677 Y2571 1678 AF163 1679 AF163 1680 AK024 1681 AF019 1692 AJ243 1683 Z6936 1684 X9491 1685 AF286 1686 AF191 1688 AJ275 1688 AJ275 1688 AJ275 1689 X07311 1690 AF2406 1691 AJ2720 1693 AF1779 1694 AF2635 1695 AF2226 1696 AK0001 1697 AB0410 1698 AB0410 1699 AF0257 1700 Y44676 1701 AK0224 1702 AB0245 1703 AF0550 1704 AF1980 1705 AE0035		Homo sapiens	Human protein clone HP10563.	109	30
1678 AF163 1679 AF163 1680 AK024 1681 AF019 1682 AJ243 1683 Z6936 1684 X9491 1685 AF286 1686 AF191 1687 AJ275 1688 AJ275 1689 X0731 1690 AF2404 1691 AJ2720 1693 AF1779 1694 AF2635 1695 AF2226 1696 AK0001 1697 AB0410 1698 AB0410 1699 AF0257 1700 Y44676 1701 AK0224 1702 AB0245 1703 AF1980 1704 AF1980		Homo sapiens	Human secreted protein encoded from gene 2.	3043	99
1679 AF163 1680 AK024 1681 AF019 1692 AJ243 1683 Z6936 1684 X9491 1685 AF286 1686 AF191 1687 AJ275 1688 AJ275 1689 X07311 1690 AF2406 1691 AJ2720 1692 AJ2720 1693 AF1773 1694 AF2635 1695 AF2226 1696 AK0001 1697 AB0410 1698 AB0410 1699 AF0257 1700 Y44676 1701 AK0224 1702 AB0245 1703 AF0550 1704 AF1980 1705 AE0035	_	Homo sapiens	Human secreted protein encoded from gene 2.	1580	91
1680 AK024 1681 AF019 1682 AJ243 1683 Z6936 1684 X9491 1685 AF286 1686 AF191 1688 AJ275 1688 AJ275 1689 X07311 1690 AF2406 1691 AJ2720 1693 AF1779 1694 AF2635 1695 AF2226 1696 AK0001 1697 AB0410 1698 AB0410 1699 AF0257 1700 Y44676 1701 AK0224 1702 AB0245 1703 AF0550 1704 AF1980 1705 AE0035		Homo sapiens	dentin sialophosphoprotein precursor	170	17
1681 AF019 1692 AJ243 1683 Z6936 1684 X94910 1685 AF286 1686 AF1913 1688 AJ2753 1689 X07313 1690 AF2404 1691 AJ2720 1693 AF1779 1694 AF2635 1695 AF2226 1696 AK0001 1697 AB0410 1698 AB0410 1699 AF0257 1700 Y44676 1701 AK0224 1702 AB0245 1703 AF1980 1704 AF1980		Homo sapiens	dentin sialophosphoprotein precursor	170	17
1682 AJ243 1683 Z6936 1684 X9491 1685 AF286 1686 AF191 1687 AJ275 1688 AJ275 1689 X07313 1690 AF2404 1691 AJ2720 1693 AF1779 1694 AF2635 1695 AF2226 1696 AK0001 1697 AB0410 1698 AB0410 1699 AF0257 1700 Y44676 1701 AK0224 1702 AB0245 1703 AF1980 1704 AF1980		Homo sapiens	FLJ00045 protein	1349	100
1683 Z6936. 1684 X9491 1685 AF286. 1686 AF191: 1687 AJ275! 1688 AJ275! 1689 X07311 1690 AF2406 1691 AJ2720 1692 AJ2720 1693 AF1775 1694 AF2635 1695 AF2226 1696 AK0001 1697 AB0410 1698 AB0410 1698 AB0410 1699 AF0257 1700 Y44676 1701 AK0224 1702 AB0245 1703 AF0550 1704 AF1980 1705 AE0035		Dictyosteliu m discoideum	TipD	613	34
1684 X9491 1685 AF286 1686 AF191 1687 AJ275 1688 AJ275 1689 X07311 1690 AF2406 1691 AJ2720 1692 AJ2720 1693 AF1773 1694 AF2635 1695 AF2226 1696 AK0001 1697 AB0410 1698 AB0410 1699 AF0257 1700 Y44676 1701 AK0224 1702 AB0245 1703 AF0550 1704 AF1980 1705 AE0035		Leishmania major	proteophosphoglycan	153	26
1685 AF286 1686 AF191 1687 AJ275 1688 AJ275 1689 X07311 1690 AF2404 1691 AJ2720 1692 AJ2720 1693 AF1773 1694 AF2635 1695 AF2226 1696 AK0001 1697 AB0410 1698 AB0410 1699 AF0257 1700 Y44676 1701 AK0224 1702 AB0245 1703 AF0550 1704 AF1980 1705 AE0035	69	Schizosaccha romyces pombe	putative GTP-binding protein	560	46
1686 AF191: 1687 AJ275: 1688 AJ275: 1689 X0731: 1690 AF2404 1691 AJ2720 1692 AJ2720 1693 AF1775 1694 AF2635 1695 AF2226 1696 AK0001 1697 AB0410 1698 AB0410 1699 AF0257 1700 Y44676 1701 AK0224 1702 AB0245 1703 AF0550 1704 AF1980 1705 AE0035		Homo sapiens	ERp28	1334	100
1687 AJ2751 1688 AJ2751 1689 X07311 1690 AF2404 1691 AJ2720 1692 AJ2720 1693 AF1775 1694 AF2635 1695 AF2226 1696 AK0001 1697 AB0410 1698 AB0410 1699 AF0257 1700 Y44676 1701 AK0224 1702 AB0245 1703 AF0550 1704 AF1980 1705 AE0035	6475	Takifugu	retinitis pigmentosa GTPase	196	19
1687 AJ2751 1688 AJ2751 1689 X07311 1690 AF2404 1691 AJ2720 1692 AJ2720 1693 AF1775 1694 AF2635 1695 AF2226 1696 AK0001 1697 AB0410 1698 AB0410 1699 AF0257 1700 Y44676 1701 AK0224 1702 AB0245 1703 AF0550 1704 AF1980 1705 AE0035		rubripes	regulator-like protein		**
1688 AJ275 1689 X07311 1690 AF2404 1691 AJ2720 1692 AJ2720 1693 AF1779 1694 AF2635 1695 AF2226 1696 AK0001 1697 AB0410 1698 AB0410 1699 AF0257 1700 Y44676 1701 AK0224 1702 AB0245 1703 AF0550 1704 AF1980 1705 AE0035		Homo sapiens	vacuolar sorting protein 35	4087	100
1689 X07313 1690 AF2404 1691 AJ2720 1692 AJ2720 1693 AF1779 1694 AF2635 1695 AF2226 1696 AK0001 1697 AB0410 1698 AB0410 1699 AF0257 1700 Y44676 1701 AK0224 1702 AB0245 1703 AF0550 1704 AF1980 1705 AE0035		Homo sapiens	transcription factor	2958	100
1691 AJ2720 1692 AJ2720 1693 AF1775 1694 AF2635 1695 AF2226 1696 AK0001 1697 AB0410 1698 AB0410 1699 AF0257 1700 Y44676 1701 AK0224 1702 AB0245 1703 AF0550 1704 AF1980 1705 AE0035		Drosophila	transcription factor heat shock protein	1886	88
1691 AJ2720 1692 AJ2720 1693 AF1775 1694 AF2635 1695 AF2226 1696 AK0001 1697 AB0410 1698 AB0410 1699 AF0257 1700 Y44676 1701 AK0224 1702 AB0245 1703 AF0550 1704 AF1980 1705 AE0035	0463	melanogaster Rattus	LIS1-interacting protein	138	43
1692 AJ2720 1693 AF1773 1694 AF2635 1695 AF2226 1696 AK0001 1697 AB0410 1698 AB0410 1699 AF0257 1700 Y44676 1701 AK0224 1702 AB0245 1703 AF0550 1704 AF1980 1705 AE0035		norvegicus Homo sapiens	NUDE1	1383	83
1693 AF1779 1694 AF2635 1695 AF2226 1696 AK0001 1697 AB0410 1698 AB0410 1699 AF0257 1700 Y44676 1701 AK0224 1702 AB0245 1703 AF0550 1704 AF1980 1705 AE0035		Homo sapiens	APOBEC-1 stimulating protein APOBEC-1 stimulating protein	1256	68
1695 AF2226 1696 AK0001 1697 AB0410 1698 AB0410 1699 AF0257 1700 Y44676 1701 AK0224 1702 AB0245 1703 AF0550 1704 AF1980 1705 AE0035	942	Xenopus	katanin p60	1336	60
1695 AF2226 1696 AK0001 1697 AB0410 1698 AB0410 1699 AF0257 1700 Y44676 1701 AK0224 1702 AB0245 1703 AF0550 1704 AF1980 1705 AE0035	_ (laevis	poo	1004	66
1696 AK0001 1697 AB0410 1698 AB0410 1699 AF0257 1700 Y44676 1701 AK0224 1702 AB0245 1703 AF0550 1704 AF1980 1705 AE0035		Homo sapiens	arginine N-methyltransferase	1774	100
1697 AB0410 1698 AB0410 1699 AF0257 1700 Y44676 1701 AK0224 1702 AB0245 1703 AF0550 1704 AF1980 1705 AE0035		Homo sapiens	protein arginine N- methyltransferase 1-variant 2	1182	81
1698 AB0410 1699 AF0257 1700 Y44676 1701 AK0224 1702 AB0245 1703 AF0550 1704 AF1980 1705 AE0035		Homo sapiens	unnamed protein product	1060	100
1699 AF0257 1700 Y44676 1701 AK0224 1702 AB0245 1703 AF0550 1704 AF1980 1705 AE0035		Homo sapiens	kidney superoxide-producing NADPH oxidase	3122	100
1700 Y44676 1701 AK0224 1702 AB0245 1703 AF0550 1704 AF1980 1705 AE0035		Homo sapiens	kidney superoxide-producing NADPH oxidase	2181	100
1701 AK0224 1702 AB0245 1703 AF0550 1704 AF1980 1705 AE0035		Homo sapiens	C2H2 zinc finger protein	488	54
1702 AB0245 1703 AF0550 1704 AF1980 1705 AE0035	-	Homo sapiens	Human ARF-Related Protein-1 (HARP-1).	938	97
1703 AF0550 1704 AF1980 1705 AE0035	407	Homo sapiens	unnamed protein product	315	98
1704 AF1980 1705 AE0035		Homo sapiens	GTP-binding like protein 2	1172	100
1705 AE0035		Homo sapiens Mus musculus	zinc finger protein 42	421	52
1706 AB0363	573	Drosophila	RP42 CG12474 gene product	1057	77 33
1 .	345	melanogaster Drosophila	aquaporin	164	24
1707 Y55927		melanogaster	Wilman CMI Va		
1708 U27121	1	Danio rerio	Human STLK2 protein. G12	2146	100
1709 AL3917:	710		putative protein		47 50

TABLE 2

SEO	ACCESSION	SPECIES	DESCRIPTION	SMITH-	1 - · · · · · · · · · · · · · · · · · ·
ID	NUMBER	0.5022	DESCRIPTION .	WATERMAN	IDENTITY
NO:				SCORE	IDEMITIE
		thaliana			
1710	B01311	Homo sapiens	Human PRO241 polypeptide.	1649	97
1711	U40750	Mus musculus	formin binding protein 30	4561	85
1712	AJ011118	Mus musculus	skeletal muscle and cardiac protein	1490	89
1713	AF255303	Homo sapiens	membrane-associated nucleic acid binding protein	4416	99
1714	AF255303	Homo	membrane-associated nucleic	2960	100
1715	U08227	sapiens Rattus	acid binding protein Ras-related protein	511	51
1716	AF168795	norvegicus Rattus	schlafen-4	1129	
1717	AF196304	norvegicus			44
1718	AL355737	Homo sapiens	SUMO-1-specific protease	5804	99
1719	AB029333	Homo sapiens	HMG20A	1.782	100
		Halocynthia roretzi	HrPET-1	1069	46
1720	AF071317	Mus musculus	COP9 complex subunit 7b	1297	97
1721	AJ272215	Homo sapiens	HEYL protein	1681	99
1722	G01982	Homo sapiens	Human secreted protein, SEQ ID NO: 6063.	718	100
1723	AL032643	Caenorhabdit is elegans	similar to Uncharacterized protein family UPF0034,	825	41
1724	G01972	Homo sapiens	Human secreted protein, SEQ	586	92
1725	Y94441	Homo sapiens	Human Adipose Specific Protein 1.	1231	100
1726	AF255443	Homo sapiens	CGI-201 protein	4397	99
1727	AF183426	Homo sapiens	HT004 protein	1810	99
1728	D10884	Bos taurus	neurocalcin	1002	99
1729	Z18529	Gallus gallus	tensin	1411	84
1730	273423	Caenorhabdit is elegans	cDNA EST EMBL:Z14908 comes from this gene~cDNA EST this gene	233	41
1732	AF090891	Homo sapiens	PR00105	470	30
1733	AJ277724	Homo sapiens	histone deacetylase 8	2015	100
1734	G04050	Homo sapiens	Human secreted protein, SEQ ID NO: 8131.	503	95
1735	D45913	Mus musculus	leucine-rich-repeat protein	3531	94
1736	AF096709	Drosophila virilis	failed axon connections	276	32
1737	AF195120	Homo sapiens	dynactin p62 subunit	2417	99
1738	L15314	Caenorhabdit	contains similarity to Pfam	206	37
1739	X54618	is elegans	family PF01772 N=1		
1/39	X54618	Listeria monocytogene s	phosphadidylinositol specific phospholipase C	134	27
1740	AL031658	Homo sapiens	dJ310013.4 (novel protein similar to predicted C. elegans an C. intestinalis proteins)	123	31
1741	Y35924	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 173.	1013	99
1742	AC013354	Arabidopsis thaliana	F15H18.15	202	32
1743	W75771	Homo sapiens	Human GTP binding protein APD08.	1932	59
1744	W75771	Homo sapiens	Human GTP binding protein APD08.	1854	61
1745	AF221098	Homo sapiens	Ral guanine nucleotide exchange factor RalGPS1A	1224	70
1746	Y99372	Homo sapiens	Human PRO1430 (UNQ736) amino acid sequence SEQ ID NO:116.	1332	99
1747	Y94294	Homo sapiens	Human coenzyme A-utilising	842	100

SEO	ACCESSION	SPECIES			•
ID	NUMBER	SPECIES	DESCRIPTION	SMITH-	8
NO:			,	WATERMAN	IDENTITY
			enzyme CoAEN-2.	SCORE	
1748	AK024436	Homo sapiens			
1749	AE000877	Methanobacte		1619	100
	12200011	rium	conserved protein	231	36
1		thermoautotr		1	
1		ophicum			1
1750	AF101361	Drosophila			1.
		melanogaster	Abnormal X segregation	193	33
1751	¥15067	Homo sapiens			
1752	AF251038	Homo sapiens		889	100
1753	AC003093			822	100
1 - 7 - 3 - 3	Acousoss	Homo sapiens		352	57
i			45% similarity to P22059		
1754	X690B9	Homo sapiens	(PID:g129308)	[1
1755	AL049795	Nomo sapiens		5703	99
1756	AL031393	Homo sapiens		1039	100
1 1730	ALUSISSS	Homo sapiens	1 (Dance tanger	2765	100
1757	AB040672		protein)	1	
1/3/	AB040672	Homo sapiens	UDP-GalNAc: polypeptide N-	2020	99
ł		Ī	acetylgalactosaminyltransfera		
1250	33000		58	ı	· [
1758	AL022238	Homo sapiens	dJ1042K10.4 (novel protein)	776	43
1760	AF117653	Homo sapiens	double homeobox protein	375	54
	¥12065	Homo sapiens	hNop56	2959	99
1761	AL049712	Homo sapiens	dJ686C3.2 (nucleolar protein	2595	99
		<u> </u>	hNop56)		1 33
1762	AC002394	Ното	Gene product with similarity	1542	51
		sapiens	to dynein beta subunit	1 -512	1 31
1763	AF169017	Homo sapiens	formiminotransferase	877	100
			cyclodeaminase	1	100
1764	U91541	Homo sapiens	human formiminotransferase	596	100
			cyclodeaminase (ftcd)protein		100
			carboxy-terminal end	i	
1765	AB013365	Bacillus	YlqF	350	34
		halodurans	1	100	1 34
1766	Y38421	Homo sapiens	Human secreted protein	145	71
1767			encoded by gene No. 36.		/ *
1/6/	AC009176	Arabidopsis	putative ribulose-1,5-	216	27
		thaliana	bisphosphate	1	- '
			carboxylase/oxygenase small	.]	
1768	27/0000		subunit N-methyltransferage T		
1769	AK000647	Homo sapiens	unnamed protein product	737	99
1770	AJ238982	Homo sapiens	VNN3 protein	2665	99
_	U73522	Homo sapiens	AMSH	1214	56
1771	U89435	Mus musculus	unknown	829	86
1772	S70011	Rattus sp.	tricarboxylate carrier	1604	95
1773	AL035086	Homo sapiens	dJ44A20.2 (novel protein)	2036	100
1774	Y99426	Homo sapiens	Human PRO1604 (UNO785) amino	1057	
			acid sequence SEQ ID NO:308.	·	99
1775	AF110330	Homo sapiens	glutaminase	3146	100
1776	AJ269529	Homo sapiens	glycerol 3-phosphate permease	2787	100
1777	Z81579	Caenorhabdit	cDNA EST yk76f1.5 comes from	232	31
		is elegans	this gene		
1778	AY007239	Homo sapiens	monooxygenase X	1875	99
1779	AL109608	Schizosaccha	oxysterol-binding protein	644	38
	ľ	romyces	family	-33	30
		pombe	-		
1780	AF254260	Homo sapiens	tuftelin 1	1729	100
1781	L07924	Mus musculus	guanine nucleotide	247	
		ļ	dissociation stimulator		50
1782	AF295773	Homo	ral guanine nucleotide	142	
	1	sapiens	dissociation stimulator	142	49.
1783	AK024475	Homo sapiens	FLJ00068 protein	4222	
1784	AK024475	Homo sapiens	FLJ00068 protein	4333	100
1785	G03933		Human secreted protein, SEQ	3996	93
	1		ID NO: 8014.	570	100
1786	S82637	Homo sapiens	Ig lambda-like gene/beta-	3.5	
			-3	247	100

TABLE 2

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	ક
ID	NUMBER			WATERMAN	IDENTITY
NO:				SCORE	
			glucuronidase exon 11 homolog		

TRADOCS:1416280.1(%CT401!.DOC)

SEQ ID N	O: ACCESSION NO.	DESCRIPTION	RESULTS*
2	BL00240	Receptor tyrosine kinase class III proteins.	BL00240B 24.70 8.250e- 12 157-181
3	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109D 17.04 8.085e- 13 358-381
4	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 9.400e- 10 1129-1146 BL00028 16.07 1.257e-09 820- 837
5	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 8.920e- 33 413-450 BL00023 24.31 4.545e-27 353- 390
6	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 8.920e- 33 413-450 BL00023 24.31 4.545e-27 353- 390
7	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 8.920e- 33 413-450 BL00023 24.31 4.545e-27 353- 390
8	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 8.920e- 33 413-450 BL00023 24.31 4.545e-27 353- 390
9	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 5.119e- 09 863-917
10	PR00464	E-CLASS P450 GROUP II SIGNATURE	PR00464D 17.40 6.182e- 12 294-312 PR00464G 12.41 4.231e-11 377- 393
11	PR00734	GLYCOSYL HYDROLASE FAMILY 7 SIGNATURE	PR00734I 11.46 4.296e- 09 502-520
12	PF00023	Ank repeat proteins.	PF00023B 14.20 6.500e- 10 99-99 PF00023B 14.20 2.636e-09 56-66
14	DM00031	IMMUNOGLOBULIN V REGION.	DM00031B 15.41 3.848e- 09 79-113
15	PR00208	GLIADIN AND LMW GLUTENIN SUPERFAMILY SIGNATURE	PR00208A 12.59 9.868e- 10 517-535 PR00208A 12.59 2.233e-09 520- 538
17	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.200e- 14 282-295 PD00066 13.92 9.400e-14 477- 490 PD00066 13.92 6.500e-13 505-518 PD00066 13.92 9.500e- 13 254-267 PD00066 13.92 1.429e-12 393- 406 PD00066 13.92 6.571e-12 421-434
18	BL00845	CAP-Gly domain proteins.	PL00845 16.43 2.200e- 25 55-80
20	BL00487	IMP dehydrogenase / GMP reductase proteins.	BL00487E 16.12 5.737e- 26 154-199 BL00487F 18.79 8.984e-22 235- 276 BL00487G 26.82 4.082e-12 287-329
21	BL00487	IMP dehydrogenase / GMP reductase proteins.	BL00487E 16.12 5.737e- 26 154-199 BL00487F 18.79 8.984e-22 235- 276 BL00487G 26.82
22	BL00107	Protein kinases ATP- binding region proteins.	4.082e-12 348-390 BL00107A 18.39 3.250e- 26 302-333

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
23	BL00107	Protein kinases ATP-	BL00107A 18.39 3.250e-
25	BL00115	binding region proteins. Eukaryotic RNA polymerase II heptapeptide repeat proteins.	26 302-333 BL00115T 8.45 7.273e- 29 1208-1242 BL00115Q 18.08 2.776e-21 953- 983 BL00115Y 11.86 8.000e-17 1604-1650 BL00115M 19.19 8.130e- 16 731-774 BL00115H 14.34 9.392e-16 463- 496 BL00115A 15.44 7.414e-15 43-82 BL00115R 6.50 6.128e- 14 983-1010 BL00115J 16.71 9.289e-14 591- 617 BL00115I 8.33 4.336e-13 535-590 BL00115L 12.25 5.939e- 13 662-694 BL00115G 11.65 6.011e-13 435- 463 BL00115K 15.03 3.417e-10 617-659 BL00115O 16.76 5.805e- 10 863-913 BL00115P 11.54 7.538e-10 913- 953 BL00115S 18.24 7.968e-10 1010-1052
26	BL00420	Speract receptor repeat	BL00115U 10.34 4.475e- 09 1242-1265 BL00420A 20.42 4.109e- 11 81-110 BL00420A
27	BL00050	proteins. Ribosomal protein L23	20.42 8.820e-10 84-113 BL00050A 23.71 9.250e-
	2250000	proteins.	27 94-127 BL00050B 14.81 8.125e-12 133-
28	PR00925	NONHISTONE CHROMOSOMAL PROTEIN HMG17 FAMILY SIGNATURE	PR00925B 3.73 3.089e- 10 41-54
29	PF00756	Putative esterase.	PF00756C 14.12 1.108e- 09 486-516
32	BL00557	FMN-dependent alpha- hydroxy acid dehydrogenases proteins.	BL00557D 17.76 5.065e- 37 274-316 BL00557A 35.08 8.909e-29 24-73 BL00557C 15.59 1.000e- 28 227-257 BL00557B 21.27 8.898e-22 130- 169
34	PR00629	SHC PHOSPHOTYROSINE INTERACTION DOMAIN SIGNATURE	PR00629E 9.90 5.886e- 35 299-328 PR00629F 10.95 8.364e-32 334- 361 PR00629B 13.66 3.786e-27 224-247 PR00629A 13.45 8.364e- 21 206-222 PR00629C 3.80 4.000e-12 249-261 PR00629D 12.45 3.739e- 11 276-286
35	PD01270	RECEPTOR FC IMMUNOGLOBULIN AFFIN.	PD01270A 17.22 1.000e- 40 39-79 PD01270B 22.18 2.875e-38 94-131 PD01270D 24.66 3.700e- 34 171-207 PD01270C 19.54 3.455e-30 137- 166
36	PD01270	RECEPTOR FC IMMUNOGLOBULIN AFFIN.	PD01270A 17.22 1.000e- 40 39-79 PD01270B 22.18 2.875e-38 94-131

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			PD01270D 24.66 3.700e- 34 171-207 PD01270C 19.54 3.455e-30 137- 166
37	BL00412	Neuromodulin (GAP-43) proteins.	BL00412C 10.28 9.241e- 10 264-298
38	BL00412	Neuromodulin (GAP-43) proteins.	BL00412C 10.28 9.24le- 10 264-298
39	BL00412	Neuromodulin (GAP-43) proteins.	BL00412C 10.28 9.241e- 10 264-298
40	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380B 12.64 7.366e- 14 342-360 PR00380C 13.18 6.927e-13 375- 394 PR00380D 9.93 2.180e-12 429-451 PR00380A 14.18 5.154e- 12 143-165
44	BL00345	Ets-domain proteins.	BL00345B 21.28 1.000e- 40 239-290 BL00345A 13.96 2.452e-14 204- 223
45	BL00345	Ets-domain proteins.	BL00345B 21.28 1.000e- 40 215-266 BL00345A 13.96 2.452e-14 180- 199
46	DM01551	kw OSTEOINDUCTIVE YOPM MEMBRANE OUTER.	DM01551A 15.63 3.538e- 26 172-202 DM01551C 14.62 3.571e-17 232- 252 DM01551B 8.84 4.750e-11 214-226
47	PR00876	NEMATODE METALLOTHIONEIN SIGNATURE	PR00876B 7.66 9.328e-
48	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 4.231e- 33 6-45
50	BL00972	Ubiquitin carboxyl- terminal hydrolases family 2 proteins.	BL00972D 22.55 7.750e- 19 994-1019 BL00972A 11.93 7.120e-18 216- 234 BL00972E 20.72 9.471e-14 1020-1042 BL00972C 16.48 7.000e- 13 360-375 BL00972B 9.45 8.269e-10 302-312
51	BL00972	Ubiquitin carboxyl- terminal hydrolases family 2 proteins.	BL00972D 22.55 7.750e- 19 990-1015 BL00972A 11.93 7.120e-18 216- 234 BL00972E 20.72 9.471e-14 1016-1038 BL00972C 16.48 7.000e- 13 360-375 BL00972B 9.45 8.269e-10 302-312
52	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 3.063e- 14 10-54
53	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 8.500e- 17 20-38 PR00988F 12.23 7.828e-15 196- 210 PR00988C 13.64 6.108e-14 104-120 PR00988E 8.27 3.872e- 11 174-186 PR00988D 5.95 6.878e-10 160-171 PR00988B 11.60 2.915e- 09 57-69
55	PR00762	CHLORIDE CHANNEL SIGNATURE	PR00762C 9.29 4.682e- 21 294-314 PR00762D 11.29 4.103e-19 509- 530 PR00762A 14.22 9.333e-18 199-217

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			PR00762F 15.12 3.100e-
			16 563-583 PR00762B
			12.12 6.063e-16 230-
			250 PR00762E 12.07
		1	2.286e-15 545-562
	1		PR00762G 14.13 6.276e-
56	BL00216	Sugar transport	13 601-616
56	BD00516	proteins.	BL00216B 27.64 8.800e- 10 153-203
58	PF00791	Domain present in ZO-1	PF00791B 28.49 2.049e-
36	1100,91	and Unc5-like netrin	10 1080-1135
		receptors.	
59	PF00791	Domain present in ZO-1	PFC0791B 28.49 2.049e-
		and Unc5-like nctrin receptors.	10 1062-1117
61	PD01929	KINASE TYPE RESISTANCE	PD01929E 10.76 9.018e-
		ANTIBIOTIC TRANSFERASE	09 206-221
68	PR00360	C2 DOMAIN SIGNATURE	PR00360A 14.59 7.395e-
			09 680-693
69	PR00360	C2 DOMAIN SIGNATURE	PR00360A 14.59 7.395e-
			09 670-683
70	PF00651	BTB (also known as BR-	PF00651 15.00 8.714e-
		C/Ttk) domain proteins.	10 51-64
72	DM00179	w KINASE ALPHA ADHESION	DM00179 13.97 5.304e-
73	BL00239	T-CELL.	09 108-118
73	BT00533	Receptor tyrosine kinase class II proteins.	BL00239B 25.15 7.075e-
74	BL00790	Receptor tyrosine kinase	BL00790N 13.25 6.116e-
14	200130	class V proteins.	10 93-120
76	DM00471	0 PROKARYOTIC DNA	DM00471A 11.73 9.357e-
,0	Dividua / 1	TOPOISOMERASE I.	13 53-66 DM00471B
			8.45 4.857e-12 70-81
80	PD02876	DECARBOXYLASE	PD02876C 8.80 2.723e-
		PHOSPHATIDYLSERINE.	13 223-236 PD02876D
			12.13 2.588e-12 334-
81	PD02876	DECARBOXYLASE	351 PD02876C 8.80 2.723e-
01	PD02076	PHOSPHATIDYLSERINE.	13 282-295 PD02876D
		PHOSPHALIDIESERINE.	12.13 2.588e-12 393-
			410
83	BL00708	Prolyl endopeptidase	BL00708B 24.91 7.197e-
		family serine proteins.	12 570-601
84	PR00014	FIBRONECTIN TYPE III	PR00014C 15.44 8.043e-
		REPEAT SIGNATURE	09 985-1004
86	PR00678	PI3 KINASE P85	PR00678H 9.13 1.379e-
	1	REGULATORY SUBUNIT	09 246-269
	<u> </u>	SIGNATURE	
89	PR00320	G-PROTEIN BETA WD-40	PR00320C 13.01 8.200e-
	1	REPEAT SIGNATURE	09 264-279 PR00320B
			12.19 8.650e-09 264-
02	DE OOASS	Dutantan and bearing	279
93	BL00455	Putative AMP-binding domain proteins.	BL00455 13.31 2.588e-
95	BL00107	Protein kinases ATP-	14 316-332 BL00107A 18.39 4.000e-
ور	PHOOTO	binding region proteins.	10 123-154
96	BL00107	Protein kinases ATP-	BL00107A 18.39 4.000e-
J.0	1,00010	binding region proteins.	10 212-243
97	PR00081	GLUCOSE/RIBITOL	PR00081B 10.38 6.318e-
		DEHYDROGENASE FAMILY	13 134-146 PR00081A
		SIGNATURE	10.53 2.500e-12 54-72
98	.PR00380	KINESIN HEAVY CHAIN	PR00380A 14.18 5.500e-
		SIGNATURE	24 401-423 PR00380D
			9.93 7.188e-20 613-635
			PR00380B 12.64 7.517e-
	1		16 529-547 PR00380C
			13.18 2.756e-13 560-
			579

SEQ ID N	O: ACCESSION NO.	DESCRIPTION	RESULTS*
102	PR00300	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT SIGNATURE	PR00300A 9.56 7.545e-
104	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 6.786e- 18 298-314 BL00479A 19.86 4.913e-16 155- 178 BL00479A 19.86 4.300e-13 272-295 BL00479B 12.57 6.294e- 12 181-197
106	BL01019	ADP-ribosylation factors family proteins.	BL01019A 13.20 8.013e- 12 43-83
107	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 5.000e-
108	BL00191	Cytochrome b5 family, heme-binding domain proteins.	3L00191K 17.38 4.951e- 27 238-282 BL00191J 11.37 6.447e-17 182- 204
109	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 4.938e- 37 8-47
110	BL01138	Scorpion short toxins proteins.	BL01138A 10.96 8.297e- 10 38-50
113	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 5.800e- 23 156-187 BL00107B 13.31 9.100e-14 225- 241
117	BL00214	Cytosolic fatty-acid binding proteins.	BL00214B 26.51 1.000e- 17 46-91 BL00214A 21.17 7.052e-11 5-31
118	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 8.560e- 13 36-67
119	PR00529	GONADOTROPHIN RELEASING HORMONE RECEPTOR SIGNATURE	PR00529C 11.03 7.506e- 10 158-177
120	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 9.400e-
121	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 9.400e-
127	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 7.158e- 13 216-241
128	BL01032	Protein phosphatase 2C proteins.	BL01032C 6.14 3.195e- 12 147-157 BL01032H 11.25 5.680e-11 318- 331 BL01032G 8.33 8.932e-11 282-296 BL01032I 10.42 8.902e- 09 379-389
129	BL01310	ATPIGI / PLM / MAT8 family proteins.	BL01310 14.74 6.694e- 26 28-64
130	PR00990	RIBOKINASE SIGNATURE	PR00990B 12.32 9.534e- 15 47-67 PR00990A 16.23 5.500e-14 20-42 PR00990C 12.62 2.412e- 09 119-133
133	BL00880	Acyl-CoA-binding protein.	BL00880 17.52 5.576e- 26 72-122
134	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 9.308e- 14 18-37
135	PR00215	NEUROMODULIN SIGNATURE	PR00215C 13.98 6.779e- 10 475-496
136	BL01310	ATP1G1 / PLM / MAT8 family proteins.	BL01310 14.74 2.432e- 29 71-107
140	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.882e- 14 214-231 BL00028 16.07 9.471e-14 102- 119 BL00028 16.07 2.800e-13 18-35

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		BL00028 16.07 5.500e-
			13 74-91 BL00028
	1		16.07 9.100e-13 186-
	-		203 BL00028 16.07
			8.043e-12 46-63
			BL00028 16.07 8.435e-
			12 130-147 BL00028
			16.07 9.217e-12 270-
			287 BL00028 16.07
			6.192e-11 242-259
			BL00028 16.07 4.000e-
			10 158-175
141	BL00501	Signal peptidases I	BL00501D 16.69 9.538e-
		serine proteins.	14 113-133 BL00501C 9.61 8.688e-10 89-101
143	Dr 01000	SAR1 family proteins.	BL01020C 15.35 7.722e-
143	BL01020	SARI Tamily processs.	20 79-130
146	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 6.400e-
140	ED0T000	ZINC-FINGER METAL-	25 335-374
		BINDING NU.	
149	BL00126	3'5'-cyclic nucleotide	BL00126C 22.07 1.450e-
		phosphodiesterases	25 509-550 BL00126E
		proteins.	35.22 3.951e-16 654-
			709 BL00126D 25.50
			1.360e-15 565-604
			BL00126B 15.20 8.200e-
	İ		11 483-495 BL00126A
			27.56 8.269e-11 442-
			479
151	BL00632	Ribosomal protein S4	BL00632 23.79 5.271e- 20 106-149
154	BL00559	proteins. Eukaryotic molybdopterin	BL00559I 13.63 5.304e-
124	PD00223	oxidoreductases	19 29-58 BL00559K
	1	proteins.	13.17 2.957e-18 172-
	1 .	proterns.	199 BL00559J 19.63
	1		8.385e-13 99-151
		1	BL00559L 13.60 5.814e-
		ł	12 241-259
155	PR00449	TRANSFORMING PROTEIN P21	PR00449A 13.20 1.692e-
		RAS SIGNATURE	13 13-35
157	BL00406	Actins proteins.	BL00406D 12.58 2.547e-
	1	}	18 275-330 BL00406A 9.95 5.776e-16 15-50
	1	1	BL00406B 5.47 7.429e-
			12 69-124 BL00406C
			6.75 9.682e-12 128-183
160	BL00132	Zinc carboxypeptidases,	BL00132A 26.07 7.000e-
		zinc-binding region 1	14 22-63 BL00132C
		proteins.	21.35 3.466e-12 104-
ı		}	145
165	PR00109	TYROSINE KINASE	PR00109B 12.27 9.043e-
		CATALYTIC DOMAIN	13 139-158
		SIGNATURE	
168	BL00362	Ribosomal protein S15	BL00362 24.67 9.700e-
		proteins.	15 129-172
169	BL00039	DEAD-box subfamily ATP-	BL00039D 21.67 1.000e-
109	PE00033		
109	BE00039	dependent helicases	35 640-686 BL00039A
109	PE00033	dependent helicases proteins.	18.44 1.964e-13 212- ·
103	BE00039		18.44 1.964e-13 212- · 251 BL00039B 19.19
109	8100039		18.44 1.964e-13 212- 251 BL00039B 19.19 4.553e-13 378-404
109	BE00039		18.44 1.964e-13 212 251 BL00039B 19.19 4.553e-13 378-404 BL00039C 15.63 8.773e-
		proteins.	18.44 1.964e-13 212 251 BL00039B 19.19 4.553e-13 378-404 BL00039C 15.63 8.773e- 12 465-489
175	PR00449	proteins. TRANSFORMING PROTEIN P21	18.44 1.964e-13 212 251 BL00039B 19.19 4.553e-13 378-404 BL00039C 15.63 8.773e- 12 465-489 PR00449A 13.20 3.721e-
175	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	18.44 1.964e-13 212- 251 BL00039B 19.19 4.553e-13 378-404 BL00039C 15.63 8.773e- 12 465-489 PR00449A 13.20 3.721e- 12 14-36
		TRANSFORMING PROTEIN P21 RAS SIGNATURE ATPIG1 / PLM / MAT8	18.44 1.964e-13 212- 251 BL00039B 19.19 4.553e-13 378-404 BL00039C 15.63 8.773e- 12 465-489 PR00449A 13.20 3.721e- 12 14-36 BL01310 14.74 2.432e-
175	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	18.44 1.964e-13 212- 251 BL00039B 19.19 4.553e-13 378-404 BL00039C 15.63 8.773e- 12 465-489 PR00449A 13.20 3.721e- 12 14-36

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
ļ	NO.	BINDING NU:	
180	DDOOGG		
180	PR00007	COMPLEMENT C1Q DOMAIN SIGNATURE	PR00007B 14.16.7.429e- 20 160-180 PR00007A 19.33 4.938e-19 133- 160 PR00007C 15.60 1.225e-15 206-228 PR00007D 9.64 6.885e- 11 238-249
3.83.	BL00027	'Homeobox' domain proteins.	BL00027 25.43 9.526e- 24 280-323
182	BL00027	'Homeobox' domain proteins.	BL00027 26.43 9.526e- 24 263-306
183	BL00027	'Homeobox' domain proteins.	BL00027 26.43 9.526e- 24 280-323
184	BL00027	'Homeobox' domain proteins.	BL00027 26.43 9.526e- 24 263-306
188	PR00929	AT-HOOK-LIKE DOMAIN SIGNATURE	PR00929C 5.26 3.328e- 09 460-471
189	PR00929	AT-HOOK-LIKE DOMAIN SIGNATURE	PR00929C 5.26 3.328e-
190	PR00450	Tyrosine specific protein phosphatases proteins.	09 440-451 BL00383F 15.51 7.188e- 17 666-682 BL00383A 13.34 8.714e-17 162- 177 BL00383E 10.35 1.000e-14 333-344 BL00383E 10.35 7.300e- 14 628-639 BL00383F 15.51 1.720e-13 371- 387 BL00383C 10.10 3.000e-13 217-228 BL00383D 11.92 7.000e- 13 295-308 BL00383B 7.61 1.692e-11 187-196 BL00383C 10.10 1.750e- 09 509-520 BL00383D 11.92 4.000e-09 589- 602 BL00383B 7.61 8.000e-09 479-488 PR00450C 12.22 7.911e-
193	PF00564	SIGNATURE Octicosapeptide repeat	15 83-105 PR00450C 12.22 6.286e-13 47-69
		proteins.	PF00564B 24.74 6.164e- 16 227-278
194	PR00503	BROMODOMAIN SIGNATURE	PR00503D 20.81 9.156e- 15 204-224 PR00503B 9.96 9.571e-13 170-187
195	BL00901	Cysteine synthase/cystathionine beta-synthase P- phosphate att.	BL00901C 20.63 3.429e- 18 67-117
197	BL00636	Nt-dnaJ domain proteins.	BL00636A 8.07 6.211e- 17 40-57 BL00636B 15.11 2.000e-13 67-88
198	PR00690	ADHESIN FAMILY SIGNATURE	PR00690A 10.86 9.866e- 09 463-482
199	BL01131	Ribosomal RNA adenine dimethylases proteins.	BL01131A 26.62 2.343e- 12 84-130
201	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 8.352e-
203	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 2.286e- 10 39-72
206	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE	PR00261A 11.02 4.462e- 19 65-87 PR00251C 11.37 9.308e-19 65-87 PR00261D 12.47 2.667e- 18 65-87 PR00261B 14.12 4.000e-18 143- 165 PR00261A 11.02

SEQ ID 1	NO: ACCESSION NO.	DESCRIPTION	RESULTS*
	140,		4.833e-18 143-165
	ļ		PR00261D 12.47 7.500e-
			18 143-165 PR00261B
		'	14.12 5.065e-16 65-87
			PR00261C 11.37 8.967e-
			16 143-165 PR00261F
i			11.57 4.938e-13 143- 165 PR00261E 11.08
			7.188e-13 65-87
			PR00261F 11.57 7.188e-
			13 65-87 PR00261E
			11.08 1.643e-11 143- 165
209	PF00791	Domain present in ZO-1	PF00791B 28.49 6.143e-
		and Unc5-like netrin	13 118-173 PF00791C
		receptors.	20.98 7.680e-10 132-
211	DD00007		171
211	PR00007	COMPLEMENT CLO DOMAIN SIGNATURE	PR00007A 19.33 5.781e-
		SIGNATURE	19 131-158 PR00007B 14.16 4.115e-18 158-
		1	178 PR00007C 15.60
		.	1.675e-15 201-223
			PR00007D 9.64 7.231e-
			11 233-244
212	BL00183	Ubiquitin-conjugating	BL00183 28.97 1.545e-
213	BL00183	enzymes proteins.	30 43-91
213	PERMIT	Ubiquitin-conjugating enzymes proteins.	BL00183 28.97 1.545e-
215	BL00039	DEAD-box subfamily ATP-	30 43-91 BL00039D 21.67 1.900e-
		dependent helicases	29 568-614 BL00039A
	[proteins.	18.44 1.871e-23 21-60
			BL00039C 15.63 1.720e-
		1	11 364-388 BL00039B
	· ·		19.19 4.064e-11 277- 303
217	BF00100	Chloramphenicol	BL00100D 17.22 8.484e-
		acetyltransferase	09 68-106
219	PR00213	proteins.	
223	FROUZES	MYELIN PO PROTEIN SIGNATURE	PR00213C 15.94 3.969e-
222	BL00678	Trp-Asp (WD) repeat	11 199-227 BL00678 9.67 1.947e-09
		proteins proteins.	144-155
224	PR00875	MOLLUSC METALLOTHIONEIN	PR00875A 5.83 1.000e-
225	BL00636	SIGNATURE	09 901-913
ل شد سه	959000	Nt-dnaJ domain proteins.	BL00636B 15.11 8.200e-
226	BL00636	Nt-dnaJ domain proteins.	19 18-39
•		and domain proceins.	BL00636A 8.07 1.000e- 21 21-38 BL00636B
			15.11 8.200e-19 45-66
229	PR00301	70 KD HEAT SHOCK PROTEIN	PR00301F 13.98 7.563e-
		SIGNATURE	13 329-346 PR00301G
			13.78 4.300e-12 361-
230	BL00460	Classification	382
230	5500460	Glutathione peroxidases selenocysteine proteins.	BL00460A 28.67 8.773e-
		boxenocysterne proteins.	20 35-70 BL00460B 9.73 7.429e-16 78-96
			BL00460C 14.35 2.831e-
			12 111-134 BL00460D
	1		16.89 8.773e-11 140-
			160
231	PR00647	SENR ORPHAN RECEPTOR	PR00647B 10.19 8.522e-
233	BL00292	SIGNATURE Cycling proteins	09 273-287
		Cyclins proteins.	BL00292B 20.31 7.429e- 27 244-275 BL00292A
			27 244-275 BL00292A 22.87 7.750e-27 201-
			235
234	PR00449	TRANSFORMING PROTEIN P21	PR00449A 13.20 6.308e-
	<u> </u>	RAS SIGNATURE	13 7-29 PR00449C
			L

SEQ ID N		DESCRIPTION	RESULTS*
-	NO.		17.27 4.462e-11 47-70
			PR00449D 10.79 7.120e- 11 109-123
235	PR00019	LEUCINE-RICH REPEAT	PR00019B 11.36 7.300e-
		SIGNATURE	10 251-265 PR00019B 11.36 5.320e-09 119-
			133 PR00019B 11.36
236	PR00019	LEUCINE-RICH REPEAT	1.000e-08 229-243
230	FR00013	SIGNATURE	PR00019B 11.36 7.300c 10 245-259 PR00019B
j	•		11.36 5.320e-09 113-
			127 PR00019B 11.36 1.000e-08 223-237
237	PD00289	PROTEIN SH3 DOMAIN	PD00289 9.97 8.448e-09
240		REPEAT PRESYNA.	67-81
240	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011D 14.03 3.492e- 10 616-635
241	PR00011	TYPE III EGF-LIKE	PR00011D 14.03 3.492e-
244	Pr.00003	SIGNATURE	10 616-635
232	BL00903	Cytidine and deoxycytidylate	BL00903 12.93 8.941e- 12 54-64
		deaminases zinc-binding	
245	DM00179	region s. w KINASE ALPHA ADHESION	·
213	Drioo173	T-CELL.	DM00179 13.97 8.043e- 09 124-134
248	BL00246	Wnt-1 family proteins.	BL00246D 23.97 1.000e-
			40 186-239 BL00246E
			20.32 1.000e-40 305- 351 BL00246B 13.69
			4.176e-36 105-140
			BL00246A 15.75 2.286e- 24 70-90 BL00246C
		ļ	15.56 4.857e-22 150-
250	PR00927	I DOWN THE NAME OF THE PARTY OF	175
230	PR00927	ADENINE NUCLEOTIDE TRANSLOCATOR 1 SIGNATURE	PR00927E 14.93 5.114e- 10 253-275
254	BL00674	AAA-protein family	BL00674B 4.46 1.000e-
255	PD01796	proteins. PROTEIN TRANSMEMBRANE	09 223-245 PD01796 15.01 6.045e-
		COBALT ZINC CADMIU.	09 61-88
255	BL50002	Src homology 3 (SH3)	BL50002B 15.18 2.800e-
258	PR00094	domain proteins profile. ADENYLATE KINASE	10 421-435 PR00094C 12.94 2.200e-
	·	SIGNATURE	18 87-104 PR00094D
			12.52 2.731e-14 161-
			177 PR00094A 10.31 5.500e-14 11-25
			PR00094B 11.01 4.115e-
			13 39-54 PR00094E 11.25 7.333e-13 178-
		<u> </u>	193
259	BL00892	HIT family proteins.	BL00892A 18.17 5.500e-
262	BL00388 ·	Proteasome A-type	13 60-91 BL00388A 23.14 1.000e-
		subunits proteins.	40 8-54 BL00388B
			31.38 3.864e-33 66-108
		1	BL00388D 20.71 1.000e- 21 153-184 BL00388C
		1	18.79 8.147e-16 126-
264	BL00903	Cytidine and	148
		deoxycytidylate	BL00903 12.93 5.821e- 09 91-101
		deaminases zinc-binding	
267	BL00107	region s. Protein kinases ATP-	PL00107P 12 21 2 500
		binding region proteins.	BL00107B 13.31 1.529e- 09 241-257
270	BL00226	Intermediate filaments	BL00226D 19.10 1.000e-
		proteins.	37 362-409 BL00226B

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			23.86 8.043e-35 196- 244 BL00226C 13.23 7.000e-20 261-292
271	PD02952	KINASE TRANSFERASE	BL00226A 12.77 6.143e- 15 96-111 PD02952C 15.76 9.731e-
		CHOLINE PROTEIN MULTIGENE FAMI.	16 235-265 PD02952B 15.57 5.625e-09 215-
272	PD02929	ADHESION GLYCOPROTEIN PRECURSOR I.	PD02929A 28.27 1.000e- 40 106-160 PD02929B 18.36 8.800e-17 179- 199
274	BL01027	Glycosyl hydrolases family 39 proteins.	BL01027B 15.34 3.486e-
275	PR00424	ADENOSINE RECEPTOR SIGNATURE	PR00424D 14.32 6.451e-
277	BL00052	Ribosomal protein S7 proteins.	BL00052A 27.85 6.000e- 13 137-184 BL00052B 15.17 5.143e-12 208- 235
279	BL00790	Receptor tyrosine kinase class V proteins.	BL00790N 13.25 5.659e- 13 267-294
280	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319D 11.64 6.625e- 23 107-125 PR00319C 13.41 1.000e-21 89-105 PR00319A 15.27 8.364e- 21 51-68 PR00319B 11.47 8.200e-19 70-85
281	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319D 11.64 6.625e- 23 94-112 PR00319C 13.41 1.000e-21 76-92 PR00319A 15.27 8.364e- 21 38-55 PR00319B
287	PF00929	Exonuclease.	11.47 8.200e-19 57-72 PF00929D 16.17 7.366e- 09 149-163
291	BL00326	Tropomyosins proteins.	BL00326A 14.01 2.360e- 09 93-127
292	BL00326	Tropomyosins proteins.	BL00326A 14.01 2.360e- 09 93-127
294	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.714e- 12 203-216
295	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 5.500e- 15 322-339 BL00028 16.07 9.471e-14 433- 450 BL00028 16.07 4.600e-13 648-665 BL00028 16.07 5.500e- 13 760-777 BL00028 16.07 9.550e-13 788- 805 BL00028 16.07 3.348e-12 704-721 BL00028 16.07 6.478e- 12 461-478 BL00028 16.07 8.435e-12 844- 861 BL00028 16.07 1.692e-11 593-610 BL00028 16.07 2.038e- 11 211-228 BL00028 16.07 5.154e-11 732- 749 BL00028 16.07 5.846e-11 377-394 BL00028 16.07 6.885e- 11 816-833 BL00028 16.07 7.231e-11 676- 693 BL00028 16.07 9.654e-11 564-581

SEQ ID N	O: ACCESSION NO.	DESCRIPTION	RESULTS*
			BL00028 16.07 4.086e- 09 517-534 BL00028 16.07 7.429e-09 489- 506
296	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 8.333e- 16 111-136 BL00215A 15.82 2.723e-11 10-35 BL00215B 10.44 9.526e- 11 152-165 BL00215B 10.44 7.375e-10 59-72 BL00215A 15.82 9.824e-
302	PF00953	Glycosyl transferase.	10 205-230 PF00953C 19.70 8.773e- 34 236-269 PF00953A 19.68 5.000e-25 102- 129 PF00953B 6.17
304	PF00152	tRNA synthetases class	1.000e-13 182-194 PF00152D 21.30 8.364e- 28 422-461 PF00152C 28.03 9.250e-21 220- 257 PF00152B 15.67 2.658e-13 159-184 PF00152A 19.68 5.714e- 11 44-67
305	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 8.250e- 35 37-76
305	PD02784	PROTEIN NUCLEAR RIBONUCLEOPROTEIN.	PD02784B 26.46 5.840e-
307	PR00454	ETS DOMAIN SIGNATURE	PR00454C 11.24 7.808e- 09 1167-1186
308	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237E 13.03 5.091e- 13 188-212 PR00237G 19.63 7.207e-13 268- 295 PR00237A 11.48 4.375e-11 24-49 PR00237C 15.69 3.057e- 10 101-124 PR00237D 8.94 4.750e-10 137-159 PR00237F 13.57 5.364e- 10 230-255 PR00237B 13.50 9.438e-10 57-79
309	BL00522	DNA polymerase family X proteins.	BL00522C 11.90 7.577e- 24 315-339 BL00522F 14.90 1.310e-15 470- 494 BL00522A 25.52 1.265e-14 179-226 BL00522E-19.63 8.615e- 14 430-460 BL00522B 27.30 9.625e-12 267- 313
310	BL00326	Tropomyosins proteins.	BL00326D 8.76 5.235e-
312	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 4.706e- 14 151-174 BL00290B 13.17 9.000e-12 211- 229
313	BL00345	Ets-domain proteins.	BL00345B 21.28 1.000e- 40 34-85 BL00345A 13.96 9.217e-16 1-20
315	PF00651	BTB (also known as BR- C/Ttk) domain proteins.	PF00651 15.00 5.091e- 15 63-76
317	BL01020	SAR1 family proteins.	BL01020C 15.35 3.198e- 17 79-130
318	BL00216	Sugar transport proteins.	BL00216B 27.64 4.696e- 11 164-214
320	PR00109	TYROSINE KINASE	PR00109B 12.27 4.814e-

SEQ ID N	O: ACCESSION NO.	DESCRIPTION	RESULTS*
		SIGNATURE	
321	BL00027	'Homeobox' domain proteins.	BL00027 26.43 5.688e- 10 329-372
322	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 8.765e- 12 558-577
324	BL01241	Link domain proteins.	BL01241 35.81 8.313e- 30 183-236 BL01241 35.81 3.222c-13 282- 335
326	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 4.000e- 12 515-566 BL00412D 16.54 5.705e-11 516- 567 BL00412D 16.54 7.848e-10 518-569 BL00412D 16.54 1.827e- 09 514-565 BL00412D 16.54 1.918e-09 513- 564 BL00412D 16.54 2.102e-09 520-571
328	BL00232	Cadherins extracellular repeat proteins domain proteins.	BL00232B 32.79 9.557e- 20 151-199 BL00232B 32.79 2.246e-18 41-89 BL00232B 32.79 5.985e- 18 370-418 BL00232B 32.79 5.500e-16 258- 306 BL00232B 32.79 9.384e-15 475-523 BL00232C 10.65 2.537e- 12 256-274 BL00232C 10.65 4.326e-11 368- 386 BL00232C 10.65 7.261e-11 473-491 BL00232C 10.65 7.457e- 11 39-57
330	PR00454	ETS DOMAIN SIGNATURE	PR00454C 11.24 7.808e- 09 1167-1186
331	BL00598	Chromo domain proteins.	BL00598 14.45 8.393e- 18 27-49
333	BL01016	Glycoprotease family proteins.	BL01016C 22.84 3.925e- 32 70-115 BL01016E 14.88 5.286e-19 149- 177 BL01016H 13.71 7.577e-13 291-301 BL01016D 8.86 3.298e- 11 127-140 BL01016G 7.14 5.622e-10 261-271 BL01016A 5.65 7.167e- 10 4-19 BL01016F 13.34 1.563e-09 200- 212 BL01016B 8.93 8.855e-09 38-50
339	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 5.500e- 11 17-61
340	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 1.231e- 33 10-49
341	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 5.042e- 09 55-109
342	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 2.400e- 30 16-55
343	DM00031	IMMUNOGLOBULIN V REGION.	DM00031A 16.80 1.000e- 40 20-68
346	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 4.764e- 11 135-154
347	PR00109	TYROSINE KINASE	PR00109B 12.27 4.764e-

SEQ ID I		DESCRIPTION	RESULTS*
	NO.	CATALYTIC DOMAIN	
		SIGNATURE	11 135-154
351	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.	BL01187B 12.04 1.783e- 13 100-116 BL01187B 12.04 8.435e-13 276- 292 BL01187B 12.04 8.800e-11 13-29 BL01187B 12.04 7.429e- 10 54-70 BL01187B 12.04 5.725e-09 231- 247 BL01187A 9.98
352	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	7.000e-09 255-267 PD00078B 13.14 5.950e- 10 366-379 PD00078B 13.14 4.522e-09 168- 181
354	BL00380	Rhodanese proteins.	BL00380F 9.76 6.694e-
355	PF00628	PHD-finger.	11 542-553 PF00628 15.84 1.000e-
356	PR00587	SOMATOSTATIN RECEPTOR TYPE 1 SIGNATURE	PR00587A 8.06 9.700e-
359	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	09 17-37 PD00066 13.92 4.462e- 15 261-274 PD00066 13.92 6.500e-13 233- 246 PD00066 13.92 4.300e-09 289-302
361	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 9.604e- 13 54-109 PF00791B 28.49 1.095e-12 21-76 PF00791A 27.85 1.432e- 09 71-126 PF00791B 28.49 7.440e-09 184- 239
362	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 2.273e- 11 279-334
363	PR00450	RECOVERIN FAMILY SIGNATURE	PR00450C 12.22 5.080e- 10 73-95 PR00450C 12.22 3.278e-09 109-
364	PF00242	DNA polymerase (viral) N-terminal domain proteins.	131 PF00242Q 13.51 2.328e- 09 22-68
365	PF00242	DNA polymerase (viral) N-terminal domain proteins.	PF00242Q 13.51 2.328e- 09 22-68
366	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 6.644e- 09 1038-1092
367	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 1.360e- 09 229-243 PR00019B 11.36 6.040e-09 91-105 PR00019A 11.19 8.667e- 09 370-384
368	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011D 14.03 9.000e- 15 30-49 PR00011A 14.06 9.830e-15 30-49 PR00011B 13.08 4.500e- 14 30-49 PR00011C 24.25 5.143e-09 6-35
369	BL01032	Protein phosphatase 2C proteins.	BL01032H 11.25 4.150e- 09 417-430
372	BL00478	LIM domain proteins.	BL00478B 14.79 7.750e- 12 410-425
373	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 9.757e- 34 26-65
376	PR00170	SODIUM CHANNEL SIGNATURE	PR00170E 6.48 2.739e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			10 88-118
380	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 1.000e- 23 276-307 BL00107B 13.31 1.692e-12 342- 358
381	BL00455	Putative AMP-binding domain proteins.	BL00455 13.31 5.714e- 12 50-66
382	PR00624	HISTONE HS SIGNATURE	PR00624G 4.08 4.900e- 09 524-544
384	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 5.950e- 10 366-379 PD00078B 13.14 4.522e-09 168-
385	PR00511	TEKTIN SIGNATURE	PR00511D 7.11 5.371e-
386	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.	PD02870B 18.83 6.000e-
388	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 5.000e- 13 516-529
389	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 7.667e- 09 151-174
390	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 5.200e- 15 221-246 BL00215A 15.82 7.618e-14 20-45 BL00215A 15.82 8.851e- 11 123-148 BL00215B 10.44 9.526e-11 69-82 BL00215B 10.44 7.300e- 09 272-285 BL00215B 10.44 8.500e-09 165- 178
394	BL00674	AAA-protein family proteins.	BL00674B 4.46 2.723e- 16 299-321
397	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 8.579e-
398	PR00761	BINDIN PRECURSOR SIGNATURE	PR00761B 9.93 6.764e-
399	BL00240	Receptor tyrosine kinase class III proteins.	BL00240B 24.70 7.907e- 10 118-142
401	PF00676	Dehydrogenase E1 component.	PF00676B 24.71 8.071e- 18 331-369 PF00676D 14.40 3.854e-15 486- 506 PF00676C 16.88 9.182e-14 454-478
402	BL00514	Fibrinogen beta and gamma chains C-terminal domain proteins.	BL00514C 17.41 4.673e- 28 4432-4469 BL00514G 15.98 6.092e-14 4555- 4585 BL00514D 15.35 2.532e-12 4473-4486 BL00514F 11.65 4.288e- 10 4519-4534 BL00514H 14.95 4.955e-10 4584- 4609
403	PF00992	Troponin.	PF00992A 16.67 5.974e- 09 105-140
404	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 1.450e- 10 73-87 PR00019A 11.19 8.043e-10 76-90 PR00019B 11.36 1.000e- 09 50-64 PR00019B 11.36 1.000e-09 96-110
405	BL00232	Cadherins extracellular repeat proteins domain proteins.	BL00232B 32.79 9.557e- 20 139-187 BL00232B 32.79 2.246e-18 29-77 BL00232B 32.79 5.985e- 18 358-406 BL00232B 32.79 5.500e-16 246-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			294 BL00232B 32.79 9.384e-15 463-511
			BL00232C 10.65 2.537e- 12 244-262 BL00232C
			10.65 4.326e-11 356-
		·	374 BL00232C 10.65 7.261e-11 461-479
			BL00232C 10.65 7.457e-
407	PF00426	Outer Capsid protein VP4	PF00426S 15.67 5.634e-
409	BL01160	(Hemagglutinin). Kinesin light chain	09 902-940 BL01160B 19.54 9.695e-
410	BL00741	repeat proteins.	09 126-180
410	BB00741	dissociation stimulators CDC24 family sign.	BL00741B 14.27 2.731e- 09 252-275
411	PF00646	F-box domain proteins.	PF00646A 14.37 6.344e- 09 86-100
412	BL00603	Thymidine kinase	BL00603B 11.39 8.500e-
415	BL00866	Carbamoyl-phosphate	09 542-557 BL00866B 36.29 3.571e-
		synthase subdomain proteins.	31 245-291 BL00866C 23.26 9.000e-25 331-
			366
41.8	PR00239	MOLLUSCAN RHODOPSIN C- TERMINAL TAIL SIGNATURE	PR00239E 1.58 6.114e- 09 590-602
421	PF00791	Domain present in 20-1	PF00791B 28.49 7.955e-
		and Unc5-like netrin receptors.	14 23-78 PF00791B 28.49 3.653e-12 273-
		_	328 PF00791B 28.49
			4.273e-11 156-211 PF00791B 28.49 7.818e-
			11 89-144 PF00791B 28.49 1.524e-10 56-111
			PF00791C 20.98 3.559e-
	,		09 37-76 PF00791C 20.98 5.235e-09 170-
			209 PF00791C 20.98
			5.235e-09 381-420 PF00791B 28.49 6.202e-
]		09 189-244 PF00791B
			28.49 7.028e-09 435- 490 PF00791B 28.49
424	DM00892	3 RETROVIRAL PROTEINASE.	8.679e-09 367-422
			DM00892C 23.55 7.207e- 28 1645-1679
425	PR00109	TYROSINE KINASE CATALYTIC DOMAIN	PR00109D 17.04 5.881e-
		SIGNATURE	10 220 231
429	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 4.600e- 11 31-40
431	BL00039	DEAD-box subfamily ATP-	BL00039D 21.67 1.844e-
		dependent helicases proteins.	34 490-536 BL00039A 18.44 5.615e-19 205-
		1	244 BL00039B 19.19
			8.920e-16 251-277 BL00039C 15.63 5.781e-
432	PR00452	SH3 DOMAIN SIGNATURE	15 333-357 PR00452B 11.65 7.652e-
			12 169-185
433	PR00828	FORMIN SIGNATURE	PR00828B 5.23 8.218e- 10 382-405
436	BL00415	Synapsins proteins.	BL00415N 4.29 8.643e-
			11 195-239 BL00415N 4.29 3.036e-09 809-853
443	PR00834	HTRA/DEGO PROTEASE FAMILY SIGNATURE	PR00834F 10.91 6.040e-
446	PF01140	Matrix protein (MA),	11 221-234 PF01140D 15.54 9.663e-

SEQ ID N	O: ACCESSION	DESCRIPTION	RESULTS*
ļ	NO.		
		p15.	10 183-218 PF01140D 15.54 3.093e-09 246- 281
449	PR00568	DOPAMINE D3 RECEPTOR SIGNATURE	PRC0568G 13.95 5.551e- 09 39-53
451	PF00084	Sushi domain proteins (SCR repeat proteins.	PF00084B 9.45 3.813e- 10 47-59
452	BL00790	Receptor tyrosine kinase class V proteins.	BL00790I 20.01 2.821e-
456	PR0038C	KINESIN HEAVY CHAIN SIGNATURE	09 618-649 PR00380A 14.18 1.000e- 25 77-99 PR00380D 9.93 1.000e-21 281-303 PR00380C 13.18 8.286e- 17 230-249 PR00380B 12.64 4.724e-16 194-
457	PR00253	GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE	PR00253A 9.15 9.143e- 24 246-267 PR00253B 13.47 2.000e-23 272- 294 PR00253C 13.85 7.000e-23 306-328 PR00253D 16.68 5.950e-
467	PR00849	GLYCOSYL HYDROLASE FAMILY 58 SIGNATURE	21 452-473 PR00849D 9.77 9.236e-
471	BL00678	Trp-Asp (WD) repeat proteins proteins.	09 910-937 BL00678 9.67 8.200e-12
472	BL00226	Intermediate filaments proteins.	33-44 BL00226B 23.86 3.721e-
473	BL00344	GATA-type zinc finger	09 282-330 BL00344 17.99 7.000e-
474	BL00481	domain proteins. Thiol-activated	12 814-852 BL00481E 13.07 8.909e-
479	PR00319	cytolysins proteins. BETA G-PROTEIN	09 173-199 PR00319B 11.47 2.571e-
480	PD01066	(TRANSDUCIN) SIGNATURE PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	09 393-408 PD01066 19.43 1.900e- 38 8-47
481	PR00405	HIV REV INTERACTING PROTEIN SIGNATURE	PR00405C 19.41 1.000e- 19 451-473 PR00405B 11.83 4.333e-18 430- 448 PR00405A 17.71 4.971e-18 411-431
482	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PRO0049D 0.00 9.286e- 10 959-974 PR00049D 0.00 9.857e-10 958-973 PR00049D 0.00 1.305e- 09 937-952 PR00049D 0.00 8.322e-09 939-954
486	PR00007	COMPLEMENT C1Q DOMAIN SIGNATURE	PR00007B 14.16 8.615e- 23 653-673 PR00007A 19.33 6.192e-22 626- 653 PR00007C 15.60 5.846e-19 698-720 PR00007D 9.64 3.647e- 13 732-743
487	PD00567	PROTEIN RNA-BINDING RNA REPEAT HYD.	PD00567B 18.23 2.853e- 09 200-214
488	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 4.569e-
489	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-	PD01066 19.43 4.882e- 27 30-69 PD01066
490	PR00049	BINDING NU. WILM'S TUMOUR PROTEIN	19.43 3.430e-10 71-110 PR00049D 0.00 7.864e-
492	BL01128	SIGNATURE Shikimate kinase	09 663-678 BL01128A 18.84 6.464e-
497	PF00429	proteins. ENV polyprotein (coat	17 58-92 PF00429 31.08 7.171e-

SEQ ID NO	O: ACCESSION NO.	DESCRIPTION	RESULTS*
		polyprotein).	15 22 22
498	BL00120	Lipases, serine	15 21-71 BL00120B 11.37 7.923e-
		proteins.	09 185-200
500	BL00030	Eukaryotic RNA-binding	BL00030A 14.39 7.353e-
		region RNP-1 proteins.	11 299-318
501	BL01159	WW/rsp5/WWP domain	BL01159 13.85 8.579e-
505	BL00021	proteins.	12 131-146
303	B200021	Kringle domain proteins.	BL00021B 13.33 3.739e- 17 492-510
508	PR00120	H+TRANSPORTING ATPASE	PR00120C 9.90 5.800e-
	}	(PROTON PUMP) SIGNATURE	19 705-722
509	DM01417	6 kw INDUCING XPMC2	DM01417E 20.62 2.938e-
		MUSHROOM SPAC22G7.04.	16 362-395 DM01417D
			11.08 3.800e-13 322-
510	PF00534	Glycosyl transferases	338
Í		group 1.	PF00534B 14.47 6.625e- 09 346-370
511	PF00534	Glycosyl transferases	PF00534B 14.47 6.625e-
		group 1.	09 293-317
512	PF00534	Glycosyl transferases	PF00534B 14.47 6.625e-
513	PD01841	group 1. PHOSPHORYLASE KINASE	09 366-390
		ALPHA MUSCL.	PD01841A 21.71 1.000e- 40 110-160 PD01841B
			14.35 1.000e-40 181-
			222 PD01841D 17.87
			1.000e-40 243-295
			PD01841F 13.36 1.000e-
			40 333-382 PD01841G 24.26 1.000e-40 386-
			440 PD01841L 18.42
			1.000e-40 968-1010
			PD01841I 23.00 4.545e-
	-		37 762-804 PD01841E
			18.60 3.750e-36 295- 333 PD01841J 14.94
	·		6.023e-35 851-888
			PD01841H 21.30 2.909e-
			33 490-527 PD01841K
			14.81 7.088e-33 924- 954 PD01841C 13.78
	ļ		9.386e-23 222-243
			PD01841M 10.82 8.594e-
			21 1054-1073 PD01841I
			23.00 2.667e-13 549-
514	PR00153	CYCLOPHILIN PEPTIDYL-	591 PR00153C 11.01 7.188e-
		PROLYL CIS-TRANS	13 95-111 PR00153E
<u> </u>		ISOMERASE SIGNATURE	9.10 4.150e-12 122-138
515	BL00740	MAM domain proteins.	BL00740A 13.87 7.188e-
516	DM00892	3 DRWDOVIDAY SOOMS	12 410-423
	DM00832	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 6.087e-
517	BL00242	Integrins alpha chain	12 1018-1052 BL00242C 16.86 8.320e-
		proteins.	09 12-42
523	DM00031	IMMUNOGLOBULIN V REGION.	DM00031A 16.80 3.750e-
			39 20-68 DM00031B
525	BL00319	Dm. 2 a / 3	15.41 1.000e-25 84-118
	2500313	Amyloidogenic glycoprotein	BL00319C 17.12 8.375e-
		extracellular domain	10 61-95
		proteins.	
526	PF00789	Domain present in	PF00789B 19.70 3.308e-
	1	ubiquitin-regulatory	12 322-343 PF00789C
		proteins.	20.98 5.269e-09 367-
			392
528	BL01162	Quinone ovidereduction	I
528	BL01162	Quinone oxidoreductase / zeta-crystallin	BL01162C 22.80 1.500e- 16 120-164

SEQ ID NO	: ACCESSION NO.	DESCRIPTION	RESULTS*
529	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 3.893e- 09 60-73
532	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 4.000e- 17 11-36 BL00215A 15.82 8.660e-11 123- 148
533	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 4.000e- 17 11-36 BL00215A 15.82 8.660e-11 97-122
534	BL00098	Thiolases acyl-enzyme intermediate proteins.	BL00098C 21.65 2.800e- 38 181-227 BL00098B 32.59 5.345e-38 86-141 BL00098D 26.30 8.364e- 35 245-288 BL00098E 22.12 1.000e-34 314- 352 BL00098F 10.18 4.971e-22 365-386 BL00098A 10.60 6.455e- 11 38-50
535	PR00370	FLAVIN-CONTAINING MONOOXYGENASE (FMO) SIGNATURE	PR00370E 11.96 7.429e- 22 321-340 PR00370D 16.33 6.143e-21 185- 204 PR00370F 17.75 6.559e-21 376-396 PR00370B 10.91 9.591e- 21 27-46 PR00370C 12.72 3.500e-20 140- 157 PR00370A 3.35 6.442e-17 4-20
536	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.429e- 16 285-302 BL00028 16.07 6.294e-14 341- 358 BL00028 16.07 1.346e-11 369-386 BL00028 16.07 1.692e- 11 397-414 BL00028 16.07 4.462e-11 453- 470 BL00028 16.07 7.231e-11 425-442 BL00028 16.07 4.300e- 10 313-330
537	BL00762	WHEP-TRS domain proteins.	BL00762A 23.43 9.419e- 15 844-881
538	BL00762	WHEP-TRS domain proteins.	BL00762A 23.43 9.419e- 15 819-856
539	BL00762	WHEP-TRS domain proteins.	BL00762A 23.43 9.419e- 15 822-859
540	PR00985	LEUCYL-TRNA SYNTHETASE SIGNATURE	PR00985A 12.10 9.000e- 10 357-375
541	PD02102	SUBUNIT E V-ATPASE VACUOLAR ATP SYNTHASE HYDROL.	PD02102A 16.74 1.000e- 40 3-47 PD02102B 18.28 4.375e-34 57-100 PD02102D 21.69 1.923e- 30 179-218 PD02102C 26.34 8.929e-26 100- 146
543	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 1.000e- 10 48-65 BL00028 16.07 6.400e-10 193- 210 BL00028 16.07 1.000e-09 343-360 BL00028 16.07 6.914e- 09 78-95
545	BL00250	TGF-beta family , proteins.	BL00250A 21.24 8.000e- 31 293-329 BL00250B 27.37 5.286e-24 354- 390
547	PR00319	BETA G-PROTEIN	PR00319B 11.47 2.714e-

SEQ ID NO		DESCRIPTION	RESULTS*
	NO.	(TRANSDUCIN) SIGNATURE	
			09 186-201 PR00319A 15.27 7.344e-09 210- 227
548	BL01204	NF-kappa-B/Rel/dorsal domain proteins.	BL01204A 17.74 1.000e- 40 8-56 BL01204D 16.42 1.000e-40 177- 221 BL01204E 13.83 7.652e-30 225-250 BL01204C 13.93 8.714e- 22 141-160 BL01204B 15.41 4.333e-16 102-
549	PR00326	GTP1/OBG GTP-BINDING	116 PR00326A 8.75 8.364e-
551	PF00632	PROTEIN FAMILY SIGNATURE	15 255-276
331	PF00632	HECT-domain (ubiquitin- transferase).	PF00632C 20.66 3.302e- 23 1569-1601 PF00632B 18.45 3.700e-21 1515- 1543
554	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290B 13.17 1.600e- 14 187-205 BL00290A 20.89 2.059e-14 130- 153
557	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 6.339e- 09 846-879
559	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.	DM01111L 11.93 3.762e- 09 7-35
562	PF00658	Poly-adenylate binding protein, unique domain proteins.	PF00658C 16.33 9.455e- 32 118-155
564	BL00141	Eukaryotic and viral aspartyl proteases proteins.	BL00141A 12.10 4.150e- 10 472-488
566	PF00855	PWWP domain proteins.	PF00855 13.75 5.667e- 15 272-289
567	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 4.977e- 13 229-268
569	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 7.000e- 19 118-149 BL00107B 13.31 5.500e-15 183-
570	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 7.000e- 19 118-149 BL00107B 13.31 5.500e-15 183-
572	PR00193	MYOSIN HEAVY CHAIN SIGNATURE	199 PR00193D 14.36 1.857e- 34 454-483 PR00193C 12.60 2.636e-31 223- 251 PR00193B 11.69 7.750e-29 171-197 PR00193A 15.41 2.588e- 22 115-135 PR00193E 19.47 6.559e-19 508- 537
573	PR00193	MYOSIN HEAVY CHAIN SIGNATURE	PR00193D 14.36 1.857e- 34 470-499 PR00193C 12.60 2.636e-31 239- 267 PR00193B 11.69 7.750e-29 171-197 PR00193A 15.41 2.588e- 22 115-135 PR00193E 19.47 6.559e-19 524- 553
575	BL00752	XPA protein.	BL00752B 19.17 9.703e- 10 885-929
576	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 7.000e- 09 276-295
577	BL00116	DNA polymerase family B	BL00116A 12.81 5.737e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		proteins.	13 864-877 BL00116B 11.82 1.529e-12 952-
578	BL00195	Glutaredoxin proteins.	965 BL00195B 15.31 7.158e- 09 121-141
579	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PRO0019B 11.36 9.000e- 11 217-231 PR00019B 11.36 1.360e-09 386- 400 PR00019A 11.19 3.333e-09 389-403 PR00019B 11.36 8.920e- 09 363-377
580	PR00253	GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE	PR00253A 9.15 2.125e- 25 275-296 PR00253B 13.47 7.923e-24 301- 323 PR00253D 16.68 5.846e-23 444-465 PR00253C 13.85 2.241e- 20 335-357
583	PR00343	SELECTIN SUPERFAMILY COMPLEMENT-BINDING REPEAT SIGNATURE	PR00343C 16.85 2.286e- 11 1233-1252 PR00343C 16.85 5.500e-11 333- 352 PR00343C 16.85 5.500e-11 783-802 PR00343C 16.85 4.246e- 10 1491-1510 PR00343C 16.85 8.230e-10 1686- 1705
584	DM01537	kw SKI2W SKI2 NUCLEOLAR HELICASE.	DM01537B 21.63 1.878e- 37 79-126 DM01537B 21.63 9.491e-30 916- 963 DM01537A 15.14 3.196e-11 784-804
586	PFC0013	KH domain proteins family of RNA binding proteins.	PF00013 5.78 1.450e-09 124-136
587	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 4.409e- 13 262-296
589	BL00478	LIM domain proteins.	BL00478B 14.79 1.643e- 13 261-276 BL00478B 14.79 7.709e-09 321- 336
590	PF00855	PWWP domain proteins.	PF00855 13.75 8.000e- 15 931-948
591	PF00855	PWWP domain proteins.	PF00855 13.75 8.000e-
593	PF00628	PHD-finger.	PF00628 15.84 3.455e- 12 424-439
594	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 2.241e- 16 558-576 PR00205A 14.73 9.308e-13 542- 558 PR00205C 13.65 5.304e-12 594-609 PR00205B 11.39 4.273e- 10 336-354
596	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 4.789e- 18 307-338
598	PD01675	GLYCOPROTEIN MAJOR ENVELOPE PROBABLE U3.	PD01675C 19.89 2.330e- 10 55-89
600	BL00242	Integrins alpha chain proteins.	BL00242E 9.03 9.591e- 27 985-1014 BL00242C 16.86 4.115e-26 286- 316 BL00242D 13.57 4.150e-25 357-382 BL00242B 8.13 7.353e- 12 189-199 BL00242D 13.57 3.455e-11 421- 446 BL00242A 13.80

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			5.000e-11 61-73 BL00242D 13.57 4.986e- 10 291-316
601	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 5.610e- 09 198-213
602	PR00278	PANCREATIC HORMONE SIGNATURE	PR00278A 12.43 4.569e- 10 331-348
603	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479C 12.01 3.250e- 12 170-183
604	BL00315	Dehydrins proteins.	BL00315A 9.35 1.672e- 09 424-452
605	BL00415	Synapsins proteins.	BL00415N 4.29 9.794e- 10 295-339
606	PR00926	MITOCHONDRIAL CARRIER PROTEIN SIGNATURE	PR00926F 17.75 1.000e-
608	PF00855	PWWP domain proteins.	PF00855 13.75 5.167e- 15 265-282
609	PF00855	PWWP domain proteins.	PF00855 13.75 5.167e-
612	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	15 211-228 DMO1206B 10.69 7.411e- 10 877-897 DM01206B 10.69 8.027e-10 861- 881 DM01206B 10.69 9.137e-10 873-893 DM01206B 10:69 1.456e- 09 859-879 DM01206B 10.69 1.797e-09 879- 899 DM01206B 10.69 4.076e-09 865-885 DM01206B 10.69 7.038e- 09 898-918 DM01206B 10.69 7.949e-09 871- 891 DM01206B 10.69 8.291e-09 767-787
615	PD02699	PROTEIN DNA-BINDING BINDING DNA.	PD02699A 8.91 2.023e- 28 129-158 PD02699C 24.84 1.000e-27 317- 364 PD02699B 18.28 1.000e-17 158-182
616	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PRO0380A 14.18 4.086e- 22 288-310 PR00380D 9.93 3.721e-17 486-508 PR00380B 12.64 2.241e- 16 410-428 PR00380C 13.18 2.976e-13 436- 455'
617	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 4.086e- 22 288-310 PR00380D 9.93 3.721e-17 486-508 PR00380B 12.64 2.241e- 16 410-428 PR00380C 13.18 2.976e-13 436- 455
618	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM012C6B 10.69 5.143e- 12 531-551 DM01206B 10.69 2.603e-10 535- 555
621	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE	PR00700B 16.80 3.160e-
622	BL00239	Receptor tyrosine kinase class II proteins.	BL00239F 28.15 3.222e- 10 647-692 BL00239C 18.75 8.304e-10 543-
623	PR00407	EUKARYOTIC MOLYBDOPTERIN DOMAIN SIGNATURE	PR00407K 9.94 8.448e- 09 326-339
	BL00641	Respiratory-chain NADH	V 320-337

SEO ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		
		subunit proteins.	24.37 1.000e-40 255- 308 BL00641F 33.12 1.000e-40 571-623 BL00641A 17.15 1.818e- 37 48-80 BL00641B 12.62 5.846e-34 113- 139 BL00641D 13.23
627	PR00103	CAMP-DEPENDENT PROTEIN KINASE SIGNATURE	9.308e-29 216-240 PR00103E 17.80 2.500e- 18 367-380 PR00103B 13.39 2.080e-14 297- 312 PR00103A 9.59 2.957e-14 282-297 PR00103D 10.83 3.077e- 12 346-358 PR00103C 15.68 1.000e-11 334- 344 PR00103B 13.39 1.450e-11 175-190 PR00103A 9.59 1.720e- 10 160-175
630	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE	PR00081A 10.53 6.211e- 16 4-22
631	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 8.500e-
632	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 2.233e- 10 1324-1344 DM01206B 10.69 4.822e-10 1276- 1296 DM01206B 10.69 7.658e-10 1328-1348 DM01206B 10.69 8.274e- 10 1280-1300 DM01206B 10.69 4.532e-09 1320- 1340 DM01206B 10.69 7.266e-09 1326-1346
635	3L00107	Protein kinascs ATP- binding region proteins.	BL00107A 18.39 7.600e- 23 145-176 BL00107B 13.31 2.636e-13 211- 227
636	BL00657	Fork head domain proteins.	BL00657A 19.39 1.545e- 30 101-143 BL00657B 22.27 7.750e-26 149- 192
637	BL00107	Protein kinases ATP- binding region proteins.	BL00107B 13.31 1.000e- 10 607-623
643	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 4.913e-09 199-212
647	PF00628	PHD-finger.	PF00628 15.84 2.350e- 13 385-400 PF00628 15.84 3.455e-12 464- 479
648	BL01129	Hypothetical yab0/yceC/sfhB family proteins.	BL01129E 13.25 4.000e- 25 332-357 BL01129C 25.56 8.200e-23 236- 279 BL01129B 12.51 6.118e-13 191-212
649	BL01228	Hypothetical cof family proteins.	BL0122BD 17.44 3.908e- 10 455-480
650	BL00027	'Homeobox' domain proteins.	BL00027 26.43 6.684e- 13 771-814
651	BL50002	Src homology 3 (SH3) domain proteins profile.	BL50002A 14.19 1.750e- 12 1026-1045
653	PR00253	GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE	PR00253A 9.15 4.000e- 24 253-274 PR00253C 13.85 8.800e-24 313- 335 PR00253B 13.47 3.143e-22 279-301 PR00253D 16.68 7.652e-

SEQ ID N	O: ACCESSION NO.	DESCRIPTION	RESULTS*
			20 422-443
654	PD01719	PRECURSOR GLYCOPROTEIN SIGNAL RE.	PD01719A 12.89 4.452e- 11 969-997 PD01719A 12.89 3.961e-10 128- 156 PD01719A 12.89 7.395e-10 1276-1304 PD01719A 12.89 1.222e- 09 1220-1248
657	BL00354	HMG-I and HMG-Y DNA- binding domain proteins (Ahook).	BL00354C 6.61 8.397e- 09 563-578
658	BL00354	HMG-I and HMG-Y DNA- binding domain proteins (Ahook).	BL00354C 6.61 8.397e- 09 580-595
659	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 2.174e- 13 539-572 DM00215 19.43 4.750e-12 549- 582 DM00215 19.43 9.824e-11 551-584 DM00215 19.43 2.929e- 10 548-581 DM00215 19.43 4.054e-1C 550- 583 DM00215 19.43 5.339e-10 552-585 DM00215 19.43 7.107e- 10 544-577
660	PR00688	XYLOSE ISOMERASE SIGNATURE	PR00688I 13.78 9.518e- 09 224-236
661	BL00027	'Homeobox' domain proteins.	BL00027 26.43 5.950e- 23 249-292
662	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.158e-
663	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.158e- 10 596-610
664	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.158e- 10 596-610
666	PR00819	CEXX/CFQX SUPERFAMILY SIGNATURE	PR00819B 10.83 8.988e- 10 704-720
667	BL50040	Elongation factor 1 gamma chain profile.	BL50040C 22.62 2.143e- 16 135-178
668	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 1.360e- 09 139-153 PR00019A 11.19 1.667e-09 94-108 PR00019B 11.36 4.600e- 09 163-177
670	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 3.250e-10 681-694 BL00018 7.41 6.400e-10 717-730
672	PD00131	ATP-BINDING TRANSPORT TRANSMEMBR.	PD00131B 34.97 1.000e- 34 356-410 PD00131C 19.59 1.346e-26 504- 542
673	PR30667	RETINAL PIGMENT EPITHELIUM-RETINAL GPCR SIGNATURE	PRC0667G 15.33 7.557e- 10 106-123
674	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 4.857e- 13 593-608 PR00320B 12.19 4.115e-12 635- 650 PR00320C 13.01 8.435e-11 717-732 PR00320C 13.01 2.800e- 10 635-650 PR00320C 13.01 6.400e-10 593- 608 PR00320B 12.19 3.250e-09 593-608
675	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 4.857e- 13 572-587 PR00320B 12.19 4.115e-12 614-

SEQ ID I	NO: ACCESSION	DESCRIPTION	RESULTS*
	NO.		
			629 PR00320C 13.01
			8.435e-11 696-711 PR00320C 13.01 2.800e-
	į		10 614-629 PR00320C
}			13.01 6.400e-10 572-
}			587 PR00320B 12.19
676	PPOGGIO		3.250e-09 572-587
070	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 9.667e-
679	PF00642	Zinc finger C-x8-C-x5-C-	09 249-263
		x3-H type (and similar).	PF00642 11.59 3.700e- 16 225-236 PF00642
		of the contract,	11.59 7.900e-12 187-
		i	198
680	PR00308	TYPE I ANTIFREEZE	PR00308C 3.83 8.754e-
681	BL00019	PROTEIN SIGNATURE	10 286-296
001	BECOOLS	Actinin-type actin-	BL00019D 15.33 4.200e-
682	PR00700	binding domain proteins. PROTEIN TYROSINE	19 227-257
	12200700	PHOSPHATASE SIGNATURE	PR00700D 12.47 4.000e-
687	PR00049	WILM'S TUMOUR PROTEIN	09 99-118 PR00049D 0.00 8.500e-
		SIGNATURE	10 538-553
689	BL01024	Protein phosphatase 2A	BL01024A 10.26 1.000e-
		regulatory subunit PR55	40 22-69 BL01024B
		proteins.	8.91 1.000e-40 86-127
			BL01024C 7.80 1.000e-
			40 146-185 BL01024D
			13.22 1.000e-40 185- 222 BL01024E 11.96
			1.000e-40 222-266
			BL01024F 9.42 1.000e-
			40 266-317 BL01024G
			11.09 1.000e-40 317-
		ľ	349 BL01024H 13.88
691	BL00027	'Homeobox' domain	1.000e-40 389-442 BL00027 26.43 8.071e-
692	77 000	proteins.	31 152-195
69%	BL00211	ABC transporters family	BL00211A 12.23 5.050c-
693	BL00211	ABC transporters family	09 45-57
•	2500221	proteins.	BL00211A 12.23 5.050e- 09 45-57
694	BL00211	ABC transporters family	BL00211A 12.23 5.050e-
		proteins.	09 58-70
696	BL00680	Methionine	BL00680 14.37 5.304e-
		aminopepticase subfamily	17 173-195
697	BL00741	1 proteins.	
	P2000 141	Guanine-nucleotide dissociation stimulators	BL00741B 14.27 3.418e-
		CDC24 family sign.	11 242-265
698	DM01930	2 kw FINGER SMCX SMCY	DM01930E 15.41 1.367e-
		YDR096W.	37 170-215 DM01930F
	1		14.16 B.232e-28 267-
			303 DM01930B 19.86
700	PRODUCE	DV2 POLICE	9.163e-10 37-71
. 30	PR00869	DNA-POLYMERASE FAMILY X	PR00869A 12.80 1.281e-
701	PR00048	SIGNATURE C2H2-TYPE ZINC FINGER	16 245-263
		SIGNATURE	PR0004BA 10.52 2.174e-
			10 77-91 PR00048A 10.52 6.870e-10 133-
			147 PR00048A 10.52
	<u> </u>	1	8.826e-10 105-119
			PR00048A 10.52 5.320e-
702	PI COESS	0.16	09 161-175
	BL00523	Sulfatases proteins.	BL00523E 19.27 2.565e-
		1	25 326-356 BL00523A
			13.36 5.050e-16 38-55 BL00523B 8.64 5.909e-
			15 86-98 BL00523C
		_ [12.64 5.500e-13 137-

SEQ ID NO	: ACCESSION NO.	DESCRIPTION	RESULTS*
	·		148 BL00523D 9.89 1.844e-11 290-302 BL00523G 9.46 5.500e- 10 513-523 BL00523F 10.85 6.351e-09 413-
703	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 8.412e- 12 376-390 PR00048B 6.02 1.000e-10 334-344
707	PD00787	SYNTHASE BIOSYNTHESIS	PR00048B 6.02 1.474e- 09 364-374 PD00787A 14.84 8.941e-
708	PR00761	TRANSFERASE. BINDIN PRECURSOR	14 66-82 PR00761E 14.32 8.500e-
712	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.	10 822-841 DM01354Y 10.69 4.977e- 38 425-465 DM01354X 13.86 7.300e-34 376- 415 DM01354V 12.97 4.923e-17 311-358 DM01354W 12.64 5.596e-
713	BL00039	DEAD-box subfamily ATP- dependent helicases proteins.	10 356-376 BL00039D 21.67 7.545e- 27 450-496 BL00039A 18.44 2.537e-18 147- 186 BL00039C 15.63 2.216e-14 280-304 BL00039B 19.19 1.947e-
715	BL00383	Tyrosine specific protein phosphatases proteins.	13 194-220 BL00383E 10.35 4.981e- 10 150-161
717	PF00777	Sialyltransferase family.	PF00777C 18.60 4.035e- 21 106-161
718	DM00031	IMMUNOGLOBULIN V REGION.	DM00031A 16.80 3.750e- 39 20-68 DM00031B 15.41 2.688e-28 84-118 DM00031C 12.79 1.300e- 12 131-142
719	BL00243	Integrins beta chain cysteine-rich domain proteins.	BL00243B 17.54 1.000e- 40 131-172 BL00243C 16.42 1.000e-40 172- 208 BL00243D 24.07 1.000e-40 222-274 BL00243F 22.63 1.000e- 40 314-358 BL00243I 31.77 6.571e-39 607- 650 BL00243E 16.70 3.077e-35 274-304 . BL00243G 21.38 3.625e- 34 358-400 BL00243H 17.53 5.235e-29 567- 593 BL00243A 17.61 3.250e-21 63-84 BL00243H 17.53 7.167e- 16 477-503 BL00243H 17.53 2.304e-11 524- 550 BL00243H 17.53 5.304e-11 606-632 BL00243I 31.77 1.380e-
720	PR00217	43 KD POSTSYNAPTIC	09 610-653 PR00217C 10.91 8.022e-
722	PR00704	PROTEIN SIGNATURE CALPAIN CYSTEINE PROTEASE (C2) FAMILY SIGNATURE	09 20-36 PR00704D 11.05 5.909e- 34 135-161 PR00704F 13.61 7.000e-26 190- 218 PR00704E 12.55 8.071e-26 165-189

SEQ ID N	O: ACCESSION NO.	DESCRIPTION	RESULTS*
			PR00704B 17.94 2.241e- 23 75-98 PR00704A 14.68 4.094e-19 30-54 PR00704C 11.88 1.871e-
725	PR00194	TROPOMYOSIN SIGNATURE	18 99-116 PR00194A 7.86 7.652e- 09 169-187
726	PR00194	TROPOMYOSIN SIGNATURE	PR00194A 7.86 7.652e- 09 169-187
727	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 2.125e- 13 277-292 PR00320A 16.74 1.310e-11 277- 292 PR00320C 13.01 4.522e-11 323-338 PR00320A 16.74 6.586e- 11 323-338 PR00320B 12.19 4.343e-10 323- 338 PR00320B 12.19 6.914e-10 277-292
731	PR00195	DYNAMIN SIGNATURE	PR00195A 11.94 8.627e- 16 288-307 PR00195E 9.82 3.912e-11 457-474
733	PF00642	Zinc finger C-x8-C-x5-C- x3-H type (and similar).	PF00642 11.59 9.082e-
738	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039A 18.44 2.565e- 28 26-65 BL00039D 21.67 2.105e-20 338- 384 BL00039C 15.63 9.100e-13 160-184 BL00039B 19.19 9.617e- 11 73-99
739	BL01289	TSC-22 / dip / bun family proteins.	BL01289A 12.18 8.909e- 31 326-353 BL01289B 10.45 9.571e-17 353- 383
742	BL01019	ADP-ribosylation factors family proteins.	BL01019A 13.20 7.078e-
743	BL00965	Phosphomannose isomerase type I proteins.	BL00965C 23.78 1.000e- 40 256-305 BL00965B 17.77 1.600e-25 126- 153 BL00965A 10.57 6.400e-19 94-113
747	BL00021	Kringle domain proteins.	BL00021D 24.56 4.563e- 25 231-273 BL00021B 13.33 5.345e-21 60-78
748	BL00612	Osteonectin domain proteins.	BL00612B 11.35 2.034e- 11 93-126
749	PR00450	RECOVERIN FAMILY SIGNATURE	PR00450C 12.22 6.880e- 10 135-157
752	BL00795	Involucrin proteins.	BL00795C 17.06 6.000e- 11 384-429 BL00795C 17.06 9.444e-11 370- 415
754	BL00051	Ribosomal protein L39e proteins.	BL00051 20.92 1.935e- 16 4-50
755	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 7.723e- 09 171-184
760	BL01020	SAR1 family proteins.	BL01020C 15.35 9.020e- 12 99-150
762	3L00046	Histone H2A proteins.	BL00046 12.95 1.000e- 40 33-88
763	PD02411	PROTEIN TRANSCRIPTION REGULATION NUCLEAR.	PD02411 21.89 9.137e- 10 206-240
764	BL00027	'Homeobox' domain proteins.	BL00027 26.43 8.800e- 29 417-460
767	BL01208	VWFC domain proteins.	BL01208B 15.83 6.063e- 10 309-324 BL01208B 15.83 8.031e-10 165-

SEQ ID I	NO: ACCESSION	DESCRIPTION	RESULTS*
	NO.		
			180 BL01208B 15.83 4.162e-09 85-100
770	BL00031	Nuclear hormones	BL00031A 19.55 9.571e-
		receptors DNA-binding	32 ·208-241 BL00031B
i		region proteins.	22.25 5.500e-27 242-
772	PR00449	TRANSFORMING PROTEIN P21	274
ĺ		RAS SIGNATURE	PR00449A 13.20 1.450e- 18 4-26 PR00449E
		İ	13.50 3.520e-14 142-
l			165 PR00449C 17.27
			3.032e-13 44-67
			PR00449D 10.79 8.579e- 13 107-121 PR00449B
			14.34 3.455e-11 27-44
773	BL00523	Sulfatases proteins.	BL00523E 19.27 9.333e-
			23 299-329 BL00523A
		1	13.36 2.200e-13 47-64 BL00523B 8.64 2.607e-
			13 91-103 BL00523D
			9.89 7.923e-12 224-236
			BL00523C 12.64 4.512e-
			10 141-152 BL00523F 10.85 5.821e-10 373-
775	DY COOL		384
773	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.686e-
776	BL00028	Zinc finger, C2H2 type,	09 568-585 BL00028 16.07 7.686e-
777	N. A. C. C. C. C. C. C. C. C. C. C. C. C. C.	domain proteins.	09 621-638
,,,	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.686e-
778	BL00030	Eukaryotic RNA-binding	09 595-612 BL00030A 14.39 8.412e-
		region RNP-1 proteins.	11 322-341 BL00030A
			14.39 7.000e-10 220-
779	PR00079	GLUCOSE-6-PHCSPHATE	239 PR00079B 12.98 2.929e-
		DEHYDROGENASE SIGNATURE	26 193-222 PR00079E
			16.65 4.150e-23 348-
	1		375 PR00079C 8.68
			6.351e-16 246-264 PR00079D 13.51 7.070e-
			16 264-281 PR00079A
			16.12 6.769e-13 169-
781	BL00215	Mitochondrial energy	183 BL00215A 15.82 9.250e-
		transfer proteins.	17 10-35 BL00215A
			15.82 6.000e-16 221-
			246 BL00215A 15.82
-			7.857e-12 108-133 BL00215B 10.44 9.526e-
702			11 168-181
783	PD00239	PROTEIN SH3 DOMAIN REPEAT PRESYNA.	PD00289 9.97 6.276e-09
785	BL00690	DRAH-box subfamily ATP-	159-173 BL00690B 13.38 1.000e-
		dependent helicases	12 147-165 BL00690A
	- 1	proteins.	6.87 5.320e-10 114-124
			BL00690C 7.51 3.189e- 09 218-228
786	PR00449	TRANSFORMING PROTEIN P21	PR00449C 17.27 8.500e-
		RAS SIGNATURE	16 50-73 PR00449A
			13.20 5.235e-14 8-30
			PR00449E 13.50 2.853e- 11 150-173 PR00449D
			10.79 1.545e-09 111-
788	DMOTOGO		125
, 50	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 8.767e-
790	BL00915	Phosphatidylinositol 3-	10 1-21 BL00915C 22.43 9.182e-
		and 4-kinases proteins.	39 725-764 BL00915B

25

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	,		22.78 5.050e-33 633- 671 BL00915D 27.02
791	PR00208		1.529e-21 795-831 BL00915A 10.09 1.000e- 13 395-407
,31	PR00208	GLIADIN AND LMW GLUTENIN SUPERFAMILY SIGNATURE	PR00208A 12.59 6.294e- 10 120-138 PR00208A 12.59 6.294e-10 121-
			139 PR00208A 12.59 6.294e-10 122-140 PR00208A 12.59 6.294e-
			10 123-141 PR00208A 12.59 6.294e-10 124- 142 PR00208A 12.59
			6.294e-10 125-143 PR00208A 12.59 6.294e-
			10 126-144 PR00208A 12.59 6.294e-10 127- 145 PR00208A 12.59
			6.294e-10 128-146 PR00208A 12.59 6.294e- 10 129-147 PR00208A
	,		12.59 7.411e-09 130- 148 PR00208A 12.59 7.658e-09 131-149
			PR00208A 12.59 7.904e- 09 132-150 PR00208A 12.59 8.274e-09 118-
795	PR00205	CADHERIN SIGNATURE	136 PR00208A 12.59 8.274e-09 119-137 PR00205B 11.39 5.034e-
			16 302-320 PR00205A 14.73 1.257e-11 284- 300 PR00205C 13.65
796	BL00412	Neuromodulin (GAP-43) proteins.	1.333e-11 337-352 BL00412D 16.54 4.000c- 12 196-247 BL00412D
			16.54 5.705e-11 197- 248 BL00412D 16.54 7.848e-10 199-250
			BL00412D 16.54 1.827e- 09 195-246 BL00412D 16.54 1.918e-09 194-
797	BL00021	Kringle domain proteins.	245 BL00412D 16.54 2.102e-09 201-252 BL00021B 13.33 6.339e-
799	BL01052	Calponin family repeat	13 40-58
		proteins.	BL01052C 18.51 1.000e- 40 87-127 BL01052A 16.12 1.529e-32 3-35
•			BL01052B 15.31 1.257e- 25 52-78 BL01052D 10.26 5.737e-25 174-
800	BL00348	p53 tumor antigen	194 BL00348F 23.19 3.714e-
801	BL00309	Proteins. Vertebrate galactoside-	09 197-240 BL00309C 18.65 1.621e-
802	PR00245	binding lectin proteins. OLFACTORY RECEPTOR SIGNATURE	09 62-87 PR00245D 10.47 5.224e- 09 187-199
804	PF00774	Dihydropyridine sensitive L-type calcium channel (Beta subuni.	PF00774A 16.47 8.457e- 10 110-156
808	PR00667	RETINAL PIGMENT EPITHELIUM-RETINAL GPCR	PR00667C 11.71 9.875e- 09 12-28
810	PD02346	SIGNATURE PHOTOSYSTEM II PROTEIN PRECURSOR	PD02346F 12.89 4.340e- 09 317-354

SEQ ID NO	ACCESSION NO.	DESCRIPTION	RESULTS*
		PHOTOSYNTHESIS.	<u> </u>
811	BL00685	CBF-A/NF-YB subunit proteins.	BL00685B 14.41 6.779e- 14 54-95 BL00685A 11.22 4.798e-13 5-54
812	PR00080	ALCOHOL DEHYDROGENASE SUPERFAMILY SIGNATURE	PR00080A 9.32 9.419e- 10 93-105
813	BL00357	Histone H2B proteins.	BL00357 7.74 1.988e-17 22-65
815	PD00066	PROTEIN ZINC-FINGER MÉTAL-BINDI.	PD00066 13.92 7.923e- 15 158-171 PD00066 13.92 5.200e-14 46-59 PD00066 13.92 7.000e- 14 18-31 PD00066 13.92 7.000e-13 130- 143 PD00066 13.92 7.500e-13 214-227 PD00066 13.92 9.000e- 13 102-115 PD00066 13.92 4.429e-12 186- 199 PD00066 13.92 1.783e-11 74-87
816	BL01195	Peptidyl-tRNA hydrolase proteins.	BL01195C 20.12 3.348e- 20 100-139
820	BLC0520	Interleukin-10 family proteins.	BL00520A 6.21 6.471e-
822	BL00972	Ubiquitin carboxyl- terminal hydrolases family 2 proteins.	BL00972A 11.93 8.113e- 09 224-242
825	PR00876	NEMATODE METALLOTHIONEIN SIGNATURE	PR00876B 7.66 2.268e-
829	PD02855	FLAVOPROTEIN PROTEIN DNA/PANTOTHEN.	PD02855A 18.37 4.732c- 28 88-124 PD02855B 8.36 6.478e-09 132-142
830	PRO0405	HIV REV INTERACTING PROTEIN SIGNATURE	PR00405B 11.83 7.000e- 21 44-62 PR00405C 19.41 1.000e-13 65-87 PR00405A 17.71 7.283e- 13 25-45
831	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 1.000e- 09 47-61 PR00019B 11.36 1.720e-09 136- 150 PR00019B 11.36 3.880e-09 44-58
832	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011B 13.08 3.438e- 16 164-183 PR00011D 14.03 6.850e-16 164- 183 PR00011A 14.06 8.364e-14 164-183 PR00011C 24.25 5.415e- 12 231-260 PR00011D 14.03 9.852e-11 212- 231
834	PD00306	PROTEIN GLYCOPROTEIN PRECURSOR RE.	PD00306A 10.26 7.000e- 12 232-246
835	PD00306	PROTEIN GLYCOPROTEIN PRECURSOR RE.	PD00306A 10.26 4.000e- 10 290-304
836	PD00306	PROTEIN GLYCOPROTEIN PRECURSOR RE.	PD00306A 10.26 7.000e- 12 216-230
837	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 3.898e- 09 78-111
839	PD02784	PROTEIN NUCLEAR RIBONUCLEOPROTEIN.	PD02784B 26.46 8.302e- 09 73-116
840	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE	PRO0700B 16.80 5.091e- 22 369-390 PR00700D 12.47 5.765e-21 491- 510 PR00700C 13.17 4.750e-14 449-467 PR00700F 11.18 8.500e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			11 538-549 PR00700E 17.57 3.100e-10 522-
841	PR00109	TYROSINE KINASE	538
	2.00105	CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 5.404a- 13 134-153
844	PD02785	PROTEIN RIBOSOMAL 60S L22 RNA-BINDING HEP.	PD02785B 14.43 1.000e- 40 58-112 PD02785A
845	BLC0826	MARCKS family proteins.	15.23 1.915e-28 8-57 BL00826C 7.63 6.738e- 09 203-230
846	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 4.429e- 10 15-24
849	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 1.000e- 08 340-349
850	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308A 5.90 6.506e- 09 12-27
851	PD02411	PROTEIN TRANSCRIPTION REGULATION NUCLEAR.	PD02411 21.89 7.000e- 16 246-280
853	BL00420	Speract receptor repeat proteins domain proteins.	BL00420B 22.67 1.000e- 40 723-778 BL00420B 22.67 1.321e-38 933- 988 BL00420B 22.67 8.457e-28 482-537 BL00420B 22.67 4.500e- 27 587-642 BL00420B 22.67 9.625e-27 270- 325 BL00420B 22.67 4.205e-26 163-218 BL00420B 22.67 5.731e- 23 55-110 BL00420B 22.67 6.464e-20 377- 432 BL00420B 22.67 2.800e-15 830-885 BL00420C 11.90 1.900e- 13 355-366 BL00420C 11.90 1.900e-12 808- 819 BL00420C 11.90 3.550e-12 248-259 BL00420C 11.90 2.831e- 11 141-152 BL00420C 11.90 5.119e-11 1018- 1029 BL00420C 11.90 7.955e-10 567-578
	BL00420	Speract receptor repeat proteins domain proteins.	BL00420B 22.67 1.000e- 40 756-811 BL00420B 22.67 1.321e-38 966- 1021 BL00420B 22.67 8.457e-28 482-537 BL00420B 22.67 4.500e- 27 620-675 BL00420B 22.67 9.625e-27 270- 325 BL00420B 22.67 4.205e-26 163-218 BL00420B 22.67 5.731e- 23 55-110 BL00420B 22.67 6.464e-20 377- 432 BL00420B 22.67 2.800e-15 863-918 BL00420C 11.90 1.900e- 13 355-366 BL00420C 11.90 1.900e-12 841- 852 BL00420C 11.90 3.550e-12 248-259 BL00420C 11.90 2.831e- 11 141-152 BL00420C 11.90 5.119e-11 1051-

SEO ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.	JESCHII I I GN	
857	PR00388		7.955e-10 567-578
85/	PR00388	3',5'-CYCLIC NUCLEOTIDE	PR00388A 10.45 2.778e-
		PHOSPHODIESTERASE	09 64-83
		SIGNATURE	
859	BL00030	Eukaryotic RNA-binding	BL00030A 14.39 2.929e-
	1-20000	region RNP-1 proteins.	13 37-56 BL00030B
		region kmr-r processis.	7.03 1.900e-11 167-177
			BL00030A 14.39 2.000e-
	1	·	10 128-147
861	PR00988	URIDINE KINASE SIGNATURE	PR00988A 5.39 4.250e-
		1	17 23-41 PR00988C
			13.64 8.714e-16 107-
	•		123 PR00988F 12.23
		,	7.828e-15 198-212
			PR00988E 8.27 9.769e-
			12 176-188 PR00988D
			5.95 8.250e-11 163-174
			PR00988B 11.60 4.512e-
063	DI GOOTE		10 60-72
863	BL00215	Mitochondrial energy	BL00215B 10.44 8.071e-
864	PR00775	transfer proteins. 90 KD HEAT SHOCK PROTEIN	12 41-54
004	PRUU//5	90 KD HEAT SHOCK PROTEIN SIGNATURE	PR00775E 8.06 1.000e-
		SIGNATURE	24 198-221 PR00775B
			3.52 1.837e-23 107-130
			PRO0775D 8.91 4.484e-
			17 171-189 PR00775A 9.90 8.342e-17 86-107
		i	PR00775C 10.68 9.379e-
			17 153-171 PR00775G
]		10.64 6.850e-15 267-
	l		286 PR00775F 12.76
			6.769e-14 249-267
866	DM01688	2 POLY-IG RECEPTOR.	DM01688G 16.45 9.460e-
		!	09 89-121
867	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 5.596e-
		ZINC-FINGER METAL-	29 14-53
		BINDING NU.	
868	BL01287	RNA 3'-terminal	BL01287A 17.95 2.688e-
	1	phosphate cyclase	26 16-48
869	DM00215	PROLINE-RICH PROTEIN 3.	
003	DMOZIS	PROLINE-RICH PROTEIN 3.	DM00215 19.43 6.464e-
872	BL00046	Histone H2A proteins.	10 304-337
***	D200040	Alscone HZA proceins.	BL00046 12.95 1.000e- 40 30-85
874	BL00188	Biotin-requiring enzymes	BL00188 30.29 9.036e-
		attachment site	32 665-711
		proteins.	25 882-111
876	BL00028	Zinc finger, C2H2 type,	BL00028 16.07 7.686e-
		domain proteins.	09 298-315
877	PD02102	SUBUNIT E V-ATPASE	PD02102A 16.74 4.176e-
	–	VACUOLAR ATP SYNTHASE	10 97-141
		HYDROL.	10 57-4-11
879	BL01189	Ribosomal protein S12e	BL01189A 14.27 1.000e-
		proteins.	40 35-71 BL01189B
			13.49 1.000e-40 71-125
882	BL00284	Serpins proteins.	BL00284C 28.56 6.400e-
			25 62-104 BL00284B
			17.99 6.182e-12 35-56
889	BL00216	Sugar transport	BL00216B 27.64 4.375e-
		proteins.	21 35-85
896	PR00391	PHOSPHATIDYLINOSITOL	PR00391E 12.50 7.785e-
		TRANSFER PROTEIN	15 211-231 PR00391B
		1	
i		SIGNATURE	8.39 1.000e-13 83-104
		SIGNATURE	8.39 1.000e-13 83-104 PR00391D 12.21 9.328e-
		SIGNATURE	8.39 1.000e-13 83-104 PR00391D 12.21 9.328e- 13 191-207 PR00391A
897	PR00327	SIGNATURE	PR00391D 12.21 9.328e-

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		RESULIS*
		SIGNATURE	09 313-328
898	BL00039	DEAD-box subfamily ATF- dependent helicases proteins.	BL00039D 21.67 7.800e- 26 386-432 BL00039A 18.44 6.674e-16 113- 152 BL00039B 19.19 1.947e-13 153-179 BL00039C 15.63 9.460e-
901	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	11 236-260 PD00066 13.92 8.200e- 16 254-267 PD00066 13.92 8.200e-16 282- 295 PD00066 13.92 8.200e-16 310-323 PD00066 13.92 8.200e- 16 366-379 PD00066 13.92 8.200e-16 394-
			407 PD00066 13.92 8.200e-14 338-351
902	BI:01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 9.321e- 11 6-50
903	PR00806	VINCULIN SIGNATURE	PR00806B 4.28 9.160e- 09 97-111
904	PR00381	KINESIN LIGHT CHAIN SIGNATURE	PR00381E 8.75 6.586e- 25 335-356 PR00381B 18.17 2.667e-24 204- 224 PR00381A 9.55 2.800e-24 107-125 PR00381C 12.48 4.522e- 24 226-245 PR00381D 13.94 1.084e-22 291- 309 PR00381F 9.13 3.288e-22 370-392 PR00381F 9.13 7.181e- 13 286-308 PR00381E 8.75 4.066e-11 251-272 PR00381E 8.75 7.033e- 11 293-314 PR00381E 8.75 8.364e-10 377-398 PR00381D 13.94 5.230e- 09 333-351 PR00381C 12.48 7.120e-09 310- 329
906	PR00345	STATHMIN FAMILY SIGNATURE	PR00345C 4.54 8.557e- 09 525-549
908	PR00345	STATHMIN FAMILY SIGNATURE	PR00345C 4.54 8.557e- 09 513-537
910	PD01066	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 9.308e-11 144-155
	* DOTO P	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 2.800e- 30 48-87
912	BL01104	Ribosomal protein L13e proteins.	BL01104C 15.14 6.000e- 09 364-392
922	3L00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 3.842e-09 500-511
923	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 2.500e- 09 323-338 PR00320C 13.01 5.500e-09 187- 202
924	PD02181 BL00019	PROTOCHLOROPHYLLIDE REDUCTASE PHOTOSYNT. Actinin-type actin- binding domain proteins.	PD02181D 12.85 8.609e- 09 36-54 BL00019C 14.66 7.453e- 25 108-144 BL00019B 13.34 6.510c-11 61-84 BL00019D 15.33 9.338e-
j			11 205-235 BL00019A 12.56 2.373e-10 34-45

	: ACCESSION	DESCRIPTION	RESULTS*
	NO.		1000000
		proteins proteins.	273-284 BL00678 9.67
1	1		1.600e-10 314-325
			BL00678 9.67 7.600e-10
1		1	360-371 BL00678 9.67 8.579e-09 206-217
929	BL00518	Zinc finger, C3HC4 type	BL00518 12.23 1.857e-
		(RING finger), proteins.	10 137-146
930	BL01085	Ribulose-phosphate 3-	BL01085D 16.55 4.600e-
]	epimerase family	24 134-165 BL01085B
ł		proteins.	10.15 5.680e-22 30-52
			BL01085E 18.87 8.676e-
}			20 172-202 BL01085C
			21.81 2.038e-14 66-97
931	BL01085	Ribulose-phosphate 3-	BLC1085D 16.55 4.600e-
		epimerase family	24 152-183 BL01085B
		proteins.	10.15 5.680e-22 30-52
			BL01085E 18.87 8.676e-
ļ		1	20 190-220 BL01085C 21.81 2.038e-14 66-97
933	PD90301	PROTEIN REPEAT MUSCLE	PD00301A 10.24 6.400e-
i	-	CALCIUM-BI.	09 160-171
936	PF00168	C2 domain proteins.	PF00168C 27.49 4.000e-
		_	12 336-362
937	BL00415	Synapsins proteins.	BL00415N 4.29 9.519e-
			10 5-49
940	PR00862	PROLYL OLIGOPEPTIDASE	PR00862D 16.17 4.086e-
		SERINE PROTEASE (S9A)	09 63-84
945	BL01230	RNA methyltransferase	
, ,,,	BB01230	trmA family proteins.	BL01230B 11.62 2.373e-
948	BL00479	Phorbol esters /	BL00479B 12.57 7.429e-
		diacylglycerol binding	18 52-68 BL00479A
	}	domain proteins.	19.86 2.200e-13 26-49
949	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 1.474e-09
		proteins proteins.	100-111
954	PD01311	PROTEIN OXIDOREDUCTASE	PD01311A 30.23 5.909e-
		NAD INTERGENIC RE.	10 66-111
955	PF00651	BTB (also known as BR-	PF00651 15.00 3.250e-
956	PF00651	C/Ttk) domain proteins. BTB (also known as BR-	12 47-60
	1100031	C/Ttk) domain proteins.	PF00651 15.00 3.250e-
957	BL00379	CDP-alcohol	BL00379 24.64 1.610e-
		phosphatidyltransferases	15 111-148
		proteins.	
959		<u> </u>	
JJJ	BL01115	GTP-binding nuclear	BL01115A 10.22 1.884e-
		protein ran proteins.	BL01115A 10.22 1.884e- 10 31-75
960	BL01115	protein ran proteins. GTP-binding nuclear	10 31-75 BL01115A 10.22 3.438e-
960	BL01115	protein ran proteins. GTP-binding nuclear protein ran proteins.	10 31-75 BL01115A 10.22 3.438e- 14 110-154
		protein ran proteins. GTP-binding nuclear protein ran proteins. Short-chain	10 31-75 BL01115A 10.22 3.438e- 14 110-154 BL00061B 25.79 6.586e-
960	BL01115	protein ran proteins. GTP-binding nuclear protein ran proteins. Short-chain dehydrogenases/reductase	10 31-75 BL01115A 10.22 3.438e- 14 110-154
960	BL01115	protein ran proteins. GTP-binding nuclear protein ran proteins. Short-chain dehydrogenases/reductase s family proteins.	10 31-75 BL01115A 10.22 3.438e- 14 110-154 BL00061B 25.79 6.586e- 13 198-236
960	BL01115	protein ran proteins. GTP-binding nuclear protein ran proteins. Short-chain dehydrogenases/reductase	10 31-75 BL01115A 10.22 3.438e- 14 110-154 BL00061B 25.79 6.586e- 13 198-236 PR00502A 15.06 8.200e-
960	BL01115 BL00061 PR00502	protein ran proteins. GTP-binding nuclear protein ran proteins. Short-chain dehydrogenases/reductase s family proteins. MUTT DOMAIN SIGNATURE	10 31-75 BL01115A 10.22 3.438e- 14 110-154 BL00061B 25.79 6.586e- 13 198-236 PR00502A 15.06 8.200e- 11 210-225
960 962 963	BL01115	protein ran proteins. GTP-binding nuclear protein ran proteins. Short-chain dehydrogenases/reductase s family proteins. MUTT DOMAIN SIGNATURE TYPE I ANTIFREEZE	10 31-75 BL01115A 10.22 3.438e- 14 110-154 BL00061B 25.79 6.586e- 13 198-236 PR00502A 15.06 8.200e- 11 210-225 PR00308A 5.90 7.035e-
960 962 963	BL01115 BL00061 PR00502	protein ran proteins. GTP-binding nuclear protein ran proteins. Short-chain dehydrogenases/reductase s family proteins. MUTT DOMAIN SIGNATURE TYPE I ANTIFREEZE PROTEIN SIGNATURE	10 31-75 BL01115A 10.22 3.438e- 14 110-154 BL00061B 25.79 6.586e- 13 198-236 PR00502A 15.06 8.200e- 11 210-225 PR00308A 5.90 7.035e- 09 55-70
960 962 963 966	BL01115 BL00061 PR00502 PR00308	protein ran proteins. GTP-binding nuclear protein ran proteins. Short-chain dehydrogenases/reductase s family proteins. MUTT DOMAIN SIGNATURE TYPE I ANTIFREEZE	10 31-75 BL01115A 10.22 3.438e- 14 110-154 BL00061B 25.79 6.586e- 13 198-236 PR00502A 15.06 8.200e- 11 210-225 PR00308A 5.90 7.035e- 09 55-70 DM01206B 10.69 1.286e-
960 962 963 966	BL01115 BL00061 PR00502 PR00308	protein ran proteins. GTP-binding nuclear protein ran proteins. Short-chain dehydrogenases/reductase s family proteins. MUTT DOMAIN SIGNATURE TYPE I ANTIFREEZE PROTEIN SIGNATURE CORONAVIRUS NUCLEOCAPSID	10 31-75 BL01115A 10.22 3.438e- 14 110-154 BL00061B 25.79 6.586e- 13 198-236 PR00502A 15.06 8.200e- 11 210-225 PR00308A 5.90 7.035e- 09 55-70 DM01206B 10.69 1.286e- 12 104-124 DM01206B
960 962 963 966	BL01115 BL00061 PR00502 PR00308	protein ran proteins. GTP-binding nuclear protein ran proteins. Short-chain dehydrogenases/reductase s family proteins. MUTT DOMAIN SIGNATURE TYPE I ANTIFREEZE PROTEIN SIGNATURE CORONAVIRUS NUCLEOCAPSID	10 31-75 BL01115A 10.22 3.438e- 14 110-154 BL00061B 25.79 6.586e- 13 198-236 PR00502A 15.06 8.200e- 11 210-225 PR00308A 5.90 7.035e- 09 55-70 DM01206B 10.69 1.286e-
960 962 963 966	BL01115 BL00061 PR00502 PR00308	protein ran proteins. GTP-binding nuclear protein ran proteins. Short-chain dehydrogenases/reductase s family proteins. MUTT DOMAIN SIGNATURE TYPE I ANTIFREEZE PROTEIN SIGNATURE CORONAVIRUS NUCLEOCAPSID	10 31-75 BL01115A 10.22 3.438e- 14 110-154 BL00061B 25.79 6.586e- 13 198-236 PR00502A 15.06 8.200e- 11 210-225 PR00308A 5.90 7.035e- 09 55-70 DM01206B 10.69 1.286e- 12 104-124 DM01206B 10.69 5.299e-11 23-43
960 962 963 966	BL01115 BL00061 PR00502 PR00308	protein ran proteins. GTP-binding nuclear protein ran proteins. Short-chain dehydrogenases/reductase s family proteins. MUTT DOMAIN SIGNATURE TYPE I ANTIFREEZE PROTEIN SIGNATURE CORONAVIRUS NUCLEOCAPSID	10 31-75 BL01115A 10.22 3.438e- 14 110-154 BL00061B 25.79 6.586e- 13 198-236 FR00502A 15.06 8.200e- 11 210-225 PR00308A 5.90 7.035e- 09 55-70 DM01206B 10.69 1.286e- 12 104-124 DM01206B 10.69 5.299e-11 23-43 DM01206B 10.69 8.274e-
960 962 963 966	BL01115 BL00061 PR00502 PR00308	protein ran proteins. GTP-binding nuclear protein ran proteins. Short-chain dehydrogenases/reductase s family proteins. MUTT DOMAIN SIGNATURE TYPE I ANTIFREEZE PROTEIN SIGNATURE CORONAVIRUS NUCLEOCAPSID	10 31-75 BL01115A 10.22 3.438e- 14 110-154 BL00061B 25.79 6.586e- 13 198-236 PR00502A 15.06 8.200e- 11 210-225 PR00308A 5.90 7.035e- 09 55-70 DM01206B 10.69 1.286e- 12 104-124 DM01206B 10.69 5.299e-11 23-43 DM01206B 10.69 8.274e- 10 73-93 DM01206B
960 962 963 966 967	BL01115 BL00061 PR00502 PR00308 DM01206	protein ran proteins. GTP-binding nuclear protein ran proteins. Short-chain dehydrogenases/reductase s family proteins. MUTT DOMAIN SIGNATURE TYPE I ANTIFREEZE PROTEIN SIGNATURE CORONAVIRUS NUCLEOCAPSID PROTEIN.	10 31-75 BL01115A 10.22 3.438e- 14 110-154 BL00061B 25.79 6.586e- 13 198-236 PR00502A 15.06 8.200e- 11 210-225 PR00308A 5.90 7.035e- 09 55-70 DM01206B 10.69 1.286e- 12 104-124 DM01206B 10.69 5.299e-11 23-43 DM01206B 10.69 8.274e- 10 73-93 DM01206B 10.69 3.962e-09 108- 128 DM01206B 10.69 5.671e-09 38-58
960 962 963 966	BL01115 BL00061 PR00502 PR00308	protein ran proteins. GTP-binding nuclear protein ran proteins. Short-chain dehydrogenases/reductase s family proteins. MUTT DOMAIN SIGNATURE TYPE I ANTIFREEZE PROTEIN SIGNATURE CORONAVIRUS NUCLEOCAPSID PROTEIN.	10 31-75 BL01115A 10.22 3.438e- 14 110-154 BL00061B 25.79 6.586e- 13 198-236 PR00502A 15.06 8.200e- 11 210-225 PR00308A 5.90 7.035e- 09 55-70 DM01206B 10.69 1.286e- 12 104-124 DM01206B 10.69 5.299e-11 23-43 DM01206B 10.69 8.274e- 10 73-93 DM01206B 10.69 3.962e-09 108- 128 DM01206B 10.69 5.671e-09 38-58 PF01008B 25.59 4.724e-
960 962 963 966 967	BL01115 BL00061 PR00502 PR00308 DM01206	protein ran proteins. GTP-binding nuclear protein ran proteins. Short-chain dehydrogenases/reductase s family proteins. MUTT DOMAIN SIGNATURE TYPE I ANTIFREEZE PROTEIN SIGNATURE CORONAVIRUS NUCLEOCAPSID PROTEIN.	10 31-75 BL01115A 10.22 3.438e- 14 110-154 BL00061B 25.79 6.586e- 13 198-236 PR00502A 15.06 8.200e- 11 210-225 PR00308A 5.90 7.035e- 09 55-70 DM01206B 10.69 1.286e- 12 104-124 DM01206B 10.69 5.299e-11 23-43 DM01206B 10.69 8.274e- 10 73-93 DM01206B 10.69 3.962e-09 108- 128 DM01206B 10.69 5.671e-09 38-58 PF01008B 25.59 4.724e- 31 417-460 PF01008C
960 962 963 966 967	BL01115 BL00061 PR00502 PR00308 DM01206	protein ran proteins. GTP-binding nuclear protein ran proteins. Short-chain dehydrogenases/reductase s family proteins. MUTT DOMAIN SIGNATURE TYPE I ANTIFREEZE PROTEIN SIGNATURE CORONAVIRUS NUCLEOCAPSID PROTEIN.	10 31-75 BL01115A 10.22 3.438e- 14 110-154 BL00061B 25.79 6.586e- 13 198-236 PR00502A 15.06 8.200e- 11 210-225 PR00308A 5.90 7.035e- 09 55-70 DM01206B 10.69 1.286e- 12 104-124 DM01206B 10.69 5.299e-11 23-43 DM01206B 10.69 8.274e- 10 73-93 DM01206B 10.69 3.962e-09 108- 128 DM01206B 10.69 5.671e-09 38-58 PF01008B 25.59 4.724e- 31 417-460 PF01008C 12.25 5.333e-18 506-
960 962 963 966 967	BL01115 BL00061 PR00502 PR00308 DM01206	protein ran proteins. GTP-binding nuclear protein ran proteins. Short-chain dehydrogenases/reductase s family proteins. MUTT DOMAIN SIGNATURE TYPE I ANTIFREEZE PROTEIN SIGNATURE CORONAVIRUS NUCLEOCAPSID PROTEIN.	10 31-75 BL01115A 10.22 3.438e- 14 110-154 BL00061B 25.79 6.586e- 13 198-236 PR00502A 15.06 8.200e- 11 210-225 PR00308A 5.90 7.035e- 09 55-70 DM01206B 10.69 1.286e- 12 104-124 DM01206B 10.69 5.299e-11 23-43 DM01206B 10.69 8.274e- 10 73-93 DM01206B 10.69 3.962e-09 108- 128 DM01206B 10.69 5.671e-09 38-58 PF01008B 25.59 4.724e- 31 417-460 PF01008C

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
970	BL01277	Ribonuclease PH	
	BEGIZY	proteins.	BL01277C 10.18 7.648e- 10 112-143 BL01277A
975	BL01159	WW/rsp5/wwP domain	17.39 9.806e-10 40-78
		proteins.	BL01159 13.85 3.605e-
			12 130-145 BL01159 13.85 4.122e-10 171-
			186
977	PF00791	Domain present in ZO-1	PF00791C 20.98 2.235e-
		and Unc5-like netrin	09 55-94
978	BL01167	receptors.	
•	DECTION .	Ribosomal protein L17 proteins.	BL01167B 20.66 8.258e-
979	BL00478	LIM domain proteins.	19 B8-127 BL00478B 14.79 9.357e-
		processio.	13 33-48 BL00478B
			14.79 7.250e-12 98-113
980	PR00312	CALSEQUESTRIN SIGNATURE	PRO0312E 8.32 3.423e-
			36 169-199 PR00312I
			15.78 5.286e-35 332-
			361 PR00312F 15.06
			5.865e-35 199-229 PR00312H 13.31 8.313e-
			35 263-291 PR00312J
	ł	ļ	13.73 5.688e-34 363-
	1		392 PR00312D 9.43
	1		2.636e-33 128-158
			PR00312C 15.14 8.839e-
		1	33 92-122 PR00312B 15.08 8.941e-33 62-92
			PR00312G 11.11 6.657e-
			32 230-258 PR00312A
981	PF00992		11.70 6.914e-27 35-59
361	PF00992	Troponin.	PF00992A 16.67 8.816e-
982	PR00299	ALPHA CRYSTALLIN	09 414-449
		SIGNATURE	PR00299F 13.20 2.367e- 09 127-149
983	BL01150	Respiratory-chain NADH	BL01150B 17.16 1.000e-
		dehydrogenase 20 Kd	40 156-202 BL01150A
		subunit proteins.	14.10 8.200e-39 100-
986	BL00795	Involucrin proteins.	138
		involución procesna.	BL00795C 17.06 7.211e- 14 4-49 BL00795C
			17.06 1.778e-11 1-46
			BL00795C 17.06 3.407e-
			10 14-59 BL00795C
		1	17.06 7.802e-10 2-47
			BL00795C 17.06 8.640e- 10 19-64 BL00795C
			17.06 7.400e-09 11-56
		1	BL00795C 17.06 7.800e-
987	21.0000		09 3-48
³⁶ ′	BL00939	Ribosomal protein Lle	BL00939F 17.27 5.393e-
988	PR00452	proteins. SH3 DOMAIN SIGNATURE	09 810-840
	11100102	SH3 DOMAIN SIGNATURE	PR00452B 11.65 6.538e-
989	PR00452	SH3 DOMAIN SIGNATURE	11 525-541 PR00452B 11.65 6.538e-
			11 497-513
994	BL00027	'Homeobox' domain	BL00027 26.43 2.500e-
997	77.0100	proteins.	25 146-189
,,,	BL01304	ubiH/COQ6 monooxygenase	BL01304A 8.05 3.893e-
998	DM01767	family proteins. 5 TRANSMITTER DOMAIN.	11 65-79
- 1		- AMMONITIER DUMAIN.	DM01767B 10.07 7.868e-
1000	PR00926	MITOCHONDRIAL CARRIER	09 22-39 PR00926C 16.07 1.750e-
i		PROTEIN SIGNATURE	24 73-94 PR00926D
1			10.53 3.250e-23 126-
		1	145 PR00926F 17.75
1		1	6.211e-23 217-240
		1	PR00926E 11.70 6.625e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			20 174-193 PR00926B 16.07 2.125e-18 24-39 PR00926A 10.41 1.00Ce- 15 11-25 PR00926F 17.75 5.565e-09 120-
1005	BL00406	Actins proteins.	BL00406B 5.47 1.000e- 40 88-143 BL00406C 6.75 1.000e-40 147-202 BL00406D 12.58 3.700e- 40 270-325 BL00406E 8.44 7.375e-38 327-377 BL00406A 9.95 3.348e- 29 11-46
1006	BL00406	Actins proteins.	BL00406B 5.47 1.000e- 40 88-143 BL00406C 6.75 1.000e-40 147-202 BL00406E 8.44 1.000e- 35 248-298 BL00406A 9.95 3.348e-29 11-46
1007	PR00304	TAILLESS COMPLEX POLYPEPTIDE 1 (CHAPERONE) SIGNATURE	PRO0304D 11.04 8.714e- 22 384-407 PR00304C 8.69 4.667e-20 98-118 PR00304B 11.60 7.577e- 19 68-87 PR00304A 9.20 3.382e-16 46-63 PR00304E 7.79 6.870e- 13 418-431
1009	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL BINDING NU.	PD01066 19.43 2.929e- 32 9-48
1011	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 2.929e- 32 68-107
1012	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 6.143e- 10 64-73
1016	PD01168	SYNTHETASE LIGASE PROTEIN ALANYL	PD01168H 12.08 1.000e-
1018	PD00930	PROTEIN GTPASE DOMAIN ACTIVATION.	11 174-194 PD00930B 33.72 1.391e- 32 261-302 PD00930A 25.62 9.550e-22 157- 183
1022	BL00175	Phosphoglycerate mutase family phosphohistidine proteins.	BL00175A 15.42 5.179e- 12 6-26 BL00175C 23.75 8.062e-10 79-111
1025	PR00305	14-3-3 PROTEIN ZETA SIGNATURE	PR00305D 16.34 1.439e-
1026	BL00353	HMG1/2 proteins.	BL00353B 11.47 2.436e- 18 238-288 BL00353C 14.83 8.844e-ll 288- 335
1028	BL00183	Ubiquitin-conjugating enzymes proteins.	BL00183 28.97 1.310e- 33 43-91
1033	PF00580	UvrD/REP helicase.	PF00580A 13.37 4.720e- 09 111-133
1034	PR00413	HALOACID DEHALOGENASE/EPOXIDE HYDROLASE FAMILY SIGNATURE	PR00413E 15.78 3.429e- 09 154-171
1037	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 9.657e- 09 5-44
1038	PD01796	PROTEIN TRANSMEMBRANE COBALT ZINC CADMIU.	PD01796 15.01 4.259e- 11 55-82
1039	BL00299	Ubiquitin domain proteins.	BL00299 28.84 9.036e- 09 17-69
1040	PR00970	ARGININE ADP- RIBOSYLTRANSFERASE	PR00970A 17.73 6.143e- 20 56-78 PR00970D

	: ACCESSION	DESCRIPTION	RESULTS*
	NO.		
ŀ		SIGNATURE	9.96 2.154e-18 154-171
			PR00970F 12.30 1.000e- 16 224-241 PR00970G
			9.97 9.229e-15 242-258
Ĭ			PR00970B 16.37 1.290e-
			13 86-105 PR00970C
			11.05 1.643e-11 115-
			130 PR00970E 11.23
1042	BL00678	Trp-Asp (WD) repeat	9.820e-11 202-218
L		proteins proteins.	BL00678 9.67 2.200e-10 243-254
1043	PR00048	C2H2-TYPE ZINC FINGER	PR00048A 10.52 6.786e-
		SIGNATURE	13 114-128 PR00048A
	-		10.52 1.000e-09 172-
1045	BL00615		186
1015	PP00012	C-type lectin domain proteins.	BL00615A 16.68 1.720e-
		proceins.	11 218-236 BL00615B
			12.25 1.857e-10 317-
1046	BL01092	Adenylate cyclases	BL01092N 13.54 8.924e-
2000		class-I proteins.	10 3-40
1047	BL01216	ATP-citrate lyase /	BL01216D 21.75 4.316e-
		succinyl-CoA ligases	28 314-344 BL01216A
1049	DM00031	family proteins.	13.91 1.000e-10 97-112
	20001	IMMUNOGLOBULIN V REGION.	. DM00031B 15.41 7.618e-
1050	BL01073	Ribosomal protein L24e	12 102-136
		proteins.	BL01073 24.30 1.000e- 40 12-62
1054	BL00571	Amidases proteins.	BL00571 25.69 5.875e-
1055			31 160-212
1055	BL00030	Eukaryotic RNA-binding	BL00030A 14.39 5.235e-
		region RNP-1 proteins.	11 98-117 BL00030B
1058	BL00223	Annexins repeat proteins	7.03 4.316e-09 137-147
•		domain proteins.	BL00223C 24.79 8.754e- 23 262-317 BL00223A
			15.59 9.478e-14 46-80
		1	BL00223A 15.59 5.557e-
1060	BL00027		11 118-152
1000	BL00027	'Homeobox' domain	BL00027 26.43 3.455e-
1064	BL00455	proteins. Putative AMP-binding	35 158-201
1064		racactve Amending	BL00455 13.31 6.211e-
1064	8500455	domain proteins	17 200 200
1064	PR00019 .	domain proteins.	13 280-296
			PR00019A 11.19 2.000e-
1065	PR00019 .	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 2.000e- 09 115-129 PR00019B 11.36 3.880e-09 87-101
		LEUCINE-RICH REPEAT SIGNATURE GTP1/OBG GTP-BINDING	PR00019A 11.19 2.000e- 09 115-129 PR00019B 11.36 3.880e-09 87-101 PR00326A 8.75 4.600e-
1065	PR00019 .	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 2.000e- 09 115-129 PR00019B 11.36 3.880e-09 87-101 PR00326A 8.75 4.600e- 16 151-172 PR00326C
1065	PR00019 .	LEUCINE-RICH REPEAT SIGNATURE GTP1/OBG GTP-BINDING	PR00019A 11.19 2.000e- 09 115-129 PR00019B 11.36 3.880e-09 87-101 PR00326A 8.75 4.600e- 16 151-172 PR00326C 9.79 1.290e-14 200-216
1065	PR00019 .	LEUCINE-RICH REPEAT SIGNATURE GTP1/OBG GTP-BINDING	PR00019A 11.19 2.000e- 09 115-129 PR00019B 11.36 3.880e-09 87-101 PR00326A 8.75 4.600e- 16 151-172 PR00326C 9.79 1.290e-14 200-216 PR00326B 16.74 8.548e-
1065	PR00019 .	LEUCINE-RICH REPEAT SIGNATURE GTP1/OBG GTP-BINDING	PR00019A 11.19 2.000e- 09 115-129 PR00019B 11.36 3.880e-09 87-101 PR00326A 8.75 4.600e- 16 151-172 PR00326C 9.79 1.290e-14 200-216 PR00326B 16.74 8.548e- 14 172-191 PR00326D
1066	PR00019 .	LEUCINE-RICH REPEAT SIGNATURE GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00019A 11.19 2.000e- 09 115-129 PR00019B 11.36 3.880e-09 87-101 PR00326A 8.75 4.600e- 16 151-172 PR00326C 9.79 1.290e-14 200-216 PR00326B 16.74 8.548e-
1065	PR00019 .	LEUCINE-RICH REPEAT SIGNATURE GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE RECEPTOR INTERLEUKIN-1	PR00019A 11.19 2.000e- 09 115-129 PR00019B 11.36 3.880e-09 87-101 PR00326A 8.75 4.600e- 16 151-172 PR00326C 9.79 1.290e-14 200-216 PR00326B 16.74 8.548e- 14 172-191 PR00326D 19.09 1.257e-13 217- 236 PD02870B 18.83 8.518e-
1066	PR00019 PR00326 PD02870	LEUCINE-RICH REPEAT SIGNATURE GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE RECEPTOR INTERLEUKIN-1 PRECURSOR.	PR00019A 11.19 2.000e- 09 115-129 PR00019B 11.36 3.880e-09 87-101 PR00326A 8.75 4.600e- 16 151-172 PR00326C 9.79 1.290e-14 200-216 PR00326B 16.74 8.548e- 14 172-191 PR00326D 19.09 1.257e-13 217- 236 PD02870B 18.83 8.518e- 11 164-197
1066	PR00019 .	LEUCINE-RICH REPEAT SIGNATURE GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE RECEPTOR INTERLEUKIN-1	PR00019A 11.19 2.000e- 09 115-129 PR00019B 11.36 3.880e-09 87-101 PR00326A 8.75 4.600e- 16 151-172 PR00326C 9.79 1.290e-14 200-216 PR00326B 16.74 8.548e- 14 172-191 PR00326D 19.09 1.257e-13 217- 236 PD02870B 18.83 8.518e- 11 164-197 PF00856A 26.14 5.976e-
1066	PR00019 PR00326 PD02870	LEUCINE-RICH REPEAT SIGNATURE GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE RECEPTOR INTERLEUKIN-1 PRECURSOR. SET domain proteins.	PR00019A 11.19 2.000e- 09 115-129 PR00019B 11.36 3.880e-09 87-101 PR00326A 8.75 4.600e- 16 151-172 PR00326C 9.79 1.290e-14 200-216 PR00326B 16.74 8.548e- 14 172-191 PR00326D 19.09 1.257e-13 217- 236 PD02870B 18.83 8.518e- 11 164-197 PF00856A 26.14 5.976e- 09 350-387
1065 1066 1071	PR00019 PR00326 PD02870 PF00856	LEUCINE-RICH REPEAT SIGNATURE GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE RECEPTOR INTERLEUKIN-1 PRECURSOR. SET domain proteins.	PR00019A 11.19 2.000e- 09 115-129 PR00019B 11.36 3.880e-09 87-101 PR00326A 8.75 4.600e- 16 151-172 PR00326C 9.79 1.290e-14 200-216 PR00326B 16.74 8.548e- 14 172-191 PR00326D 19.09 1.257e-13 217- 236 PD02870B 18.83 8.518e- 11 164-197 PF00856A 26.14 5.976e- 09 350-387 BL01009D 14.19 4.300e-
1065 1066 1071	PR00019 PR00326 PD02870 PF00856	LEUCINE-RICH REPEAT SIGNATURE GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE RECEPTOR INTERLEUKIN-1 PRECURSOR. SET domain proteins.	PR00019A 11.19 2.000e- 09 115-129 PR00019B 11.36 3.880e-09 87-101 PR00326A 8.75 4.600e- 16 151-172 PR00326C 9.79 1.290e-14 200-216 PR00326B 16.74 8.548e- 14 172-191 PR00326D 19.09 1.257e-13 217- 236 PD02870B 18.83 8.518e- 11 164-197 PF00856A 26.14 5.976e- 09 350-387 BL01009D 14.19 4.300e- 20 127-148 BL01009A
1065 1066 1071	PR00019 PR00326 PD02870 PF00856	LEUCINE-RICH REPEAT SIGNATURE GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE RECEPTOR INTERLEUKIN-1 PRECURSOR. SET domain proteins. Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7	PR00019A 11.19 2.000e- 09 115-129 PR00019B 11.36 3.880e-09 87-101 PR00326A 8.75 4.600e- 16 151-172 PR00326C 9.79 1.290e-14 200-216 PR00326B 16.74 8.548e- 14 172-191 PR00326D 19.09 1.257e-13 217- 236 PD02870B 18.83 8.518e- 11 164-197 PF00856A 26.14 5.976e- 09 350-387 BL01009D 14.19 4.300e- 20 127-148 BL01009A 13.75 6.586e-13 57-75
1065 1066 1071 1072	PR00019 PR00326 PD02870 PF00856 BL01009	LEUCINE-RICH REPEAT SIGNATURE GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE RECEPTOR INTERLEUKIN-1 PRECURSOR. SET domain proteins. Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7	PR00019A 11.19 2.000e- 09 115-129 PR00019B 11.36 3.880e-09 87-101 PR00326A 8.75 4.600e- 16 151-172 PR00326C 9.79 1.290e-14 200-216 PR00326B 16.74 8.548e- 14 172-191 PR00326D 19.09 1.257e-13 217- 236 PD02870B 18.83 8.518e- 11 164-197 PF00856A 26.14 5.976e- 09 350-387 BL01009D 14.19 4.300e- 20 127-148 BL01009A 13.75 6.586e-13 57-75 BL01009E 13.50 1.439e-
1065 1066 1071	PR00019 PR00326 PD02870 PF00856	LEUCINE-RICH REPEAT SIGNATURE GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE RECEPTOR INTERLEUKIN-1 PRECURSOR. SET domain proteins. Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 proteins. CARBOXYPEPTIDASE C	PR00019A 11.19 2.000e- 09 115-129 PR00019B 11.36 3.880e-09 87-101 PR00326A 8.75 4.600e- 16 151-172 PR00326C 9.79 1.290e-14 200-216 PR00326B 16.74 8.548e- 14 172-191 PR00326D 19.09 1.257e-13 217- 236 PD02870B 18.83 8.518e- 11 164-197 PF00856A 26.14 5.976e- 09 350-387 BL01009D 14.19 4.300e- 20 127-148 BL01009A 13.75 6.586e-13 57-75 BL01009E 13.50 1.439e- 11 159-175
1065 1066 1071 1072	PR00019 PR00326 PD02870 PF00856 BL01009	LEUCINE-RICH REPEAT SIGNATURE GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE RECEPTOR INTERLEUKIN-1 PRECURSOR. SET domain proteins. Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 proteins. CARBOXYPEPTIDASE C SERINE PROTEASE (S10)	PR00019A 11.19 2.000e- 09 115-129 PR00019B 11.36 3.880e-09 87-101 PR00326A 8.75 4.600e- 16 151-172 PR00326C 9.79 1.290e-14 200-216 PR00326B 16.74 8.548e- 14 172-191 PR00326D 19.09 1.257e-13 217- 236 PD02870B 18.83 8.518e- 11 164-197 PF00856A 26.14 5.976e- 09 350-387 BL01009D 14.19 4.300e- 20 127-148 BL01009A 13.75 6.586e-13 57-75 BL01009E 13.50 1.439e-
1065 1066 1071 1072	PR00019 PR00326 PD02870 PF00856 BL01009 PR00724	LEUCINE-RICH REPEAT SIGNATURE GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE RECEPTOR INTERLEUKIN-1 PRECURSOR. SET domain proteins. Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 proteins. CARBOXYPEPTIDASE C SERINE PROTEASE (S10) FAMILY SIGNATURE	PR00019A 11.19 2.000e- 09 115-129 PR00019B 11.36 3.880e-09 87-101 PR00326A 8.75 4.600e- 16 151-172 PR00326C 9.79 1.290e-14 200-216 PR00326B 16.74 8.548e- 14 172-191 PR00326D 19.09 1.257e-13 217- 236 PD02870B 18.83 8.518e- 11 164-197 PF00856A 26.14 5.976e- 09 350-387 BL01009D 14.19 4.300e- 20 127-148 BL01009A 13.75 6.586e-13 57-75 BL01009E 13.50 1.439e- 11 159-175 PR00724A 10.91 1.000e- 08 366-379
1065 1066 1071 1072 1075	PR00019 PR00326 PD02870 PF00856 BL01009	LEUCINE-RICH REPEAT SIGNATURE GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE RECEPTOR INTERLEUKIN-1 PRECURSOR. SET domain proteins. Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 proteins. CARBOXYPEPTIDASE C SERINE PROTEASE (S10) FAMILY SIGNATURE Mitochondrial energy	PR00019A 11.19 2.000e- 09 115-129 PR00019B 11.36 3.880e-09 87-101 PR00326A 8.75 4.600e- 16 151-172 PR00326C 9.79 1.290e-14 200-216 PR00326B 16.74 8.548e- 14 172-191 PR00326D 19.09 1.257e-13 217- 236 PD02870B 18.83 8.518e- 11 164-197 PF00856A 26.14 5.976e- 09 350-387 BL01009D 14.19 4.300e- 20 127-148 BL01009A 13.75 6.586e-13 57-75 BL01009E 13.50 1.439e- 11 159-175 PR00724A 10.91 1.000e- 08 366-379 BL00215A 15.82 1.000e-
1065 1066 1071 1072 1075	PR00019 PR00326 PD02870 PF00856 BL01009 PR00724	LEUCINE-RICH REPEAT SIGNATURE GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE RECEPTOR INTERLEUKIN-1 PRECURSOR. SET domain proteins. Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 proteins. CARBOXYPEPTIDASE C SERINE PROTEASE (S10) FAMILY SIGNATURE	PR00019A 11.19 2.000e- 09 115-129 PR00019B 11.36 3.880e-09 87-101 PR00326A 8.75 4.600e- 16 151-172 PR00326C 9.79 1.290e-14 200-216 PR00326B 16.74 8.548e- 14 172-191 PR00326D 19.09 1.257e-13 217- 236 PD02870B 18.83 8.518e- 11 164-197 PF00856A 26.14 5.976e- 09 350-387 BL01009D 14.19 4.300e- 20 127-148 BL01009A 13.75 6.586e-13 57-75 BL01009E 13.50 1.439e- 11 159-175 PR00724A 10.91 1.000e- 08 366-379

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		
1001		proteins proteins.	298-309
1081	BL00326	Tropomyosins proteins.	BL00326A 14.01 7.398e- 10 23-57
1094	BI-00460	Glutathione peroxidases	BL00460A 28.67 3.204e-
i		selenocysteine proteins.	18 57-92 BL00460B
			9.73 6.400e-13 100-118
	}		BL00460D 16.89 9.143e-
			12 162-182 BL00460C
			14.35 5.500e-09 133-
1095	PD02811		156
1095	PD05811	PROTEIN PEPTIDE	PD02811A 20.67 3.017e-
		REDUCTASE MG448 PILB FIMBRIA TRAN.	22 67-105 PD02811B
		THERE I IVE	17.07 2.263e-21 118- 151 PD02811C 13.25
			5.696e-13 154-167
1096	PD02811	PROTEIN PERTIDE	PD02811A 20.67 3.017e-
		REDUCTASE MG448 PILB	22 60-98 PD02811B
		FIMBRIA TRAN.	17.07 2.263e-21 111-
			144 PD02811C 13.25
1000			5.696e-13 147-160
1097	BL00479	Phorbol esters /	BL00479B 12.57 6.143e-
		diacylglycerol binding domain proteins.	09 200-216
1105	PF00881	1	
-200	2 7 0 0 0 0 1	Nitroreductase family.	PF00881A 27.15 9.229e-
1109	PR00449	TRANSFORMING PROTEIN P21	PR00449A 13.20 3.077e-
		RAS SIGNATURE	10 15-37 PR00449E
			13.50 1.857e-09 185-
		İ	208 PR00449D 10.79
			8.364e-09 131-145
1115	PR00405	HIV REV INTERACTING	PR00405B 11.83 5.737e-
		PROTEIN SIGNATURE	20 42-60 PROG405A
			17.71 2.703e-17 23-43
			PR00405C 19.41 6.902e-
1116	BL00355	HMG14 and HMG17	10 63-85 BL00355 5.97 2.528e-25
	İ	proteins.	20-51
1117	BL00355	HMG14 and HMG17	BL00355 5.97 2.528e-25
		proteins.	20-51
1120	BL00107	Protein kinases ATP-	BL00107B 13.31 4.857e-
1100		binding region proteins.	10 290-306
1123	PR00412	EPOXIDE HYDROLASE	PR00412F 18.76 9.526e-
1125	PR00186	SIGNATURE	12 301-324
	PROUISS	HEMERYTHRIN SIGNATURE	PR00186A 13.62 2.800e-
1129	BL00170	Cyclophilin-type	09 87-101 BL00170C 18.49 3.077e-
	-500	peptidyl-prolyl cis-	33 84-129 BL00170B
		trans isomerase	20.97 6.838e-25 37-77
		signatur.	BL00170A 17.08 3.455e-
			15 10-37
1131	BL00636	Nt-dnaJ domain proteins.	BL00636A 8.07 5.304e-
	1		15 29-46 BL00636B
1132	PT 00C30	III David	15.11 1.360e-14 59-80
1176	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 6.211e-09
1133	BL00678	proteins proteins.	29-40
	-2000/6	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 6.211e-09
1136	BL00990	Clathrin adaptor	29-40 BL00990C 18 78 4 1750
		complexes medium chain	BL00990C 18.78 4.176e- 38 235-269 BL00990A
	1	proteins.	21.44 4.316e-36 94-132
	}	1-	BL00990B 20.15 2.125e-
			27 157-187 BL00990D
			16.13 5.320e-18 403-
			422
1137	PR00314	CLATHRIN COAT ASSEMBLY	PR00314B 15.68 8.000e-
		PROTEIN SIGNATURE	34 100-128 PR00314D
			9.66 3.531e-33 233-261 PR00314C 16.05 8.909e-

SEQ ID NO	D: ACCESSION NO.	DESCRIPTION	RESULTS*
			32 159-188 PR00314A
1139	BL01115	GTP-binding nuclear	14.53 1.281e-22 13-34 BL01115A 10.22 6.364e-
1141	BL00107	protein ran proteins. Protein kinases ATP-	13 13-57 BL00107A 18.39 4.000e-
		binding region proteins.	13.31 3.077e-12 519-
1148	PR00685	TRANSCRIPTION INITIATION	1 1.00,00
1155	PD01652	FACTOR IIB SIGNATURE RECEPTOR CELL NK	09 21-42 PD01652B 8.50 9.396e-
1157		GLYCOPROTEIN IMMUNOGLOB.	10 522-574 PD01652B 8.50 9.463e-10 740-792
1157	PD02894	HYDROLASE N4- PRECURSOR PROTEIN SIGNAL BE.	PD02894A 21.96 7.873e- 28 81-127 PD02894B 13.93 1.188e-27 178-
1159	BL00623	GMC oxidoreductases	211 BL00623E 15.00 3.531e-
		proteins.	20 391-414 BL00623C 10.86 4.240e-20 155-
1161	PD01937	DNA PROTEIN POLYMERASE ENDONUCLEASE DNA	PD01937A 6.68 3.475e-
1162	PD01937	DNA PROTEIN POLYMERASE ENDONUCLEASE DNA	09 330-341 PD01937A 6.68 3.475e-
1163	PR00624	HISTONE H5 SIGNATURE	09 221-232 PR00624D 11.94 7.455e-
			10 214-239 PR00624D 11.94 1.961e-09 312- 337
1167	BL00226	Intermediate filaments proteins.	BL00226B 23.86 7.384e- 09 302-350
1177	BL01032	Protein phosphatase 2C proteins.	BL01032G 8.33 1.422e-
1178	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	10 34-48 PR00320A 16.74 1.794e- 10 205-220 PR00320C 13.01 7.840e-10 205- 220 PR00320B 12.19 8.457e-10 35-50 PR00320A 16.74 7.146e- 09 35-50 PR00320B
1180	PR00454	ETS DOMAIN SIGNATURE	12.19 9.100e-09 79-94 PR00454D 10.89 4.150e-
1181	BL00291	Prion protein.	19 765-784 BL00291A 4.49 8.962e-
1184	BL00720	Guanine-nucleotide dissociation stimulators CDC25 family sign.	11 152-187 BL00720B 16.57 4.103e- 18 1089-1113
1185	BLC0215	Mitochondrial energy transfer proteins.	BL00215A 15.82 4.553e- 13 204-229 BL00215A 15.82 1.429e-12 11-36 BL00215A 15.82 9.809e-
L187	BL00983	Ly-6 / u-PAR domain	11 104-129 BL00983C 12.69 2.761e-
.188	BL00878	proteins. Orn/DAP/Arg decarboxylases family 2 pyridoxal-P attachment si.	10 77-93 BL00878B 10.95 6.000e- 16 189-204 BL00878C 17.74 8.435e-15 225- 245 BL00878F 19.67 3.625e-13 379-402 BL00878D 16.56 1.621e-
191	PD02939	PROTEIN GLUTATHIONE SYNTHETASE SY.	09 270-289 PD02939B 10.10 2.723e- 12 203-220 PD02939C 20.01 1.000e-11 224-
193	PR00345	STATHMIN FAMILY SIGNATURE	PR00345B 7.12 2.800e- 28 72-101 PR00345B

SEQ ID NO	ACCESSION NO.	DESCRIPTION	RESULTS*
			8.54 7.652e-28 149-174 PR00345C 4.54 9.100e- 28 101-125 PR00345D 10.97 1.964e-24 125- 149 PR00345A 13.46 5.645e-16 43-62
1194	PR00345	STATHMIN FAMILY SIGNATURE	PR00345B 7.12 2.800c- 28 108-137 PR00345E 8.54 7.652e-28 185-210 PR00345C 4.54 9.100e- 28 137-161 PR00345D 10.97 1.964e-24 161-
1195	PF00995	Secl family.	185 PR00345A 13.46 5.645e-16 79-98 PF00995B 17.37 1.120e-
1196	BL00932	Bacterial-type phytoene	13 224-264 BL00982A 18.41 6.738e-
1197	BL01298	Dihydrodipicolinate reductase proteins.	11 15-47 BL01298A 13.90 5.959c
1203	BL00061	Short-chain dehydrogenases/reductase s family proteins.	09 51-73 BL00061B 25.79 1.000e- 14 152-190
1204	PR00118	BETA-LACTAMASE CLASS A SIGNATURE	PRO0118F 16.42 9.386e-
1206	BL01183	ubiE/COQ5 methyltransferase family proteins.	BL01183B 21.31 1.429e- 37 184-229 BL01183D 27.71 8.535e-27 264- 307 BL01183A 13.25 3.250e-23 51-73 BL01183C 10.77 5.295e- 09 246-258
1208	BL00979	G-protein coupled receptors family 3 proteins.	BL00979L 20.63 2.485e- 09 105-146
1209	PFC0023	Ank repeat proteins.	PF00023A 16.03 4.857e- 11 49-65 PF00023B 14.20 1.818e-09 45-55
1212	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 7.750e- 14 227-241 PR00048A 10.52 4.316e-11 199-
1213	PR00450	RECOVERIN FAMILY SIGNATURE	PR00450C 12.22 1.720e- 10 20-42 PR00450C 12.22 3.506e-09 56-78 PR00450D 16.58 6.769e- 09 44-64
1216	BL00412 PR00456	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 5.598e- 10 179-230
1222		RIBOSOMAL PROTEIN P2 SIGNATURE	PR00456E 3.06 5.348e- 11 249-264
	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 7.231e- 15 295-308 PD00066 13.92 7.231e-15 406- 419 PD00066 13.92 2.286e-12 378-391 PD00066 13.92 7.857e- 12 434-447 PD00066 13.92 3.348e-11 350- 363
1223	BL50058	G-protein gamma subunit profile.	BL50058 27.23 1.000e- 40 13-61
1226	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 8.439e- 09 279-330
1227	BL00437	Catalase proximal heme- ligand proteins.	BL00437A 18.82 1.000e- 40 49-101 BL00437B 16.28 1.000e-40 114- 168 BL00437C 21.86

SEQ ID NO	NO.	DESCRIPTION	RESULTS*
			1.000e-40 190-239
			BL00437D 25.72 1.000e-
1			40 248-301 BL00437E
	1		23.95 1.000e-40 327-
1230	BL01160	Kinesin light chain	379
		repeat proteins.	BL01160B 19.54 8.297e- 10 5-60
1231	PR00735	GLYCOSYL HYDROLASE	PR00735A 11.19 6.857e-
		FAMILY 8 SIGNATURE	09 391-405
1232	PR00497	NEUTROPHIL CYTOSOL	PR00497A 6.92 5.553e-
1233	PR00497	FACTOR P40 SIGNATURE	10 158-176
	PROOTS	NEUTROPHIL CYTOSOL FACTOR P40 SIGNATURE	PR00497A 6.92 5.553e-
1235	BL00866	Carbamoyl-phosphate	10 158-176
		synthase subdomain	BL00866B 36.29 2.776e- 09 75-121
		proteins.	05 75-121
1237	BL00027	'Homeobox' domain	BL00027 26.43 1.818e-
1243	PR00403	proteins.	21 36-79
	PR00403	WW DOMAIN SIGNATURE	PR00403B 12.19 1.184e-
1246	PD01168	SYNTHETASE LIGASE	11 10-25
		PROTEIN ALANYL.	PD01168L 9.47 2.837e- 10 31-46 PD01168L
			9.47 4.490e-10 174-189
			PD01168L 9.47 7.612e-
1249	BL00018		10 183-198
	2000019	EF-hand calcium-binding domain proteins.	BL00018 7.41 2.800e-10
1254	BL00183	Ubiquitin-conjugating	183-196
		enzymes proteins.	BL00183 28.97 2.440e- 36 96-144
1255	BL01115	GTP-binding nuclear	BL01115A 10.22 5.670e-
1256	BL00373	protein ran proteins.	11 8-52
1230	БП003./3	Phosphoribosylglycinamid	BL00373C 10.35 3.348e-
		e formyltransferase proteins.	12 143-156
1258	PR00011	TYPE III EGF-LIKE	PR00011B 13.08 3.217e-
1050		SIGNATURE	10 174-193
1259	BL00518	Zinc finger, C3HC4 type	BL00518 12.23 8.286e-
1261	PR00070	(RING finger), proteins.	10 31-40
	12800070	DIHYDROFOLATE REDUCTASE SIGNATURE	PR00070D 11.63 1.000e-
			15 112-127 PR00070C 13.09 9.500e-15 51-63
			PR00070A 12.92 5.500e-
1262	Proof Co		12 16-27
1202	BL00462	Gamma -	BL00462A 20.89 6.438e-
		glutamyltranspeptidase proteins.	24 140-183 BL00462B
			17.88 5.500e-20 230- 267 BL00462C 27.41
1060			2.023e-11 292-347
1263	BL00038	Myc type, helix-loop-	BL00038B 16.97 9.455e-
		helix' dimerization domain proteins.	11 62-83
1264	BL01115	GTP-binding nuclear	DY 0
		protein ran proteins.	BL01115A 10.22 5.670e- 11 17-61
1266	PR00837	ALLERGEN V5/TPX-1 FAMILY	PR00837C 17.21 2.714e-
	1	SIGNATURE	18 165-182 PRO0837A
			14.77 4.512e-12 86-105
			PR00837D 11.12 7.577e-
1269	PR00449	TRANSFORMING PROTEIN P21	12 201-215
		RAS SIGNATURE	PR00449C 17.27 9.308e- 22 40-63 PR00449E
	1	1	13.50 1.000e-16 137-
		1	160 PR00449D 10.79
270	BL00276	Change 1 feet	3.520e-11 102-116
· -	1 22002/6	Channel forming colicins proteins.	BL00276A 8.87 1.500e-
275	PD02327	GLYCOPROTEIN ANTIGEN	09 17-29
	1		PD02327C 15.47 9.769e-
.276	PR00412	PRECURSOR IMMUNOGLO. EPOXIDE HYDROLASE	09 228-243

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
·		SIGNATURE	12 119-135 PR00412C 11.30 1.857e-11 165- 179 PR00412A 13.23 3.400e-11 100-119
1277	PF00756	Putative esterase.	PF00756C 14.12 9.538e- 10 127-157
1279	BL00134	Serine proteases, trypsin family, histidine proteins.	BL00134A 11.96 9.325e- 13 128-145
1280	BL01220	Phosphatidylethanolamine -binding protein family proteins.	BL01220C 14.75 9.348e- 15 248-276
1285	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 2.286e- 10 33-42
1287	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 7.182e- 11 288-343
1292	PR00802	SERUM ALBUMIN FAMILY SIGNATURE	PR00802B 16.51 1.610e- 10 81-105
1297	PR00716	M-PHASE INDUCER PHOSPHATASE SIGNATURE	PR00716C 17.65 5.696e-
1298	BL00478	LIM domain proteins.	BL00478B 14.79 6.478e- 14 268-283
1301	BL00127	Pancreatic ribonuclease family proteins.	BL00127C 31.49 3.571e- 28 82-126 BL00127B 26.57 8.800e-28 23-68
1302	PR00637	TYPE 3 BOMBESIN RECEPTOR SIGNATURE	PR00637E 11.27 4.250e- 09 290-306
1307	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 5.500e- 17 13-38 BL00215A 15.82 1.000e-16 226- 251 BL00215A 15.82 2.658e-13 107-132
1308	PRC0898	VASOPRESSIN V2 RECEPTOR SIGNATURE	PR00898H 11.34 4.682e-
1309	PD00301	PROTEIN REPEAT MUSCLE CALCIUM-BI.	PD00301B 5.49 2.731e- 09 390-401
1310	BL00983	Ly-6 / u-PAR domain proteins.	BL00983C 12.69 9.654e- 13 73-89 BL00983B 8.19 3.132e-09 12-22
1313	BL00194	Thioredoxin family proteins.	BL00194 12.16 1.900e- 11 15-28
1314	BL00594	Aromatic amino acids permeases proteins.	BL00594A 16.75 8.969e-
1316	BL00134	Serine proteases, trypsin family, histidine proteins.	10 53-97 BL00134A 11.96 9.325e- 13 128-145
1320	BL00783	Ribosomal protein L13 proteins.	BL00783C 22.43 6.559e- 24 87-117 BL00783A 14.55 1.600e-19 8-33 BL00783B 12.76 3.500e- 12 74-86
1327	PF00514	Armadillo/beta-catenin- like repeat proteins.	PF00514A 31.30 7.268e- 11 82-120
1329	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 6.294e- 11 129-148 BL00030B 7.03 4.789e-09 168-178
1331	PR00497	NEUTROPHIL CYTOSOL FACTOR P40 SIGNATURE	PR00497A 6.92 7.239e- 09 25-43
1332	PR00161	NICKEL-DEPENDENT HYDROGENASE/B-TYPE CYTOCHROME SIGNATURE	PR00161C 9.51 4.930e- 09 317-337
1333	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 6.769e- 33 10-49
1336	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE	PR00700D 12.47 2.200e- 09 262-281
1337	PR00700	PROTEIN TYROSINE	PR00700D 12.47 2.200e-

SEQ ID NO	ACCESSION NO.	DESCRIPTION	RESULTS*
		PHOSPHATASE SIGNATURE	
1340	PR00860	VERTEBRATE SIGNATURE	09 211-230
		METALLOTHIONEIN	PR00860A 5.46 5.034e-
		SIGNATURE	13 5-18
1341	BL00893	mutT domain proteins.	BL00893 18.99 6.750e-
			16 46-71
1343	BL01282	BIR repeat proteins.	BL01282B 30.49 5.974e-
			21 383~422
1344	DM00099	4 kw A55R REDUCTASE	DM00099B 14.73 8.313e-
		TERMINAL	09 417-427
1345		DIHYDROPTERIDINE.	1 12 12 1
1345	BL00923	Aspartate and glutamate	BL00923B 11.41 5.935e-
1348	7700	racemases proteins.	10 135-146
1340	PF00651	BTB (also known as BR-	PF00651 15.00 7.231e-
1350	7770	C/Ttk) domain proteins.	13 44-57
1350	PR00193	MYOSIN HEAVY CHAIN	PR00193D 14.36 3.571e-
		SIGNATURE	32 416-445 PR00193C
	Ì		12.60 6.318e-31 179-
			207 PR00193B 11.69
			3.571e-24 133-159
			PR00193E 19.47 9.069e-
	1	1	22 470-499 PR00193A
1352	PR00447	Manual Control of the	15.41 1.783e-20 77-97
	FR00447	NATURAL RESISTANCE-	PR00447E 9.73 1.554e-
		ASSOCIATED MACROPHAGE	15 299-319 PR00447D
		PROTEIN SIGNATURE	13.54 3.408e-15 200-
		1	224 PR00447A 12.73
			6.357e-11 97-124
		İ	PR00447G 6.69 9.877e-
1353	BL00303	S-100/ICaBP type calcium	10 353-373
r		binding protein.	BL00303A 21.77 6.667e-
•		process.	26 45-82 BL00303B
1355	BL00039	DEAD-box subfamily ATP-	26.15 1.000e-24 93-130
		dependent helicases	BL00039D 21.67 5.950e-
		proteins.	29 375-421 BL00039A
		-	18.44 7.136e-29 99-138 BL00039C 15.63 4.000e-
			18 225-249 BL00039B
		1	19.19 3.182e-14 141-
1357		<u> </u>	167
1357	PF00615	Regulator of G protein	PF00615B 16.25 2.216e-
]	signalling domain	12 84-101 PF00615C
		proteins.	10.06 8.412e-12 162-
1360	PD01066		176
.500	PDOTOGG	PROTEIN ZINC FINGER	PD01066 19.43 9.234e-
		ZINC-FINGER METAL-	29 10-49
361	PR00925	BINDING NU.	
	1	NONHISTONE CHROMOSOMAL	PR00925A 5.47 5.091e-
		DDOTRIN INCO.	1 3.0316
•		PROTEIN HMG17 FAMILY	18 14-29 PR00925B
		PROTEIN HMG17 FAMILY SIGNATURE	18 14-29 PR00925B 3.73 6.143e-14 29-42
•		PROTEIN HMG17 FAMILY SIGNATURE	18 14-29 PR00925B 3.73 6.143e-14 29-42 PR00925C 5.57 4.789e-
		PROTEIN HMG17 FAMILY SIGNATURE	18 14-29 PR00925B 3.73 6.143e-14 29-42 PR00925C 5.57 4.789e- 12 53-64 PR00925D
362		SIGNATURE	18 14-29 PR00925B 3.73 6.143e-14 29-42 PR00925C 5.57 4.789e- 12 53-64 PR00925D 6.56 1.857e-10 76-87
362	BL01272	Glucokinase regulatory	18 14-29 PR00925B 3.73 6.143e-14 29-42 PR00925C 5.57 4.789e- 12 53-64 PR00925D 6.56 1.857e-10 76-87 BL01272B 19.61 6.870e-
362		SIGNATURE	18 14-29 PR00925B 3.73 6.143e-14 29-42 PR00925C 5.57 4.789e- 12 53-64 PR00925D 6.56 1.857e-10 76-87 BL01272B 19.61 6.870e- 30 136-171 BL01272C
362		Glucokinase regulatory	18 14-29 PR00925B 3.73 6.143e-14 29-42 PR00925C 5.57 4.789e- 12 53-64 PR00925D 6.56 1.857e-10 76-87 BL01272B 19.61 6.870e- 30 136-171 BL01272C 11.68 3.314e-25 249-
362		Glucokinase regulatory	18 14-29 PR00925B 3.73 6.143e-14 29-42 PR00925C 5.57 4.789e- 12 53-64 PR00925D 6.56 1.857e-10 76-87 BL01272B 19.61 6.870e- 30 136-171 BL01272C 11.68 3.314e-25 249- 274 BL01272A 6.49
362		Glucokinase regulatory protein family proteins.	18 14-29 PR00925B 3.73 6.143e-14 29-42 PR00925C 5.57 4.789e- 12 53-64 PR00925D 6.56 1.857e-10 76-87 BL01272B 19.61 6.870e- 30 136-171 BL01272C 11.68 3.314e-25 249- 274 BL01272A 6.49 1.231e-18 99-117
	BL01272	Glucokinase regulatory protein family proteins.	18 14-29 PR00925B 3.73 6.143e-14 29-42 PR00925C 5.57 4.789e- 12 53-64 PR00925D 6.56 1.857e-10 76-87 BL01272B 19.61 6.870e- 30 136-171 BL01272C 11.68 3.314e-25 249- 274 BL01272A 6.49 1.231e-18 99-117 BL01272B 19.61 6.870e-
	BL01272	Glucokinase regulatory protein family proteins.	18 14-29 PR00925B 3.73 6.143e-14 29-42 PR00925C 5.57 4.789e- 12 53-64 PR00925D 6.56 1.857e-10 76-87 BL01272B 19.61 6.870e- 30 136-171 BL01272C 11.68 3.314e-25 249- 274 BL01272A 6.49 1.231e-18 99-117 BL01272B 19.61 6.870e- 30 113-148 BL01272C
	BL01272	Glucokinase regulatory protein family proteins.	18 14-29 PR00925B 3.73 6.143e-14 29-42 PR00925C 5.57 4.789e- 12 53-64 PR00925D 6.56 1.857e-10 76-87 BL01272B 19.61 6.870e- 30 136-171 BL01272C 11.68 3.314e-25 249- 274 BL01272A 6.49 1.231e-18 99-117 BL01272B 19.61 6.870e- 30 113-148 BL01272C 11.68 3.314e-25 226-
363	BL01272	Glucokinase regulatory protein family proteins.	18 14-29 PR00925B 3.73 6.143e-14 29-42 PR00925C 5.57 4.789e- 12 53-64 PR00925D 6.56 1.857e-10 76-87 BL01272B 19.61 6.870e- 30 136-171 BL01272C 11.68 3.314e-25 249- 274 BL01272A 6.49 1.231e-18 99-117 BL01272B 19.61 6.870e- 30 113-148 BL01272C 11.68 3.314e-25 226- 251 BL01272A 6.49
	BL01272	Glucokinase regulatory protein family proteins. Glucokinase regulatory protein family proteins.	18 14-29 PR00925B 3.73 6.143e-14 29-42 PR00925C 5.57 4.789e- 12 53-64 PR00925D 6.56 1.857e-10 76-87 BL01272B 19.61 6.870e- 30 136-171 BL01272C 11.68 3.314e-25 249- 274 BL01272A 6.49 1.231e-18 99-117 BL01272B 19.61 6.870e- 30 113-148 BL01272C 11.68 3.314e-25 226- 251 BL01272A 6.49 1.231e-18 76-94
363	BL01272	Glucokinase regulatory protein family proteins. Glucokinase regulatory protein family proteins. w KINASE ALPHA ADHESION	18 14-29 PR00925B 3.73 6.143e-14 29-42 PR00925C 5.57 4.789e- 12 53-64 PR00925D 6.56 1.857e-10 76-87 BL01272B 19.61 6.870e- 30 136-171 BL01272C 11.68 3.314e-25 249- 274 BL01272A 6.49 1.231e-18 99-117 BL01272B 19.61 6.870e- 30 113-148 BL01272C 11.68 3.314e-25 226- 251 BL01272A 6.49 1.231e-18 76-94 DM00179 13.97 5.304e-
363	BL01272	Glucokinase regulatory protein family proteins. Glucokinase regulatory protein family proteins. W KINASE ALPHA ADHESION T-CELL.	18 14-29 PR00925B 3.73 6.143e-14 29-42 PR00925C 5.57 4.789e- 12 53-64 PR00925D 6.56 1.857e-10 76-87 BL01272B 19.61 6.870e- 30 136-171 BL01272C 11.68 3.314e-25 249- 274 BL01272A 6.49 1.231e-18 99-117 BL01272B 19.61 6.870e- 30 113-148 BL01272C 11.68 3.314e-25 226- 251 BL01272A 6.49 1.231e-18 76-94 DM00179 13.97 5.304e- 09 167-177
363	BL01272 BL01272 DM00179	Glucokinase regulatory protein family proteins. Glucokinase regulatory protein family proteins. W KINASE ALPHA ADHESION T-CELL. POTASSIUM CHANNEL	18 14-29 PR00925B 3.73 6.143e-14 29-42 PR00925C 5.57 4.789e- 12 53-64 PR00925D 6.56 1.857e-10 76-87 BL01272B 19.61 6.870e- 30 136-171 BL01272C 11.68 3.314e-25 249- 274 BL01272A 6.49 1.231e-18 99-117 BL01272B 19.61 6.870e- 30 113-148 BL01272C 11.68 3.314e-25 226- 251 BL01272A 6.49 1.231e-18 76-94 DM00179 13.97 5.304e-

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.	DESCRIPTION .	RESULIS*
			10 1-19
1371	BL00242	Integrins alpha chain	BL00242B 8.13 8.615e-
1372	PR00625	proteins. DNAJ PROTEIN FAMILY	09 469-479
1372	PR00625	SIGNATURE	PR00625B 13.48 7.353e-
		DIGINITORE	19 46-67 PR00625A 12.84 1.39le-16 14-34
1373	BL00434	HSF-type DNA-binding	BL00434C 23.85 3.778e-
		domain proteins.	09 90-130
1374	PR00962	LETHAL (2) GIANT LARVAE	PR00952C 8.00 6.337e-
1375	PD02475	PROTEIN SIGNATURE	09 505-526
1373	PD02475	MUCIN EPITHELIAL TUMOR- ASSOCIATE.	PD02475A 23.18 8.552e-
1376	PD01066	PROTEIN ZINC FINGER	10 1111-1150 PD01066 19.43 9.571e-
		ZINC-FINGER METAL-	32 24-63
		BINDING NU.	
1380	BL00194	Thioredoxin family	BL00194 12.16 8.333e-
1381	DM01970	proteins.	12 48-61
1301	DMOISTO	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 1.458e-
1383	BL00678	Trp-Asp (WD) repeat	15 1123-1136 BL00678 9.67 7.600e-10
		proteins proteins.	243-254
1384	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 7.600e-10
1205	0.00000	proteins proteins.	271-282
1385	BL00303	S-100/ICaBP type calcium	BL00303B 26.15 6.203e-
1386	BL01160	binding protein. Kinesin light chain	10 95-132
	2201100	repeat proteins.	BL01160B 19.54 5.042e- 09 1574-1628
1387	BL00518	Zinc finger, C3HC4 type	BL00518 12.23 1.000e-
		(RING finger), proteins.	11 52-61
1389	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 3.600e-
		ZINC-FINGER METAL-	30 10-49
1390	PD01066	PROTEIN ZINC FINGER	DD01066 10 42 2 512
		ZINC-FINGER METAL-	PD01066 19.43 3.512e- 31 32-71
		BINDING NU.	
1392	PR00308	TYPE I ANTIFREEZE	PR00308C 3.83 9.723e-
1393	PR00380	PROTEIN SIGNATURE KINESIN HEAVY CHAIN	10 127-137
2333	PROUSEO	SIGNATURE	PR00380A 14.18 9.625e- 25 88-110 PR00380D
		D TOWN TO KE	9.93 2.406e-20 304-326
		1	PR00380B 12.64 4.414e-
			16 208-226 PR00380C
			13:18 6.538e-16 243-
1394	PD00066	PROTEIN ZINC-FINGER	PD00066 13.92 3.400e-
		METAL-BINDI.	14 462-475 PD00066
			13.92 8.800e-14 348-
			361 PD00066 13.92
			9.571e-12 405-418
			PD00066 13.92 6.087e- 11 490-503 PD00066
			13.92 B.043e-11 320-
			333
1398	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 6.786c-
	1	ZINC-FINGER METAL-	32 10-49
1400	DM01206	BINDING NU. CORONAVIRUS NUCLEOCAPSID	DM0120CP 10 CT
		PROTEIN.	DM01206B 10.69 7.038e- 09 270-290
1406	PD00930	PROTEIN GTPASE DOMAIN	PD00930A 25.62 7.324e-
		ACTIVATION.	15 363-389
1407	BL00030	Eukaryotic RNA-binding	BL00030A 14.39 7.500e-
		region RNP-1 proteins.	10 457-476
1408	PROCES		
1408	PR00019	LEUCINE-RICH REPEAT	PR00019A 11.19 9.550e-
1408	PR00019		PR00019A 11.19 9.550e- 11 179-193 PR00019A
1408	PR00019	LEUCINE-RICH REPEAT	PR00019A 11.19 9.550e- 11 179-193 PR00019A 11.19 8.826e-10 228-
1408	PR00019	LEUCINE-RICH REPEAT	PR00019A 11.19 9.550e- 11 179-193 PR00019A

SEQ ID N	O: ACCESSION	DESCRIPTION	RESULTS*
	NO.		RESULTS*
1409	DD00540		09 176-190
1405	PR00510	NEBULIN SIGNATURE	PR00510A 9.09 4.150e-
ł			12 182-202 PR00510B
			12.96 8.767e-12 210-
1			230 PR00510F 9.88
1			8.172e-10 58-75
1	ļ	}	PR00510D 9.21 2.367e-
1410	PD00078	REPEAT PROTEIN ANK	09 251-267 PD00078B 13.14 5.696e-
		NUCLEAR ANKYR.	09 31-44
1412	BL00358	Ribosomal protein L5	BL00358B 22.76 1.00Ce-
		proteins.	40 57-103 BL00358C
			13.75 6.087e-14 122-
			136 BL00358D 14.26
			5.500e-13 143-158
			BL00358A 13.06 1.931e-
1414	BL00282	Kamal control	11 33-44
İ	2200202	Kazal serine protease inhibitors family	BL00282 16.88 7.338e-
1		proteins.	10 511-534
1415	BL00023	Type II fibronectin	
		collagen-binding domain	BL00023 24.31 4.300e- 29 40-77
		proteins.	25 40-77
1417	PR00681	RIBOSOMAL PROTEIN S1	PR00681G 12.54 2.149e-
1410		SIGNATURE	09 38-60
1418	DM00973	3 kw RESISTANCE BENOMYL	DM00973A 21.17 1.462e-
1419		YLL028W CYCLOHEXIMIDE.	09 171-208
1419	PR00319	BETA G-PROTEIN	PR00319B 11.47 1.571e-
1420	PD01941	(TRANSDUCIN) SIGNATURE	09 428-443
1120	PD01941	TRANSMEMBRANE	PD01941A 14.81 1.000e-
		COTRANSPORTER SYMP.	40 142-196 PD01941B
			15.02 7.049e-30 400-
			447 PD01941E 15.92
			2.475e-20 817-864
			PD01941C 19.96 3.118e- 19 488-543 PD01941D
		į	27.18 9.614e-18 641-
			690 PD01941F 28.52
1422			5.382e-15 1038-1093
1422	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 8.043e-
1423	PR00209		12 199-217
	FR00209	ALPHA/BETA GLIADIN	PR00209B 4.88 6.318e-
1424	BL50002	FAMILY SIGNATURE	11 1009-1028
	3230002	Src homology 3 (SH3)	BL50002A 14.19 8.200e-
		domain proteins profile.	14 367-386 BL50002A
	-		14.19 9.250e-12 298-
	ì	<u>}</u>	317 BL50002A 14.19
			4.462e-11 208-227 BL50002B 15.18 1.000e-
			09 244-258
1425	PF00628	PHD-finger.	PF00628 15.84 3.045e-
1406			12 330-345
1426	PF00628	PHD-finger.	PF00628 15.84 3.045e-
1427	- I DDO = 1 = =		12 377-392
1427	PR00405	HIV REV INTERACTING	PR00405B 11.83 5.114e-
		PROTEIN SIGNATURE	16 281-299 PR00405A
	1	1	17.71 4.306e-14 262-
1428	BL00039	DEAD	282
-	2200033	DEAD-box subfamily ATP-	BL00039D 21.67 5.219e-
		dependent helicases proteins.	34 147-193
1429	PR00320	G-PROTEIN BETA WD-40	
		REPEAT SIGNATURE	PR00320C 13.01 8.920e-
	PR00378	INOSITOL PHOSPHATASE	10 577-592
1430	*******		UUUUU 10 00 00 00 00 00 00 00 00 00 00 00 00
1430	1.00376	SIGNATURE	PR00378D 16.86 7.563e-
1430	1200376	SIGNATURE	12 295-314 PR00378B
1430	1200376	SIGNATURE	

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	NO.	PROTEIN SIGNATURE	10 103-124
1433	BL01113	Clq domain proteins.	BL01113B 18.26 7.049e- 15 14-50 BL01113C
1434	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	13.18 7.000e-12 82-102 PR00319B 11.47 7.983e- 10 135-150
1436	BL00030	Eukaryotic RNA-binding	BL00030A 14.39 1.000e-
1438	BL00290	region RNP-1 proteins. Immunoglobulins and	12 84-103 BL00290B 13.17 2.500e-
		major histocompatibility complex proteins.	09 250-268 BL00290A 20.89 4.000e-09 188- 211
1440	PR00806	VINCULIN SIGNATURE	PR00806B 4.28 4.960e-
1441	PR00806	VINCULIN SIGNATURE	PR00806B 4.28 4.960e-
1444	BL00422	Granins proteins.	BL00422D 19.48 1.000e- 08 114-138
1445	PD01841	PHOSPHORYLASE KINASE ALPHA MUSCL.	PD01841A 21.71 1.000e- 40 73-123 PD01841B 14.35 1.000e-40 144- 185 PD01841D 17.87 1.000e-40 206-258 PD01841F 13.36 1.000e- 40 296-345 PD01841G 24.26 1.000e-40 349- 403 PD01841I 23.00 1.000e-40 494-536 PD01841J 14.94 1.000e- 40 895-932 PD01841L 18.42 1.000e-40 1083- 1125 PD01841E 18.60 9.719e-38 258-296 PD01841K 14.81 1.000e- 35 1041-1071 PD01841H 21.30 3.189e-31 435- 472 PD01841C 13.78 1.000e-25 185-206 PD01841M 10.82 1.250e-
1446	PF00816	H-NS histone family.	20 1175-1194 PF00816B 13.84 8.875e-
1447	PR00048	C2H2-TYPE ZINC FINGER	09 190-220 PR00048A 10.52 2.080e-
1440		SIGNATURE	09 402-416
1448	DM00315	072 RIBONUCLEASE INHIBITOR.	DM00315D 18.40 7.393e- 09 23-67
1451	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030B 7.03 2.800e- 10 94-104
1454	DM01688	2 POLY-IG RECEPTOR.	DM01688D 13.44 7.146e- 09 382-405
1455	PF00777	Sialyltransferase family.	PF00777C 18.60 2.929e- 22 4-59
1457	BL00927	Trehalase proteins.	BL00927C 10.83 8.085e-
1460	BL00545	Aldose 1-epimerase proteins.	BL00545C 11.28 7.353e- 17 169-182 BL00545A 10.20 2.071e-15 73-89 BL00545B 13.10 3.942e- 09 140-153
1466	PR00097	ANTHRANILATE SYNTHASE COMPONENT II SIGNATURE	PR00097C 9.42 9.069e- 09 233-245
1472	BL01129	Hypothetical yabO/yceC/sfhB family proteins.	BL01129E 13.25 5.250e- 22 170-195 BL01129C
1473	BL00790	Receptor tyrosine kinase class V proteins.	25.56 9.526e-18 63-106 BL00790I 20.01 2.821e-
1475	PF00686	Starch binding domain proteins.	09 2114-2145 PF00686A 13.45 9.100e- 09 267-277

SEQ ID N	O: ACCESSION NO.	DESCRIPTION	RESULTS*
1477	PF00566	Probable rabGAP domain	PF00566A 12.64 7.333e-
1478	BL00030	proteins. Eukaryotic RNA-binding	10 466-476 BL00030B 7.03 9.400e-
1479	DM00406	region RNP-1 proteins. GLIADIN.	10 43-53 DM00406 7.73 8.541e-10
1480	BL00290	Immunoglobulins and	292-305 BL00290B 13.17 2.385c-
1481	PR00350	major histocompatibility complex proteins.	20.89 5.09le-11 12-35
1482	PR00150	PHOSPHOENOLPYRUVATE CARBOXYLASE SIGNATURE	PR00150F 10.45 9.039e- 09 21-51
1462	PF00780	Domain found in NIK1- like kinases, mouse citron and yeast ROM.	PF00780I 14.69 4.825e- 09 107-137
1483	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 1.153e- 09 108-162
1485	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 5.909e- 25 17-56
1486	BL00107	Protein kinases ATP- binding region proteins.	BL00107B 13.31 1.529e-
1488	BL00039	DEAD-box subfamily ATP- dependent helicases	09 34-50 BL00039D 21.67 9.586e- 10 116-162
1490	BL00166	proteins. Enoyl-CoA hydratase/isomerase proteins.	BL00166D 22.87 2.607e- 24 190-226 BL00166C 18.93 5.500e-14 140- 167 BL00166B 16.92
1491	BL00452	Guanylate cyclases proteins.	9.357e-11 93-115 BL00452D 28.59 3.700e- 31 63-106 BL00452E 11.92 3.045e-13 115-
1492	PR00019	LEUCINE-RICH REPEAT SIGNATURE	131 PR00019A 11.19 3.667e- 09 532-546
1497	BL00107	Protein kinases ATP- binding region proteins.	BL00107B 13.31 1.000e- 11 384-400 BL00107A 18.39 5.345e-11 322-
1500	PF00876	Ogre family.	353 PF00876E 7.99 1.947e-
1502	BL00027	'Homeobox' domain proteins.	10 107-117 BL00027 26.43 4.789e-
1503	BL00027	'Homeobox' domain proteins.	24 112-155 BL00027 26.43 4.789e-
1505	BL01177	Anaphylatoxin domain proteins.	24 112-155 BL01177E 20.64 5.800e- 24 448-475 BL01177C 17.39 5.333e-19 402- 421 BL01177B 13.61 7.840e-16 155-171 BL01177D 17.50 1.900e- 15 427-445
1506	BL00972	Ubiquitin carboxyl- terminal hydrolases family 2 proteins.	BL00972D 22.55 5.500e- 14 311-336 BL00972A 11.93 7.429e-14 48-66 BL00972E 20.72 8.759e- 10 341-363
1512	BL00523	Sulfatases proteins.	BL00523E 19.27 4.536e- 22 76-106 BL00523D 9.89 1.563e-11 40-52 BL00523F 10.85 4.162e- 09 159-170 BL00523G 9.46 5.333e-09 256-266
1516	BL00914	Syntaxin / epimorphin family proteins.	BL00914 24.91 7.045e- 14 168-218
1518	BL00600	Aminotransferases class- III pyridoxal-phosphate attachment si.	BL00600A 17.98 6.143e- 19 98-122 BL00600E 16.43 1.771e-17 302-

SEO ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		
			331 BL006C0G 12.43
			9.625e-17 377-396
			BL00600B 19.60 5.091e-
	1		15 160-186 BL00600C
			16.18 6.04Ce-12 190-
	}		206 BL006COF 8.77
			1.000e-11 343-356
			BL00600D 8.71 1.000e-
1523	PD00930	PROTEIN GTPASE DOMAIN	1
1523	PD30930	ACTIVATION.	PD00930B 33.72 9.600e-
1528	PR00320	G-PROTEIN BETA WD-40	PR00320B 12.19 4.774e-
	1.00520	REPEAT SIGNATURE	11 192-207 PR00320B
			12.19 8.839e-11 272-
			287 PR00320B 12.19
			9.743e-10 106-121
	ł	1	PR00320A 16.74 1.878e-
			09 192-207 PR00320A
			16.74 2.317e-09 106-
			121 PR00320A 16.74
		1	8.683e-09 272-287
			PR00320C 13.01 8.800e-
1536	D1401070	o la greca de venas en	09 106-121
1538	DM01970	0 kw ZK632.12 YDR313C	DM01970B 8.60 4.508e-
1539	PF00781	ENDOSOMAL III. Diacylglycerol kinase	15 171-184 PF00781D 11.11 7.593e-
1539	PF00781	catalytic domain	10 103-127
		proteins (presumed).	10 103-127
1540	PR00965	OCULAR ALBINISM TYPE 1	PR00965H 10.73 1.231e-
1210	TROOSOS	PROTEIN SIGNATURE	29 312-334 PR00965E
			12.93 5.846e-29 172-
			195 PR00965F 5.98
			1.123e-28 209-231
			PR00965C 15.04 1.000e-
			27 131-151 PR00965D
			5.84 1.000e-27 150-170
			PR00965G 8.52 2.440e-
		1	27 258-279 PR00965B
			4.80 8.650e-26 88-109
			PR00965A 12.52 1.000e-
			25 35-55 PR009651 3.91 6.442e-25 385-406
1541	BL01013	Oxysterol-binding	BL01013D 26.81 9.719e-
1241	BE01013	protein family proteins.	17 163-207
1543	PD02699	PROTEIN DNA-BINDING	PD02699C 24.84 1.000e-
	- 202055	BINDING DNA.	40 599-646 PD02699A
			8.91 2.286e-34 219-248
			PD02699B 18.28 6.143e-
			21 485-509
1544	PR00049	WILM'S TUMOUR PROTEIN	PR00049D 0.00 7.857e-
		SIGNATURE	10 182-197 PR00049D
	_		0.00 7.102e-09 67-82
1547	BL00951	ER lumen protein	BL00951C 19.35 1.000e-
	1	retaining receptor	40 93-142 BL00951D
	1	proteins.	13.94 8.714e-40 142-
	1		177 BL00951A 15.10
			1.000e-38 2-38 .
	I		BL00951B 14.23 6.250e-
2540			33 38-69
1548	BL00536	Ubiquitin-activating	BL00536F 13.65 8.920e-
		enzyme proteins.	30 279-318 BL00536D
			22.91 5.737e-24 21-65
	1	1	BL00536E 16.94 4.696e-
1549	PERCOLAG	1	18 248-279
1343	PR00139	ASPARAGINASE/GLUTAMINASE	PR00139C 11.72 9.679e-
1553	PR00049	FAMILY SIGNATURE	09 550-569
	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 5.119e- 09 58-73
	i.	I SIGNATURE	I V2 35-/3

SEQ ID NO	ACCESSION NO.	DESCRIPTION	RESULTS*
1556	BL00061	Short-chain	
	2200001	dehydrogenases/reductase s family proteins.	BL00061B 25.79 6.276e- 13 67-105
1557	BL01228	Hypothetical cof family proteins.	BL01228D 17.44 8.105e-
1558	BL01228	Hypothetical cof family	12 107-132 BL01228D 17.44 8.105e-
1559	BL01228	proteins. Hypothetical cof family	12 107-132 BL01228D 17.44 8.105e-
1562	BL00522	DNA polymerase family X	12 107-132
		proteins.	BL00522C 11.90 6.600e- 18 412-436 BL00522B 27.30 1.738e-16 364- 410 BL00522A 25.52 6.000e-16 279-326 BL00522E 19.63 6.123e- 14 502-532 BL00522F 14.90 2.385e-13 551- 575
1563	PF00651	BTB (also known as BR-	PF00651 15.00 1.947c-
1564	BL00299	C/Ttk) domain proteins. Ubiquitin domain	11 46-59 BL00299 28.84 2.823e-
1566		proteins.	10 324-376
1366	BL01013	Oxysterol-binding	BL01013D 26.81 8.594e-
		protein family proteins.	17 184-228 BL01013C 9.97 4.906e-12 14-24
1567	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 3.400e-10 378-389 BL00678 9.67 5.800e-10 418-429 BL00678 9.67 8.800e-10
1570	BL00479		295-306
		Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 5.235e- 17 297-313 BL00479A 19.86 6.625e-15 271- 294 BL00479A 19.86 2.667e-14 147-170 BL00479B 12.57 6.294e- 12 173-189
1576	PRODESS	OXYTOCIN RECEPTOR SIGNATURE	PR00665G 12.36 4.673e- 24 364-384 PR00665D 9.93 1.200e-22 138-155 PR00665F 11.73 4.000e- 22 337-354 PR00665C 5.89 1.000e-20 65-80 PR00665B 5.29 4.337e- 19 24-39 PR00665E 5.60 2.929e-15 246-260 PR00665A 5.99 5.622e- 15 11-25
1577	DM00099	4 kw A55R REDUCTASE TERMINAL DIHYDROPTERIDINE.	DM00099B 14.73 9.308e- 10 127-137
1579	BL00524	Somatomedin B domain	BL00524A 9.65 6.776e-
1580	PD02894	PROTEIN SIGNAL BE.	14 52-73 PD02894B 13.93 6.959e- 16 182-215 PD02894A
.581	BL00411	Kinesin motor domain proteins.	21.96 2.125e-10 57-103 BL00411C 15.04 5.292e- 12 32-54 BL00411H 15.66 4.441e-11 245- 276
.582	PR00604	CLASS IA AND IB	PR00604A 11.13 2.440e-
584	PF00651	CYTOCHROME C SIGNATURE BTB (also known as BR-	09 79-87 PF00651 15.00 1.000e-
I I		C/Ttk) domain proteins.	10 225-238
585	DM01551		DM01551C 14.62 9.455e-

SEQ ID NO:	ACCESSION	DESCRIPTION	I BROTT MOA
	NO.		RESULTS*
1587	PR00072	MALIC ENZYME SIGNATURE	PR00072B 13.77 7.955e-
			33 180-210 PR00072A
			12.75 6.040e-25 120- 145 PR00072C 11.42
			2.286e-24 216-239
			PR00072D 10.77 3.400e-
			22 276-295 PR00072E
			10.54 1.360e-19 301-
}			318 PR00072G 10.45
			5.304e-19 433-450
			PR00072F 8.87 5.935e-
1589	BL00191	Cytochrome b5 family,	BL00191H 15.64 1.537e-
		heme-binding domain	22 61-113 BL00191K
		proteins.	17.38 9.027e-12 398-
			442
1590	DM01970	0 kw ZK632.12 YDR313C	DM01970B 8.60 7.716e-
		ENDOSOMAL III.	13 211-224 DM01970B 8.60 2.157e-12 94-107
1591	DM00517	5 kw NUCLEAR 60.7 NUP1	DM00517B 10.96 6.625e-
•		CHROMOSOME.	16 1175-1193 DM00517A
			8.21 1.000e-11 1015-
			1026
1592	BL00037	Myb DNA-binding domain	BL00037B 15.92 3.250e-
		proteins repeat proteins proteins.	27 116-142 BL00037A 16.68 2.500e-24 83-107
		proceins.	BL00037A 16.68 3.250e-
			12 31-55 BL00037B
	•		15.92 3.526e-11 64-90
		· · ·	BL00037C 16.86 9.654e-
1505	DY COOC		10 146-164
1595	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 1.514e- 09 110-127
1598	PF00628	PHD-finger.	PF00628 15.84 3.250e-
			11 1667-1682
1599	PR00014	FIBRONECTIN TYPE III	PR00014D 12.04 5.500e-
1600	77.00510	REPEAT SIGNATURE	09 980-995
1600	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 6.571e- 10 30-39
1602	BL00412	Neuromodulin (GAP-43)	BL00412D 16.54 5.402e-
		proteins.	10 136-187
1605	PF00651	BTB (also known as BR-	PF00651 15.00 3.571e-
		C/Ttk) domain proteins.	10 44-57
1607	BL00252	Interferon alpha, beta and delta family	BL00252A 18.49 6.657e-
		proteins.	23 20-57 BL00252B 19.78 9.125e-16 58-109
1610	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 1.000e-
			08 61-94
1611	BL00904	Protein	BL00904C 8.98 7.353e-
		prenyltransferases alpha	10 91-125 BL00904D
		subunit repeat proteins	1.47 6.018e-09 127-168
1612	PF00168	proteins. C2 domain proteins.	PF00168C 27.49 3.250e-
	1	or domain processis.	09 365-391
1613	BL00412	Neuromodulin (GAP-43)	BL00412D 16.54 6.051e-
		proteins.	09 932-983 BL00412D
			16.54 7.153e-09 933-
1614	BLOOSED		984
1014	BL00559	Eukaryotic molybdopterin oxidoreductases	BL00559I 13.63 3.531e-
	1	proteins.	25 54-83 BL00559K
		processis.	224 BL00559J 19.63
	1		6.870e-16 124-176
			BL00559L 13.60 9.000e-
1616	PROF. SEE		16 266-284
1615	PD01427	TRANSFERASE	PD01427B 22.45 3.025e-
	1	METHYLTRANSFERASE BI.	22 500-541 PD01427A 19.94 8.773e-18 439-
	_l		AD. 24 0. //38-18 439-

SEQ ID N	•	DESCRIPTION	RESULTS*
	NO.		472
1616	BL00115	Eukaryotic RNA	472
	ł	polymerase II	BL00115Z 3.12 7.485e-
		heptapeptide repeat	09 152-201 BL00115Z 3.12 9.603e-09 145-194
		proteins.	3.12 9.603E-09 145-194
1617	BL00303	S-100/ICaBP type calcium	
)	binding protein.	
	1	binding procein.	32 51-88 BL00303A
1618	BL01254	Potential E-12	21.77 1.947e-31 4-41
	DEVIEST	Fetuin family proteins.	BL01254F 10.02 8.754e-
1619	PD01888		09 137-147
1015	*D01998	PEPTIDE REDUCTASE	PD01888B 25.10 1.000e-
		PROTEIN METHI.	40 47-97 PD01888C
	1	!	21.56 7.000e-30 125-
	Ì		155 PD01888A 12.84
			8.800e-15 7-23
1621	PR00239	MOLLUSCAN RHODOPSIN C-	PR00239E 1.58 3.455e-
		TERMINAL TAIL SIGNATURE	09 692-704 PR00239E
		l service services	1.58 4.580e-09 697-709
	1		
			PR00239E 1.58 1.580e-
			09 702-714 PR00239E
1622	PR00860	VERTEBRATE	1.58 5.193e-09 703-715
	1		PR00860B 7.04 1.900e-
		METALLOTHIONEIN	18 27-41 PR00860C
		SIGNATURE	9.61 1.474e-14 41-51
			PR00860A 5.46 1.720e-
1624	770000		14 5-18
1624	PR00784	MITOCHONDRIAL BROWN FAT	PR00784D 15.86 8.027e-
		UNCOUPLING PROTEIN	11 77-95
		SIGNATURE	
1626	BL00325	Actin-depolymerizing	BL00325B 21.66 1.000e-
	[proteins.	40 93-139 BLC0325A
_	- 1	_	24.83 6.786e-23 61-93
1631	BL00064	L-lactate dehydrogenase	24.63 6.7866-23 61-93
	ľ	proteins.	BL00064B 23.57 1.000e-
		process.	40 82-130 BL00064C
			17.28 1.000e-40 137-
	1		182 BL00064E 27.20
			1.000e-40 223-275
	i i		BL00064F 25.14 7.882e-
			36 286-331 BL00064A
	į		21.16 1.000e-33 22-60
	ł		BL00064D 14.19 6.500e-
1632			31 182-212
1032	PR00063	RIBOSOMAL PROTEIN L27	PR00063B 15.24 9.700e-
	i	SIGNATURE	11 59-84 PR00063A
		1	11.71 1.614e-09 34-59
1634	PR00239	MOLLUSCAN RHODOPSIN C-	PR00239D 0.00 1.105e-
		TERMINAL TAIL SIGNATURE	11 36-49 PR00239C
			3 F3 O F30: 00 05 45
1636	BL01210	Caveolins proteins.	3.51 2.538e-09 37-45
			BL01210B 13.92 9.531e-
1637	BL00982	Do-hard I	10 133-183
	2200982	Bacterial-type phytoene	BL00982A 18.41 5.388e-
1639	DI 01103	dehydrogenase proteins.	11 11-43
-039	BL01183	ubiE/COQ5	BL01183B 21.31 8.144e-
	1	methyltransferase family	12 132-177
		proteins.	
L640	PR00015	GRAM-POSITIVE COCCUS	PR00015B 9.84 8.468e-
	1	SURFACE PROTEIN ANCHOR	10 128-149
		SIGNATURE	250-743
641	PR00320	G-PROTEIN BETA WD-40	Phoop do
		REPEAT SIGNATURE	PR00320B 12.19 5.935e-
		DAI SIGNATURE	11 364-379 PR00320A
		, ,	16.74 7.828e-11 364~
		1	379 PR00320C 13.01
		į l	2.800e-10 279-294
		1	PR00320C 13.01 2.800e-
	1	1	10 364-379 PR00320B
	1	1	12.19 5.114e-10 279-
	1	1	294 PRO0320A 16.74
	į	1	7 FEGG 00 272 224
			1.659e-09 279-294

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	NO.		PR00320A 16.74 2.098e-
	1		09 229-244
1642	PF00023	Ank repeat proteins.	PF00023A 16.03.6.464e-
1643	PR00169	POTASSIUM CHANNEL SIGNATURE	PR00169A 16.77 1.806e- 11 74-94
1644	BL00678	Trp-Asp (WD) repeat proteins proteins	BL00678 9.67 2.200e-10 109-120 BL00678 9.67 5.737e-09 528-539
1645	BL01108	Ribosomal protein L24 proteins.	BL01108A 20.33 7.366e- 17 56-89
1646	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PRO0380A 14.18 9.270e- 21 103-125 PR00380D 9.93 6.30Be-18 386-408 PR00380C 13.18 7.923e- 16 332-351 PR00380B 12.64 6.657e-15 292- 310
1647	DM01242	3 THREONINETRNA LIGASE.	DMO1242C 17.15 9.791e- 37 340-381 DM01242E 23.00 5.071e-31 463- 505 DM01242D 23.29 3.925e-30 420-463 DM01242B 23.57 8.054e- 18 265-314 DM01242F 10.61 7.618e-14 526-
1649	PD00126	PROTEIN REPEAT DOMAIN TPR NUCLEA.	PD00126A 22.53 5.500e- 10 13-34
1651	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 6.720e- 11 431-485
1652	BL00933	FGGY family of carbohydrate kinases proteins.	BL00933A 17.50 4.673e- 12 11-35 BL00933E 13.80 9.217e-09 456- 472
1653	BL00795	Involucrin proteins.	BL00795C 17.06 2.988e- 10 70-115
1654	BL00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 7.750e- 17 302-334
1655	BL00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 7.750e- 17 282-314
1656	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 1.391e- 16 607-630
1657	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 7.938e- 11 114-136
1658	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 8.889e-
1659	BL00972	Ubiquitin carboxyl- terminal hydrolases family 2 proteins.	BL00972D 22.55 4.140e- 12 376-401 BL00972E 20.72 5.629e-09 446- 468
1660	BL00406	Actins proteins.	BL00406D 12.58 8.767e- 15 188-243
1661	PR00105	CYTOSINE-SPECIFIC DNA METHYLTRANSFERASE SIGNATURE	PR00105A 10.36 4.900e- 13 1140-1157 PR00105B 12.32 2.800e-12 1259- 1274 PR00105C 10.86 1.000e-10 1305-1319
1662	BL00280	Pancreatic trypsin inhibitor (Kunitz) family proteins.	BL00280 24.61 3.172e- 33 3119-3163
1663	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319D 11.64 6.625e- 23 107-125 PR00319C 13.41 5.714e-20 89-105 PR00319A 15.27 5.286e- 19 51-68 PR00319B 11.47 8.200e-19 70-85

SEQ ID N	O: ACCESSION NO.	DESCRIPTION	RESULTS*
1664	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 5.050e-10
1667	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	489-502 PD01066 19.43 8.500e- 38 7-46
1669	BL01153	NOL1/NOP2/sun family proteins.	BL01153D 19.69 1.188e- 17 115-141 BL01153C 13.67 8.977e-15 66-80 BL01153B 20.52 1.885e- 10 13-37
1671	PR00678	PI3 KINASE P85 REGULATORY SUBUNIT SIGNATURE	PR00678H 9.13 3.100e- 10 1146-1169
1672	BL00598	Chromo domain proteins.	BL00598 14.45 8.500e-
1673	PR00326	GTP1/OBG GTP-BINDING	20 27-49 PR00326A 8.75 8.329e-
1674	PR00049	PROTEIN FAMILY SIGNATURE WILM'S TUMOUR PROTEIN SIGNATURE	09 686-707 PR0C049D 0.00 7.580e- 11 343-358 PR00049D
1676	PR00747	GLYCOSYL HYDROLASE FAMILY 47 SIGNATURE	0.00 1.286e-10 342-357 PR00747H 12.76 8.636e- 19 427-448 PR00747G 14.50 2.286e-18 368- 393 PR00747C 12.06 7.500e-18 112-131 PR00747A 14.05 4.600e- 17 42-63 PR00747D 15.23 8.759e-17 163- 183 PR00747E 15.13 8.244e-15 254-272 PR00747B 7.65 5.355e- 13 75-90 PR00747F 13.56 8.714e-10 311- 328
1677	PR00747	GLYCOSYL HYDROLASE FAMILY 47 SIGNATURE	PR00747H 12.76 8.636e- 19 309-330 PR00747G 14.50 2.286e-18 250- 275 PR00747C 12.06 7.500e-18 112-131 PR00747A 14.05 4.600e- 17 42-63 PR00747B 7.65 5.355e-13 75-90 PR00747F 13.56 8.714e-
1680	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 4.600e-10 406-417 BL00678 9.67
1681	BL00678	Trp-Asp (WD) repeat proteins proteins.	6.684e-09 320-331 BL00678 9.67 4.600e-10 329-340 BL00678 9.67 6.684e-09 243-254
1683	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 1.346e- 13 389-410
1685	PR00646	RDC1 ORPHAN RECEPTOR SIGNATURE	PR00646H 6.32 4.188e-
1690	BL01160	Kinesin light chain	09 755-771 BL01160B 19.54 6.644e-
1691	PR00456	repeat proteins. RIBOSOMAL PROTEIN PZ SIGNATURE	PR00456E 3.06 7.281e- 10 418-433 PR00456E 3.06 7.281e-10 419-434 PR00456E 3.06 8.125e-
1692	PR00456	RIBOSOMAL PROTEIN P2 SIGNATURE	PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e-10 488-503 PR00456E 3.06 8.125e-
1693	BL00674	AAA-protein family proteins.	10 489-504 BL00674C 22.60 8.043e- 24 274-317 BL00674B

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
<u> </u>	NO.		KESOBIS.
			4.46 4.000e-23 241-263
			BL00674D 23.41 8.560e-
			18 338-385 BL00674E
			15.24 1.720e-15 414- 434
1697	PR00409	PHTHALATE DIOXYGENASE	PR00409F 12.70 4.388e-
1 2031	1100403	REDUCTASE FAMILY	10 427-447
		SIGNATURE	10 42/-44/
1698	PR00466	CYTOCHROME B-245 HEAVY	PR00466C 10.17 3.443e-
	1	CHAIN SIGNATURE	13 187-208 PR00466B
			5.03 5.500e-11 162-186
}	ļ	1	PR00466F 9.16 6.159e-
			09 498-517
1699	BL00028	Zinc finger, C2H2 type,	BL00028 16.07 9.217e-
	1	domain proteins.	12 283-300 BL00028
			16.07 3.769e-11 255-
	1		272 BL00028 16.07
			5.154e-11 171-188
			BL00028 16.07 5.500e-
			11 227-244 BL00028
	ł		16.07 1.600e-10 199-
1700	BL01019	ADD with a seed and	216
1,00	Lange	ADP-ribosylation factors	BL01019A 13.20 3.348e-
		family proteins.	15 62-102 BL01019B 19.49 4.000e-15 107-
			19.49 4.000e-15 107-
1703	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 2.484e-
		ZINC-FINGER METAL-	12 200-239
		BINDING NU.	200 233
1707	PR00109	TYROSINE KINASE	PR00109B 12.27 4.558e-
		CATALYTIC DOMAIN	14 134-153
		SIGNATURE	
1710	PR00019	LEUCINE-RICH REPEAT	PR00019A 11.19 2.565e-
		SIGNATURE	10 116-130 PR00019B
			11.36 4.600e-09 113-
			127 PR00019B 11.36
1711	BL01159	WW/rsp5/WWP domain	7.120e-09 204-218
	BEGILDS	proteins.	BL01159 13.85 6.523e- 11 232-247 BL01159
		process.	13.85 5.408e-10 613-
			628
1712	PF00023	Ank repeat proteins.	PF00023A 16.03 7.000e-
	j		10 187-203
1713	PF00642	Zinc finger C-x8-C-x5-C-	PF00642 11.59 9.550e-
		x3-H type (and similar).	11 230-241
1714	PF00642	Zinc finger C-x8-C-x5-C-	PF00642 11.59 9.550e-
		x3-H type (and similar).	11 230-241
1715	BL01115 .	GTP-binding nuclear	BL01115A 10.22 7.129e-
1718	Process:	protein ran proteins.	09 7-51
T.TD	BL00353	HMG1/2 proteins.	BL00353C 14.83 6.018e-
	1		10 136-183 BL00353B
1719	BL00412	Neuromodulin (GAP-43)	11.47 8.866e-09 86-136
		proteins.	BL00412D 16.54 5.408e- 09 432-483
			1 VV TV4 TUJ
1721	BL00038		BI-00038B 16 97 9 449-
1721	BL00038	Myc-type, 'helix-loop-	BL00038B 16.97 8.448e-
1721	BL00038		12 79-100 BL00038A
1721	BL00038	Myc-type, 'helix-loop- helix' dimerization domain proteins.	12 79-100 BL00038A 13.61 4.000e-11 52-68
		Myc-type, 'helix-loop- helix' dimerization	12 79-100 BL00038A
		Myc-type, 'helix-loop- helix' dimerization domain proteins. PROTEIN RNA-BINDING RNA	12 79-100 BL00038A 13.61 4.000e-11 52-68 PD00567C 9.17 8.500e-
1723	PD00567	Myc-type, 'helix-loop- helix' dimerization domain proteins. PROTBIN RNA-BINDING RNA REPEAT HYD.	12 79-100 BL00038A 13.61 4.000e-11 52-68 PD00567C 9.17 8.500e- 09 418-428
1723	PD00567	Myc-type, 'helix-loop-helix' dimerization domain proteins. PROTEIN RNA-BINDING RNA REPEAT HYD. Protein-L-isoaspartate(D-aspartate) 0-	12 79-100 BL00038A 13.61 4.000e-11 52-68 PD00567C 9.17 8.500e- 09 418-428 BL01279A 24.27 5.663c-
1723	PD00567	Myc-type, 'helix-loop-helix' dimerization domain proteins. PROTEIN RNA-BINDING RNA REPEAT HYD. Protein-L-isoaspartate(D-aspartate) O-methyltransferase signa.	12 79-100 BL00038A 13.61 4.000e-11 52-68 PD00567C 9.17 8.500e- 09 418-428 BL01279A 24.27 5.663c-
1723	PD00567	Myc-type, 'helix-loop-helix' dimerization domain proteins. PROTBIN RNA-BINDING RNA REPEAT HYD. Protein-L-isoaspartate(D-aspartate) 0-methyltransferase signa. EF-hand calcium-binding	12 79-100 BL00038A 13.61 4.000e-11 52-68 PD00567C 9.17 8.500e- 09 418-428 BL01279A 24.27 5.663c-
1723	PD00567	Myc-type, 'helix-loop-helix' dimerization domain proteins. PROTEIN RNA-BINDING RNA REPEAT HYD. Protein-L-isoaspartate(D-aspartate) O-methyltransferase signa.	12 79-100 BL00038A 13.61 4.000e-11 52-68 PD00567C 9.17 8.500e- 09 418-428 BL01279A 24.27 5.663c- 12 233-281
1723 1724 1728	PD00567 BL01279 BL00018	Myc-type, 'helix-loop-helix' dimerization domain proteins. PROTEIN RNA-BINDING RNA REPEAT HYD. Protein-L-isoaspartate(D-aspartate) O-methyltransferase signa. EF-hand calcium-binding domain proteins.	12 79-100 BL00038A 13.61 4.000e-11 52-68 PD00567C 9.17 8.500e- 09 418-428 BL01279A 24.27 5.663e- 12 233-281 BL00018 7.41 2.059e-11
1723	PD00567	Myc-type, 'helix-loop-helix' dimerization domain proteins. PROTBIN RNA-BINDING RNA REPEAT HYD. Protein-L-isoaspartate(D-aspartate) 0-methyltransferase signa. EF-hand calcium-binding	12 79-100 BL00038A 13.61 4.000e-11 52-68 PD00567C 9.17 8.500e- 09 418-428 BL01279A 24.27 5.663e- 12 233-281 BL00018 7.41 2.059e-11 73-86 BL00018 7.41

SEQ ID N	NO.	DESCRIPTION	RESULTS*
1731	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 9.676e- 10 296-350
1732	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 9.676e- 10 316-370
1733	PF00850	Histone deacetylase family.	PF00850F 15.70 4.349e- 22 246-279 PF00850D 14.76 6.850e-20 177- 201 PF00850E 8.88 8.691e-18 209-235 PF00850G 22.75 4.098e-
1734	BL00354	HMG-I and HMG-Y DNA- binding domain proteins (Ahook)	14 281-323 BL00354C 6.61 5.932e- 09 292-307
1735	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 5.263e- 10 492-502
1743	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PRO0449A 13.20 1.188e- 11 5-27 PR00449D 10.79 2.241e-10 109- 123 PR00449E 13.50
1744	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	9.289e-10 144-167 PR00449A 13.20 1.188e- 11 5-27 PR00449D 10.79 2.241e-10 109- 123 PR00449E 13.50
1745	BL00720	Guanine-nucleotide dissociation stimulators CDC25 family sign.	9.289e-10 144-167 BL00720B 16.57 8.297e- 15 136-160
1746	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE	PR00081B 10.38 6.727e- 11 45-57 PR00081E 17.54 3.935e-10 150-
1747	BL00439	Acyltransferases ChoActase / COT / CPT family proteins.	168 BL00439H 18.24 8.435e- 14 65-91 BL00439G
1749	PR00819	CBXX/CFQX SUPERFAMILY SIGNATURE	13.40 2.895e-12 3-14 PR00819B 10.83 7.158e- 11 4-20
1751	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 3.400e- 14 33-46 PD00066 13.92 1.000e-13 89-102 PD00066 13.92 7.000e- 13 61-74 PD00066 13.92 6.571e-12 117- 130
1753	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 6.516e-
1754	BL00790	Receptor tyrosine kinase class V proteins.	BL00790I 20.01 2.393e- 09 490-521 BL00790I 20.01 2.821e-09 60-91 BL00790I 20.01 6.357e- 09 287-318
1756	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 9.750e- 35 10-49
1758	DM00406	GLIADIN.	DM00406 7.73 7.600e-09 653-666
1762	PD02929	ADHESION GLYCOPROTEIN PRECURSOR I.	PD02929A 28.27 4.529e- 09 224-278
1765	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 5.950e- 11 146-167
1775	PF00023	Ank repeat proteins.	PF00023A 16.03 3.077e- 14 523-539
1776	BL00942	glpT family of transporters proteins.	BL00942F 15.07 4.343e- 10 371-389 BL00942B
1777	DM00215	PROLINE-RICH PROTEIN 3.	20.36 8.040e-09 94-137 DM00215 19.43 2.373e- 09 279-312

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1778	BL00084	Copper type II, ascorbate-dependent monooxygenases proteins.	BL00084D 25.11 3.700e- 20 169-224 BL00084B 24.26 8.134e-16 10-58 BL00084C 27.71 8.412e- 11 107-158
1779	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 3.758e- 18 611-655 BL01013A 25.14 2.891e-15 344- 380 BL01013C 9.97 6.308e-13 435-445 BL01013B 11.33 3.717e- 12 409-420
1783	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 8.138e- 13 492-515
1784	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 8.138e- 13 492-515

^{*} results include in order: accession number subtype; raw score; p-value; postion of signature in amino acid sequence.

TRADOCS:1416223.1(%CRJ0!!.DOC)

TABLE 4

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM
2	ig	Immunoglobulin domain		SCORE
3	pkinase	Eukaryotic protein kinase	2.1e-32	109.5
	•	domain protein kinase	1.3e-29	110.7
4	zf-C2H2	Zinc finger, C2H2 type		
5	fn3	Fibronectin type III domain	1.6e-21	84.9
6	fn3	Fibronectin type III domain	0	1097.
7	fn3	Pibronectin type III domain	0	1035.
8	fn3	Fibronectin type III domain	0	1090.
9	TBC	Fibronectin type III domain	0	1097.
10		TBC domain	4e-40	146.7
12	p450	Cytochrome P450	9.5e-17	62.0
	ank	Ank repeat	6e-20	79.7
14	ig	Immunoglobulin domain	1.7e-05	22.7
15	zf-MYND	MYND finger	1.3e-06	
16	zf-MYND	MYND finger		35.4
17	zf-C2H2	Zinc finger, C2H2 type	1.3e-06	35.4
18	CAP GLY	CAP-Gly domain	1.7e-99	343.9
20	IMPDH C	CAP-Gly domain	1.2e-25	98.7
	IMPDH_C	IMP dehydrogenase / GMP	1.6e-119	410.5
21	71/5	reductase C terminus		12013
21	IMPDH_C	IMP dehydrogenase / GMP	4.3e-102	352.6
		reductase C terminus	1.50 102	332.6
22	pkinase	Eukaryotic protein kinase	2.4e-79	1222 5
	1	domain	2.46-79	277.0
23	pkinase	Eukaryotic protein kinase		
	i -	domain	8.4e-74	258.6
25	RNA_pol_A			1
26	Clq	RNA polymerase alpha subunit	0	1077.7
27	Ribosomal L2	cig domain	1.9e-10	44.4
	3	Ribosomal protein L23	7.8e-32	111.2
28			Ĭ	
20	Ribosomal_L2	Ribosomal protein L23	le-29	104.2
	3	<u> </u>		104.2
30	zf-A20	A20-like zinc finger	1.5e-10	48.5
31	zf-A20	A20-like zinc finger	1.5e-10	48.5
32	FMN_dh	FMN-dependent dehydrogenace	5.4e-179	
34	PID	Phosphotyrosine interaction	3.8e-59	608.1
	ł	domain (PTB/PID)	3.86-59	209.9
35	ig	Immunoglobulin domain		
6	ig	Immunoglobulin domain	1.4e-13	48.8
0	kinesin	Kinesin motor domain	1.4e-13	48.8
4	Ets	Ets-domain	6.7e-76	265.6
5	Ets		1.4e-56	182.1
6	LRR	Ets-domain	1.4e-56	182.1
8		Leucine Rich Repeat	1.7e-13	58.3
	zf-C2H2	Zinc finger, C2H2 type	2.3e-162	552.8
9	ITAM	Immunoreceptor tyrosine-based	1.4e-05	
		activation mot	1.46-05	31.9
0	UCH-2	Ubiquitin carboxyl-terminal	 	
1		hydrolase family	1.1e-26	102.0
1	UCH-5	Ubiquitin carboxyl-terminal		11
		hydrolase family	1.1e-26	102.0
2	ras	Ras family		
3	PRK	Ras ramily	8.5e-45	162.3
4	<u> </u>	Phosphoribulokinase	2.1e-65	230.7
-	myb_DNA-	Myb-like DNA-binding domain	0.096	15.2
	binding			~~
	voltage_CLC	Voltage gated chloride channels	3.3e-186	631.9
5	sugar_tr	Sugar (and other) transporter		
	TBC	TBC domain	0.00015	-64.3
	ank	Ank repeat	2.2e-37	137.6
-	ank	Ank repeat	5.9e-25	96.3
, — —	PMP22 Claudi		5.9e-25	96.3
i i	-	PMP-22/EMP/MP20/Claudin family	7.9e-49	175.6
	n			2.2.0
	CZ	C2 domain	7.9e-54	192.2
	C2	C2 domain	2.3e-54	
	Kelch	Kelch motif		194.0
	ig	Immunoglobulin domain	9.4e-99	341.5
	pkinase	Eukaryotic protein kinase	8.2e-28	94.7
		- analyoute protein kinase	8e-69	242.1

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:			p value	SCORE
		domain		
74	pkinase	Eukaryotic protein kinase domain	2.8e-38	140.6
76	zf- C4_Topoisom	Topoisomerase DNA binding C4 zinc fing	5.4e-54	192.8
83	Peptidase_S9	Prolyl oligopeptidase family	4.3e-10	36.8
84	fn3	Fibronectin type III domain	4.1e-51	183.2
86	SH2	Src homology domain 2	3.1e-22	67.7
88	ig	Immunoglobulin domain	0.0091	14.0
89 92	WD40	WD domain, G-beta repeat	2.1e-21	84.6
93	laminin_G AMP-binding	Laminin G domain	6.1e-27	98.5
95	pkinase	AMP-binding enzyme	2.4e-13	-37.2
		Eukaryotic protein kinase domain	1.4e-59	211.4
96	pkinase	Eukaryotic protein kinase domain	2.6e-51	183.9
97	adh_short	short chain dehydrogenase	2e-61	217.5
98	kinesin	Kinesin motor domain	2.2e-86	300.4
101	IRS	PTB domain (IRS-1 type)	5.4e-36	133.0
102	AAA	ATPases associated with various cellular act	6.8e-05	-5.2
104	pkinase	Eukaryotic protein kinase domain	2.7e-73	256.9
106	ras	Ras family	8.3e-24	92.5
107	FYVE	FYVE zinc finger	5.4e-27	100.7
108	Cyt_reductas e	FAD/NAD-binding Cytochrome reductase	7.7e-61	215.5
109	zf-C2H2	Zinc finger, C2H2 type	2.3e-122	420.0
113	pkinase	Eukaryotic protein kinase domain	4e-88	306.2
116	PH	PH domain	3.1e-11	45.2
117	lipocalin	Lipocalin / cytosolic fatty- acid binding pr	2.4e-14	53.5
118	pkinase	Eukaryotic protein kinase domain	4.5e-20	76.3
120	WD40	WD domain, G-beta repeat	2.4e-14	61.1
121	WD40	WD domain, G-beta repeat	2.4e-14	61.1
123	IF5_eIF4_eIF 2	eIF4-gamma/eIF5/eIF2-epsilon	1e-32	122.2
124	ig	Immunoglobulin domain	6.5e-08	30.6
127	mito_carr	Mitochondrial carrier proteins	3e-16	58.6
128	PP2C	Protein phosphatase 2C	2.2e-71	250.6
129	ATP1G1_PLM_M AT8	ATPIGI/PLM/MAT8 family	3.1e-20	80.6
130	pfkB	pfkB family carbohydrate kinase	4.5e-42	137.1
133 134	ACBP	Acyl CoA binding protein	4.6e-22	86.7
	rrm	RNA recognition motif.	1.2e-31	118.5
135 136	IQ	IQ calmodulin-binding motif	2.6e-08	41.0
	ATPIG1_PLM_M AT8	ATP1G1/PLM/MAT8 family	9.3e-22	85.7
139	WH2	Wiskott Aldrich syndrome homology region 2	0.0067	23.1
140	zf-C2H2	Zinc finger, C2H2 type	1.7e-82	287.5
141	Peptidase_S2	Signal peptidase I	5.7e-10	35.7
143	arf	ADP-ribosylation factor family	1.2e-39	145.2
146	KRAB	KRAB box	7.3e-30	112.6
L48	DUF6	Integral membrane protein DUF6	0.096	8.0
149	PDEase	3'5'-cyclic nucleotide phosphodiesterase	3.8e-80	231.1
51	S4	S4 domain	1.1e-08	122
.53	tRNA-synt_1d	tRNA synthetases class I (R)	3.8e-103	42.3
.54	Cyt_reductas e	FAD/NAD-binding Cytochrome reductase	7.8e-60	356.1 212.2
.55	ras	Ras family	3 6: 55	
.57	actin	Actin	3.6e-28	107.0
	·		3.8e-26	87.1

SEQ ID	PFAM NAME	DESCRIPTION		
NO:	FFAM NAME	DESCRIPTION	p-value	PFAM
158	Jacalin	Jacalin-like lectin domain	0.09	SCORE
160	Zn_carbOpept	Zinc carboxypeptidase		-24.9
165	pkinase	Eukaryotic protein kinase	5e-138	471.9
167	zf-C3IIC4	domain	5.1e-67	236.1
	ZE-C311C4	Zinc finger, C3HC4 type (RING finger)	5.3e-07	27.0
168	Ribosomal_S1 5	Ribosomal protein S15	1.1e-06	29.0
169	DEAD	DEAD/DEAH box helicase	le-48	157.0
171	DUF59	Domain of unknown function DUF59	0.07	-17.4
172	pkinase	Eukaryotic protein kinase domain	3.7e-15	58.6
173	globin	Globin	1	
174	WW	WW domain	4.6e-18	67.4
175	ras	Ras family	7.3e-06	32.9
178	ATPIG1 PLM M		le-31	118.8
	AT8	ATP1G1/PLM/MAT8 family	2.5e-17	71.0
179	2f-C2H2	Zinc finger, C2H2 type	1.5e-99	344.2
180	Clq	Clq domain	8.8e-72	251.9
190	Y phosphatas e	Protein-tyrosine phosphatase	4.9e-287	967.0
191	efhand	EF hand	7.5e-16	66.1
193	pkinase	Eukaryotic protein kinase domain	6.5e-82	285.6
194	bromodomain	Bromodomain	5.8e-31	111.4
195	PALP	Pyridoxal-phosphate dependent	2.5e-64	227.1
197	DnaJ	enzyme		
199	RrnaAD	DnaJ domain	1.6e-38	141.4
133	RTNAMD	Ribosomal RNA adenine dimethylases	0.00018	16.9
200	acid_phospha t	Histidine acid phosphatase	2.5e-10	37.2
201	WH2	Wiskott Aldrich syndrome homology region 2	0.00048	26.9
204	vATP- synt_AC39	ATP synthase (C/AC39) subunit	1.3e-159	543.7
205	VATP- synt AC39	ATP synthase (C/AC39) subunit	1.6e-139	476.9
206	ldl_recept_a	Low-density lipoprotein receptor domain	2.4e-25	97.6
209	ank	Ank repeat	1.4e-19	78.4
210	Rhomboid	Rhomboid family	0.0035	1.2
211	Clq	Clg domain	1.6e-70	247.7
212	UQ con	Ubiquitin-conjugating enzyme	7.4e-74	258.8
213	UQ con	Ubiquitin-conjugating enzyme	1e-53	191.9
215	DEAD	DEAD/DEAH box helicase	1.8e-43	140.4
216	PMP22_Claudi n	PMP-22/EMP/MP20/Claudin family	4.5e-21	83.4
218	Glycos_trans f_2	Glycosyl transferases	4e-21	83.6
219	iq	Immunoglobulin domain	0 002	107
222	WD4 0	WD domain, G-beta repeat	0.092	10.7
224	TPR	TPR Domain	7.4e-23	89.4
225	DnaJ_CXXCXGX	DnaJ central domain (4 repeats)	1.2e-08 1.5e-38	42.1 141.5
226	DnaJ_CXXCXGX G	DnaJ central domain (4 repeats)	1.5e-38	141.5
229	HSP70	Hsp70 protein	1 4 - 54	1.04
230	GSHPx		2.4e-54	194.0
231	tsp 1	Glutathione peroxidases	3.4e-47	170.2
233	cyclin	Thrombospondin type 1 domain	0.0075	17.1
234	_ 	Cyclin	4.6e-144	492.0
234	ras	Ras family	4.8e-50	179.7
236	LRR	Leucine Rich Repeat	1.2e-30	115.3
ا 10	LRR	Leucine Rich Repeat	6.7e-29	109.4
237	PDZ	PDZ domain (Also known as DHR	1.7e-09	45.0

SEQ ID	L DEEM MAN			
NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
244	dCMP_cyt_dea	Cytidine and deoxycytidylate deaminase	2.5e-05	31.1
245	ig	Immunoglobulin domain	6.7e-08	30.5
248	wnt	wnt family of developmental signaling protei	9.1e-270	742.6
250	mito carr	Mitochondrial carrier proteins	1.3e-55	
254	adenylatekin	Adenylate kinase	1.3e-55	193.6
255	ase			55.7
	Cation_efflu x	Cation efflux family	2.8e-33	124.0
256	SH3	SH3 domain	3.9e-14	60.4
257	Aa_trans	Transmembrane amino acid transporter protein	2.6e-52	187.2
258	adenylatekin ase	Adenylate kinase	2.1e-110	380.2
259	HIT	HIT family		
260	Bacterial PO	PQQ enzyme repeat	8.2e-07	25.3
	Q	1	1.6e-15	65.0
262	proteasome	Proteasome A-type and B-type	6.5e-64	225.7
267	pkinase	Eukaryotic protein kinase domain	6.3e-27	101.0
270	filament	Intermediate filament proteins	3.2e-150	512.5
271	Choline_kina se	Choline/ethanolamine kinase	2e-67	237.4
277	Ribosomal S7	Ribosomal protein S7p/S5e	3.3e-20	80.6
279	pkinase	Eukaryotic protein kinase	3.3e-77	269.9
280	WD40	WD domain, G-beta repeat	17.0-73	
281	WD40	WD domain, G-beta repeat	7.8e-73 7.8e-73	255.4
284	zf-DHHC	DHHC zinc finger domain	4.6e-24	255.4 93.4
287	Exonuclease	Exonuclease	1.4e-67	238.0
291	SAM	SAM domain (Sterile alpha	0.034	11.2
292	SAM	motif) SAM domain (Sterile alpha motif)	0.034	11.2
294	zf-C2H2	Zinc finger, C2H2 type	1.4e-29	111.7
295	zf-C2H2	Zinc finger, C2H2 type	2.2e-125	430.0
296	mito_carr	Mitochondrial carrier proteins	4.1e-59	205.5
297	HMG_box	HMG (high mobility group) box	6.7e-29	109.4
302	Glycos_trans f_4	Glycosyl transferase	5e-87	302.5
304	tRNA-synt_2	tRNA synthetases class II (D, K and N)	1.1e-84	294.8
305	KRAB	KRAB box	2e-44	161.0
306	rrm	RNA recognition motif.	2.7e-44	160.6
308	7tm_1	7 transmembrane receptor (rhodopsin family)	5.2e-39	126.1
309	DNA_polymera seX	DNA polymerase X family	2.4e-64	227.2
311	F-box	F-box domain.	9.5e-08	39.2
312	ig	Immunoglobulin domain	6.8e-19	65.9
313	Ets	Ets-domain	8.le-60	192.3
315	Kelch	Kelch motif	1.3e-106	367.6
317	arf	ADP-ribosylation factor family	3.2e-35	130.4
318	sugar_tr	Sugar (and other) transporter	0.0003	-73.1
320	pkinase	Eukaryotic protein kinase domain	8.1e-83	288.6
322	pkinase	Eukaryotic protein kinase domain	4.9e-81	282.6
			1	L
324	Xlink	Extracellular link domain	4.5e-143	331.5
326	ARID	Extracellular link domain ARID DNA binding domain	4.5e-143 5.1e-37	331.5 136.4
326 327	ARID HMG_box	ARID DNA binding domain	5.1e-37	136.4
326 327 328	ARID HMG_box cadherin	Extracellular link domain ARID DNA binding domain HMG (high mobility group) box Cadherin domain	5.1e-37 6.7e-29	136.4 109.4
326 327	ARID HMG_box	ARID DNA binding domain HMG (high mobility group) box	5.1e-37	136.4

SEQ II NO:		DESCRIPTION	p-value	PFAM
335	vwa	von Willebrand factor type A	2.3e-07	37.9
339	ras	Ras family		
340	zf-C2H2	Zinc finger, C2H2 type	7.8e-07	-59.1
342	zf-C2H2	Zinc linger, CZHZ type	8.2e-64	225.4
343	ig	Zinc finger, C2H2 type	2.4e-85	297.0
346	pkinase	Immunoglobulin domain	0.0005	18.0
340	prinase	Eukaryotic protein kinase domain	6.5e-65	229.1
347	pkinase	Eukaryotic protein kinase	6.5e-65	229.1
351	EGF	domain EGF-like domain		
352	ank	Ank repeat	8.5e-20	79.2
354	TBC	TBC domain	2.5e-101	350.0
355	PHD		5.le-15	63.3
358	DUF6	PHD-finger	3.2e-07	37.4
359		Integral membrane protein DUF6	0.033	15.8
	zf-C2H2	Zinc finger, C2H2 type	7.4e-20	79.4
361	ank	Ank repeat	6.6e-34	126.1
362	ArfGap	Putative GTP-ase activating	4.7e-53	E
	i	protein for Arf	1.76-53	189.7
363	efhand	EF hand		
367	LRR	Leucine Rich Repeat	5.4e-10	46.6
368	laminin_G	Laminin G domain	8.8e-44	158.9
369	PP2C	Danielli G domain	1.5e-33	121.7
372	LIM	Protein phosphatase 2C	5.3e-20	73.9
373	KRAB	LIM domain containing proteins	9.9e-15	57.1
76		KRAB box	4.8e-23	90.0 .
	ion_trans	Ion transport protein	2.9e-09	-4.2
77	Beach	Beige/BEACH domain	4.9e-208	,
80	pkinase	Eukaryotic protein kinase	1.6e-94	704.5 327.5
81	AMP-binding	domain	J	1
82	HECT	AMP-binding enzyme	1.4e-07	-140.3
.02	HECT	HECT-domain (ubiquitin- transferase).	1.3e-07	-13.5
84	ank		1	1
86		Ank repeat	2.5e-101	350.0
88	ig	Immunoglobulin domain	9.5e-05	23.6
	zf-C2H2	Zinc finger, C2H2 type	1.7e-42	154.6
89	ig	Immunoglobulin domain	2.8e-15	54.3
90	mito_carr	Mitochondrial carrier proteins	3.5e-67	
92	TPR	TPR Domain	6.1e-17	233.2
93	SH3	SH3 domain		69.7
94	AAA	ATPases associated with various	3.5e-09 4.le-21	83.6
96		Cellular act		03.6
	spectrin	Spectrin repeat	2.1e-67	237.3
97	zf-C2H2	Zinc finger, C2H2 type	0.0066	
9	fn3	Fibronectin type III domain		23.1
00	WD40	WD domain, G-beta repeat	4.1e-102	352.6
)1	El_dehydrcg	Dehydrogenase El component	0.00049	26.8
02	fn3	Fibronectin type III domain	3e-119	409.6
)4	LRR	Leugine Bigh	0	1719.6
15	cadherin	Leucine Rich Repeat	2.1e-10	48.0
6	zf-CXXC	Cadherin domain	8.1e-81	281.9
0		CXXC zinc finger	5e-15	63.4
	RhoGEF	RhoGEF domain	1.1e-23	92.1
.1	F-box	F-box domain.	4.2e-06	_
2	SNF2_N	SNF2 and others N-terminal	5.8e-16	33.7 61.6
.5	CPSase_L_cha	domain		1
	in	Carbamoyl-phosphate synthase (CPSase)	1.5e-172	586.6
8	LRR	Leucine Rich Repeat		
9	DENN	DENN (AEX-3) domain	3.8e-24	93.6
0	RasGEF	Bacoma domain	2e-58	207.5
1		RasGEF domain	8.1e-43	155.7
4	ank	Ank repeat	1.4e-153	523.7
	G-patch	G-patch domain	le-19	
5	pkinase	Eukaryotic protein kinase	2.2e-31	78.9
6	Playin	domain	2.22-31	117.1
٠	Plexin_repea t	Plexin repeat	0.0023	24.6

SCORE	SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
Since Finger, Chief type (RING 6.5e-11 39.2	NO:			P value	
131 DEAD DEAD/DEAH box helicase 1e-66 214.0	429	i -	Zing finger Called him (DING		
SH3			finger)	8.6e-11	39.2
33 GFP_CDC Coll division protein 2.1.e-114 333.5 436 Collagen Collagen triple helix repeat 4.6e-194 558.1 438 Ricin_B_lect Similarity to lectin domain of 0.0085 10.5 10 In Ricin_B_lect Similarity to lectin domain of 0.0085 10.5 11 In Ricin_B_lect Similarity to lectin domain of 0.0085 10.5 12 Alpha_adapti Alpha adaptin carboxyl-terminal 1.2e-256 866.0 442 Alpha_adapti Alpha adaptin carboxyl-terminal 1.8e-235 795.7 443 FDZ FDZ DDZ domain (Also known as DHR 0.00011 20.1 445 LON AFP-dependent protease La (LON) 0.00012 -17.1 446 19 Inmunoglobulin domain 0.00011 20.1 445 19 Inmunoglobulin domain 0.00011 20.1 446 19 Inmunoglobulin domain 1.5e-06 35.2 451 Sushi Sushi domain (SCR repeat) 1.4e-18 75.2 452 In FDZ FDZ domain 1.5e-06 35.2 454 Pyridoxal_de Fyridoxal_dependent 6.3e-14 55.3 455 Rinesin Fyridoxal_dependent 6.3e-14 55.3 456 Kinesin Neurotxansmitter-gated ion 1e-175 557.1 457 Neur_chan Neurotxansmitter-gated ion 1e-175 557.1 458 Josephin Josephin Josephin 1.7e-07 31.8 459 DZIP DZIP transcription factor 1.7e-07 31.8 470 NTP_transfer Nouleotidyl transferase 6.3e-06 -26.3 471 ROTE				1e-66	214.0
1.				3.4e-16	67.2
			Cell division protein	2.1e-114	393.5
### Ricin Blect Similarity to lectin domain of 10.085 10.	436	Collagen	Collagen triple helix repeat (20 copies)		
Alpha adapti Alpha adaptin carboxyl-terminal 1.2e-256 866.0 n.C	438		Similarity to lectin domain of	0.0085	10.5
Alpha adapti Alpha adaptin carboxyl-terminal 1.8e-235 795.7 domai PDZ PDZ domain (Also known as DHR 1.9e-65 230.9 445 LON ATP-dependent protease la (LON) 0.00012 -17.1 446 Ig Immunoglobulin domain 0.00011 20.1 20	441		Alpha adaptin carboxyl-terminal	1.2e-256	866.0
PDZ	442	Alpha_adapti	Alpha adaptin carboxyl-terminal	1.8e-235	795.7
ATP-dependent protease La (LON) 0.00012 -17.1	443		PDZ domain (Also known as DHR	1.9e-65	230.9
domain d	445	LON		0.00012	-17.1
Sushi Sushi Sushi Gomain Sck repeat 1.4e-18 75.2			domain		
Sushi			Immunoglobulin domain	0.00011	20.1
151	•		Sushi domain (SCR repeat)	1.4e-18	
Syridoxal_decarboxylase conse S.3e-14 So.3			Fibronectin type III domain		
C decarboxylase conse A.9e-217 734.4	454		Pyridoxal-dependent		
		Į -	decarboxylase conse		1 55.5
Neurochansmitter-gated ion-channel 1e-175 597.1		kinesin	Kinesin motor domain	4.96-217	734 4
Channel Josephin	457	neur_chan	Neurotransmitter-gated ion-		
According to According A		<u> </u>	channel	5	757.3
Magnetic Magnetic		Josephin	Josephin	0.0002	18 7
NTP_transfer ase ase And	468	bZIP	bzIP transcription factor	. 1	
A73	470		Nucleotidyl transferase		
LIM	471	WD40	WD domain, G-beta repeat	20-20	102.0
2f-RanBP	473	LIM	LIM domain containing proteins		
WD WD Momain, G-beta repeat 6.5e-18 73.0	477	zf-RanBP	Zn-finger in Ran binding	. 2	
RRAB KRAB	479	WD40	protein and others.		
ArfGap	_				_L
SH2 SH2 Src homology domain 2 0.011 11.4					
11.4 11.4			protein for Arf	8.4e-66	232.0
			Src homology domain 2	0.011	11.4
### ### ### ### ### #### #### #### #####			Clq domain	4.3e-74	259.6
Alpha adapti n_C domai		dsrm	motif	1.1e-47	171.9
Alpha_adapti			Zinc finger, C2H2 type	4.8e-153	521 9
# 1.2e-10	490		Alpha adaptin carboxyl-terminal		
ENV_polyprot ein	492	SKI	Shikimate kinase	1 20 10	
ein polyprotein) abhydrolase_ 2 Phospholipase/Carboxylesterase 0.041 -48.1 500 rrm RNA recognition motif. 5.4e-34 126.4 501 WW WW domain 4.6e-18 73.4 502 ig Immunoglobulin domain 1.1e-10 39.5 504 abhydrolase alpha/beta hydrolase fold 0.045 -3.6 505 vwa von Willebrand factor type A 7.1e-62 219.0 508 Na_K_ATPase_ C Na+/K+ ATPase C-terminus 2.3e-145 496.3 509 Exonuclease Exonuclease 1.3e-56 201.5 510 Glycos_trans Glycosyl transferases group 1 2.9e-06 27.0 511 Glycos_trans Glycosyl transferases group 1 2.9e-06 27.0 512 Glycos_trans Glycosyl transferases group 1 1.9e-09 38.5 514 pro_isomeras Cyclophilin type peptidyl- 1.8e-63 221.4	497	ENV polyprot			
2	498	ein	polyprotein)		
WW WW domain 4.6e-18 73.4 126.4 126.4 126.2 13 136.4 136.5		2			
1		3	RIVE TECOGNITION motif.		
1.1e-10 39.5					73.4
Von Willebrand factor type A 7.1e-62 219.0			immunoglobulin domain		39.5
domain			aipha/beta hydrolase fold	0.045	-3.6
C			domain	7.1e-62	219.0
Glycos_trans Glycosyl transferases group 1 2.9e-06 27.0 2			Na+/K+ ATPase C-terminus	2.3e-145	496.3
Glycos_trans Glycosyl transferases group 1 2.9e-06 27.0	509	Exonuclease	Exonuclease	1 30-56	201 5
Glycos_trans Glycosyl transferases group 1 2.9e-06 27.0 2	510				<u>L</u>
Glycos_trans Glycosyl transferases group 1 1.9e-09 38.5 1 1 1.9e-09 1.8e-63 221.4 1.8e-63 221.4	511	Glycos_trans	Glycosyl transferases group 1	2.9e-06	27.0
pro_isomeras Cyclophilin type peptidyl- 1.8e-63 221.4	512	Glycos_trans	Glycosyl transferases group 1	1.9e-09	38.5
prolyl cis-tr	514	pro_isomeras	Cyclophilin type peptidyl-	1.8e-63	221.4
		e	prolyl cis-tr		

SEQ ID	Done synes			
NO:	PFAM NAME	DESCRIPTION	p-value	PFAM
515	EGF	EGF-like domain		SCORE
516	Surp	Surp module	1.9e-18	74.7
523	ig		4.3e-38	140.0
526	UBX	Immunoglobulin domain	3.3e-06	25.0
528	adh zinc	UBX domain	1.le-34	128.6
530	SAM	Zinc-binding dehydrogenases	2.7e-34	127.4
1 330	SAM	SAM domain (Sterile alpha	0.046	10.0
531	adh_short	motif)		
532	mito carr	short chain denydrogenase	0.0025	-34.1
533	mito_carr	Mitochondrial carrier proteins	2.5e-8I	281.7
534		Mitochondrial carrier proteins	2e-61	213.5
535	thiolase	Thiolase	3.5e-183	622.0
235	FMO-like	Flavin-binding monooxygenase-	0	1153.7
536		like		
	SCAN	SCAN domain	4e-55	196.6
537	tRNA-synt_1	tRNA synthetases class I (I, L,	3.1e-136	466.0
		M and V)		
538	tRNA-synt_1	tRNA synthetases class I (I, L,	3.le-136	466.0
		M and V)		100.0
539	tRNA-synt_1	tRNA synthetases class I (I, L,	1.9e-117	403.6
		M and V)		100.0
540	tRNA-synt_1	tRNA synthetases class I (I, L,	3.1e-136	466.0
		M and V)		1.50.0
541	vATP-synt_E	ATP synthase (E/31 kDa) subunit	5.9e-85	295.7
543	2f-C2H2	Zinc finger, C2H2 type	5.5e-69	242.6
544	DUF101	Protein of unknown function	8.5e-38	139.0
		DUF101	1 0.00	133.0
545	TGFb_propept	TGF-beta propeptide	1.1e-67	238.2
	ide		1.10-07	230.2
547	WD40	WD domain, G-beta repeat	2.6e-32	120 8
548	RHD	Rel homology domain (RHD)	1.6e-238	686.2
549	MMR_HSR1	GTPase of unknown function	5.4e-67	236.0
551	HECT	HECT-domain (ubiquitin-	4.3e-127	435.6
		transferase).	1.36-12/	433.6
554	MHC_II_alpha	Class II histocompatibility	3.5e-74	259.8
	-	antigen, alp	3.32-74	259.8
5 55	zf-UBR1	Putative zinc finger in N-	3.3e-16	67.3
		recognin	3.30 10	07.3
5 56	Kelch	Kelch motif	5.5e-29	109.7
561	AMP-binding	AMP-binding enzyme	2.8e-06	-163.7
562	PABP	Poly-adenylate binding protein,	4.9e-38	139.8
		unique domai	1	133.0
564	Gag_p30	Gag P30 core shell protein	1.2e-67	238.2
566	PWWP	PWWP domain	8.1e-16	66.0
567	SCAN	SCAN domain	7.3e-68	238.9
569	pkinase	Eukaryotic protein kinase	1.5e-84	294.3
	1	domain	1.56-84	294.3
570	pkinase	Eukaryotic protein kinase	1.5e-84	204 2
		domain	1.76-04	294.3
571	CN_hydrolase	Carbon-nitrogen hydrolase	0.00081	70 7
572	myosin_head	Myosin head (motor domain)	0.00081	-79.7
573	myosin head	Myosin head (motor domain)	0	1495.2
575	Surp	Surp module		1490.4
576	Surp	Surp module	1.7e-23	91.5
577	DNA pol B	DNA polymerase family B	1.7e-23	91.5
578	PDZ	PDZ domain (Also known as DHR	0	1138.6
	1	or GLGF).	8.3e-09	42.7
579	LRR	Leucine Rich Repeat		L
580	neur chan	Neurotransmitter-gated ion-	4.9e-21	83.3
		channel	5.9e-177	601.3
	 	Sushi domain (SCR repeat)		
583	l sushi	(SCK repeat)	0	1673.0
	sushi DEAD	DEAD /DEAU how have		
584	DEAD	DEAD/DEAH box helicase	7.3e-36	116.3
584 586	DEAD KH-domain	DEAD/DEAH box helicase KH domain		116.3 57.5
584 586 587	DEAD KH-domain G-patch	DEAD/DEAH box helicase KH domain G-patch domain	7.3e-36	
584 586 587 589	DEAD KH-domain G-patch LIM	DEAD/DEAH box helicase KH domain G-patch domain LIM domain containing proteins	7.3e-36 2.9e-13	57. 5
583 584 586 587 589 590	DEAD KH-domain G-patch	DEAD/DEAH box helicase KH domain G-patch domain	7.3e-36 2.9e-13 2.3e-14	57.5 61.2

SEO ID	PFAM NAME	DESCRIPTION	T	
NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
592	hormone rec	Ligand-binding domain of	3.5e-22	87.1
	_	nuclear hormone		
593	PHD	PHD-finger	3.8e-12	53.8
594	cadherin	Cadherin domain	4.2e-99	342.7
596	pkinase	Eukaryotic protein kinase domain	5e-92	319.2
597	WD40	WD domain, G-beta repeat	0.00054	26.7
600	FG-GAP	FG-GAP repeat	4.3e-75	262.9
602	G_Adapt_CT	Gamma-adaptin, C-terminus	1.1e-53	191.8
603	pkinase	Eukaryotic protein kinase domain	2.3e-86	300.4
605	Collagen	Collagen triple helix repeat (20 copies)	8e-42	152.4
606	mito_carr	Mitochondrial carrier proteins	6.3e-67	232.3 .
608	PWWP	PWWP domain	2.6e-28	107.5
609	PWWP	PWWP domain	2.6e-28	107.5
613	CAP_GLY	CAP-Gly domain	0.0046	20.1
615	RFX_DNA_bind ing	RFX DNA-binding domain	5.2e-54	192.9
616	kinesin	Kinesin motor domain	1.1e-81	284.8
617	kinesin	Kinesin motor domain	8.4e-80	278.5
618	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.0098	13.1
620	MATH	MATH domain	7.8e-05	22.2
621	Y_phosphatas e	Protein-tyrosine phosphatase	1.4e-32	121.6
622	pkinase	Eukaryotic protein kinase domain	4.4e-40	146.6
623 .	BNR	BNR repeat	2.1e-11	51.3
624	molybdopteri n	Prokaryotic molybdopterin oxidoreductas	1.4e-12	42.2
625	TPR	TPR Domain	1.1e-17	72.2
627	cNMP_binding	Cyclic nucleotide-binding domain	3.7e-58	206.6
630	adh_short	short chain dehydrogenase	5e-17	70.0
631	zf-C2H2	Zinc finger, C2H2 type	2.1e-88	307.1
632	rrm	RNA recognition motif.	4e-05	30.5
635	pkinase	Eukaryotic protein kinase domain	1.6e-104	360.7
636	Fork_head	Fork head domain ,	5.9e-27	103.0
637	pkinase	Eukaryotic protein kinase domain	3.8e-70	246.5
642	TPR	TPR Domain	4.8e-08	40.1
643	efhand	EF hand	1.9e-27	104.6
647	SNF2_N	SNF2 and others N-terminal	1.2e-101	351.1
CAC	D	domain		1
648	PseudoU_synt h_2	RNA pseudouridylate synthase	1.9e-55	197.6
650	h_2 zf-C2H2	RNA pseudouridylate synthase Zinc finger, C2H2 type	0.0087	22.7
650 651	h_2 zf-C2H2 ank	RNA pseudouridylate synthase Zinc finger, C2H2 type Ank repeat	0.0087 1.3e-17	22.7
650 651 652	h_2 zf~C2H2 ank I_LWEQ	RNA pseudouridylate synthase Zinc finger, C2H2 type Ank repeat I/LWEQ domain	0.0087 1.3e-17 9.5e-101	22.7 71.9 341.0
650 651 652 653	h_2 zf-C2H2 ank I_LWEQ neur_chan	RNA pseudouridylate synthase Zinc finger, C2H2 type Ank repeat I/LWEQ domain Neurotransmitter-gated ion- channel	0.0087 1.3e-17 9.5e-101 4.1e-171	22.7 71.9 341.0 581.8
650 651 652 653	h_2 zf-C2H2 ank I_LWEQ neur_chan tsp_1	RNA pseudouridylate synthase Zinc finger, C2H2 type Ank repeat I/LWEQ domain Neurotransmitter-gated ion- channel Thrombospondin type 1 domain	0.0087 1.3e-17 9.5e-101 4.1e-171	22.7 71.9 341.0 581.8
650 651 652 653 654 659	h_2 zf-C2H2 ank I_LWEQ neur_chan tsp_1 FH2	RNA pseudouridylate synthase Zinc finger, C2H2 type Ank repeat I/LWEQ domain Neurotransmitter-gated ion- channel Thrombospondin type 1 domain Formin Homology 2 Domain	0.0087 1.3e-17 9.5e-101 4.1e-171 4.1e-47 1e-107	22.7 71.9 341.0 581.8 169.9 371.2
650 651 652 653 654 659	h_2 zf-C2H2 ank I_LWEQ neur_chan tsp_1 FH2 pou	RNA pseudouridylate synthase Zinc finger, C2H2 type Ank repeat I/LWEQ domain Neurotransmitter-gated ion- channel Thrombospondin type 1 domain Formin Homology 2 Domain Pou domain - N-terminal to homeobox domain	0.0087 1.3e-17 9.5e-101 4.1e-171 4.1e-47 1e-107 5.3e-45	22.7 71.9 341.0 581.8 169.9 371.2 162.9
650 651 652 653 654 659 661	h_2 zf-C2H2 ank I_LWEQ neur_chan tsp_1 FH2 pou	RNA pseudouridylate synthase Zinc finger, C2H2 type Ank repeat I/LWEQ domain Neurotransmitter-gated ion- channel Thrombospondin type 1 domain Formin Homology 2 Domain Pou domain - N-terminal to homeobox domain C2 domain	0.0087 1.3e-17 9.5e-101 4.1e-171 4.1e-47 1e-107 5.3e-45	22.7 71.9 341.0 581.8 169.9 371.2 162.9
650 651 652 653 654 659 661	h_2 zf-C2H2 ank I_IWEQ neur_chan tsp_1 FH2 pou C2 C2	RNA pseudouridylate synthase Zinc finger, C2H2 type Ank repeat I/LWEQ domain Neurotransmitter-gated ion- channel Thrombospondin type 1 domain Formin Homology 2 Domain Pou domain - N-terminal to homeobox domain C2 domain C2 domain	0.0087 1.3e-17 9.5e-101 4.1e-171 4.1e-47 1e-107 5.3e-45 6.7e-19 6.7e-19	22.7 71.9 341.0 581.8 169.9 371.2 162.9
650 651 652 653 654 659 661 662 663 664	h_2 zf-C2H2 ank I_LWEQ neur_chan tsp_1 FH2 pou C2 C2 C2	RNA pseudouridylate synthase Zinc finger, C2H2 type Ank repeat I/LWEQ domain Neurotransmitter-gated ion- channel Thrombospondin type 1 domain Formin Homology 2 Domain Pou domain - N-terminal to homeobox domain C2 domain C2 domain C2 domain C2 domain	0.0087 1.3e-17 9.5e-101 4.1e-171 4.1e-47 1e-107 5.3e-45 6.7e-19 6.7e-19 6.7e-19	22.7 71.9 341.0 581.8 169.9 371.2 162.9 76.2 76.2
650 651 652 653 654 659 661 662 663 664 667	h_2 zf-C2H2 ank I_LWEQ neur_chan tsp_1 FH2 pou C2 C2 C2 C2 GST	RNA pseudouridylate synthase Zinc finger, C2H2 type Ank repeat I/LWEQ domain Neurotransmitter-gated ion- channel Thrombospondin type 1 domain Formin Homology 2 Domain Pou domain - N-terminal to homeobox domain C2 domain C2 domain C2 domain C2 domain C2 domain C1 domain C2 domain C2 domain C3 domain C4 domain	0.0087 1.3e-17 9.5e-101 4.1e-171 4.1e-47 1e-107 5.3e-45 6.7e-19 6.7e-19 6.7e-19 9.3e-34	22.7 71.9 341.0 581.8 169.9 371.2 162.9 76.2 76.2 76.2
650 651 652 653 654 659 661 662 663 664 667 668	h_2 zf-C2H2 ank I_LWEQ neur_chan tsp_1 FH2 pou C2 C2 C2 C2 GST LRR	RNA pseudouridylate synthase Zinc finger, C2H2 type Ank repeat I/LWEQ domain Neurotransmitter-gated ion- channel Thrombospondin type 1 domain Formin Homology 2 Domain Pou domain - N-terminal to homeobox domain C2 domain C2 domain C2 domain C2 domain C2 domain C1 domain C2 domain C2 domain C2 domain C2 domain C2 domain C2 domain C3 domain C4 domain C5 domain C6 domain C7 domain C8 domain C9 domain C9 domain	0.0087 1.3e-17 9.5e-101 4.1e-171 4.1e-47 1e-107 5.3e-45 6.7e-19 6.7e-19 6.7e-19 9.3e-34 9.3e-31	22.7 71.9 341.0 581.8 169.9 371.2 162.9 76.2 76.2 76.2 114.4 115.6
650 651 652 653 654 659 661 662 663 664 667 668	h_2 zf-C2H2 ank I_LWEQ neur_chan tsp_1 FH2 pou C2 C2 C2 C2 C4 GST LRR spectrin	RNA pseudouridylate synthase Zinc finger, C2H2 type Ank repeat I/LWEQ domain Neurotransmitter-gated ion- channel Thrombospondin type 1 domain Formin Homology 2 Domain Pou domain - N-terminal to homeobox domain C2 domain C2 domain C2 domain C2 domain C3 domain C4 domain C5 domain C5 domain C6 domain C9 domain	0.0087 1.3e-17 9.5e-101 4.1e-171 4.1e-47 1e-107 5.3e-45 6.7e-19 6.7e-19 9.3e-34 9.3e-31 4e-57	22.7 71.9 341.0 581.8 169.9 371.2 162.9 76.2 76.2 76.2 114.4 115.6 203.2
650 651 652 653 654 659 661 662 663 664 667 668	h_2 zf-C2H2 ank I_LWEQ neur_chan tsp_1 FH2 pou C2 C2 C2 C2 GST LRR	RNA pseudouridylate synthase Zinc finger, C2H2 type Ank repeat I/LWEQ domain Neurotransmitter-gated ion- channel Thrombospondin type 1 domain Formin Homology 2 Domain Pou domain - N-terminal to homeobox domain C2 domain C2 domain C2 domain C2 domain C2 domain C1 domain C2 domain C2 domain C2 domain C2 domain C2 domain C2 domain C3 domain C4 domain C5 domain C6 domain C7 domain C8 domain C9 domain C9 domain	0.0087 1.3e-17 9.5e-101 4.1e-171 4.1e-47 1e-107 5.3e-45 6.7e-19 6.7e-19 6.7e-19 9.3e-34 9.3e-31	22.7 71.9 341.0 581.8 169.9 371.2 162.9 76.2 76.2 76.2 76.2 114.4 115.6

SEQ ID	PFAM NAME	DESCRIPTION	L	Table.
NO:			p-value	PFAM
675	WD40	WD domain, G-beta repeat		SCORE
676	LRR	Leucine Rich Repeat	4.8e-24	93.3
679	zf-CCCH	Zing finger C - C	0.0015	25.2
- , 2	22 CCCH	Zinc finger C-x8-C-x5-C-x3-H	2.6e-29	107.7
680	zf-C2H2	type		
681	CH	Zinc finger, C2H2 type	5.2e-05	30.1
682	DSPC	Calponin homology (CH) domain	2.4e-17	71.1
002	DSPC	Dual specificity phosphatase,	4.3e-43	156.6
		catalytic doma		
683	zf-C3HC4	Zinc finger, C3HC4 type (RING	0.051	10.8
		finger)		1 20.0
687	Synapsin	Synapsin	 0	1000
689	PR55	Protein phosphatase 2A	0	1890.8
	1	regulatory subunit PR	0	1038.8
691	homeobox	Homeobox domain		
696	Peptidase_M2		8.5e-30	112.4
	4	metallopeptidase family M24	2.6e-59	210.5
697	RhoGEF		1	ı
698		RhoGEF domain	9.5e-35	128.9
	PHD	PHD-finger	0.008	9.3
701	zf-C2H2	Zinc finger, C2H2 type	5.5e-123	422.0
702	Sulfatase	Sulfatase	3e-231	781.6
703	zf-C2H2	Zinc finger, C2H2 type	5.7e-20	
707	Acyl transf	Acyl transferase domain		79.8
708	WD40	WD domain, G-beta repeat	1.le-22	88.8
710	Ran BP1	WD domain, G-Deta repeat	4.8e-19	76.7
713	DEAD	RanBP1 domain.	8.4e-06	-7.3
714		DEAD/DEAH box helicase	9.9e-42	134.9
	PH	PH domain	1.6e-09	39.0
715	DSPc	Dual specificity phosphatase,	1.5e-37	138.2
	_	catalytic doma	1 2.30 37	130.2
717	Sialyltransf	Sialyltransferase family	7.5e-31	1
718	ig	Immunoglobulin domain		115.9
719	integrin B	Integrins, beta chain	1e-29	100.8
720	zf-C3HC4	7ing fine Card	0	1125.4
	22 0303	Zinc finger, C3HC4 type (RING	1.1e-08	32.4
722	Peptidase C2	finger)	İ	
,	repridase_C2	Calpain family cysteine	3e-145	495.9
723		protease	1	1
	ig	Immunoglobulin domain	2.2e-05	22.4
724	F-box	F-box domain.	0.007	23.0
725	Nop	Putative snoRNA binding domain	8.1e-58	205.5
726	Nop	Putative snoRNA binding domain	8.1e-58	
727	WD40	WD domain, G-beta repeat		205.5
730	dsrm	Double-stranded RNA binding	7.5e-26	99.3
	1	motif	0.027	12.1
731	dynamin	Dynamin family		1
733	zf-CCCH	Dynamin ramily	4.2e-16	66.9
	21-CCCH	Zinc finger C-x8-C-x5-C-x3-H	2.8e-10	41.7
735	CDP-	type		
135		CDP-alcohol	4.2e-26	100.1
	OH_P_transf	phosphatidyltransferase		
738	DEAD	DEAD/DEAH box helicase	8.6e-57	1103 5
739	TSC22	TSC-22/dip/bun family	6.5e-32	182.5
42	ras	Ras family		119.5
743	PMI_typeI	Phosphomannosc isomerase type I	2.2e-100	346.9
47	trypsin	Trimein	1.2e-243	822.9
48	kazal	Trypsin	6.4e-88	279.4
		Kazal-type serine protease	2.2e-52	187.4
149	1	inhibitor domain	1	ł
	efhand	EF hand	6.3e-06	33.1
51	PHD	PHD-finger	4.9e-16	66.7
52	zf-C2H2	Zinc finger, C2H2 type	3.2e-21	
53	Hydrolase	haloacid dehalogenase-like		83.9
		hydrolase	6.le-11	49.8
54	Ribosomal L3	Pihonemal 130		
-	9	Ribosomal L39 protein	0.00018	26.7
	1		1	i
55	PH	PH domain	3.6e-14	55.7
58	SCAN	SCAN domain	1.4e-53	
59	PA	PA domain		191.5
60	arf	ADP-ribosylation factor family	0.0065	23.1
61	CIDE-N	CIDE-N domain	2.2e-19	77.8
		VAULTR GOMAIN	2.2e-40	147.6

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:	- 			SCORE
763	histone	Core histone H2A/H2B/H3/H4	9.9e-53	188.6
764	zf-MYND	MYND finger	4.1e-14	60.3
764	bon	Pou domain - N-terminal to	1e-52	188.6
767	Vwc	homeobox domain		
/0/) vwc	von Willebrand factor type C domain	2.9e-34	127.3
769	efhand	EF hand		
770	zf-C4	Zinc finger, C4 type (two	4.8e-11	50.1
1	22 04	domains)	2.4e-53	181.6
772	ras	Ras family	7- 00	
773	Sulfatase	Sulfatase	7e-90	312.0
775	zf-C2H2	Zinc finger, C2H2 type	le-142	487.5
776	zf-C2H2	Zinc finger, C2H2 type	1.1e-12	55.5
777	zf-C2H2	Zinc finger, C2H2 type	1.1e-12	55.5
778	rrm	RNA recognition motif.	1.1e-12	55.5
779	G6PD ·	Glucose-6-phosphate	2.1e-32	121.1
		dehydrogenase	1.5e-76	236.6
780	spectrin	Spectrin repeat	3.7e-29	
781	mito carr	Mitochondrial carrier proteins	4.6e-57	110.3
782	SCAN	SCAN domain	1.3e-24	198.5
783	PDZ	PDZ domain (Also known as DHR	1.3e-24 4.1e-07	95.2 37.1
		or GLGF).	1.16-0/	137.1
785	DEAD	DEAD/DEAH box helicase	6e-06	121.7
786	ras	Ras family	5.3e-39	143.0
787	RNase HII	Ribonuclease HII	2.5e-67	237.1
790	PI3 PI4 kina	Phosphatidylinositol 3- and 4-	5.4e-108	372.2
	se	kinases	3.40-100	3/2.2
795	cadherin	Cadherin domain	2.5e-40	147.4
796	ARID	ARID DNA binding domain	1.6e-20	81.6
797	trypsin	Trypsin	9.9e-20	64.8
799	СН	Calponin homology (CH) domain	3.7e-15	63.8
801	Gal-	Vertebrate galactoside-binding	4.1e-25	88.7
	bind_lectin	lectin		
803	WD40	WD domain, G-beta repeat	0.00082	26.1
806	TBC	TBC domain	1.8e-26	101.4
807	TBC	TBC domain	1.8e-26	101.4
808	CN_hydrolase	Carbon-nitrogen hydrolase	8.8e-80	278.5
811	CBFD_NFYB_HM	Histone-like transcription	6e-14	59.8
812	F	factor	1	
814	adh_short	short chain dehydrogenase	8.1e-20	79.3
815		Domain of unknown function	3.3e-71	250.0
816	zf-C2H2	Zinc finger, C2H2 type	8.2e-66	232.1
010	Pept_tRNA_hy	Peptidyl-tRNA hydrolase	1.6e-37	138.0
817		1010 Day		
91,		ARID DNA binding domain	2.5e-18	74.3
826	ARID	GTE4 /- YEE7		
826	IF5_eIF4_eIF	eIF4-gamma/eIF5/eIF2-epsilon	1.6e-32	121.5
	IFS_eIF4_eIF 2	eIF4-gamma/eIF5/eIF2-epsilon	1.6e-32	121.5
826 830	IF5_eIF4_eIF	eIF4-gamma/eIF5/eIF2-epsilon Putative GTP-ase activating		
	IF5_eIF4_eIF 2 ArfGap	eIF4-gamma/eIF5/eIF2-epsilon Putative GTP-ase activating protein for Arf	1.6e-32 1.5e-53	121.5
830 831	IF5_eIF4_eIF 2 ArfGap LRR	eIF4-gamma/eIF5/eIF2-epsilon Putative GTP-ase activating protein for Arf Leucine Rich Repeat	1.6e-32 1.5e-53 2.1e-26	121.5 191.3
830	IF5_eIF4_eIF 2 ArfGap	Putative GTP-ase activating protein for Arf Leucine Rich Repeat Laminin EGF-like (Domains III	1.6e-32 1.5e-53	121.5
830 831	IF5_eIF4_eIF 2 ArfGap LRR laminin_EGF	eIF4-gamma/eIF5/eIF2-epsilon Putative GTP-ase activating protein for Arf Leucine Rich Repeat Laminin EGF-like (Domains III and V)	1.6e-32 1.5e-53 2.1e-26 2e-57	121.5 191.3 101.1 204.2
830 831 832	IF5_eIF4_eIF 2 ArfGap LRR laminin_EGF	eIF4-gamma/eIF5/eIF2-epsilon Putative GTP-ase activating protein for Arf Leucine Rich Repeat Laminin EGF-like (Domains III and V) RNA recognition motif.	1.6e-32 1.5e-53 2.1e-26 2e-57 1.3e-22	121.5 191.3 101.1 204.2 88.5
830 831 832	IF5_eIF4_eIF 2 ArfGap LRR laminin_EGF	eIF4-gamma/eIF5/eIF2-epsilon Putative GTP-ase activating protein for Arf Leucine Rich Repeat Laminin EGF-like (Domains III and V)	1.6e-32 1.5e-53 2.1e-26 2e-57	121.5 191.3 101.1 204.2
830 831 832	IF5_eIF4_eIF 2 ArfGap LRR laminin_EGF rrm Y_phosphatas e	eIF4-gamma/eIF5/eIF2-epsilon Putative GTP-ase activating protein for Arf Leucine Rich Repeat Lamine EGF-like (Domains III and V) RNA recognition motif. Protein-tyrosinc phosphatase	1.6e-32 1.5e-53 2.1e-26 2e-57 1.3e-22 2.6e-119	121.5 191.3 101.1 204.2 88.5 409:8
831 832 839 840	IF5_eIF4_eIF 2 ArfGap LRR laminin_EGF	eIF4-gamma/eIF5/eIF2-epsilon Putative GTP-ase activating protein for Arf Leucine Rich Repeat Lamin EGF-like (Domains III and V) RNA recognition motif. Protein-tyrosine phosphatase Eukaryotic protein kinase	1.6e-32 1.5e-53 2.1e-26 2e-57 1.3e-22	121.5 191.3 101.1 204.2 88.5
831 832 839 840	IF5_eIF4_eIF 2 ArfGap LRR laminin_EGF rrm Y_phosphatas e	eIF4-gamma/eIF5/eIF2-epsilon Putative GTP-ase activating protein for Arf Leucine Rich Repeat Laminin EGF-like (Domains III and V) RNA recognition motif. Protein-tyrosine phosphatase Eukaryotic protein kinase domain	1.6e-32 1.5e-53 2.1e-26 2e-57 1.3e-22 2.6c-119	121.5 191.3 101.1 204.2 88.5 409.8
830 831 832 839 840	IF5_eIF4_eIF 2 ArfGap LRR laminin_EGF rrm Y_phosphatas e pkinase	eIF4-gamma/eIF5/eIF2-epsilon Putative GTP-ase activating protein for Arf Leucine Rich Repeat Lamin EGF-like (Domains III and V) RNA recognition motif. Protein-tyrosine phosphatase Eukaryotic protein kinase	1.6e-32 1.5e-53 2.1e-26 2e-57 1.3e-22 2.6e-119	121.5 191.3 101.1 204.2 88.5 409:8
830 831 832 839 840	IF5_eIF4_eIF 2 ArfGap LRR laminin_EGF rrm Y_phosphatas e pkinase Ribosomal_L2	eIF4-gamma/eIF5/eIF2-epsilon Putative GTP-ase activating protein for Arf Leucine Rich Repeat Laminin EGF-like (Domains III and V) RNA recognition motif. Protein-tyrosine phosphatase Eukaryotic protein kinase domain Ribosomal L22e protein family	1.6e-32 1.5e-53 2.1e-26 2e-57 1.3e-22 2.6c-119 3.4e-100	121.5 191.3 101.1 204.2 88.5 409:8 346.3
830 831 832 839 840 841	IF5_eIF4_eIF 2 ArfGap LRR laminin_EGF rrm Y_phosphatas e pkinase Ribosomal_L2 2e IBR	eIF4-gamma/eIF5/eIF2-epsilon Putative GTP-ase activating protein for Arf Leucine Rich Repeat Laminin EGF-like (Domains III and V) RNA recognition motif. Protein-tyrosine phosphatase Eukaryotic protein kinase domain Ribosomal L22e protein family IBR domain	1.6e-32 1.5e-53 2.1e-26 2e-57 1.3e-22 2.6e-119 3.4e-100 1e-64	121.5 191.3 101.1 204.2 88.5 409:8 346.3 228.4
830 831 832 839 840 841 844	IF5_eIF4_eIF 2 ArfGap LRR laminin_EGF rrm Y_phosphatas e pkinase Ribosomal_L2 2e	eIF4-gamma/eIF5/eIF2-epsilon Putative GTP-ase activating protein for Arf Leucine Rich Repeat Laminin EGF-like (Domains III and V) RNA recognition motif. Protein-tyrosine phosphatase Eukaryotic protein kinase domain Ribosomal L22e protein family IBR domain Zinc finger, C3HC4 type (RING	1.6e-32 1.5e-53 2.1e-26 2e-57 1.3e-22 2.6c-119 3.4e-100	121.5 191.3 101.1 204.2 88.5 409:8 346.3
830 831 832 839 840 841 844	IF5_eIF4_eIF 2 ArfGap LRR laminin_EGF rrm Y_phosphatas e pkinase Ribosomal_L2 2e IBR zf-C3HC4	Putative GTP-ase activating protein for Arf Leucine Rich Repeat Laminin EGF-like (Domains III and V) RNA recognition motif. Protein-tyrosinc phosphatase Eukaryotic protein kinase domain Ribosomal L22e protein family IBR domain Zinc finger, C3HC4 type (RING finger)	1.6e-32 1.5e-53 2.1e-26 2e-57 1.3e-22 2.6e-119 3.4e-100 1e-64 9e-15 7.4e-07	121.5 191.3 101.1 204.2 88.5 409:8 346.3 228.4 62.5 26.5
830 831 832 839 840 841 844 846	IF5_eIF4_eIF 2 ArfGap LRR laminin_EGF rrm Y_phosphatas e pkinase Ribosomal_L2 2e IBR	Putative GTP-ase activating protein for Arf Leucine Rich Repeat Laminin EGF-like (Domains III and V) RNA recognition motif. Protein-tyrosinc phosphatase Eukaryotic protein kinase domain Ribosomal L22e protein family IBR domain Zinc finger, C3HC4 type (RING finger) Zinc finger, C3HC4 type (RING	1.6e-32 1.5e-53 2.1e-26 2e-57 1.3e-22 2.6e-119 3.4e-100 1e-64	121.5 191.3 101.1 204.2 88.5 409:8 346.3 228.4
830 831 832 839 840 841 844 846	IF5_eIF4_eIF 2 ArfGap LRR laminin_EGF rrm Y_phosphatas e pkinase Ribosomal_L2 2e IBR zf-C3HC4	Putative GTP-ase activating protein for Arf Leucine Rich Repeat Laminin EGF-like (Domains III and V) RNA recognition motif. Protein-tyrosinc phosphatase Eukaryotic protein kinase domain Ribosomal L22e protein family IBR domain Zinc finger, C3HC4 type (RING finger)	1.6e-32 1.5e-53 2.1e-26 2e-57 1.3e-22 2.6e-119 3.4e-100 1e-64 9e-15 7.4e-07	121.5 191.3 101.1 204.2 88.5 409:8 346.3 228.4 62.5 26.5

SEQ I	D PFAM NAME	DESCRIPTION	p-value	PFAM
	- 			SCORE
853	SRCR	rich domain		
	- CALOR	Scavenger receptor cysteine- rich domain	0	1025.
857	lactamase B	Metallo-beta-lactamase		
	_	superfamily	0.012	-6.0
858	COX6A	Cytochrome c oxidase subunit	3.4e-58	
200		VIa	3.4e-58	206.7
859 861	rrm	RNA recognition motif.	5.4e-45	162.9
863	PRK	Phosphoribulokinase	5.1e-62	219.4
864	mito_carr HSP90	Mitochondrial carrier proteins	2.9e-53	185.5
866	iq	Hsp90 protein	4.7e-158	538.5
867	zf-C2H2	Immunoglobulin domain	4e-12	44.1
872	histone	Zinc finger, C2H2 type	7e-135	461.5
874	CPSase L cha	Core histone H2A/H2B/H3/H4	4.9e-41	149.8
	in	Carbamoyl-phosphate synthase (CPSase)	2.1e-218	739.0
879	Ribosomal S1			1
	2e	Ribosomal protein S12e	2.1e-98	340.3
882	serpin	Serpins (serine protease		
		inhibitors)	2.5e-42	145.7
883	Patatin	Patatin	+	
884	RA	Ras association (RalGDS/AF-6)	1.2e-51 0.044	182.0
		domain	i	8.0
887	DUF92	Integral membrane protein DUF92	2.7e-12	
889	sugar_tr	Sugar (and other) transporter	8.2e-63	54.3
893	DUF28	Domain of unknown function	1.3e-43	222.1
225		DUF28	1.36-43	158.3
896	IP_trans	Phosphatidylinositol transfer	6.5e-98	338,7
898	1000	protein	0.50	330.7
899	DEAD	DEAD/DEAH box helicase	1.5e-48	156.5
900	KE2	KE2 family protein	7e-61	215.7
901	zf-C2H2	KE2 family protein	4.3e-51	183.2
902	ras	Zinc finger, C2H2 type	2.7e-57	203.8
904	TPR	Ras family	2.3e-75	263.8
906	GBP	TPR Domain	3.2e-22	87.2
907	GBP	Guanylate-binding protein	8.9e-253	853.1
908	WD40	Guanylate-binding protein	1.1e-239	809.6
909	PH	WD domain, G-beta repeat PH domain	2.6e-26	100.8
10	2f-C2H2	Zinc finger, C2H2 type	1.3e-09	39.4
13	Epimerase	NAD dependent	2.5e-39	144.1
		epimerase/dehydratase family	5e-07	-88.5
21	TBC	TBC domain		
22	WD40	WD domain, G-beta repeat	1.5e-09	30.7
23	WD40	WD domain, G-beta repeat	1.6e-25	98.2
24	Hydrolase	haloacid dehalogenase-like	8.2e-07	36.1
~=		hydrolase	2.9e-05	29.1
25	UQ_con	Ubiquitin-conjugating enzyme	0.00033	22
26	CH	Calponin homology (CH) domain	3.3e~53	-27.6
28	WD40	WD domain, G-beta repeat	5.9e-48	190.2
29	zf-C3HC4	Zinc finger, C3HC4 type (RING	3.1e-10	172.7
30	-	finger)	~.∓E-T0	37.4
30	Ribul_P_3_ep	Ribulose-phosphate 3 epimerase	7.2e-105	361.8
31	im	family	7.22 203	361.8
31	Ribul_P_3_ep	Ribulose-phosphate 3 epimerase	1.2e-96	334.4
36	im C2	tamily		334.4
37		C2 domain	2.2e-62	220.7
	NAP_family	Nucleosome assembly protein	1.1e-22	84.6
10	abhydrolase	(NAP)	1	· -
4	Tropomyosin	alpha/beta hydrolase fold	0.011	3.1
8	pkinase	Tropomyosins	3.2e-07	25.1
. •	Putmase	Bukaryotic protein kinase	3.4e-75	263.2
9	WD40	domain	ľ	
0	Acyltransfer	WD domain, G-beta repeat Acyltransferase	1.8e-27	104.7
			1.6e-07	

SEQ ID	PFAM NAME	DESCRIPTION		
NO:			p-value	PFAM
951	SAM	SAM domain (Sterile alpha	0.014	14.5
954	GFO IDH MOCA	motif)		
955	BTB BTB	Oxidoreductase family BTB/POZ domain	1.3e-11	52.0
956	BTB	BTB/POZ domain	7e-22	86.1
957	CDP-	CDP-alcohol	0.053	-22.2
	OH_P_transf	phosphatidyltransferase	10.055	-24.2
959	ras	Ras family	2.4e-97	336.8
960	ras	Ras family	8.4e-43	155.6
961	Acetyltransf	Acetyltransferase (GNAT) family	1.2e-08	42.2
962 963	adh_short	short chain dehydrogenase	2.4e-31	117.6
969	IF-2B	Bacterial mutT protein	5.6e-06	26.2
, , ,	16-25	Initiation factor 2 subunit family	8.4e-193	653.9
970	RNase PH	3' exoribonuclease family	9e-24	92.4
975	WW	WW domain	5.7e-25	96.4
977	PDZ	PDZ domain (Also known as DHR	3.6e-21	83.7
		or GLGF).] 53.7
978	Ribosomal_L1	Ribosomal protein L17	2.4e-20	81.0
979	LIM	LTM domain and domain		
980	Calsequestri	LIM domain containing proteins Calsequestrin	5.8e-42	152.8
	n	Schroettii	1.7e-297	1001.7
982	HSP20	Hsp20/alpha crystallin family	1.2e-10	43.2
983	oxidored_q6	NADH ubiquinone oxidoreductase,	4.8e-63	222.9
		20 Kd sub		555.5
988	TBC	TBC domain	2.2e-50	180.8
989	TBC	TBC domain	2.2e-50	180.8
993	tRNA_int_end	tRNA intron endonuclease	0.0017	-34.2
994	homeobox	Homeobox domain		
997	pyr redox	Pyridine nucleotide-disulphide	4e-18	73.6
		oxidoreducta	0.012	11.8
1000	mito_carr	Mitochondrial carrier proteins	9.7e-123	421.2
1001	RA	Ras association (RalGDS/AF-6)	1.2e-15	65.4
1004	DUF81	domain		
1004	DUF81	Domain of unknown function	0.099	10.2
1005	actin	Actin		<u> </u>
1006	actin	Actin	1.3e~174 3.1e-130	574.3
1007	cpn60 TCP1	TCP-1/cpn60 chaperonin family	3.7e-130	428.6
1008	TPR	TPR Domain	8.1e-44	159.0
1009	zf-C2H2	Zinc finger, C2H2 type	3.6e-61	216.6
1011	zf-C2H2	Zinc finger, C2H2 type	3.6e-61	216.6
1012	zf-C3HC4	Zinc finger, C3HC4 type (RING	4.7e-15	53.1
1016	FDM -	finger)		
1018 1018	tRNA-synt_2c	tRNA synthetases class II (A)	2.3e-15	55.2
1022	RhoGAP PGAM	Rhogap domain	1.6e-78	274.3
1026	HMG box	Phosphoglycerate mutase family HMG (high mobility group) box	3.8e-18	69.7
1027	TBC	TBC domain	8.4e-20 7.3e-45	79.2
1028	UQ_con	Ubiquitin-conjugating enzyme	1.4e-49	162.5 178.1
1032	PDZ	PDZ domain (Also known as DHR	0.028	16.3
102:		or GLGF).		1
1034	Hydrolase	haloacid dehalogenasc-like	2e-21	84.6
1037	KRAB	hydrolase		
1037	Cation_efflu	KRAB box	4.8e-06	32.4
	x	Cation efflux family	7.1e-42	152.5
1040	ART	NAD:arginine ADP-	4 75 43	156.2
		ribosyltransferase	4.7e-47	169.1
1042	WD40	WD domain, G-beta repeat	1.9e-18	74.7
1043	zf-C2H2	Zinc finger, C2H2 type	3.7e-24	93.7
1045	lectin_c	Lectin C-type domain	1.9e-28	108.0
1046	Glucosamine_	Glucosamine-6-phosphate	0.00013	-25.1
	iso	isomerase	•	I

NO:	D PFAM NAME	DESCRIPTION	p-value	PFAM
1047			p varue	SCORE
1047	ligase-CoA	CoA-ligases	4.5e-80	279.4
1050	ig	Immunoglobulin domain	1.7e-09	35.6
1030	Ribosomal L2	Ribosomal protein L24e	2e-33	124.5
1054	Amidase			
1055	rrm	Amidase	4.3e-152	518.7
1058	annexin	RNA recognition motif.	3.8e-26	100.3
1059	PMP22_Claudi	Annexin	6 05 44	159.2
	n n	PMP-22/EMP/MP20/Claudin family	0.023	-23.6
1060	homeobox		ļ	
1062	Acyltransfer	Homeobox domain	3.2e-31	117.2
	ase	Acyltransferase	0.00065	10.5
1064	AMP-binding	AMP-binding enzyme		
1065	LRR	Leucine Rich Repeat	6.6e-100	345.3
1066	GTP1 OBG	GTP1/OBG family	3.3e-14	60.6
1071	ig	Transport	4.8e-41	141.8
1072	PHD	Immunoglobulin domain PHD-finger	8.4e-48	159.1
1074	DENN	DENN (AEX-3) domain	6.8e-07	36.3
1075	SCP	DENN (AEX-3) domain	8.3e-33	121.5
1077	OLF	SCP-like extracellular protein Olfactomedin-like domain	4.7e-41	149.8
1078	mito carr	Mitoghondy	2.2e-66	234.0
1079	WD40	Mitochondrial carrier proteins	le-42	149.3
1087	START	WD domain, G-beta repeat START domain	6.2e-45	162.7
1093	DSPc	Dual specificity phosphatase,	1.5e-48	174.7
		catalytic doma	3.3e-63	223.4
1094	GSHPx	Glutathione peroxidases		
1095	DUF25	Domain of unknown function	9.6e-41	148.8
		DUF25	2e-75	264.0
1096	.DUF25	Domain of unknown function	 	
		DUF25	6e-75	262.4
1105	Nitroreducta	Nitroreductase family	-	
	se	<u> </u>	1.3e-13	58.6
1106	PTE	Phosphotriesterase family	1 70 170	+
1107	DAGKC	Diacylglycerol kinase catalytic	1.3e-179 0.00049	610.1
		domain	0.00049	19.6
1109	ras	Ras family	1.3e-15	10.0
1115	ArfGap	Putative GTP-ase activating	9.7e-47	168.7
1116	111100	protein for Arf	3.70.47	100.7
1117	HMG14_17	HMG14 and HMG17	4.4e-21	83.5
1119	HMG14_17	HMG14 and HMG17	9.9e-12	52.4
1.1.1.5	FAA_hydrolas	Fumarylacetoacetate (FAA)	2e-83	290.6
1120	pkinase	hydrolase fam	1	1 230.0
	prinase	Eukaryotic protein kinase	1.4e-94	327.6
1123	abhydrolase	domain	{	
1129	pro_isomeras	alpha/beta hydrolase fold	9.2e-23	89.0
	e pro_isomeras	Cyclophilin type peptidyl- prolyl cis-tr	2.2e-56	197.1
131	DnaJ	Protyl Cis-tr		-
132	WD40	DnaJ domain	1.6e-30	114.9
.133	WD40	WD domain, G-beta repeat WD domain, G-beta repeat	1.3e-19	78.6
-		wu domain, G-beta repeat	1.8e-15	64.9
134	PH	DU domni-	1.86-12	04.9
.134 .136	PH Adap comp su	PH domain	0.0015	17.8
	Adap_comp_su	PH domain Adaptor complexes medium		
	Adap_comp_su b	PH domain Adaptor complexes medium subunit family	0.0015	17.8
136	Adap_comp_su	PH domain Adaptor complexes medium subunit family Adaptor complexes medium	0.0015	17.8
136	Adap_comp_su b Adap_comp_su	PH domain Adaptor complexes medium subunit family Adaptor complexes medium subunit family	0.0015 1.2e-256 2.5e-209	17.8 866.0
136 137	Adap_comp_su b Adap_comp_su b	PH domain Adaptor complexes medium subunit family Adaptor complexes medium subunit family Ras family	0.0015 1.2e-256 2.5e-209 1.5e-86	17.8 866.0 708.8
136 137 139	Adap_comp_su b Adap_comp_su b	PH domain Adaptor complexes medium subunit family Adaptor complexes medium subunit family Ras family Eukaryotic protein kinase	0.0015 1.2e-256 2.5e-209	17.8 866.0 708.8
136 137 139	Adap_comp_su b Adap_comp_su b ras pkinase	PH domain Adaptor complexes medium subunit family Adaptor complexes medium subunit family Ras family Eukaryotic protein kinase domain	0.0015 1.2e-256 2.5e-209 1.5e-86 9.4e-74	17.8 866.0 708.8
136 137 139 141	Adap_comp_su b Adap_comp_su b	PH domain Adaptor complexes medium subunit family Adaptor complexes medium subunit family Ras family Eukaryotic protein kinase	0.0015 1.2e-256 2.5e-209 1.5e-86	17.8 866.0 708.8
136 137 139 141	Adap comp su b Adap comp su b ras pkinase Acyltransfer	PH domain Adaptor complexes medium subunit family Adaptor complexes medium subunit family Ras family Eukaryotic protein kinase domain Acyltransferase	0.0015 1.2e-256 2.5e-209 1.5e-86 9.4e-74 1.2e-05	17.8 866.0 708.8 301.0 258.4
136 137 139 141	Adap_comp_su b Adap_comp_su b ras pkinase Acyltransfer ase	PH domain Adaptor complexes medium subunit family Adaptor complexes medium subunit family Ras family Eukaryotic protein kinase domain Acyltransferase PTB domain (IRS-1.type)	0.0015 1.2e-256 2.5e-209 1.5e-86 9.4e-74 1.2e-05 5.4e-55	17.8 866.0 708.8 301.0 258.4
136 137 139 141 152	Adap_comp_su b Adap_comp_su b ras pkinase Acyltransfer ase IRS	PH domain Adaptor complexes medium subunit family Adaptor complexes medium subunit family Ras family Eukaryotic protein kinase domain Acyltransferase PTB domain (IRS-1.type) Immunoglobulin domain	0.0015 1.2e-256 2.5e-209 1.5e-86 9.4e-74 1.2e-05 5.4e-55 1.3e-31	17.8 866.0 708.8 301.0 258.4
136 137 139 141 152 153	Adap_comp_su b Adap_comp_su b ras pkinase Acyltransfer ase IRS	PH domain Adaptor complexes medium subunit family Adaptor complexes medium subunit family Ras family Eukaryotic protein kinase domain Acyltransferase PTB domain (IRS-1.type)	0.0015 1.2e-256 2.5e-209 1.5e-86 9.4e-74 1.2e-05 5.4e-55	17.8 866.0 708.8 301.0 258.4 29.9
136 137 139 141 152 153	Adap_comp_su b Adap_comp_su b ras pkinase Acyltransfer ase IRS ig Asparaginase 2	PH domain Adaptor complexes medium subunit family Adaptor complexes medium subunit family Ras family Eukaryotic protein kinase domain Acyltransferase PTB domain (IRS-1.type) Immunoglobulin domain Asparaginase	0.0015 1.2e-256 2.5e-209 1.5e-86 9.4e-74 1.2e-05 5.4e-55 1.3e-31 6.4e-72	17.8 866.0 708.8 301.0 258.4 29.9 196.1 106.9 252.3
136 137 139 141 152 153 155 157	Adap_comp_su b Adap_comp_su b ras pkinase Acyltransfer ase IRS ig Asparaginase 2 GMC_oxred	PH domain Adaptor complexes medium subunit family Adaptor complexes medium subunit family Ras family Eukaryotic protein kinase domain Acyltransferase PTB domain (IRS-1.type) Immunoglobulin domain Asparaginase GMC oxidoreductases	0.0015 1.2e-256 2.5e-209 1.5e-86 9.4e-74 1.2e-05 5.4e-55 1.3e-31	17.8 866.0 708.8 301.0 258.4 29.9 196.1 106.9

SEO ID	PFAM NAME	DESCRIPTION		
NO:			p-value	PFAM SCORE
1163	linker_histo ne	linker histone H1 and H5 family	3.8e-14	60.4
1164	DED	Death effector domain	3.9e-05	30.5
1165	IRS	PTB domain (IRS-1 type)	2.6e-43	157.3
1166	IRS	PTB domain (IRS-1 type)	2.6e-43	157.3
1168	SAM	SAM domain (Sterile alpha motif)	0.04	10.5
1170	abhydrolase	alpha/beta hydrolase fold	0.098	-7.5
1174	SAP	SAP domain	3.9e-10	47.1
1177	PP2C	Protein phosphatase 2C	5.3e-31	112.5
1178	WD40	WD domain, G-beta repeat	4.7e-35	129.9
1180	Ets	Ets-domain	1.8e-09	33.3
1181	Collagen	Collagen triple helix repeat (20 copies)	0.00016	24.7
1182	TCL1_MTCP1	TCL1/MTCP1 family	9.5e-56	198.6
1184	RasGEF	RasGEF domain	1.7e-88	307.4
1185	mito_carr	Mitochondrial carrier proteins	1.5e-62	217.3
1187	UPAR_LY6	u-PAR/Ly-6 domain	0.0042	15.6
1188	Orn_DAP_Arg_ deC	Pyridoxal-dependent decarboxylase	6.2e-128	430.6
1193	Stathmin	Stathmin family	1.8e-90	314.0
1194	Stathmin	Stathmin family	1.8e-90	314.0
1195	Sec1	Sec1 family	3.2e-183	622.1
1196	pyr_redox	Pyridine nucleotide-disulphide oxidoreducta	3.1e-32	111.8
1197	Glyco_transf	Glycosyl transferase family 8	1.2e-09	45.5
1202	K_tetra	K+ channel tetramerisation domain	0.022	-16.8
1203	adh_short	short chain dehydrogenase	8.3e-45	162.3
1206	Ubie_methylt ran	ubiE/COQ5 methyltransferase family	1.3e-121	417.4
1208	7tm_3	7 transmembrane receptor	7.2e-09	29.0
1209	ank	Ank repeat	3.9e-15	63.7
1210	vATP- synt_AC39	ATP synthase (C/AC39) subunit	2.5e-128	439.7
1212	zf-C2H2	Zinc finger, C2H2 type	5.5e-17	69.9
1213	efhand	EF hand	3.2e-07	37.4
1219	rrm	RNA recognition motif.	2.1e-40	147.7
1220	DUF6	Integral membrane protein DUF6	0.015	21.5
1222	SCAN	SCAN domain	1.5e-71	251.1
1223	G-gamma	GGL domain	3.6e~36	129.5
1227	catalase	Catalase	0	1158.9
1232	PX PX	PX domain	2.2e-15	64.5
1236	FCH	PX domain	2.2e-15	64.5
1241	Peptidase_M2	Fes/CIP4 homology domain Peptidase family M20/M25/M40	3.3e-09 2e-63	44.0 224.1
1243	WW	WW done in		<u> </u>
1247	UPF0006	WW domain Metalloenzyme of unknown	0.044	17.9
		function UPF0006	6.3e-61	215.8
1248	Glycos_trans f_2	Glycosyl transferases	4.5e-10	46.9
1249	efhand	EF hand	4e-11	50.4
1254	UQ_con	Ubiquitin-conjugating enzyme	2.1e-73	257.3
1255	ras	Ras family	2.2e-62	220.7
1256	formyl_trans	Formyl transferase	4.9e-30	108.3
1259	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	5.3e-13	46.4
1261	DiHfolate_re	Dihydrofolate reductase	2.1e-69	241.7
1262	G_glu_transp ept	Gamma-glutamyltranspeptidase	1.8e-110	380.4
1263	PAS	PAS domain	1.3e-08	36.9
			~	1 1
1265	LRR	Leucine Rich Repeat	4.2e-22	86.9

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:	SCP			SCORE
1267		SCP-like extracellular protein	6e-29	108.0
	K_tetra	K+ channel tetramerisation domain	2.8e-27	104.0
1269	ras	Ras family	1.3e-85	297.9
1275	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	4.2e-10	37.0
1276	abhydrolase	alpha/beta hydrolase fold	5.4e-23	89.8
1277	abhydrolase	alpha/beta hydrolase fold	5.6e-21	83.1
1279	trypsin	Trypsin	4.4e-41	132.0
1280	PBP	Phosphatidylethanolamine- binding protein	1.3e-13	58.7
1285	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	5.6e-14	49.6
1287	ank	Ank repeat	1.7e-52	187.8
1294	fn3	Fibronectin type III domain	0.026	20.9
1295	GBP	Guanylate-binding protein	0.00026	-70.0
1296	PMP22_Claudi n	PMP-22/EMP/MP20/Claudin family	6.9e-41	149.3
1297	Rhodanese	Rhodanese-like domain	3.2e-14	60.7
1298	LIM	LIM domain containing proteins	5.8e-21	79.1
1301	rnaseA	Pancreatic ribonucleases	4.9e-43	145.2
1307	mito_carr	Mitochondrial carrier proteins	2.1e-53	186.0
1308	WD40	WD domain, G-beta repeat	1.6e-17	71.6
1310	UPAR_LY6	u-PAR/Ly-6 domain	7.1e-20	75.5
1313	thiored	Thioredoxin	3.6e-05	21.6
1314	Aa_trans	Transmembrane amino acid transporter protein	1.5e-67	237.9
1316	trypsin	Trypsin	4.4e-41	132.0
1320	Ribosomal_L1 3	Ribosomal protein L13	3.9e-62	219.8
1327	Armadillo_se	Armadillo/beta-catenin-like repeats	0.0054	23.4
1328	KRAB	KRAB box	0.052	-5.6
1329	rrm	RNA recognition motif.	2.1e-40	147.7
1330	Bcl-2	Apoptosis regulator proteins, Bcl-2 family	0.014	-1.6
1331	PX	PX domain	2.1e-10	48.0
1333	KRAB	KRAB box	1.8e-36	134.6
1334	UPP_syntheta	Putative undecaprenyl	2.3e-89	310.3
333	86	diphosphate synt		
1335	UPP_syntheta se	Putative undecaprenyl diphosphate synt	1.8e-59	211.0
1336	DSPC	Dual specificity phosphatase, catalytic doma	1.2e-31	118.6
1337	DSPc	Dual specificity phosphatase, catalytic doma	2.3e-12	54.5
1338	TPR	TPR Domain	0.00021	28.1
1340	metalthio	Metallothionein	0.013	20.3
1341	mutT	Bacterial mutT protein	5.8e-09	36.5
1343	Band 41	FERM domain (Band 4.1 family)	1.3e-38	122.5
1344	Kelch	Kelch motif	1.4e-44	161.5
1345	Antifreeze	Antifreeze protein	1.2e-10	48.8
1347	3Beta_HSD	3-beta hydroxysteroid dehydrogenase/isomera	0.086	-177.2
1348	BTB	BTB/POZ domain	5.3e-28	106.5
1349	DUF6	Integral membrane protein DUF6	0.033	15.8
1350	myosin_head	Myosin head (motor domain)	0	1088.7
1352	Nramp	Natural resistance-associated macrophage pro	1.2e-202	686.6
1353	S_100	S-100/ICaBP type calcium binding domain	5.3e-23	89.9
	1		i	
1355	DEAD		3.60-65	200 1
1356	DEAD C2	DEAD/DEAH box helicase C2 domain	3.6e-65 2.4e-15	209.0
1356 135 7	C2 RBD	DEAD/DEAH box helicase C2 domain	2.4e-15	64.4
1356	C2	DEAD/DEAH box helicase		1

SEO ID	PFAM NAME	DESCRIPTION		
NO:	TIPE MENTS	DESCRIPTION	p-value	PFAM
1362	SIS	SIS domain	3.8e-30	113.6
1363	SIS	SIS domain	1.3e-28	108.5
1364	ig	Immunoglobulin domain	0.00026	19.0
1368	K tetra	K+ channel tetramerisation	1.1e-16	68.9
	-	domain	1 - 1 - 10	1 88.9
1371	Collagen	Collagen triple helix repeat	2.2e-113	390.1
<u>L</u>		(20 copies)		330.1
1372	DnaJ	DnaJ domain	6.6e-36	132.7
1376	KRAB	KRAB box	2.1e-38	141.0
1378	ELM2	ELM2 domain	2e-23	91.3
1380	thiored	Thioredoxin	1.2e-23	82.8
1381	ank	Ank repeat	2.3e-83	290.4
1382	BTB	BTB/POZ domain	3e-11	50.8
1383	WD40	WD domain, G-beta repeat	1.6e-19	78.3
1384	WD40	WD domain, G-beta repeat	6.3e-24	92.9
1387	zf-C3HC4	Zinc finger, C3HC4 type (RING	1.1e-09	35.6
		finger)		1 33.13
1389	zf-C2H2	Zinc finger, C2H2 type	5.5e-50	179.5
1390	zf-C2H2	Zinc finger, C2H2 type	2.5e-85	296.9
1393	kinesin	Kincsin motor domain	7.8e-188	637.4
1394	zf-C2H2	Zinc finger, C2H2 type	1.2e-49	178.4
1398	KRAB	KRAB box	5.1e-22	86.6
1402	bZIP	bZIP transcription factor	0.035	13.1
1405	sugar_tr	Sugar (and other) transporter	0.003	-101.5
1406	RhoGAP	RhoGAP domain	8.9e-47	168.8
1407	rrm	RNA recognition motif.	le-35	132.1
1408	LRR	Leucine Rich Repeat	2.1e-13	58.0
1409	Nebulin_repe	Nebulin repeat	6e-54	192.6
1410	at			1
1412	.1	Ank repeat	1.6e-17	71.6
1415	Ribosomal_L5	ribosomal L5P family C-terminus	8.2e-58	205.5
1415	trypsin	/// // // // // // // // // // // // //		
1416	aminotran 1	Trypsin Aminotransferases class-I	4.7e-85	270.4
1417	S1	S1 RNA binding domain	4.4e-05	-91.2
1419	WD40	WD domain, G-beta repeat	1.6e-07	33.1
1422	cadherin	Cadherin domain	2.2e-09	44.6
1424	SH3	SH3 domain	8.3e-42	152.3
1425	PHD	PHD-finger	2.5e-80	280.3
1426	PHD	PHD-finger	3.2e-17	70.6
1427	ArfGap	Putative GTP-ase activating	3.2e-17 1e-37	70.6
	,p	protein for Arf	1e-37	138.8
1428	helicase C	Helicases conserved C-terminal	le-26	1.00 -
		domain	16-70	102.2
1429	WD40	WD domain, G-beta repeat	3.9e-07	37.2
1430	inositol P	Inositol monophosphatase family	2.5e-10	40.2
1431				
	mito_carr	Mitochondrial carrier proteins		
1433		Mitochondrial carrier proteins Clq domain	4.3e-83	287.7
1433 1434	mito_carr	Mitochondrial carrier proteins Clq domain WD domain, G-beta repeat	4.3e-83 2.9e-16	287.7 66.2
1433	mito_carr Clq	Mitochondrial carrier proteins Clq domain WD domain, G-beta repeat	4.3e-83 2.9e-16 1.6e-13	287.7 66.2 58.3
1433 1434 1435	mito_carr Clq WD40	Mitochondrial carrier proteins Clq domain	4.3e-83 2.9e-16	287.7 66.2
1433 1434 1435	mito_carr C1q WD40 Inos-1-	Mitochondrial carrier proteins Clq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif.	4.3e-83 2.9e-16 1.6e-13 7e-228	287.7 66.2 58.3 770.4
1433 1434 1435 1436 1438	mito_carr Clq WD40 Inos-1- P_synth rrm ig	Mitochondrial carrier proteins Clq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain	4.3e-83 2.9e-16 1.6e-13	287.7 66.2 58.3 770.4
1433 1434 1435 1436 1438 1440	mito_carr Clq WD40 Inos-1- P_synth rrm ig G_Adapt_CT	Mitochondrial carrier proteins Clq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus	4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12	287.7 66.2 58.3 770.4 128.3 45.6
1433 1434 1435 1436 1438 1440 1441	mito_carr Clq WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT	Mitochondrial carrier proteins Clq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif.	4.3e-83 2.9e-16 1.6e-13 7e-228	287.7 66.2 58.3 770.4 128.3 45.6 236.7
1433 1434 1435 1436 1438 1440 1441	mito_carr Clq WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT Kelch	Mitochondrial carrier proteins Clq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif	4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12 3.4e-67	287.7 66.2 58.3 770.4 128.3 45.6 236.7
1433 1434 1435 1436 1438 1440 1441 1443	mito_carr Clq WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT Kelch ARID	Mitochondrial carrier proteins Clq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif ARID DNA binding domain	4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12 3.4e-67	287.7 66.2 58.3 770.4 128.3 45.6 236.7 236.7
1433 1434 1435 1436 1438 1440 1441 1443 1446	mito_carr Clq WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT Kelch ARID zf-C2H2	Mitochondrial carrier proteins Clq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus	4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12 3.4e-67 0.00013	287.7 66.2 58.3 770.4 128.3 45.6 236.7 236.7 28.7
1433 1434 1435 1436 1438 1440 1441 1443 1446 1447	mito_carr Clq WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT Kelch ARID	Mitochondrial carrier proteins Clq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif ARID DNA binding domain Zinc finger, CZH2 type AMP-binding enzyme	4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12 3.4e-67 0.00013 1.8e-21 9.4e-28	287.7 66.2 58.3 770.4 128.3 45.6 236.7 236.7 28.7 84.7
1433 1434 1435 1436 1438 1440 1441 1443 1446 1447 1448	mito_carr Clq WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT Kelch ARID zf-C2H2	Mitochondrial carrier proteins Clq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif ARID DNA binding domain Zinc finger, CZHZ type AMP-binding enzyme RNA recognition motif.	4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12 3.4e-67 0.00013 1.8e-21 9.4e-28 2.6e-07	287.7 66.2 58.3 770.4 128.3 45.6 236.7 236.7 28.7 84.7 105.6
1433 1434 1435 1436 1438 1440 1441 1443 1446 1447 1448 1451	mito_carr Clq WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT Kelch ARID zf-C2H2 AMP-binding	Mitochondrial carrier proteins Clq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif ARID DNA binding domain Zinc finger, CZHZ type AMP-binding enzyme RNA recognition motif.	4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12 3.4e-67 0.00013 1.8e-21 9.4e-28 2.6e-07 6.5e-21	287.7 66.2 58.3 770.4 128.3 45.6 236.7 28.7 84.7 105.6 -145.1 82.9
1433 1434 1435 1436 1438 1440 1441 1443 1446 1447 1448 1451 1454	mito_carr Clq WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT Kelch ARID zf-C2H2 AMP-binding rrm	Mitochondrial carrier proteins Clq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif ARID DNA binding domain Zinc finger, CZH2 type AMP-binding enzyme	4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12 3.4e-67 0.00013 1.8e-21 9.4e-28 2.6e-07 6.5e-21 5.6e-44	287.7 66.2 58.3 770.4 128.3 45.6 236.7 236.7 28.7 84.7 105.6 -145.1 82.9
1433 1434 1435 1436 1438 1440 1441 1443 1446 1447 1448 1451 1454	mito_carr Clq WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT Kelch ARID zf-C2H2 AMP-binding rrm ig Sialyltransf Aldose_epim	Mitochondrial carrier proteins Clq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif ARID DNA binding domain Zinc finger, CZH2 type AMP-binding enzyme RNA recognition motif. Immunoglobulin domain Sialyltransferase family	4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12 3.4e-67 0.00013 1.8e-21 9.4e-28 2.6e-07 6.5e-21 5.6e-44 5.4e-21	287.7 66.2 58.3 770.4 128.3 45.6 236.7 236.7 28.7 84.7 105.6 -145.1 82.9 146.7 83.2
1433 1434 1435 1436 1438 1440 1441 1443 1446 1447 1448 1451 1454 1455	mito_carr Clq WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT Kelch ARID zf-C2H2 AMP-binding rrm ig Sialyltransf Aldose_epim C2	Mitochondrial carrier proteins Clq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif ARID DNA binding domain Zinc finger, CZH2 type AMP-binding enzyme RNA recognition motif. Immunoglobulin domain	4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12 3.4e-67 0.00013 1.8e-21 9.4e-28 2.6e-07 6.5e-21 5.6e-44	287.7 66.2 58.3 770.4 128.3 45.6 236.7 28.7 84.7 105.6 -145.1 82.9 146.7 83.2
1433 1434 1435 1436 1438 1440 1441 1443 1446 1447 1448 1451 1454	mito_carr Clq WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT Kelch ARID zf-C2H2 AMP-binding rrm ig Sialyltransf Aldose_epim	Mitochondrial carrier proteins Clq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif ARID DNA binding domain Zinc finger, CZH2 type AMP-binding enzyme RNA recognition motif. Immunoglobulin domain Sialyltransferase family Aldose 1-epimerase	4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12 3.4e-67 0.00013 1.8e-21 9.4e-28 2.6e-07 6.5e-21 5.6e-44 5.4e-21 1.9e-35	287.7 66.2 58.3 770.4 128.3 45.6 236.7 236.7 28.7 84.7 105.6 -145.1 82.9 146.7 83.2

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:	h 2		_	SCORE
1474	DENN			
1475		DENN (AEX-3) domain	1.3e-44	161.6
	Cation_efflu x	Cation efflux family	4.6e-49	176.4
1477	TBC	TBC domain	8e-47	169.0
1478	rrm	RNA recognition motif.	2e-21	84.6
1480	ig	Immunoglobulin domain	5.5e-06	24.3
1484	Telo_bind_al	Telomere-binding protein alpha	0.028	-225.9
<u></u>	pha	subuni	1 0.020	223.9
1485	zf-C2H2	Zinc finger, C2H2 type	1.8e-68	240.9
1486	pkinase	Eukaryotic protein kinase	9.5e-13	49.9
1488	helicase_C	Helicases conserved C-terminal domain	1.4e-15	65.2
1489	DUF89	Protein of unknown function DUF89	0.079	-132.4
1490	ECH	Enoyl-CoA hydratase/isomerase	5.2e-41	149.7
1491	guanylate cy	family		
1492	c LRR	Adenylate and Guanylate cyclase catalyt	1	166.1
1492	1	Leucine Rich Repeat	3.4e-19	77.2
	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	7.1e-10	36.3
1497	pkinase	Eukaryotic protein kinase domain	le-22	85.8
1500	SH3	SH3 domain	9.3e-05	27.2
1502	homeobox	Homeobox domain	0.084	13.8
1503	homeobox	Homeobox domain	0.084	13.8
1505	EGF	EGF-like domain	2.7e-23	90.8
1506	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	2.7e-21	84.2
1508	Peptidase_M2 0	Peptidase family M20/M25/M40	2.8e-28	101.8
1511	PX	PX domain	1.9e-11	51.5
1512	Sulfatase	Sulfatase	2.8e-35	130.7
1516	Syntaxin	Syntaxin	0.011	-62.3
1518	aminotran_3	Aminotransferases class-III pyridoxal-pho	9.7e-106	305.6
1520	ig	Immunoglobulin domain	0.075	11.0
1521	RA	Ras association (RalGDS/AF-6)	0.013	13.3
1523	RhoGAP	RhoGAP domain	2.5e-05	10 =
1528	WD40	WD domain, G-beta repeat	5.4e-24	18.7
1535	IMS	impB/mucB/samB family	7.8e-95	93.1
1538	FYVE	FYVE zinc finger	3.2e-27	328.5
1539	DAGKC	Diacylglycerol kinase catalytic domain	6e-07	101.5 36.5
1540	Ocular alb	Ocular albinism type 1 protein	0	1,7,7,4 ==
1653	SAP	SAP domain	6e-06	1184.7
1654	Amino_oxidas	Flavin containing amine oxidase	3.2e-43	33.2 157.0
1655	Amino_oxidas e	Flavin containing amine oxidase	3.2e-43	157.0
2000	RhoGEF	RhoGEF domain	1.4e-24	05
1656			4E-24	95.1
1656	MMR HSR1			
		GTPase of unknown function Ubiquitin carboxyl-terminal	0.0011 2.5e-11	-45.5 51.1
1657	MMR_HSR1 UCH-2	GTPase of unknown function Ubiquitin carboxyl-terminal hydrolase family	0.0011 2.5e-11	-45.5 51.1
1657 1659	MMR_HSR1 UCH-2 actin	GTPase of unknown function Ubiquitin carboxyl-terminal hydrolase family Actin	0.0011 2.5e-11 6.6e-21	-45.5 51.1 69.9
1657 1659	MMR_HSR1 UCH-2	GTPase of unknown function Ubiquitin carboxyl-terminal hydrolase family Actin BAH domain von Willebrand factor type A	0.0011 2.5e-11	-45.5 51.1
1657 1659 1660 1661 1662	MMR_HSR1 UCH-2 actin BAH vwa	GTPase of unknown function Ubiquitin carboxyl-terminal hydrolase family Actin BAH domain von Willebrand factor type A domain	0.0011 2.5e-11 6.6e-21 1.7e-82	-45.5 51.1 69.9 287.5
1657 1659 1660 1661 1662	MMR_HSR1 UCH-2 actin BAH vwa	GTPase of unknown function Ubiquitin carboxyl-terminal hydrolase family Actin BAH domain von Willebrand factor type A domain WD domain, G-beta repeat	0.0011 2.5e-11 6.6e-21 1.7e-82 0	-45.5 51.1 69.9 287.5
1657 1659 1660 1661 1662	MMR_HSR1 UCH-2 actin BAH vwa	GTPase of unknown function Ubiquitin carboxyl-terminal hydrolase family Actin BAH domain von Willebrand factor type A domain	0.0011 2.5e-11 6.6e-21 1.7e-82	-45.5 51.1 69.9 287.5 1909.4

SEQ ID No:	PFAM NAME	DESCRIPTION	p-value	PFAM
1672	chromo	'chromo' (CHRromatin	2.1e-18	SCORE 67.7
		Organization MOdifier)	2.16-10	67.7
1674	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H	0.0025	17.6
		type .	1	1
1676	Glyco_hydro_ 47	Glycosyl hydrolase family 47	1.8e-187	636.2
1677	Glyco_hydro_	Glycosyl hydrolase family 47	4.5e-74	259.5
1680	WD40	WD domain, G-beta repeat	1.1e-27	105.5
1681	WD40	WD domain, G-beta repeat	1.1e-27	105.5
1683	MMR HSR1	GTPase of unknown function	1.8e-78	274.1
1691	rrm	RNA recognition motif.	1.8e-37	137.9
1692	rrm	RNA recognition motif.	1.8e-37	137.9
1693	AAA	ATPases associated with various cellular act	1.3e-81	284.5
1697	Ferric_reduc	Ferric reductase like	8.4e-82	285.2
1698	Ferric_reduc	Ferric reductase like	3.5e-53	190.1
1600	t cour	transmembrane com	_l	
1699 1700	zf-C2H2	Zinc finger, C2H2 type	4.4e-34	126.6
1700	arf GTP EFTU	ADP-ribosylation factor family	9e-19	75.8
1702	SCAN SCAN	Elongation factor Tu family	0.014	11.4
1707	pkinase	SCAN domain	1.8e-54	194.4
	1	Eukaryotic protein kinase domain	1.2e-88	307.9
1709	WD40	WD domain, G-beta repeat	0.0035	24.0
1710	LRR	Leucine Rich Repeat	1.2e-30	115.3
1711	WW	WW domain	7.6e-12	52.8
1712	ank	Ank repeat	4.2e-34	126.7
	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	2.6e-09	38.3
1714	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	2.6e-09	38.3
1715	ras	Ras family	4.4e-41	149.9
1718	HMG_box	HMG (high mobility group) box	8.3e-21	82.6
1719	TBC	TBC domain	1.1e-45	165.2
1721	HLH	Helix-loop-helix DNA-binding domain	9.2e-10	45.9
1723	dsrm	Double-stranded RNA binding motif	2.9e-05	30.9
1724	RrnaAD	Ribosomal RNA adenine dimethylases	0.045	9.2
1725	CIDE-N	CIDE-N domain		1
1725	HAT	HAT (Half-A-TPR) repeats	5.9e-40 2.9e-44	145.2
1728	efhand	EF hand	5.1e-20	79.9
1733	Hist_deacety	Histone deacetylase family	1.7e-104	360.6
1735	LRR	Leucine Rich Repeat	4 60.31	126 6
1739	PI-PLC-X	Phosphatidylinositol-specific phospholipase	4.6e-34 0.0023	126.6
1743	ras	Ras family		
1744	ras	Ras family	3.7e-10	-21.3
1745	RasGEF	RasGEF domain	3.7e-10	-21.3
1746	adh short	short chain dehydrogenase	3.2e-49 7.1e-08	176.9
1751	zf-C2H2	Zinc finger, C2H2 type	9e-39	34.6
1754	fn3	Fibronectin type III domain	5.5e-101	348.9
1756	zf-C2H2	Zinc finger, C2H2 type	6.3e-93	322.1
1758	rrm	RNA recognition motif.	0.017	21.2
1760	Nop	Putative snoRNA binding domain	6.1e-95	328.8
1761	Nop	Putative snoRNA binding domain	6.1e-95	328.8
1765	MMR_HSR1	GTPase of unknown function	6.4e-41	149.4
1769	CN_hydrolase	Carbon-nitrogen hydrolase	3e-06	-43.9
1775	ank	Ank repeat	4.1e-07	37.1
				,
	Oxysterol_BP	Oxysterol-binding protein	4.7e-56	199.6
1779 1783 1784	RhoGEF RhoGEF	RhoGEF domain RhoGEF domain	4.7e-56 1.6e-23	199.6 91.6

SEQ ID PFAM NAME	DESCRIPTION	p-value	PFAM	1
1785 rrm	RNA recognition motif.	6.4e-14	SCORE 59.7	l

TRADOCS:1416227.1(%CRN01!.DOC)

WO 01/53312

TABLE 5

SEQ ID NO:	POSITION OF	MaxS (MAXIMUM	MeanS (MEAN
	SIGNAL IN AMINO ACID SEQUENCE	SCORE)	SCORE)
1	1-21	0.991	0.955
2	1-31	0.995	0.944
3	1-33	0.949	0.736
4	1-19	0.970	0.951
5	1-26	0.971	0.863
6	1-26	0.971	0.863
7	1-26	0.971	0.863
8	1-26	0.971	0.863
9	1-46	0.982	0.901
10	1-21	0.991	
11	1-23	0.989	0.955
12	1-25		0.899
13		0.955	0.803
14	1-18	0.932	0.625
	1-18	0.938	0.876
15	1-25	0.941	0.811
16	1-17	0.972	0.939
17	1-27	0.964	0.777
18	1-16	0.914	0.657
19	1-19	0.953	0.840
20	1-20	0.935	0.701
21	1-22	0.974	0.850
22	1-33	0.961	0.895
23	1-19	0.991	0.959
24	1-31	0.995	0.944
25	1-22	0.976	0.935
26	1-27	0.996	0.928
27	1-24	0.953	0.739
28	1-21	0.906	0.688
29	1-31	0.986	0.841
30	1-28	0.980	<u> </u>
31	1-19	0.993	0.893
32	1-22	0.998	0.976
35	1-33	0.949	0.909
36	1-33		0.736
46		0.949	0.736
67	1-19	0.570	0.951
71	1-25	0.968	0.848
	1-18	0.949	0.845
72	1-30	0.991	0.919
75	1-29	0.958	0.854
88	1-20	0.986	0.945
94	1-33	0.994	0.943
97	1-46	0.964	0.595
103	1-49	0.983	0.570
108	1-26	0.978	0.885
111	1-23	0.989	0.899
126	1-25	0.955	0.803
129	1-19	0.963	0.918
138	1-29	0.971	0.844
L43	1-18	0.914	
L48	1-20	0.969	0.628
.56	1-25		0.904
.58		0.941	0.811
.60	1-22	0.979	0.927
	1-17	0.972	0.939
61	1-48	0.903	0.571
.62	1-25	0.937	0.729
168	1-16	0.939	0.826
L71	1-27	0.964	0.777
78	1-21	0.945	0.825
.80	1-27	0.981	0.941
187	1-28	0.982	0.936
.90	1-19	0.953	0.840
.96	1-22	0.975	
	(1 0.3/3	0.916

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
199	1-20	0.935	
200	1-23	0.935	0.701
206	1-30	0.984	0.773
207	1-19	0.990	0.890
208	1-22	0.974	0.924
210	1-40	0.940	0.850
211	1-28	0.940	0.670
216	1-24	0.986	0.849
218	1-33	0.961	0.956
219	1-19	0.970	0.895
221	1-19	0.904	0.871
222	1-21	0.917	0.553
230	1-19	0.991	0.555
231	1-26	0.953	0.959
232	1-25	0.988	0.800
239	1-23	0.969	0.826
240	1-17	0.982	0.828
241	1-17		0.955
245	1-30	0.982	0.955
248	1-22		0.722
249	1-23	0.976	0.935
252	1-18	0.968	0.940
261	1-24	0.883	0.923
265	1-18		0.587
272	1-24	0.939	0.868
283	1-21	0.953	0.739
284	1-29	0.906	0.688
290	1-31	0.997	0.854
302	1-28	0.986	0.841
304	1-16	0.980	0.893
312	1-19	0.907	0.635
313	1-17	0.993	0.976
323	1-22	0.930	0.753
324	1-17	0.998	0.909
328	1-19	0.982	0.954
329	1-22	0.971	0.865
330	1-33	0.963	0.924
331	1-24	0.978	0.841
332	1-24	0.920	0.712
333	1-19	0.984	0.881
334	1-20	0.899	0.941
335	1-27	0.942	0.567
336	1-20	0.952	0.813
337	1-38	0.942	0.850
338	1-27	0.973	0.653
339	1-36	0.979	<u> </u>
340	1-27	0.888	0.804
343	1-19	0.971	0.597
344	1-22	0.994	0.865
345	1-17	0.966	0.928
346	1-19	0.936	0.687
347	1-22	0.963	0.822
349	1-24	0.982	0.924
351	1-21	0.918	0.966
352	1-31	0.918	0.815
354	1-31	0.988	0.912
355	1-29	0.974	0.839
356	1-15	0.932	0.632
357	1-33	0.935	0.969
360	1-27	<u>.l </u>	0.726
361	1-25	0.938	0.827
362	1-22		0.674
363	1-21	0.929	0.788
364	1-33	0.881	0.715
365	1-33	0.978	0.841
		0.978	0.841

SEQ ID NO:	POSITION OF	MaxS (MAXIMUM	MeanS (MEAN
}	SIGNAL IN AMINO	SCORE)	SCORE)
	ACID SEQUENCE		,
366	1-21	0.916	0.820
367	1-19	0.936	0.822
368	1-29	0.972	0.874
370	1-24	0.920	0.712
371	1-24	0.961	0.773
372	1-27	0.919	0.768
373	1-19	0.986	0.945
375	1-32	0.994	0.932
376	1-34	0.987	0.810
377	1-17	0.995	0.950
378	1-49	0.971	0.749
380	1-20	0.968	0.874
381	1-20	0.928	0.782
382	1-19	0.986	0.934
383	1-28	0.965	0.829
384	1-39	0.970	0.551
386	1-24	0.975	0.881
388	1-30	0.989	0.868
389	1-19	0.984	0.941
390	1-26	0.971	0.782
392	1-20	0.981	0.900
393	1-16	0.968	0.890
394	1-23	0.937	0.701
397	1-22	0.985	0.854
399	1-46	0.977	0.698
401	1-20	0.899	0.567
402	1-22	0.967	0.931
403	1-27	0.992	0.934
404	1-19	0.991	0.973
405	1-23	0.994	0.921
407	1-35	0.987	0.658
408	1-39	0.976	0.551
410	1-33	0.897	0.570
411	1-25	0.990	0.962
412	1-38	0.977	0.827
413	1-20	0.944	0.768
414	1-46	0.988	0.965
415	1-46	0.993	0.638
417	1-29	0.981	0.940
418	1-20	0.941	0.672
419	1-19	0.952	0.850
420	1-29	0.986	0.967
421	1-22	0.965	0.861
422	1-48	0.889	0.785
424	1-19	0.982	0.862
428	1-38		0.933
430	1-18	0.942	0.653
432	1-33	0.947	0.595
433	1-26	0.957	0.789
434	1-27	0.962	0.904
435	1-24	0.962	0.777
436	1-27		0.977
443	1-15	0.973	0.772
448	1-36	0.966	0.940
453	1-30	0.979	0.804
455	1-33	0.958	0.609
457	1-27		0.606
462	1-16	0.888	0.597
486	1-27	0.925	0.681
495	1-24	0.972	0.845
498	1-26	0.917	0.636
505	1-20	0.993	0.890
507	1-17	0.976	0.926
510	1-23	0.966	0.687
	1 2-3	0.930	0.593

SEQ ID NO:	POSITION OF	MaxS (MAXIMUM	MeanS (MEAN
	SIGNAL IN AMINO	SCORE)	SCORE)
	ACID SEQUENCE	,	1 2001127
511	1-23	0.930	0.593
512	1-23	0.020	0.593
S15	1-18	0.978	0.956
523	1-19	0.936	0.822
529	1-22	0.963	0.924
545	1-24	0.982	
550	1-30		0.966
552	1-21	0.933	0.713
554	1-23	0.973	0.912
571		0.969	0.784
574	1-21	0.918	0.815
	1-31	0.988	0.912
580	1-39	0.925	0.556
594	1-31	0.974	0.839
608	1-29	0.932	0.632
609	1-29	0.932	0.632
610	1-21	0.990	0.948
621	1-15	0.994	0.969
623	1-33	0.935	0.726
653	1-27	0.938	0.827
668	1-22	0.929	0.788
677	1-16	0.948	0.807
685	1-21	0.881	0.715
699	1-22	0.975	0.816
702	1-31	0.968	0.898
707	1-16	0.860	0.562
713	1-25	0.966	
718	1-19	0.936	0.743
719	1-20		0.822
729	1-29	0.961	0.824
735	1-46	0.972	0.874
746		0.903	0.598
747	1-14	0.916	0.730
	1-22	0.965	0.876
748	1-29	0.968	0.785
759	1-24	0.961	0.773
767	1-27	0.919	0.768
768	1-33	0.900	0.585
773	1-42	0.959	0.702
779	1-19	0.986	0.945
797	1-19	0.944	0.759
798	1-19	0.900	0.568
820	1-17	0.995	0.950
827	1-49	0.971	0.749
948	1-20	0.968	0.874
864	1-20	0.928	0.782
866	1-19	0.986	0.934
873	1-23	0.948	0.886
881	1-28	0.965	0.829
387	1-39	0.970	0.551
927	1-30	0.989	
934	1-48	0.989	0.868
939	1-39		0.777
944	1-26	0.994	0.889
950		0.971	0.782
963	1-29	0.957	0.845
	1-20	0.981	0.900
964	1-20	0.886	0.558
73	1-16	0.968	0.890
80	1-34	0.961	0.749
81	1-20	0.953	0.822
984	1-12	0.938	0.780
1015	1-22	0.985	0.854
1040	1-46	0.977	0.698
053	1-18	0.969	0.842
1052			
			
1059	1-20	0.927	0.867 0.918

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
1075	1-27	0.992	- 0.034
1080	1-19	0.931	0.934
1092	1-19	0.991	0.829
1094	2-46	0.992	0.973
1095	1-30	0.974	0.653
1105	1-23		0.929
1123		0.994	0.921
1138	1-35	0.987	0.658
1140	1-32	0.954	0.613
	1-39	0.989	0.789
1142	1-33	0.897	0.570
1152	1-25	0.990	0.962
1170	1-38	0.977	0.827
1176	1-20	0.944	0.768
1187	1-20	0.988	0.965
1189	1-35	0.967	0.839
1192	1-46	0.993	0.638
1193	1-16	0.925	
1197	1-29		0.710
1208	1-23	0.985	0.853
1225	1-23	0.981	0.940
1245	1-19	0.941	0.672
1258		0.986	0.967
1265	1-29	0.965	0.861
	1-22	0.889	0.785
1266	1-20	0.944	0.809
1276	1-48	0.982	0.862
1292	1-19	0.979	0.933
1296	1-21	0.984	0.944
1297	1-19	0.984	0.953
1332	1-38	0.942	0.653
1358	1-18	0.947	0.595
1371	1-33	0.957	
1380	1-26	0.979	0.789
1397	1-27		0.904
1399	1-23	0.962	0.777
1404	1-24	0.997	0.960
1410		0.998	0.977
1414	1-15	0.946	0.845
1415	1-24	0.913	0.588
1416	1-19	0.982	0.929
	1-12	0.931	0.891
1418	1-30	0.933	0.563
1420	1-20	0.881	0.561
1421	1-19	0.990	0.968
1423	1-17	0.968	0.863
1424	1-21	0.885	0.591
1425	1-24	0.913	0.588
1426	1-24	0.913	0.588
1428	1-25	0.967	
1430	1-34	0.977	0.899
1431	1-28	0.979	0.819
1432	1-36	J	0.923
1433	1-32	0.957	0.613
1434		0.921	0.753
1435	1-39	0.983	0.621
	1-25	0.910	0.631
1436	1-42	0.988	0.868
1437	1-22	0.998	0.980
1442	1-20	0.918	0.753
1448	1-12	0.931	0.891
1462	1-18	0.968	0.888
1490	1-20	0.881	
1518	1-17		0.561
1525	1-21	0.968	0.863
1547	1-21	0.885	0.591
1561		0.974	0.891
1580	1-25	0.967	0.899
	1-17	0.923	0.824
1593	1-28	0.979	0.923



SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
1596	1-16	0.929	0.709
1601	1-36	0.957	0.613
1606	1-22	0.979	0.831
1607	1-20	0.974	0.770
1608	1-32	0.921	0.753
1614	1-33	0.969	0.829
1616	1-20	0.959	0.869
1625	1-39	0.983	0.621
1632	1-25	0.910	0.631
1636	1-33	0.897	0.591
1639	1-42	0.988	0.868
1645	1-20	0.927	0.568
1647	1-17	0.923	0.742
1648	1-22	0.998	0.980

TRADOCS:1416234.1(%CR%01!.DOC)



TABLE 6

TABLE 6					
SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
of full-	NO: of	of contig	NO:	docket number	NO:in
length	full-	nucleotide	Of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide		sequence	priority	03/400,725
	sequence		acarcures.	1 -	
1	1787	3573	5359	application	
2	<u> </u>			784CIP2_1	1103
	1788	3574	5360	784CIP2_2	2673
3	1789	357,5	5361	784CIP2_3	4117
4	1790	3576	5362	784CIP2_4	5556
5	1791	3577	5363	784CIP2 5	5562
6	1792	3578	5364	784CIP2 6	5562
7	1793	3579	5365	784CIP2 7	5562
8	1794	3580	5366	784CIP2 8	5562
9	1795	3581	5367	784CIP2 9	
10	1796	3582	5368		5563
11	1797	.1	1	784CIP2_10	5564
	1	3583	5369	784CIP2_11	5565
12	1798	3584	5370	784CIP2_12	5689
13	1799	3585	5371	784CIP2_13	5729
14	1800	3586	5372	784CIP2 14	5745
15	1801	3587	5373	784CIP2 15	5777
16	1802	3588	5374	784CIP2 16	5777
17	1803	3589	5375	784CIP2 17	5789
18	1804	3590	5376	784CIP2 18	5792
19	1805	3591	5377	784CIP2_18	
20	1806	3592	5378		5804
21	1807		1	784CIP2_20	5805
22		3593	5379	784CIP2_21	5805
L	1808	3594	5380	784C1P2_22	5844
23	1809	3595	5381	784CIP2_23	5844
24	1810	3596	5382	784CIP2_24	5850
25	1811	3597	5383	784CIP2 25	5867
26	1812	3598	5384	784CIP2 26	5973
27	1813	3599	5385	784CIP2 27	5995
28	1814	3600	5386	784CIP2 28	5995
29	1815	3601	5387	784CIP2 29	6005
30	1815	3602	5388	784CIP2 30	
31	1817	3603	5389		6007
32	1818			784CIP2_31	6007
	L	3604	5390	784CIP2_32	6009
33	1819	3605	5391	784CIP2_33	6012
34	1820	3606	5392	784CIP2_34	6015
35	1821	3607	5393	784C1P2_35	6016
36	1822	3608	5394	784CIP2 36	6016
37	1823	3609	5395	784CIP2 37	6018
38	1824	3610	5396	784CIP2 38	6018
39	1825	3611	5397	784CIP2 39	6018
40	1826	3612	5398	784CIP2_39	6023
41	1827	3613	5399		
42	1828	3614	5400		6070
43	1829			784CIP2_42	6081
		3615	5401	784CIP2_43	6089
44	1830	3616	5402	784CIP2_44	6118
45	1831	3617	5403	784CIP2_45	6118
46	1832	3618	5404	784CIP2_46	6130
47	1833	3619	5405	784CIP2 47	6177
48	1834	3620	5406	784CIP2 48	6189
49	1835	3621	5407	784CIP2 49	6191
50	1836	3622	5408	784CIP2 50	
51	1837	3623			6204
52			5409	784CIP2_51 -	6204
	1838	3624	5410	784CIP2_52	6284
53	1839	3625	5411	784CIP2_53	6367
54	1840	3626	5412	784CIP2_54	6436
55	1841	3627	5413	784CIP2 55	6442
56	1842	3628	5414	784CIP2 56	6445
57	1843	3629	5415	784CIP2 57	6457
58	1844	3630	5416	784CIP2_57	6458
59	1845	3631	5417		
		3031	341/	784CIP2_59	6458

SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
of full-	NO: of	of contig	NO:	docket number	NO: in
length nucleotide	full-	nucleotide	of contig	corresponding	U.S.S.N.
	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide		sequence	priority	
	sequence			application	
60	1846	3632	5418	784CIP2 60	6462
61	1847	3633	5419	784CIP2 61	6472
62	1848	3634	5420	784CIP2 62	6499
63	1849	3635	5421	784CIP2 63	6499
64	1850	3636	5422	784CIP2 64	6505
65	1851	3637	5423	784CIP2 65	6534
66	1852	3638	5424	784CIP2 66	
67	1853	3639	5425	784CIP2 67	6534
68	1854	3640	5426	784CIP2_67 784CIP2_68	6540
69	1855	3641	5427		6550
70	1856	3642		784CIP2_69	6550
71	1857		5428	784CIP2_70	6592
72	1858	3643	5429	784CIP2_71	6645
73		3644	5430	784CIP2_72	6671
74	1859	3645	5431	784CIP2_73	6763
	1860	3646	5432	784CIP2 74	6763
75	1861	3647	5433	784CIP2 75	6786
76	1862	3648	5434	784CIP2 76	6824
77	1863	3649	5435	784CIP2 77	6830
78	1864	3650	5436	784CIP2 78	6831
79	1865	3651	5437	784CIP2 79	6832
80	1866	3652	5438	784CIP2 80	6834
. 81	1857	3653	5439	784CIP2 81	
82	1868	3654	5440		6834
83	1869	3655	5441	784CIP2_82 784CIP2_83	6835
84	1870	3656	5442		6837
85	1871	3657	5443	784CIP2_84	6843
86	1872	3658		784CIP2_85	6859
87	1873	3659	5444	784CIP2_86	6915
88	1874	3660	5445	784CIP2_87	6932
89	1875	3661	5446	784CIP2_88	6957
90	1876		5447	784CIP2_89	6961
91		3662	5448	784CIP2_90	6973
92	1877	3663	5449	784CIP2_91	6973
93	1878	3664	5450	784CIP2_93	7007
	. 1879	3665	5451	784CIP2_94	7018
94	1880	3666	5452	784CIP2 95	7019
95	1881	3667	5453	784CIP2 96	7020
96	1882	3668	5454	784CIP2 97	7020
97	1883	3669	5455	784CIP2 98	7021
98	1884	3670	5456	784CIP2 99	7023
99	1885	3671	5457	784CIP2 100	7027
100	1886	3672	5458	784CIP2 101	7028
101 .	1887	3673	5459	784CIP2 102	7028
102	1888	3674	5460	784CIP2 103	
103	1889	3675	5461	784CIP2 104	7031
104	1890	3676	5462		7032
105	1891	3677	5463	784CIP2_105	7033
106	1892	3678		784CIP2_106	7035
107	1893		5464	784CIP2_107	7036
108	1894	3679	5465	784CIP2_108	7039
109		3680	5466	784CIP2_109	7043
	1895	3681.	5467	784CIP2_110	7044
110	1896	3682	5468	784CIP2 111	7046
111	1897	3683	5469	784CIP2_112	7054
112	1898	3684	5470	784CIP2 113	7061
113	1899	3685	5471	784CIP2 114	7077
114	1900	3686	5472	784CIP2_115	7077
115	1901	3687	5473		
116	1902	3688		784CIP2_116	7094
117	1903	3689	5474	784CIP2_117	7106
118	1904		5475	784CIP2_118	7107
119		3690	5476	784CIP2_119	7111
120	1905	3691	5477	784CIP2_120	7123
	1906	3692 3693	5478	784CIP2_121	7142
121			5479	784CIP2 122	

SEO ID NO:

SEQ ID

SEQ ID NO:

SEQ ID

Y. .

ι. .

32

SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
of full-	NO: of	of contig	NO:	docket number	NO: in
length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide		sequence	priority	' ' ' ' '
	sequence			application	
184	1970	3756	5542	784CIP2_186	7641
185	1971	3757	5543	784CIP2_187	7642
186	1972	3758	5544	784CIP2_188	7649
187	1973	3759	5545	784CIP2_189	7656
188	1974	3760	5546	784CIP2_190	7657
189	1975	3761	5547	784CIP2_191	7657
190	1976	3762	5548	784CIP2_192	7662
191	1977	3763	5549	784CIP2_193	7668
192	1978	3764	5550	784CIP2 194	7673
193	1979	3765	5551	784CIP2_195	7690
194	1980	3766	5552	784CIP2 196	7700
195	1981	3767	5553	784CIP2 197	7709
196	1982	3768	5554	784CIP2 198	7736
197	1983	3769	5555	784CIP2 199	7737
198	1984	3770	5556	784CIP2 200	7744
199	1985	3771	5557	784CIP2 201	7771
200	1986	3772	5558	784CIP2 202	7786
201	1987	3773	5559	784CIP2 203	7791
202	1988	3774	5560	784CIP2 204	7797
203	1989	3775	5561	784CIP2 205	7806
204	1990	3776	5562	784CIP2 206	7812
205	1991	3777	5563	784CIP2 207	7812
206	1992	3778	5564	784CIP2 208	7818
207	1993	3779	5565	784CIP2 209	7822
208	1994	3780	5566	784CIP2 210	7827
209	1995	3781	5567	784CIP2 211	7830
210	1995	3782	5568	784CIP2 212	7835
211	1997	3783	5569	784CIP2 214	7840
212	1998	3784	5570	784CIP2 215	7858
213	1999	3785	5571	784CIP2 216	7858
214	2000	3786	5572	784CIP2 217	7861
215	2001	3787	5573	784CIP2 218	7866
216	2002	3788	5574	784CIP2 219	7868
217	2003	3789	5575	784CIP2 220	7896
218	2004	3790	5576	784CIP2 221	7898
219	2005	3791	5577	784CIP2 222	7900
220	2006	3792	5578	784CIP2 223	7906
221	2007	3793	5579	784CIP2 224	7908
222	2008	3794	5580	784CIP2_225	7909
223	2009	3795	5581	784CIP2_226	7917
224	2010	3796	5582	784CIP2_227	7932
225	2011	3797	5583	784CIP2_228	7940
226	2012	3798	5584	784CIP2_229	7940
227	2013	3799	5585	784CIP2_230	7984
228	2014	3800	5586	784CIP2_231	7984
229	2015	3801	5587	784CIP2_232	8001
230	2016	3802	5588	784CIP2_233	8021
231	2017	3803	5589	784CIP2_234	8029
232	2018	3804	5590	784CIP2_235	8033
233	2019	3805	5591	784CIP2_236	8040
234	2020	3806	5592	784CIP2_237	8052
235	2021	3807	5593	784CIP2_238	8096
236	2022	3808	5594	784CIP2_239	8096
237	2023	3809	5595	784CIP2_240	8113
238	2024	3810	5596	784CIP2_241	8126
239	2025	3811	5597	784CIP2_242	8132
240	2026	3812	5598	784CIP2 243	8137
241	2027	3813	5599	784CIP2 244	8137
	2028	3814	5600	784CIP2 245	8159
242					
243	2029	3815	5501	784CIP2 246	8159
		3815 3816	5501 5602	784CIP2_246 784CIP2_247	8159 8161

SEQ ID NO:	SEQ ID	1 CEO TO 110	· · · · · · · · · · · · · · · · · · ·		
of full-	NO: of	SEQ ID NO: of contig	SEQ ID	Priority	SEQ ID
length	full-	nucleotide	NO: of contig	docket number corresponding	NO:in
nucleotide	length	sequence	peptide	SEQ ID NO: in	U.S.S.N.
sequence	peptide	1011011	sequence	priority	09/488,725
	sequence			application	1
246	2032	3818	5604	784CIP2 249	8196
247	2033	3819	5605	784CIP2 250	8200
248	2034	3820	5606	784CIP2 251	8212
249	2035	3821	5607	784CIP2 252	8220
250	2036	3822	5608	784CIP2 253	8238
251	2037	3823	5609	784CTP2 254	8254
252	2038	3824	5610	784CIP2 255	8255
253	2039	3825	5611	784CIP2 256	8288
254	2040	3826	5612	784CIP2 257	8296
255	2041	3827	5613	784CIP2 258	8329
256	2042	3828	5614	784CIP2 259	8362
257	2043	3829	5615	784CIP2 260	8429
258	2044	3830	5616	784CIP2 261	8436
259	2045	3831	5617	784CIP2 262	8448
260	2046	3832	5618	784CIP2_263	8472
261	2047	3833	5619	784CIP2_264	8502
262	2048	3834	5620	784CIP2_265	8504
263	2049	3835	5621	784CIP2_266	8507
264	2050	3836	5622	784CIP2_268	8509
265	2051	3837	5623	784CIP2_269	8515
266	2052	3838	5624	784CIP2_270	8519
267	2053	3839	5625	784CIP2_271	8530
268	2054	3840	5626	784CIP2_272	8532
269 270	2055	3841	5627	784CIP2_273	8532
271	2056	3842	5628	784CIP2_274	8539
272	2057	3843	5629	784CIP2_275	8541
273	2058	3844	5630	784CIP2_276	8543
274	2059	3845	5631	784CIP2_277	8593
275	2060	3846	5632	784CIP2_278	8595
276	2062	3847 3848	5633	784CIP2_279	8615
277	2063	3849	5634	784CIPZ_280	8620
278	2064	3850	5635 5636	784CIP2_281	8621
279	2065	3851	5637	784CIP2_282	8623
280	2066	3852	5638	784CIP2 283	8625
281	2067	3853	5639	784CIP2_284	8628
282	2068	3854	5640	784CIP2_285 784CIP2_286	8628
283	2069	3855	5641	784CIP2_286 784CIP2_287	8629
284	2070	3856	5642	784CIP2_287	8630
285	2071	3857	5643	784CIP2_288 784CIP2_289	8631 8633
286	2072	3858	5644	784CIP2_289 784CIP2_290	8633 8634
287	2073	3859	5645	784CIP2_290 784CIP2_291	8634
288	2074	3860	5646	784CIP2_291 784CIP2_292	8636
289	2075	3861	5647	784CIP2_292	8659
290	2076	3862	5648	784CIP2 294	8660
291	2077	3863	5649	784CIP2 295	8667
292	2078	3864	5650	784CIP2 296	8667
293	2079	3865	5651	784CIP2 297	8685
294	2080	3866	5652	784CIP2 298	8805
295	2081	3867	5653	784CIP2 299	8896
296	2082	3868	5654	784CIP2_300	8978
297	2083	3869	5655	784CIP2 301	9046
298	2084	3870	5656	784CIP2 302	9048
299	2085	3871	5657	784CIP2 303	9116
300	2086	3872	5658	784CIP2 304	9195
301	2087	3873	5659	784CIP2 305	9201
302	2088	3874	5660	784CIP2 306	9307
303	2089	3875	5661	784CIP2 307	9321
304	2090	3876	5662	784CIP2 308	9397
305	2091	3877	5663	784CIP2 309	9405
306	2092	3878	5664	784CIP2 310	9406
307	2093	3879	5665	784CIP2 311	9422

of full-	SEQ ID NO: of	SEQ ID NO:	SEQ ID	Priority	SEQ ID
length	full-	of contig	No:	docket number_	NO:in
nucleotide	length	sequence	of contig	corresponding	U.S.S.N.
sequence	peptide	1	sequence	SEQ ID NO: in priority	09/488,72
	sequence		12420	application	
308	2094	3880	5666	784CIP2 312	9494
309	2095	3881	5667	784CIP2 313	9512
310	2096	3882	5668	784CIP2 314	9632
311	2097	3883	5669	784CIP2 315	9661
312	2098	3884	5670	784CIP2 316	9664
313	2099	3885	5671	784CIP2 317	9691
314	2100	3886	5672	784CIP2 318	9700
315	2101	3887	5673	784CIP2 319	9716
316	2102	3888	5674	784CIP2 320	9721
317	2103	3889	5675	784CIP2 321	9870
318	2104	3890	5676	784CIP2 322	9887
319	2105	3891	5677	784CIP2 323	9923
320	2106	3892 _.	5678	784CIP2_324	9938
321 322	2107	3893	5679	784CIP2 325	9964
323	2108	3894	5680	784CIP2_326	10007
323	2109	3895	5681	784CIP2_327	10009
325	2110	3896	5682	784CIP2_328	10046
326	2111	3897	5683	784CIP2_329	10156
327	2112	3898	5684	784CIP2_330	10276
328	2113 2114	3899	5685	784CIP2_331	10283
329	2114	3900	5686	784CIP2B_1	152
330	2115	3901	5687	784CIP2B_2	167
331	2117	3902	5688	784CIP2B_3	205
332	2118	3903	5689	784CIP2B_4	210
333	2119	3904	5690	784CIP2B_5	225
334	2120	3905 3906	5691	784CIP2B_6	226
335	2121	3905	5692	784CIP2B_7	264
336	2122	3908	5693	784CIP2B_8	268
337	2123	3909	5694 5695	784CIP2B_9	293
338	2124	3910	5695	784CIP2B_10	293
339	2125	3911	5697	784CIP2B_11	293
340	2126	3912	5698	784CIP2B_12	302
341	2127	3913	5699	784CIP2B_13 784CIP2B_14	311
342	2128	3914	5700		352
343	2129	3915	5701	784CIP2B_15 784CIP2B_16	358
344	2130	3916	5702	784CIP2B_17	36B 393
345	2131	3917	5703	784CIP2B 18	477
346	2132	3918	5704	784CIP2B 19	508
347	2133	3919	5705	784CIP2B_20	508
348	2134	3920	5706	784CIP2B 21	515
349	2135	3921	570 7	784CIP2B 22	578
350	2136	3922	5708	784CIP2B 23	588
351	2137	3923	5709	784CIP2B 24	591
352	2138	3924	5710	784CIP2B 25	593
353	2139	3925	5711	784CIP2B 26	594
354	2140	3926	5712	784CIP2B 27	619
355	2141	3927	5713	784CIP2B_28	620
356 357	2142	3928	5714	784CIP2B_29	654
	2143	3929	5715	784CIP2B 30	692
358 359	2144	3930	5716	784CIP2B_31	753
360	2145	3931	5717	784CIP2B_32	758
361	2146	3932	5718	784CIP2B_33	787
362	2147	3933	5719	784CIP2B_34	833
363	2148	3934	5720	784CIP2B_35	838
	2149	3935	5721	784CIP2B_36	870
364 365	2150	3936	5722	784CIP2B_37	891
366	2151	3937	5723	784CIP2B_38	891
367	2152	3938	5724	784CIP2B_39	921
368	2153	3939	5725	784CIP2B_40	924
369	2154	3940	5726	784CIP2B_41	932
	ا دریم	3941	5727	784CIP2B_42	942

SEO ID NO:	SEQ ID	SEO ID NO:	1 000 20	**************************************	
of full-	NO: of	of contig	SEQ ID	Priority	SEQ ID
length	full-	nucleotide	of contig	docket number_ corresponding	NO:in
nucleotide	length	sequence	peptide	SEQ ID NO: in	U.S.S.N.
sequence	peptide	3	sequence	priority	09/488,725
	sequence		1	application	i
370	2156	3942	5728	784CIP2B 43	958
371	2157	3943	5729	784CIP2B 44	968
372	2158	3944	5730	784CIP2B 45	992
373	2159	3945	5731	784CIP2B 46	1025
374	2160	3946	5732	784CIP2B 47	1074
375	2161	3947	5733	784CIP2B 48	1104
376	2162	3948	5734	784CIP2B 49	1114
377	2163	3949	5735	784CIP2B 50	1144
378	2164	3950	5736	784CIP2B 51	1262
379	2165	3951	5737	784CIP2B 52	1318
380	2166	3952	5738	784CIP2B 53	1319
381	2167	3953	5739	784CIP2B 54	1319
382	2168	3954	5740	784CIP2B 55	1436
383	2169	3955	5741	784CIP2B 56	1464
384	2170	3956	5742	784CIP2B 57	1584
385	2171	3957	5743	784CIP2B 58	1617
386	2172	3958	5744	784CIP2B 59	1724
387	2173	3959	5745	784CIP2B 60	1728
388	2174	3960	5746	784CIP2B_60	1772
389	2175	3961	5747	784CIP2B 62	1809
390	2176	3962	5748	784CIP2B_62	1868
391	2177	3963	5749	784CIP2B 64	1898
392	2178	3964	5750	784CIP2B 65	1926
393	2179	3965	5751	784CIP2B 66	1965
394	2180	3966	5752	784CIP2B 67	1965
395	2181	3967	5753	784CIP2B 68	1995
396	2182	3968	5754	784CIP2B 69	2005.
397	2183	3969	5755	784CIP2B 70	2003.
398	2184	3970	5756	784CIP2B_70	2027
399	2185	3971	. 5757	784CIP2B 72	2103
400	2186	3972	5758	784CIP2B 73	2106
401	2187	3973	5759	784CIP2B 74	2166
402	2188	3974	5760	784CIP2B 75	2175
403	2189	3975	5761	784CIP2B 76	2176
404	2190	3976	5762	784CIP2B 78	2236
405	2191	3977	5763	784CIP2B 79	2250
406	2192	3978	5764	784CIP2B 80	2300 .
407	2193	3979	5765	784CIP2B 81	2323
408	2194	3980	5766	784CIP2B 82	2340
409	2195	3981	5767	784CIP2B 83	2371
410	2196	3982	5768	784CIP2B 84	2399
411	2197	3983	5769	784CIP2B 85	2411
412	2198	3984	5770	784CIP2B_86	2428
413	2199	3985	5771	784CIP2B 87	2430
414	2200	3986	5772	784CIP2B 88	2439
415	2201	3987	5773	784CIP2B 89	2447
416	2202	3988	5774	784CIP2B 90	2461
417	2203	3989	5775	784CIP2B 91	2487
418	2204	3990	5776	784CIP2B 92	2492
419	2205	3991	5777	784CIP2B 93	2512
420	2206	3992	5778	784CIP2B 94	2564
421	2207	3993	5779	784CIP2B 95	2678
422	2208	3994	5780	784CIP2B 96	2816
423	2209	3995	5781	784CIP2B 97	2818
424	2210	3996	5782	784CIP2B 98	2819
425	2211	3997	5783	784CIP2B 99	2943
426	2212	3998	5784	784CIP2B 100	
427	2213	3999	5785	784CIP2B_100 784CIP2B_101	3137
428	2214	4000	5786		3137
429	2215	4001	5787	784CIP2B_102	3160
430	2216	4002	5788	784CIP2B 103	3323
431	2217	4003	5789	784CIP2B_104	3360
		1000	3,03	784CIP2B_105	3362

of full-	SEQ ID NO: of	SEQ ID NO: of contig	SEQ ID	Priority	SEQ ID
length	full-	nucleotide	of contig	docket number	
nucleotide	length	sequence	peptide		U.S.S.N.
sequence	peptide	,	sequence	SEQ ID NO: in priority	09/488,72
	sequence		-equence	application	ı
432	2218	4004	5790	784CIP2B 106	
433	2219	4005	5791		3417
434	2220	4006	5792	784CIP2B_107	3418
435	2221	4007	5793	784CIP2B_108	3442
436	2222	4008	5794	784CIP2B_109	3442
437	2223	4009		784CIP2B_110	3444
438	2224	4010	5795	784CIP2B_111	3855
439	2225	4011	5796	784CIP2B_112	3863
440	2226	4012	5797	784CIP2B_113	4090
441	2227	4012	5798	784CIP2B_114	4105
442	2228		5799	784CIP2B_115	4142
443	2229	4014	5800	784CIP2B_116	4142
444		4015	5801	784CIP2B_117	4149
445	2230	4016	5802	784CIP2B 118	4196
446	2231	4017	5803	784CIP2B 119	4202
	2232	4018	5804	784CIP2B 120	4274
447	2233	4019	5805	784CIP2B 121	4304
448	2234	4020	5806	784CIP2B 122	4306
449	2235	4021	5807	784CIP2B 123	4311
450	2236	4022	5808	784CIP2B 124	4321
451	2237	4023	5809	784CIP2B 125	4323
452	2238	4024	5810	784CIP2B 126	
453	2239	4025	5811	784CIP2B 127	4332
454	2240	4026	5812	784CIP2B 128	4488
455	2241	4027	5813	784CIP2B 129	4588
456	2242	4028	5814	784CIP2B_129	5569
457	2243	4029	5815	784CIP2B_130	5573
458	2244	4030	5816		5577
459	2245	4031	5817		5579
460	2246	4032	5818		5582
461	2247	4033	5819	784CIP2B_134	5583
462	2248	4034	5820	784CIP2B_135	5584
463	2249	4035	5821	784CIP2B_136	5585
464	2250	4036	5822	784CIP2B_137	5591
465	2251	4037	5823	784CIP2B_138	5593
466	2252	4038		784CIP2B_139	5594
467	2253	4039	5824	784CIP2B_140	5594
468	2254	4040	5825	784CIP2B_141	5598
469	2255	4041	5826	784CIP2B_142	5602
470	2256	4042	5827	784CIP2B_143	5605
471	2257		5828	784CIP2B_144	5608
472	2258	4043	5829	784CIP2B_145	5617
473	2259	4044	5830	784CIP2B_146	5620
474	2260	4045	5831	784CIP2B_147	5622
475		4046	5832	784CIP2B_148	5623
476	2261	4047	5833	784CIP2B 149	5624
	2262	4048	5834	784CIP2B_150	5625
477	2263	4049	5835	784CIP2B 151	5627
478	2264	4050	5836	784CIP2B 152	5628
479	· 2265	4051	5837	784CIP2B 153	5630
480	2266	4052	5838	784CIP2B 154	5632
481	2267	4053	5839	784CIP2B 155	5640
482	2268	4054	5840	784CIP2B 156	
483	2269	4055	5841	784CIP2B 157	5641
484	2270	4056	5842	784CIP2B 157	5643
485	2271	4057	5843		5647
486	2272	4058	5844	784CIP2B_159	5649
487	2273	4059		784CIP2B_160	5658
488	2274	4060	5845	784CIP2B_161	5659
489	2275		5846	784CIP2B_162	5667
490	2276	4061	5847	784CIP2B_163	5672
491	2277	4062	5848	784CIP2B_164	5674
492		4063	5849	784CIP2B 165	5678
493	2278	4064	5850	784CIP2B_166	5680
4 J J	2279	4065	5851	784CIP2B 167	5684

SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	T CEO TO
of full-	NO: of	of contig	NO:	docket number	SEQ ID NO:in
length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide		sequence	priority	1
	sequence			application	
494	2280	4066	5852	784CIP2B_168	5686
495	2281	4067	5853	784CIP2B_169	5694
496	2282	4068	5854	784CIP2B_170	5698
497	2283	4069	5855	784CIP2B_171	5699
498	2284	4070	5856	784CIP2B_172	5712
499	2285	4071	5857	784CIP2B_173	5719
500	2286	4072	5858	784CIP2B_174	5720
501	2287	4073	5859	784CIP2B_175	5727
502	2288	4074	5860	784CIP2B_176	5730
503	2289	4075	5861	784CIP2B_177	5734
504	2290	4076	5862	784CIP2B_178	5738
505	2291	4077	5863	784CIP2B_179	5739
506	2292	4078	5864	784CIP2B_180	5740
507	2293	4079	5865	784CIP2B_181	5744
508	2294	4080	5866	784CIP2B_182	5748
509	2295	4081	5867	784CIP2B_183	5749
510	2296	4082	5868	784CIP2B_184	5750
511	2297	4083	5869	784CIP2B_185	5750
512	2298	4084	5870	784CIP2B_186	5750
513 514	2299	4085	5871	784CIP2B_187	5761
514	2300	4086	5872	784CIP2B_188	5762
516	2301	4087	5873	784CIP2B_189	5767
517	2302 2303	4088	5874	784CIP2B_190	5773
518		4089	5875	784CIP2B_191	5783
519	2304	4090	5876	784CIP2B_192	5784
520	2306	4091 4092	5877	784CIP2B_193	5788
521	2307	4092	5878	784CIP2B_194	5798
522	2308	4094	5879 5880	784CIP2B_196	5807
523	2309	4095	5881	784CIP2B_197	5818
524	2310	4096	5881	784CIP2B_198 784CIP2B_199	5819
525	2311	4097	5883	784CIP2B_199	5827
526	2312	4098	5884	784CIP2B_200	5828
527	2313	4099	5885	784CIP2B 202	5842
528	2314	4100	5886	784CIP2B 202	5853 5861
529	2315	4101	5887	784CIP2B_203	5864
530	2316	4102	5888	784CIP2B 205	5865
531	2317	4103	5889	784CIP2B 206	5871
532	2318	4104	5890	784CIP2B 207	5873
533	2319	4105	5891	784CIP2B 208	5873
534	2320	4106	5892	784CIP2B 209	5875
535	2321	4107	5893	784CIP2B 210	5878
536	2322	4108	5894	784CIP2B 211	5879
537	2323	4109	5895	784CIP2B 212	5880
538	2324	4110	5896	784CIP2B 213	5880
539	2325	4111	5897	784CIP2B 214	5880
540	2326	4112	5898	784CIP2B 215	5880
541	2327	4113	5899	784CIP2B 216	5885
542	2328	4114	5900	784CIP2B 217	5895
543	2329	4115	5901	784CIP2B 218	5898
544	2330	4116	5902	784CIP2B 219	5902
545	2331	4117	5903	784CIP2B 220	5904
546	2332	4118	5904	784CIP2B 221	5918
547	2333	4119	5905	784CIP2B 222	5921
548	2334	4120	5906	784CIP2B 223	5927
549	2335	4121	5907	784CIP2B 224	5932
550	2336	4122	5908	784CIP2B 225	5939
551	2337	4123	5909	784CIP2B 226	5945
552	2338	4124	5910	784CIP2B 227	5946
553	2339	4125	5911	784CIP2B 228	5947
554	2340	4126	5912	784CIP2B 229	5956
555	2341	4127	5913	784CIP2B 230	5967
					JJ07

SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	
of full-	NO: of	of contig	NO:	docket number	SEQ ID
length	full-	nucleotide	of contig	corresponding	NO:in U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	
sequence	peptide	•	sequence	priority	09/488,725
	sequence	1	1	application	
556	2342	4128	5914	784CIP2B 232	5975
557	2343	4129	5915	784CIP2B 233	5977
558	2344	4130	5916	784CIP2B 234	
559	2345	4131	5917	784CIP2B_234	5978
560	2346	4132	5918	784CIP2B_235	5979
561	2347	4133	5919	784CIP2B_236	5980
562	2348	4134	5920	784CIP2B 237	5988
563	2349	4135	5921		5989
564	2350	4136	5922	784CIP2B_239	5991
565	2351	4137	5923	784CIP2B_240	5997
566	2352	4138		784CIF2B_241	5998
567	2353	4139	5924	784CIP2B_242	6003
568	2354		5925	784CIP2B_243	6004
569	2355	4140	5926	784CIP2B_244	6013
570	2356	4141	5927	784CIF2B_245	6028
571	2357	4142	5928	784CIP2B_246	6028
572	2358	4143	5929	784CIP2B_247	6029
573		4144	5930	784CIF2B_248	6031
574	2359	4145	5931	784CIP2B_249	6031
575	2360	4146	5932	784CIP2B_250	6032
	2361	4147	5933	784CIP2B 251	6037
576	2362	4148	5934	784CIP2B_252	6037
577	2363	4149	5935	784CIP2B_253	6043
578	2364	4150	5936	784CIP2B 254	6044
579	2365	4151	5937	784CIP2B_255	6046
580	2366	4152	5938	784CIP2B_256	6048
581	2367	4153	5939	784CIP2B_257	6049
582	2368	4154	5940	784CIP2B 258	6051
583	2369	4155	5941	784CIP2B 259	6053
584	2370	4156	5942	784CIP2B 260	6060
585	2371	4157	5943	784CIP2B 261	6063
586	2372	4158	5944	784CIP2B 262	6066
587	2373	4159	5945	784CIP2B 263	6067
588	2374	4160	5946	784CIP2B 264	5068
589	2375	4161	5947	784CIP2B 265	6073
590	2376	4162	5948	784CIP2B 266	6076
591	2377	4163	5949	784CIP2B 267	6076
592	2378	4164	5950	784CIP2B 268	6077
593	2379	4165	5951	784CIP2B 269	6079
594	2380	4166	5952	784CIP2B 270	6082
595	2381	4167	5953	784CIP2B 272	6088
596	2382	4168	5954	784CIP2B 273	6091
597	2383	4169	5955	784CIP2B 274	6094
598	2384	4170	5956	784CIP2B 275	6101
599	2385	4171	5957	784CIP2B_276	6103
600	2386	4172	5958	784CIP2B 277	6104
601	2387	4173	5959	784CIP2B 278	6108
602	2388	4174	5960	784CIP2B 279	6112
603	2389	4175	5961	784CIP2B 280	6121
604	2390	4176	5962	784CIP2B 281	6125
605	2391	4177	5963	784CIP2B 282	6126
606	2392	4178	5964	784CIP2B 283	6128
607	2393	4179	5965	784CIP2B 284	6129
608	2394	4180	5966	784CIP2B 285	6133
609	2395	4181	5967	784CIP2B 286	6133
610	2396	4182	5968	784CIP2B 287	6135
611	2397	4183	5969	784CIP2B 288	6139
612	2398	4184	5970	784CIP2B 289	6141
613	2399	4185	5971	784CIP2B 290	6145
614	2400	4186	5972	784CIP2B_290 784CIP2B 291	
615	2401	4187	5973	784CIP2B 291	6146
616	2402	4188	5974	784CIP2B 292	6148
617	2403 .	4189	5975	784CIP2B 293	6149
				,04C1F2B_294	6149

SEO ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
of full-	NO: of	of contig	NO:	docket number	NO:in
length .	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide		sequence	priority	', ', ', ', '
	sequence			application	
618	2404	4190	5976	784CIP2B_295	6153
619	2405	4191	5977	784CIP2B_296	6159
620	2406	4192	5978	784CIP2B 297	6164
621	2407	4193	5979	784CIP2B_298	6167
622	2408	4194	5980	784CIP2B_299	6172
623	2409	4195	5981	784CIP2B 300	6173
624	2410	4196	5982	784CIP2B 301	6190
625	2411	4197	5983	784CIP2B 302	6194
626	2412	4198	5984	784CIP2B 303	6196
627	2413	4199	5985	784CIP2B 304	6197
628	2414	4200	5986	784CIP2B 305	6198
629	2415	4201	5987	784CIP2B 306	6198
630	2416	4202	5988	784CIP2B 308	6214
631	2417	4203	5989	784CIP2B 309	6215
632	2418	4204	5990	784CIP2B 310	6219
633	2419	4205	5991	784CIP2B 311	6226
634	2420	4206	5992	784CIP2B 312	6229
635	2421	4207	5993	784CIP2B 313	6234
636	2422	4208	5994	784CIP2B 314	6237
637	2423	4209	5995	784CIP2B 315	6238
638	2424	4210	5996	784CIP2B 316	6239
639	2425	4211	5997	784CIP2B 317	6239
640	2426	4212	5998	784CIP2B 318	6239
641	2427	4213	5999	784CIP2B 319	6240
642	2428	4214	6000	784CIP2B 320	6244
643	2429	4215	6001	784CIP2B 321	6245
644	2430	4216	6002	784CIP2B 322	6250
645	2431	4217	6003	784CIP2B 323	6252
646	2432	4218	6004	784CIP2B 324	6252
647	2433	4219	6005	784CIP2B 325	6256
648	2434	4220	6006	784CIP2B 326	6260
649	2435	4221	6007	784CIP2B 327	6261
650	2436	4222	6008	784CIP2B 328	6264
651	2437	4223	6009	784CIP2B 329	6265
652	2438	4224	6010	784CIP2B 330	6266
653	2439	4225	6011	784CIP2B 331	6270
654	2440	4226	6012	784CIP2B 332	6271
655	2441	4227	6013	784CIP2B 334	6274
656	2442	4228	6014	784CIP2B 335	6276
657	2443	4229	6015	784CIP2B 336	6281
658	2444	4230	6016	784CIP2B 337	6281
659	2445	4231	6017	784CIP2B 338	628B
660	2446	4232	6018	784CIP2B 339	6292
661	2447	4233	6019	784CIP2B_340	6294
662	2448	4234	6020	784CIP2B 343	6312
663	2449	4235	6021	784CIP2B 344	6312
664	2450	4236	6022	784CIP2B 345	6312
665	2451	4237	6023	784CIP2B 346	6322
666	2452	4238	6024	784CIP2B 347	6324
667	2453	4239	6025	784CIP2B 349	6329
668	2454	1240	6026	784CIP2B 350	6331
669	2455	4241	6027	784CIP2B 351	6333
670	2456	4242	6028	784CIP2B 352	6334
671	2457	4243	6029	784CIP2B 353	6337
672	2458	4244	6030	784CIP2B 354	6339
673	2459	4245	6031	784CIP2B 355	6346
674	2460	4246	6032	784CIP2B 356	6348
675	2461	4247	6033	784CIP2B_356	6348
676	2462	4248	6034	784CIP2B 358	6350
677	2463	4249	6035	784CIP2B 359	
678	2464	4250	6036	784CIP2B 360	6351 6355
679	2465	4251	6037	784CIP2B 361	6362
				.01C1F2B_301	0302

SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
of full- length	NO: of	of contig	NO:	docket number	NOtin
nucleotide	full- length	nucleotide	Of conti	g corresponding	ี บ.ร.ร.ท
sequence	peptide	sequence	peptide	SEQ ID NO: in	09/488,725
4	sequence		sequence	priority	,
680	2466	4252		application	
681	2467	4253	603B	784CIP2B_362	6368
682	2468	4254	6039	784CIP2B_363	6369
683	2469	4255	6040	784CIP2B_364	6371
684	2470	4256	6041	784CIP2B_369	
685	2471	4257	6042	784CIP2B_366	40.5
686	2472	4258	6043	784CIP2B_367	6380
687	2473	4259	6044	784CIP2B_368	
688	2474	4260	6045	784CIP2B_369	1 0002
689	2475	4261	6046	784CIP2B_370	
690	2476	4261	6047	784CIP2B_371	6397
691	2477	4263	6048	784CIP2B_372	6400
692	2478	4264	6049	784CIP2B_373	6401
693	2479		6050	784CIP2B_374	6411
694	2480	4265 4266	6051	784CIP2B_375	6411
695	2481	4266	6052	784CIP2B_376	6411
696	2482	4268	6053	784CIP2B_377	6416
697	2483	4269	6054	784CIP2B_378	6418
698	2484	4270	6055	784CIP2B_379	. 6422
699	2485		6056	784CIP2B_380	6423
700	2486	4271 4272	6057	784CIP2B_381	6426
701	2487	4273	6058	784CIP2B_382	6427
702	2438	4274	6059	784CIP2B_383	6428
703	2489	4275	6060	784CIP2B_384	6429
704	2490	4276	6061 6062	784CIP2B_385	6430
705	2491	4277	6063	784CIP2B_386	6432
706	2492	4278	6064	784CIP2B_387	6432
707	2493	4279	6065	784CIP2B_388	6438
708	2494	4280	6066	784CIP2B_389	6441
709	2495	4281	6067	784CIP2B_390	6446
710	2496	4282	6068	784CIP2B_391 784CIP2B_392	6454
711	2497	4283	6069		6459
712	2498	4284	6070		6461
713	2499	4285	6071	784CIP2B_395 784CIP2B_396	6467
714	2500	4286	6072	784CIP2B 396	6468
715	2501	4287	6073	784CIP2B 398	6487
716	2502	4288	6074		6491
717	2503	4289	6075	784CIP2B_399 784CIP2B 401	6506
718	2504	4290	6076	784CIP2B 401	6514
719	2505	4291	6077	784CIP2B_403	6519
720	2506	4292	6078	784CIP2B 404	6521
721	2507	4293	6079	784CIP2B 405	6532 6536
722	2508	4294	6080	784CIP2B 406	
723	2509	4295	6081	784CIP2B 407	6543
724	2510	4296	6082	784CIP2B_408	6544
725	2511	4297	6083	784CIP2B 409	6548
726	2512	4298	6084	784CIP2B 410	6551
727	2513	4299	6085	784CIP2B 411	6551
728	2514	4300	6086	784CIP2B 412	6552
729	2515	4301	6087	784CIP2B_413	6554
730	2516	4302	6088	784CIP2B 414	6556
731	2517	4303	6089	784CIP2B_415	6560
732	2518	4304	6090	784CIP2B_415	6563
733	2519	4305	6091	784CIP2B 417	6564
734	2520	4306	6092	784CIP2B 418	6567
	2521	4307	6093	784CIP2B_418 784CIP2B_419	6573
735			6094	70401525 419	6575
736	2522	4308			
736 737	2522 2523	4308	·	784CIP2B 420	6577
736 737 738			6095	784CIP2B_421	6593
736 737 738 739	2523	4309	6095 6096	784CIP2B_421 784CIP2B_422	6593 6595
736 737 738 739 740	2523 2524	4309 4310	6095 6096 6097	784CIP2B 421 784CIP2B 422 784CIP2B 423	6593 6595 6599
736 737 738 739	2523 2524 2525	4309 4310 4311	6095 6096	784CIP2B_421 784CIP2B_422	6593 6595

SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID		
of full-	NO: of	of contig	NO:	Priority	SEQ ID
length	full-	nucleotide	of contig	docket number_ corresponding	
nucleotide	length	sequence	peptide	SEQ ID NO: in	U.S.S.N.
sequence	peptide	•	sequence	priority	09/488,72
	sequence		Jequence	application	
804	2590	4376	6162	784CIP2B 489	
805	2591	4377	6163	784C1P2B_489	6880
806	2592	4378		784CIP2B_490	6885
807	2593	4379	6164	784CIP2B_491	6890
808	2594	4380	6165	784CIP2B_492	6890
809	2595		6166	784CIP2B 493	6894
810	2596	4381	6167	784CIP2B_494	6901
811	2595	4382	6168	784CIP2B_495	6904
812		4383	6169	784CIP2B 496	6907
813	2598	4384	6170	784CIP2B 497	6914
	2599	4385	6171	784CIP2B 498	6917
814 ·	2600	4386	6172	784CIP2B 499	6923
815	2601	4387	6173	784CIP2B 500	6929
816	2602	4388	6174	784CIP2B 501	6931
817	2603	4389	6175	784CIP2B 502	6935
818	2604	4390	6176	784CIP2B 503	
819	2605	4391	6177	784CIP2B 504	6940
820	2606	4392	6178		6945
821	2607	4393	6179		6946
822	2608	4394	6180	784CIP2B_506	6947
823	2609	4395		784CIP2B_507	6949
824	2610	4396	6181	784CIP2B_508	6959
825	2611	4397	6182	784CIP2B_509	6960
826	2612	4398	6183	784CIP2B_510	6962
827	2613		6184	784CIP2B_511	6963
828	2614	4399	6185	784CIP2B_512	6967
829	2615	4400	6186	784CIP2B_513	6983
830		4401	6187	784CIP2B_514	6988
831	2616	4402	6198	784CIP2B_515	6996
832	2617	4403	6189	784CIP2B 516	7003
833	2618	4404	6190	784CIP2B 517	7016
834	2619	4405	6191	784CIP2B 518	7017
835	2620	4406	6192	784CIP2B 519	7025
836	2621	4407	6193	784CIP2B 520	7025
	2622	4408	6194	784CIP2B 521	7025
837	2623	4409	6195	784CIP2B 522	7050
838	2624	4410	6196	784CIP2B 523	7051
839	2625	4411	6197	784CIP2B 524	7055
840	2626	4412	6198	784CIP2B_525	
841	2627	4413	6199	784CIP2B 526	7060
842	2628	4414	6200	784CIP2B 527	7064
843	2629	4415	6201	784CIP2B 528	7067
844	2630	4416	6202		7071
845	2631	4417	6203		7072
846	2632	4418	6204	784CIP2B_530	7073
847	2633	4419		784CIP2B_531	7076
848	2634	4420	6205	784CIP2B_532	7088
849	2635	4421	6206	784CIP2B_533	7089
850	2636		6207	784CIP2B_534	7091
851	2637	4422	6208	784CIP2B_535	7091
852	2638	4423	6209	784CIP2B_536	7104
853		4424	6210	784CIP2B_537	7105
	2639	4425	6211	784CIP2B 538	7105
854	2640	4426	6212	784CIP2B_539	7109
855	2641	4427	6213	784CIP2B 540	7109
856	2642	4428	6214	784CIP2B 541	7119
857	2643	4429	6215	784CIP2B 542	
858	2644	4430	6216	784CIP2B 543	7120
859	2645	4431	6217		7121
860	2646	4432	6218	784CIP2B_544	7126
861	2647	4433		784CIP2B_545	7127
862	2648	4434	6219	784CIP2B_546	7130
863	2649		6220	784CIP2B_547	7131
864	2650	4435 4436	6221	784CIP2B_548	7144
			CO00		
865	2651	4437	6222 6223	784CIP2B 549 784CIP2B 550	7159

í	SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	Leno In
١	of full-	NO: of	of contig	NO:	docket number	SEQ ID No:in
ł	length	full-	nucleotide	of contig	corresponding	U.S.S.N.
1	nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
1	sequence	peptide	} -	sequence	priority	
1		sequence	Ì		application	Ì
ı	866	2652	4438	6224	784CIP2B 551	7175
ſ	867	2653	4439	6225	784CIP2B 552	7188
Í	868	2654	4440	6226	784CIP2B 553	7189
Ī	869	2655	4441	6227	784CIP2B_554	7190
ĺ	870	2656	4442	6228	784CIP2B_555	7191
Į	871	2657	4443	6229	784CIP2B_556	7203
I	872	2658	4444	6230	784CIP2B_557	7204
	873	2659	4445	6231	784CIP2B_558	7208
[874	· 2660	4446	6232	784CIP2B_559	7209
	875	2661	4447	6233	784CIP2B_560	7210
I	876	2662	4448	6234	784CIP2B_561	7216
l	877	2663	4449	6235	784CIP2B_562	7221
Į	878	2664	4450	6236	784CIP2B_563	7230
L	879	2665	4451	6237	784CIP2B_564	7237
	880	2666	4452	6238	784CIP2B_565	7240
L	881	2667	4453	6239	784CIP2B_566	7245
ļ	882	2668	4454	6240	784CIP2B_567	7250
1	883	2669	4455	6241	784CIP2B_568	7251
L	884	2670	4456	6242	784CIP2B_569	7255
Į.	885	2671	4457	6243	784CIP2B_570	7260
Į	886	2672	4458	6244	784CIP2B_571	7265
1	887	2673	4459	6245	784CIP2B_572	7268
ļ	888	2674	4460	6246	784CIP2B_573	7275
ŀ	889 890	2675	4461	6247	784CIP2B_574	7279
ŀ	891	2676	4462	6248	784CIP2B_575	7283
ŀ	892	2677 2678	4463	6249	784CIF2B_576	7283
ŀ	893	2679	4464 4465	6250	784CIP2B_577	7287
ł	894	2680	4466	6251 6252	784CIP2B_578	7301
ŀ	895	2681	4467	6253	784CIP2B_579 784CIP2B 580	7308
ŀ	896	2682	4468	6254	784CIP2B_580	7308 7309
ŀ	897	2683	4469	6255	784CIP2B_581 784CIP2B_582	7319
ŀ	898	2684	4470	6256	784CIP2B_582	7319
ŀ	899	2685	4471	6257	784CIP2B_583	7326
ŀ	900	2686	4472	6258	784CIP2B_584 784CIP2B_585	7326
f	901	2687	4473	6259	784CIP2B_586	7334
ŀ	902	2688	4474	6260	784CIP2B 587	7337
f	903	2689	4475	6261	784CIP2B 588	7339
t	904	2690	4476	6262	784CIP2B 589	7344
t	905	2691	4477	6263	784CIP2B 590	7355
r	906	2692	4478	6264	784CIP2B 591	7363
1	907	2693	4479	6265	784CIP2B 592	7363
r	908	.2694	4480	6266	784CIP2B 593	7365
r	909	2695	4481	6267	784CIP2B 594	7368
٢	910	2696	4482	6268	784CIP2B 595	7369
Ţ	911	2697	4483	6269	784CIP2B 596	7372
Γ	912	2698	4484	6270	784CIP2B 599	7375
r	913	2699	4485	6271	784CIP2B 600	7381
٢	914	2700	4486	6272	784CIP2B 601	7383
Γ	915	2701	4487	6273	784CIP2B 602	7387
Γ	916	2702	4488	6274	784CIP2B_603	7391
Γ	917	2703	4489	6275	784CIP2B_604	7393
Γ	918	2704	4490	6276	784CIP2B_605	7395
	919	2705	4491	6277	784CIP2B_606	7397
Γ	920	2706	4492	6278	784CIP2B_607	7399
Γ	921	2707	4493	6279	784CIP2B 608	7405
Γ	922	2708	4494	6280	784CIP2B 609	7406
٢	923	2709	4495	6281	784CIP2B 610	7406
ł	924	2710	4496	6282	784CIP2B_611	7409
r	724					
	925	2711	4497	6283	784CIP2B_612	7410
		2711 2712 2713	4497 4498	6283 6284	784CIP2B_612 784CIP2B_613	7410 7411

SEQ ID NO:	SEQ ID	SEQ ID NO:	T-0-1		
of full-	NO: of	of contig	SEQ ID	Priority	SEQ ID
length	full-	nucleotide	of contig	docket number	NO:in
nucleotide	length	sequence	peptide	SEQ ID NO: in	U.S.S.N.
sequence	peptide	1 1	sequence	priority	09/488,725
	sequence	1		application	
928	2714	4500	6286	784CIP2B_615	7418
929	2715	4501	6287	784CIP23 616	7421
930	2716	4502	6288	784CIP2B 617	7422
931	2717	4503	6289	784CIP23 618	7422
932	2718	4504	6290	784CIP2B 619	7423
933	2719	4505	6291	784CIP23 620	7424
934	2720	4506	6292	784CIP2B 621	7426
935	2721	4507	6293	784CIP29 622	7427
936	2722	4508	6294	784CIP2B 623	7428
937	2723	4509	6295	784CIP2B 624	7430
938	2724	4510	6296	784CIP2B 625	7435
939	2725	4511	6297	784CIP2B 626	7437
940	2726	4512	6298	784CIP2B 627	7439
941	2727	4513	6299	784CIP2B 628	7440
942	2728	4514	6300	784CIP23 629	7442
943	2729	4515	6301	784CIP2B 630	7450
944	2730	4516	6302	784CIP23 631	7451
945	2731	4517	6303	784CIP2B 632	7452
946	2732	4518	6304	784CIP23 633	7454
947	2733	4519	6305	784CIP2B 634	7457
948	2734	4520	6306	784CIP2B 635	7459
949	2735	4521	6307	784CIP2B 636	7461
950	2736	4522	6308	784CIP2B 637	7463
951	2737	4523	6309	784CIP2B 638	7466
952	2738	4524	6310	784CIP2B 639	7469
953	2739	4525	6311	784CIP2B 640	7473
954	2740	4526	6312	784CIP2B 641	7481
955	2741	4527	6313	784CIP2B 642	7482
956	2742	4528	6314	784CIP2B 643	7482
957	2743	4529	6315	784CIP2B_644	7483
958	2744	4530	6316	784CIP2B_645	7485
959	2745	4531	6317	784CIP2B_646	7486
960 961	2746	4532	6318	784CIP2B_647	7487
962	2747	4533	6319	784CIP2B_648	7491
962	2748	4534	6320	784CIP2B_649	7492
964	2749	4535	6321	784CIP2B_650	7494
965	2750	4536	6322	784CIP23_651	7498
966	2751 2752	4537	6323	784CIP2B_652	7504
967	2753	4538	6324	784CIP23_653	7508
968	2754	4539	6325	784CIP2B_654	7516
969	2755	4540	6326	784CIP2B_655	7518
970	2756	4541 4542	6327	784CIP2B_656	7519
971			6328	784CIP2B_657	7521
972	2757	4543 4544	6329	784CIP2B_658	7529
973	2759	4544	6330	784CIP2B_659	7532
974	2760		6331	784CIP2B_660	7533
975	2751	4546	6332	784CIP2B_661	7535
976	2762	4547	6333	784CIP2B_662	7545
977	2753	4548	6334	784CIP2B_663	7546
978	2764	4549	6335	784CIP2B_664	7552
979	2765	4550	6336	784CIP2B_665	7554
980	2766	4551	6337	784CIP2B_666	7567
981	2767	4552	6338	784CIP23_667	7569
982	2768	4553	6339	784CIP2B_668	7575
983		4554	6340	784CIP23_669	7576
984	2769	4555	6341	784CIP2B_670	7577
	2770	4556	6342	784CIP2B_671	7579
985	2771	4557	6343	784CIP23_672	7582
986	2772	4558	6344	784CIP2B_673	7587
987	2773 2774	4559	6345	784CIP2B_674	7589
		4664			
988 989	2775	4560 4561	6346	784CIP2B_675 784CIP2B_676	7597

SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	1 000
of full-	NO: of	of contig	NO:	docket number	SEQ ID
length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide		sequence	priority	100,100,100
	sequence		_	application	
990	2776	4562	6348	784CIP2B 677	7609
991	2777	4563	6349	784CIPZB 678	7609
992	2778	4564	6350	784CIP2B 679	7609
993	2779	4565	6351	784CIP2B 680	7613
994	2780	4566	6352	784CIP23 681	7623
995	2781	4567	6353	784CIP2B 682	7629
996	2782	4568	6354	784CIP2B 683	7630
997	2783	4569	6355	784CIP2B 684	7633
998	2784	4570	6356	784CIP2B 685	7635
999	2785	4571	6357	784CIP2B_686	7638
1000	2786	4572	6358	784CIP2B 687	7639
1001	2787	4573	6359	784CIP2B 688	7646
1002	2788	4574	6360	784CIP2B 689	7647
1003	2789	4575	6361	784CIP2B 690	7648
1004	2790	4576	6362	784CIP2B 691	7658
1005	2791	4577	6363	784CIP2B 692	7664
1006	2792	1578	6364	784CIP2B 693	7664
1007	2793	4579	6365	784CIP2B 695	7674
1008	2794	4580	6366	784CIP2B 696	7675
1009	2795	4581	6367	784CIP2B 697	7676
1010	2796	4582	6368	784CIP2B 698	7681
1011	2797	4583	6369	784CIP2B 699	7688
1012	2798	4584	6370	784CIP2B 700	7693
1013	2799	4585	6371	784CIP2B 701	7694
1014	2800	4586	6372	784CIP2B 702	7715
1015	2801	4587	6373	784CIP2B 703	7716
1016	2802	4588	6374	784CIP2B 704	7718
1017	2803	4589	6375	784CIP2B 705	7721
1018	2804	4590	6376	784CIP2B 706	7723
1019	2805	4591	6377	784CIP2B 707	7729
1020	2806	4592	6378	784CIP2B 708	7733
1021	2807	4593	6379	784CIP2B 709	7735
1022	2808	4594	6380	784CIP2B 710	7741
1023	2809	4595	6381	784CIP2B 711	7743
1024	2810	4596	6382	784CIP2B 712	7748
1025	2811	4597	6383	784CIP2B 713	7749
1026	2812	4598	6384	784CIP2B 714	7750
1027	2813	4599	6385	784CIP2B 715	7757
1028	2814	4600	6386	784CIP2B 716	7759
1029	2815	4601	6387	784CIP2B 717	7760
1030	2816	4602	6388	784CIP2B 718	7760
1031	2817	4603	6389	784CIP2B 719	7764
1032	2818	4604	6390	784CIP2B 720	7765
1033	2819	4605	6391	784CIP2B 721	7766
1034	2820	4606	6392	784CIP2B 722	7767
1035	2821	4607	6393	784CIP2B 723	7769
1036	2822	4608	6394	784CIP2B 724	7770
1037	2823	4609	6395	784CIP2B 725	7774
1038	2824	4610	6396	784CIP2B 726	7779
1039	2825	4611	6397	784CIP2B 727	7781
1040	2826	4612	6398	784CIP2B 728	7782
1041	2827	4613	6399	784CIP2B 729	7783
1042	2828	4614	6400	784CIP2B 730	7787
1043	2829	4615	6401	784CIP2B_731	7792
1044	2830	4616	6402	784CIP2B 732	7795
1045	2831	4617	6403	784CIP2B 733	7801
1046	2832	4618	6404	784CIP2B_733	7807
1047	2833	4619	6405	784CIP2B_734 784CIP2B_735	7808
1048	2834	4620	6406	784CIP2B_735	7819
1049	2835	4621	6407		
1050	2836	4622	6408	784CIP2B_737	7824
1051	2837	4623	6409	784CIP2B_738	7826
			0303	784CIP2B_739	7829

SEQ ID NO	SEQ ID	TOPO TO NO			
of full-	NO: OF	SEQ ID NO: of contig	1 ~	Priority	SEQ ID
length	full-	nucleotide	NO:	docket number	r_ NO:in
nucleotide	length	sequence			
sequence	peptide.	seductice	peptide	SEQ ID NO: in	09/488,725
_	sequence	1	sequence		
1052	2838	4624		application	
1053	2839		6410	784CIP2B_74	
1054	2840	4625	6411	784CIP2B_74	7839
1055	2841	4626	6412	784CIP2B 74:	
1056		4627	6413	784CIP2B 74	
1057	2842	4628	6414	784CIP2B 74	
1058	2843	4629	6415	784CIP2B 746	, , , ,
1059	2844	4630	6416	784CIP2B 74	, 05±
	2845	4631	6417	784CIP2B 748	
1060	2846	4632	6418	784CIP2B 749	,002
1061	2847	4633	6419	784CIP2B 750	
1062	2848	4634	6420		
1063	2849	4635	6421		,,,,
1064	2850	4636	6422		
1065	2851	4637	6423	784CIP2B 753	,002
1066	2852	4638		784CIP2B_754	
1067	2853	4639	6424	784CIP2B_755	
1068	2854	4640	6425	784CIP2B_756	, , , , ,
1069	2855	4641	6426	784CIP2B_757	7889
1070	2856	4641	6427	784CIP2B_758	7901
1071	2857		6428	784CIP2B 759	7910
1072	2858	4643	6429	784CIP2B 760	7911
1073	2859	4644	6430	784CIP2B 761	7921
1074		4645	6431	784CIP2B 762	7923
1075	2860	4646	6432	784CIP2B 763	7924
1076	2861	4647	6433	784CIP2B 764	7925
1077	2862	4648	6434	784CIP2B 765	7928
	2863	4649	6435	784CIP2B 766	7929
1078	2864	4650	6436	784CIP2B 767	
1079	2865	4651	6437	784CIP2B 768	7930
1080	2866	4652	6438	784CIP2B 769	7934
1081	2867	4653	6439		7938
1082	2868	4654	6440	784CIP2B_770 784CIP2B_771	7942
1083	2869	4655	6441		7945
1084	2870	4656	6442		7946
1085	2871	4657	6443	784CIP2B_773	7948
1086	2872	4658	6444	784CIP2B_774	7951
1087	2873	4659	6445	784CIP2B_775	7952
1088	2874	4660	6446	784CIP2B 776	7953
1089	2875	4661		784CIP2B_777	7954
1090	2876	4662	6447	784CIP2B_778	7957
1091	2877	4663	6448	784CIP2B_779	7958
1092	2878		6449	784CIP2B_780	7961
1093	2879	4664	6450	784CIP2B_781	7965
1094	2880	4655	6451	784CIP2B 782	7966
1095	2881	4666	6452	784CIP2B 783	7979
1096		4667	6453	784CIP2B 784	7986
1097	2882	4668	6454	784CIP2B_785	7986
1098	2883	4669	6455	784CIP2B 786	7988
	2884	4670	6456	784CIP2B 787	7991
1099	2885	4671	6457	784CIP2B 788	7991
1100	2886	4672	6458	784CIP2B 789	
1101	2887	4673	6459	784CIP2B 790	7992
1102	2888	4674	6450	784CIP2B 790	7992
1103	2889	4675	6461	704CIPZB /91	7992
1104	2890	4676	6462	784CIP2B_792	8003
1105	2891	4677	6463	784CIP2B_793	8014
1106	2892	4678		784CIP2B_794	8015
1107	2893	4679	6464	784CIP2B_795	8016
1108	2894		6465	784CIP2B_796	8017
1109	2895	4680	6466	784CIP2B_797	8019
1110	2896	4681	6467	784CIP2B_798	8020
1111		4682	6468	784CIP2B 799	8022
1112	2897	4683	6469	784CIP2B 800	8022
1113	2898	4684	6470	784CIP2B 801	8028
4113	2899	4685	6471	784CIP2B 802	8030
	_				0030

of full- length sequence seque	SEQ ID NO:	SEQ ID	I SEO ID NO:	I CDO TO		
Length Length peptide Sequence Length peptide Sequence Length peptide Sequence Length peptide Sequence Length peptide Sequence Length Sequence Length Sequence Length Sequence Length Sequence Length Sequence Length Sequence Length Sequence Length				SEQ ID	Priority	SEQ ID
mucleotide length sequence	length		_			1
Sequence Sequence	nucleotide	length		, -		
Sequence	sequence	peptide	1 -	1		03/400,725
1115			}] -		j
1115 2901 4687 6473 784CIPZB 804 8022 1116 2902 4688 6474 784CIPZB 805 8045 1117 2903 4689 6475 784CIPZB 806 8045 1118 2904 4690 6476 784CIPZB 806 8045 1119 2905 4691 6477 784CIPZB 806 8047 1120 2906 4692 6478 784CIPZB 807 8046 1119 2905 4691 6477 784CIPZB 807 1121 2907 4693 6479 784CIPZB 807 1121 2907 4693 6479 784CIPZB 809 8051 1122 2908 4694 6480 784CIPZB 809 1122 2909 4695 6481 784CIPZB 801 8059 1122 2909 4695 6481 784CIPZB 811 8064 1123 2909 4695 6481 784CIPZB 812 8069 1124 2910 4696 6482 784CIPZB 813 8069 1125 2911 4697 6483 784CIPZB 813 8077 1126 2912 4698 6484 784CIPZB 813 8077 1127 2913 4699 6485 784CIPZB 816 8079 1128 2914 4700 6486 784CIPZB 818 8078 1129 2915 4701 6487 784CIPZB 818 8078 1130 2916 4702 6488 784CIPZB 818 8088 1130 2916 4702 6488 784CIPZB 818 8088 1131 2917 4703 6489 784CIPZB 818 8088 1131 2917 4703 6489 784CIPZB 818 8088 1131 2919 4705 6491 784CIPZB 821 8099 1132 2918 4706 6492 784CIPZB 821 8099 1133 2919 4705 6491 784CIPZB 821 8099 1134 2920 4708 6492 784CIPZB 823 8100 1135 2921 4707 6493 784CIPZB 823 8100 1136 2922 4708 6494 784CIPZB 823 8100 1137 2923 4708 6494 784CIPZB 824 8102 1138 2921 4707 6493 784CIPZB 828 8103 1139 2928 4711 6497 784CIPZB 827 8104 1140 2927 4713 6499 784CIPZB 827 8104 1141 2927 4713 6499 784CIPZB 827 8104 1141 2929 4715 6500 784CIPZB 827 8104 1140 2929 4715 6500 784CIPZB 827 8104 1141 2929 4715 6500 784CIPZB 828 8103 1141 2929 4715 6500 784CIPZB 831 8117 1144 2930 4716 6500 784CIPZB 831 8117 1145 2931 4717 6503 784CIPZB 831 8117 1146 2932 4718 6500 784CIPZB 831 8117 1147 2933 4719 6500 784CIPZB 831 8117 1148 2934 4724 6510 784CIPZB 835 8143 1149 2935 4714 6500 784CIPZB 835 8143 1140 2925 4718 6500 784CIPZB 831 8117 1141 2937 4719 6500 784CIPZB 831 8117 1141 2937 4719 6500 784CIPZB 831 8117 1141 2930 4716 6500 784CIPZB 831 8117 1141 2930 4716 6500 784CIPZB 831 8117 1141 2930 4716 6500 784CIPZB 831 8117 1141 2930 4718 6500 784CIPZB 831 8119 1140 2940 4726 6512 784CIPZB 849 8188 1151 2931 4717 6503 784CIPZB 849 8188 1151 2931 4719 6500 784CIPZB 850 8199 1160 2940			4686	6472		8038
1117 7903 4689 6476 784C1P2B 806 8045 1118 3904 4690 6476 784C1P2B 806 8045 1119 2905 4691 6477 784C1P2B 807 8046 1120 2906 4692 6478 784C1P2B 809 8051 1121 2907 4693 6479 784C1P2B 809 8051 1122 2908 4694 6480 784C1P2B 810 8059 1123 2909 4695 6481 784C1P2B 812 8069 1124 2910 4696 6482 784C1P2B 812 8069 1125 2911 4697 6483 784C1P2B 813 8074 1126 2912 4698 6484 784C1P2B 814 8077 1127 2913 4699 6485 784C1P2B 814 8077 1128 2914 4700 6486 784C1P2B 815 6078 1129 2915 4701 6487 784C1P2B 818 8078 1129 2915 4701 6487 784C1P2B 818 8078 1130 2916 4702 6488 784C1P2B 818 8078 1131 2917 4703 6489 784C1P2B 818 8078 1131 2917 4703 6489 784C1P2B 818 8078 1131 2919 4704 6490 784C1P2B 818 8099 1131 2919 4706 6491 784C1P2B 818 8099 1131 2919 4706 6491 784C1P2B 821 8099 1131 2919 4706 6491 784C1P2B 821 8099 1131 2920 4706 6493 784C1P2B 823 8009 1131 2922 4708 6494 784C1P2B 823 8010 1131 2922 4708 6494 784C1P2B 828 8010 1131 2923 4708 6494 784C1P2B 828 8010 1131 2924 4710 6496 784C1P2B 828 8010 1131 2925 4711 6497 784C1P2B 828 8010 1131 2925 4711 6497 784C1P2B 828 8010 1140 2925 4711 6497 784C1P2B 828 8010 1141 2927 4713 6499 784C1P2B 83 8011 1141 2927 4713 6499 784C1P2B 83 8011 1141 2927 4713 6499 784C1P2B 83 8011 1141 2928 4714 6500 784C1P2B 83 8013 1146 2935 4712 6509 784C1P2B 83 8013 1147 2933 4716 6501 784C1P2B 83 8013 1146 2935 4712 6509 784C1P2B 83 8013 1147 2935 4726 6511 784C1P2B 83 8013 1146 2937 4728 6509 784C1P2B 83 8014 1147 2938 4726 6511 784C1P2B 849 8088 1159 2945 4736 6512			4687	6473	784CIP2B 804	<u> </u>
1117 2903 4689 6475 784CTP2B 806 8045 1118 2904 4690 6476 784CTP2B 807 8046 1119 2905 4691 6477 784CTP2B 808 8047 1120 2906 4692 6478 784CTP2B 808 8047 1121 2907 4693 6479 784CTP2B 808 8051 1121 2907 4693 6479 784CTP2B 810 8059 1122 2908 4694 6480 784CTP2B 811 8066 1124 2910 4696 6481 784CTP2B 812 8069 1124 2910 4696 6481 784CTP2B 813 8077 1126 2911 4697 6483 784CTP2B 813 8077 1126 2912 4698 6484 784CTP2B 813 8077 1127 2913 4699 6485 784CTP2B 814 8077 1128 2914 4700 6486 784CTP2B 814 8077 1129 2915 4701 6487 784CTP2B 816 8088 1130 2916 4702 6488 784CTP2B 816 8088 1131 3917 4703 6489 784CTP2B 818 8089 1132 2918 4704 6499 784CTP2B 818 8099 1133 2919 4705 6489 784CTP2B 82 8099 1134 3927 4706 6492 784CTP2B 82 8099 1135 2921 4706 6492 784CTP2B 82 8099 1136 2922 4706 6492 784CTP2B 82 8099 1137 2923 4706 6492 784CTP2B 82 8099 1138 2924 4707 6493 784CTP2B 82 8010 1136 2922 4708 6494 784CTP2B 82 8010 1137 2923 4708 6495 784CTP2B 82 8010 1138 2924 4710 6496 784CTP2B 82 8010 1140 2927 4713 6498 784CTP2B 82 8010 1141 2927 4713 6498 784CTP2B 82 8010 1140 2929 4718 6500 784CTP2B 82 8010 1141 2927 4713 6499 784CTP2B 82 8010 1140 2929 4718 6500 784CTP2B 82 8010 1141 2927 4713 6499 784CTP2B 82 8010 1140 2929 4718 6500 784CTP2B 83 8011 1141 2927 4713 6499 784CTP2B 82 8010 1141 2929 4718 6500 784CTP2B 83 8015 1149 2931 4717 6500 784CTP2B 83 8014 1140 2931 4717 6500 784CTP2B 83 8014 1141 2931 4717 6500 784CTP2B 84 8014 1148 29314 4720 6500 784CTP2B 84 8018 1149 29315 4722 6500 784CTP2B			4688	6474	784CIP2B 805	
1119		4	1	6475	784CIP2B 806	8045
1120				6476	784CIP2B 807	8046
1121			<u> </u>	6477	784CIP2B_808	8047
1122					784CIP2B_809	8051
1123			L	6479	784CIP2B_810	8059
1124				1	784CIP2B_811	8064
1125			<u>. </u>		 	8069
1126				I		8074
1127 2913 4699 6485 784CIP2B 816 8079 1128 2914 4700 6486 784CIP2B 817 8084 1129 2915 4701 6487 784CIP2B 817 8084 1130 2916 4702 6488 784CIP2B 819 8088 1131 2917 4703 6489 784CIP2B 819 8099 1131 2918 4704 6490 784CIP2B 822 8099 1132 2918 4704 6490 784CIP2B 822 8099 1133 2919 4705 6491 784CIP2B 822 8099 1134 2920 4706 6492 784CIP2B 822 8099 1135 2921 4707 6493 784CIP2B 823 8100 1136 2922 4708 6495 784CIP2B 823 8100 1137 2923 4709 6495 784CIP2B 825 8103 1138 2924 4710 6496 784CIP2B 826 8103 1139 2925 4711 6497 784CIP2B 828 8108 1140 2926 4712 6498 784CIP2B 829 8104 1140 2926 4712 6498 784CIP2B 829 8106 1141 2927 4713 6499 784CIP2B 829 8100 1141 2927 4713 6499 784CIP2B 830 8116 1142 2928 4714 6500 784CIP2B 831 8117 1143 2929 4715 5501 784CIP2B 831 8117 1144 2930 4716 6552 784CIP2B 831 8117 1147 2931 4717 6503 784CIP2B 833 8130 1146 2932 4718 6504 784CIP2B 838 8133 1147 2933 4719 6505 784CIP2B 838 8143 1147 2931 4717 6503 784CIP2B 838 8143 1149 2934 4720 6506 784CIP2B 838 8143 1149 2935 4721 6507 784CIP2B 838 8151 1150 2936 4722 6508 784CIP2B 838 8152 1151 2937 4723 6509 784CIP2B 838 8153 1152 2938 4724 6510 784CIP2B 838 8153 1159 2934 4725 6511 784CIP2B 838 8153 1159 2935 4721 6507 784CIP2B 838 8153 1159 2936 4725 6512 784CIP2B 849 8168 1159 2937 4723 6509 784CIP2B 849 8168 1159 2938 4725 6511 784CIP2B 849 8168 1159 2939 4725 6511 784CIP2B 849 8168 1159 2939 4725 6511 784CIP2B 849 8168 1159 2939 4725 6512 784CIP2B 849 8168 1159 2945 4730 6516 784CIP2B 849 8168 1160 2946 47				l		8077
1128						8078
1129	L					8079
1130 2916 4702 6488 784CIP2B 819 8090 1131 2917 4703 6489 784CIP2B 820 8091 1132 2918 4704 6490 784CIP2B 821 8099 1133 2919 4705 6491 784CIP2B 822 8099 1134 2920 4706 6491 784CIP2B 822 8099 1135 2921 4707 6493 784CIP2B 823 8100 1136 2922 4708 6494 784CIP2B 824 8102 1137 2923 4709 6495 784CIP2B 826 8103 1137 2923 4709 6495 784CIP2B 826 8103 1138 2924 4710 6496 784CIP2B 827 8103 1139 2925 4711 6497 784CIP2B 827 8104 1139 2926 4711 6497 784CIP2B 827 8104 1140 2926 4712 6498 784CIP2B 829 8108 1141 2927 4713 6499 784CIP2B 829 8110 1141 2928 4714 6550 784CIP2B 831 8117 1143 2929 4715 5501 784CIP2B 832 8123 1144 2930 4716 6552 784CIP2B 832 8130 1146 2931 4717 6503 784CIP2B 838 8130 1146 2931 4717 6503 784CIP2B 836 8143 1147 2933 4718 6504 784CIP2B 836 8143 1149 2935 4721 6507 784CIP2B 836 8143 1149 2935 4721 6507 784CIP2B 837 8154 1149 2935 4722 6508 784CIP2B 837 8154 1149 2935 4722 6508 784CIP2B 837 8154 1149 2936 4722 6508 784CIP2B 837 8154 1149 2937 4723 6509 784CIP2B 837 8154 1149 2936 4722 6508 784CIP2B 837 8154 1149 2937 4724 6510 784CIP2B 837 8154 1151 2937 4724 6510 784CIP2B 837 8154 1152 2938 4724 6510 784CIP2B 841 8172 1154 2940 4726 6512 784CIP2B 841 8172 1155 2936 4722 6508 784CIP2B 840 8163 1151 2937 4723 6509 784CIP2B 841 8172 1154 2940 4726 6512 784CIP2B 843 8179 1155 2944 4730 6516 784CIP2B 843 8179 1156 2942 4728 6511 784CIP2B 844 8182 1157 2943 4729 6515 784CIP2B 848 8187 1159 2944 4730 6516 784CIP2B 848 8187 1159 2945 4731 6517 784CIP2B 848 8187 1159 2945 4731 6517 784CIP2B 848 8187 1159 2945 4731 6517 784CIP2B 848 8187 1160 2546 4732 6518 784CIP2B 849 8188 1159 2945 4731 6517 784CIP2B 848 8187 1160 2546 4732 6518 784CIP2B 849 8188 1159 2945 4731 6517 784CIP2B 848 8187 1160 2546 4732 6518 784CIP2B 849 8188 1161 2947 4733 6519 784CIP2B 849 8188 1161 2957 4743 6520 784CIP2B 849 8188 1161 2957 4743 6520 784CIP2B 851 8199 1166 2955 4731 6527 784CIP2B 856 8199 1167 2953 4734 6520 784CIP2B 858 8199 1168 2959 4745 6528 784CIP2B 856 8199 1169 2955 4741 6527 784CIP2B 856 8199 1169 2955 4741 6527 784CIP2B 866				1		8084
1131						8088
1132 2918		1		<u> </u>		8090
1133 2919 4705 6491 784C1P2B 822 8099 1134 2920 4706 6492 784C1P2B 823 8100 1135 2921 4707 6493 784C1P2B 824 8102 1136 2922 4708 6494 784C1P2B 825 8103 1137 2923 4709 6495 784C1P2B 826 8103 1138 2924 4710 6496 784C1P2B 827 8104 1139 2925 4711 6497 784C1P2B 827 8104 1139 2925 4711 6497 784C1P2B 828 8108 1140 2926 4712 6498 784C1P2B 828 8108 1141 2927 4713 6499 784C1P2B 828 8118 1141 2927 4713 6499 784C1P2B 828 8118 1142 2928 4714 6500 784C1P2B 831 8117 1143 2929 4715 5501 784C1P2B 832 8123 1144 2930 4716 6502 784C1P2B 832 8123 1145 2931 4717 6503 784C1P2B 834 8130 1146 2932 4718 6504 784C1P2B 834 8130 1147 2933 4719 6506 784C1P2B 837 8154 1148 2934 4720 6506 784C1P2B 837 8154 1149 2935 4721 6507 784C1P2B 838 8143 1149 2935 4721 6507 784C1P2B 838 8159 1150 2936 4722 6508 784C1P2B 837 8154 1151 2937 4723 6509 784C1P2B 838 8155 1150 2936 4724 6510 784C1P2B 848 8163 1151 2937 4723 6509 784C1P2B 838 8155 1151 2937 4723 6509 784C1P2B 838 8155 1151 2937 4723 6509 784C1P2B 838 8155 1152 2938 4724 6510 784C1P2B 840 8163 1155 2938 4724 6510 784C1P2B 840 8163 1155 2941 4727 6513 784C1P2B 840 8163 1155 2941 4727 6513 784C1P2B 842 8173 1156 2942 4728 6514 784C1P2B 842 8173 1158 2940 4726 6512 784C1P2B 842 8173 1158 2944 4730 6516 784C1P2B 842 8173 1156 2942 4728 6514 784C1P2B 847 8182 1157 2943 4729 6515 784C1P2B 847 8183 1158 2944 4730 6516 784C1P2B 847 8183 1158 2944 4730 6517 784C1P2B 847 8183 1158 2944 4730 6517 784C1P2B 848 8183 1158 2944 4730 6517 784C1P2B 847 8185 1150 2948 4734 6520 784C1P2B 847 8185 1151 2957 4731 6517 784C1P2B 848 8189 1166 2952 4738 6512 784C1P2B 852 8199 1166 2954 4734 6520 784C1P2B 857 8199 1166 2954 4734 6527 784C1P2B 858 8199 1166 2954 4734 6527 784C1P2B 858 8199 1166 2954 4734 6527 784C1P2B 858 8199 1166 2955 4738 6527 784C1P2B 858 8199 1168 2959 4735 6521 784C1P2B 858 8199 1169 2955 4731 6527 784C1P2B 858 8199 1169 2955 4731 6527 784C1P2B 858 8199 1169 2957 4734 6529 784C1P2B 858 8199 1169 2958 4744 6530 784C1P2B 858 829 1170 2956 4744 6530 784C1P2B 858 829 1171 2957 4743 6529 784C1P2B 863 8				<u></u>		8091
1134					L	8099
1135 2921 4707 6493 784C1P2B 824 8100 1136 2922 4708 6494 784C1P2B 825 8103 1137 2923 4709 6495 784C1P2B 825 8103 1138 2924 4710 6496 784C1P2B 827 8104 1139 2925 4711 6497 784C1P2B 827 8104 1140 2926 4712 6498 784C1P2B 828 8108 1140 2926 4712 6498 784C1P2B 828 8106 1141 2927 4713 6499 784C1P2B 828 8106 1141 2927 4713 6499 784C1P2B 831 8117 1142 2928 4714 6500 784C1P2B 831 8117 1143 2929 4715 5501 784C1P2B 831 8117 1144 2930 4716 5502 784C1P2B 834 8130 1145 2931 4717 6503 784C1P2B 834 8130 1146 2932 4718 6504 784C1P2B 836 8143 1147 2933 4719 6505 784C1P2B 836 8143 1149 2934 4720 6506 784C1P2B 837 8154 1149 2935 4721 6507 784C1P2B 838 8153 1150 2936 4722 6508 784C1P2B 839 8162 1151 2937 4723 6509 784C1P2B 839 8162 1151 2938 4724 6510 784C1P2B 839 8162 1152 2938 4724 6510 784C1P2B 839 8162 1155 2938 4726 6501 784C1P2B 839 8162 1155 2940 4726 6512 784C1P2B 842 8173 1154 2940 4726 6512 784C1P2B 842 8173 1155 2941 4727 6513 784C1P2B 842 8173 1156 2942 4728 6514 784C1P2B 843 8189 1157 2943 4729 6515 784C1P2B 843 8179 1158 2944 4730 6516 784C1P2B 842 8173 1159 2945 4731 6517 784C1P2B 842 8173 1150 2954 4728 6514 784C1P2B 842 8173 1156 2942 4728 6514 784C1P2B 843 8189 1157 2943 4729 6515 784C1P2B 844 8182 1159 2945 4731 6517 784C1P2B 848 8187 1159 2945 4731 6517 784C1P2B 848 8187 1150 2946 4732 6518 784C1P2B 849 8185 1156 2947 4733 6519 784C1P2B 849 8189 1166 2946 4732 6518 784C1P2B 849 8189 1161 2947 4733 6519 784C1P2B 849 8189 1162 2948 4734 6520 784C1P2B 851 8199 1163 2949 4735 6521 784C1P2B 852 8199 1164 2950 4736 6522 784C1P2B 853 8199 1166 2952 4738 6522 784C1P2B 858 8199 1169 2955 4741 6527 784C1P2B 859 8203 1170 2956 4742 6528 784C1P2B 859 8203 1171 2957 4743 6529 784C1P2B 859 8203 1172 2958 4744 6530 784C1P2B 859 8203 1169 2955 4741 6527 784C1P2B 859 8203 1171 2957 4743 6527 784C1P2B 859 8203 1171 2957 4743 6527 784C1P2B 856 8199 1169 2955 4741 6527 784C1P2B 856 8199 1171 2957 4743 6531 784C1P2B 863 8217						
1136 2922 4708 6494 784CIP2B_825 8103 1137 2923 4709 6495 784CIP2B_826 8103 1138 2924 4710 6496 784CIP2B_827 8104 1139 2925 4711 6497 784CIP2B_828 8108 1140 2926 4712 6498 784CIP2B_828 8108 1141 2927 4713 6499 784CIP2B_828 8110 1141 2927 4713 6499 784CIP2B_828 8110 1142 2928 4714 6500 784CIP2B_831 8117 1143 2929 4715 5501 784CIP2B_831 8117 1144 2930 4716 6502 784CIP2B_831 8117 1144 2931 4717 6503 784CIP2B_833 8130 1145 2931 4717 6503 784CIP2B_835 8143 1146 2932 4718 6504 784CIP2B_835 8143 1147 2933 4719 6505 784CIP2B_836 8143 1148 2934 4720 6506 784CIP2B_836 8143 1149 2935 4721 6507 784CIP2B_838 8155 1150 2936 4722 6508 784CIP2B_838 8155 1151 2937 4723 6509 784CIP2B_838 8155 1151 2937 4723 6509 784CIP2B_838 8155 1151 2939 4725 6511 784CIP2B_838 8155 1155 2941 4727 6513 784CIP2B_840 8163 1154 2940 4726 6512 784CIP2B_840 8163 1155 2941 4727 6513 784CIP2B_841 8173 1155 2941 4727 6513 784CIP2B_841 8172 1155 2941 4727 6513 784CIP2B_843 8179 1155 2941 4727 6513 784CIP2B_843 8179 1155 2941 4727 6513 784CIP2B_848 8183 1159 2946 4732 6512 784CIP2B_848 8183 1159 2946 4731 6517 784CIP2B_848 8183 1159 2946 4731 6517 784CIP2B_848 8183 1159 2946 4732 6518 784CIP2B_848 8183 1159 2946 4738 6514 784CIP2B_848 8187 1160 2946 4732 6518 784CIP2B_848 8187 1160 2946 4732 6518 784CIP2B_848 8187 1160 2946 4732 6518 784CIP2B_848 8187 1161 2947 4739 6515 784CIP2B_848 8187 1162 2948 4734 6520 784CIP2B_848 8187 1163 2949 4735 6521 784CIP2B_848 8187 1160 2946 4732 6518 784CIP2B_855 8199 1164 2950 4736 6522 784CIP2B_855 8199 1165 2951 4737 6523 784CIP2B_855 8199 1166 2952 4738 6524 784CIP2B_855 8199 1166 2952 4738 6524 784CIP2B_855 8199 1168 2955 4741 6527 784CIP2B_856 8203 1170 2956 4742 6531 784CIP2B_856 8203 1171 2957 4743 6529 784CIP2B_856 8203 1171 2957 4744 6530 784CIP2B_856 8203 1171 2957 4744 6530 784CIP2B_856 8203 1171 2957 4746 6532 784CIP2B_856 8203 1171 2957 4746 6532 784CIP2B_856 8203						
1137 2923 4709 6495 784CIP2B 826 8103 1138 2924 4710 6496 784CIP2B 827 8104 1139 2925 4711 6497 784CIP2B 828 8108 1140 2926 4712 6498 784CIP2B 829 8110 1140 2926 4712 6498 784CIP2B 829 8110 1141 2927 4713 6499 784CIP2B 830 8116 1142 2928 4714 6500 784CIP2B 831 8117 1143 2929 4715 5501 784CIP2B 831 8117 1144 2930 4716 6502 784CIP2B 832 8130 1145 2931 4717 6503 784CIP2B 834 8130 1146 2932 4718 6504 784CIP2B 835 8143 1147 2933 4719 6505 784CIP2B 836 8143 1148 2934 4720 6506 784CIP2B 837 8154 1149 2935 4721 6507 784CIP2B 838 8155 1150 2936 4722 6508 784CIP2B 838 8155 1151 2937 4723 6509 784CIP2B 838 8155 1151 2937 4723 6509 784CIP2B 838 8153 1152 2938 4724 6510 784CIP2B 840 8163 1153 2939 4725 6511 784CIP2B 840 8163 1155 2941 4727 6553 784CIP2B 841 8172 1156 2940 4726 6512 784CIP2B 842 8173 1156 2941 4727 6553 784CIP2B 843 8179 1155 2941 4727 6553 784CIP2B 842 8173 1156 2942 4728 6514 784CIP2B 842 8173 1157 2943 4729 6515 784CIP2B 848 8182 1159 2945 4731 6517 784CIP2B 848 8182 1159 2945 4731 6517 784CIP2B 848 8183 1160 2946 4732 6518 784CIP2B 848 8187 1159 2945 4731 6517 784CIP2B 848 8187 1160 2946 4732 6518 784CIP2B 848 8187 1161 2947 4733 6519 784CIP2B 848 8187 1162 2948 4734 6520 784CIP2B 848 8187 1164 2950 4736 6522 784CIP2B 848 8187 1165 2945 4731 6517 784CIP2B 848 8187 1160 2946 4732 6518 784CIP2B 848 8187 1161 2947 4733 6517 784CIP2B 848 8187 1161 2947 4733 6517 784CIP2B 848 8187 1161 2948 4734 6520 784CIP2B 851 8190 1162 29548 4734 6520 784CIP2B 851 8190 1163 2949 4735 6521 784CIP2B 851 8190 1164 2950 4736 6522 784CIP2B 855 8197 1166 2952 4738 6524 784CIP2B 855 8197 1167 2953 4734 6529 784CIP2B 856 8197 1168 2954 4740 6526 784CIP2B 855 8197 1169 2955 4731 6521 784CIP2B 856 8203 1170 2956 4744 6530 784CIP2B 860 8209 1171 2957 4743 6529 784CIP2B 856 8203 1171 2957 4743 6529 784CIP2B 856 8203 1170 2956 4744 6530 784CIP2B 860 8209						
1138 2924 4710 6496 784CIPZB_827 8103 1139 2925 4711 6497 784CIPZB_828 8108 1140 2926 4712 6498 784CIPZB_828 8108 1141 2927 4713 6499 784CIPZB_830 8110 1141 2928 4714 6500 784CIPZB_831 8117 1143 2928 4714 6500 784CIPZB_831 8117 1144 2930 4716 6502 784CIPZB_833 8130 1144 2931 4717 6503 784CIPZB_833 8130 1146 2932 4718 6504 784CIPZB_835 8143 1147 2933 4719 6505 784CIPZB_835 8143 1147 2933 4719 6505 784CIPZB_836 8143 1149 2936 4720 6506 784CIPZB_838 8155 1150 2936 4722 6508 784CIPZB_838 8155 1150 2936 4722 6508 784CIPZB_839 8162 1151 2937 4723 6509 784CIPZB_839 8162 1152 2938 4724 6510 784CIPZB_839 8163 1155 2938 4724 6510 784CIPZB_838 8155 1155 2938 4724 6510 784CIPZB_839 8162 1155 2938 4724 6510 784CIPZB_839 8162 1155 2938 4724 6510 784CIPZB_840 8130 1155 2938 4724 6510 784CIPZB_840 8163 1155 2940 4726 6512 784CIPZB_840 8163 1155 2941 4727 6513 784CIPZB_841 8172 1158 2940 4726 6513 784CIPZB_844 8182 1157 2943 4729 6513 784CIPZB_848 8159 1156 2942 4728 6514 784CIPZB_848 8179 1158 2944 4730 6516 784CIPZB_848 8187 1159 2945 4731 6517 784CIPZB_848 8187 1160 2946 4732 6513 784CIPZB_848 8187 1161 2947 4733 6519 784CIPZB_848 8187 1160 2946 4732 6513 784CIPZB_848 8187 1161 2947 4733 6519 784CIPZB_848 8187 1160 2946 4734 6520 784CIPZB_848 8187 1161 2947 4733 6519 784CIPZB_848 8187 1160 2946 4734 6520 784CIPZB_848 8187 1161 2947 4733 6519 784CIPZB_848 8187 1161 2947 4733 6519 784CIPZB_848 8187 1162 2948 4734 6520 784CIPZB_848 8187 1163 2949 4735 6521 784CIPZB_855 8199 1164 2950 4736 6522 784CIPZB_856 8199 1165 2951 4737 6523 784CIPZB_858 8193 1166 2952 4738 6524 784CIPZB_856 8199 1169 2955 4741 6527 784CIPZB_856 8199 1169 2955 4741 6527 784CIPZB_856 8199 1169 2955 4741 6527 784CIPZB_856 8199 1169 2955 4741 6527 784CIPZB_858 8203 1170 2958 4744 6530 784CIPZB_856 8199 1169 2955 4731 6523 784CIPZB_856 8199 1169 2955 4741 6527 784CIPZB_856 8199 1169 2955 4741 6527 784CIPZB_856 8199 1169 2955 4741 6527 784CIPZB_856 8199 1169 2955 4744 6530 784CIPZB_856 8208 1171 2957 4743 6528 784CIPZB_866 8209						.1.
1139						
1140 2926 4712 6498 784CIP2B 829 8110 1141 2927 4713 6499 784CIP2B 830 8116 1142 2928 4714 6500 784CIP2B 831 8117 1143 2929 4715 6501 784CIP2B 832 8123 1144 2930 4716 6502 784CIP2B 833 8130 1145 2931 4717 6503 784CIP2B 834 8130 1146 2932 4718 6504 784CIP2B 835 8143 1147 2933 4719 6505 784CIP2B 836 8143 1148 2934 4720 6506 784CIP2B 836 8143 1149 2935 4721 6507 784CIP2B 838 8155 1150 2936 4722 6508 784CIP2B 839 8162 1151 2937 4723 6509 784CIP2B 839 8162 1151 2937 4723 6509 784CIP2B 839 8162 1152 2938 4724 6510 784CIP2B 840 8163 1154 2940 4726 6512 784CIP2B 841 8173 1155 2941 4727 6513 784CIP2B 842 8173 1156 2942 4728 6514 784CIP2B 843 8179 1157 2943 4730 6516 784CIP2B 848 8187 1159 2945 4731 6507 784CIP2B 848 8183 1157 2943 4729 6515 784CIP2B 848 8183 1157 2943 4730 6516 784CIP2B 848 8183 1158 2944 4730 6516 784CIP2B 848 8183 1159 2945 4731 6517 784CIP2B 848 8187 1160 2946 4732 6518 784CIP2B 849 8188 1161 2947 4733 6519 784CIP2B 848 8187 1161 2947 4733 6517 784CIP2B 848 8187 1160 2946 4732 6518 784CIP2B 849 8188 1161 2947 4733 6517 784CIP2B 848 8187 1160 2946 4732 6518 784CIP2B 849 8188 1161 2947 4733 6519 784CIP2B 849 8188 1161 2947 4733 6519 784CIP2B 849 8188 1161 2947 4733 6519 784CIP2B 849 8188 1161 2947 4733 6519 784CIP2B 849 8188 1161 2947 4733 6521 784CIP2B 849 8189 1162 2948 4734 6520 784CIP2B 851 8190 1163 2949 4735 6521 784CIP2B 851 8190 1164 2950 4736 6522 784CIP2B 851 8199 1165 2951 4737 6523 784CIP2B 854 8197 1166 2952 4738 6524 784CIP2B 858 8199 1167 2953 4741 6527 784CIP2B 858 8199 1168 2954 4740 6526 784CIP2B 858 8199 1169 2955 4741 6527 784CIP2B 858 8203 1170 2956 4742 6528 784CIP2B 858 8203 1171 2957 4743 6529 784CIP2B 860 8209 1172 2958 4744 6530 784CIP2B 860 8209 1173 2959 4745 6531 784CIP2B 860 8209 1174 2960 4746 6532 784CIP2B 860 8209				L		
1141						
1142	1141					
1143	1142					
1144	1143			<u> </u>		<u></u>
1145	1144	2930				
1146 2932 4718 6504 784CIP2B_835 8143 1147 2933 4719 6505 784CIP2B_836 8143 1148 2934 4720 6506 784CIP2B_837 8154 1149 2935 4721 6507 784CIP2B_838 8155 1150 2936 4722 6508 784CIP2B_839 8162 1151 2937 4723 6509 784CIP2B_840 8163 1152 2938 4724 6510 784CIP2B_841 8172 1153 2939 4725 6511 784CIP2B_842 8173 1154 2940 4726 6512 784CIP2B_843 8179 1155 2941 4727 6513 784CIP2B_843 8179 1156 2942 4728 6514 784CIP2B_845 8183 1157 2943 4729 6515 784CIP2B_846 8183 1157 2943 4731 6517 784CIP2B_847 <	1145	2931		L		
1147 2933 4719 6505 784CIP2B_836 8143 1148 2934 4720 6506 784CIP2B_837 8154 1149 2935 4721 6507 784CIP2B_838 8155 1150 2936 4722 6508 784CIP2B_839 8162 1151 2937 4723 6509 784CIP2B_840 8163 1152 2938 4724 6510 784CIP2B_842 8173 1153 2939 4725 6511 784CIP2B_842 8173 1154 2940 4726 6512 784CIP2B_842 8173 1155 2941 4727 6513 784CIP2B_843 8179 1155 2942 4728 6514 784CIP2B_844 8182 1157 2943 4729 6515 784CIP2B_846 8184 1158 2944 4730 6516 784CIP2B_847 8185 1159 2945 4731 6517 784CIP2B_849 <	1146	2932	4718			l
1148 2934 4720 6506 784CIP2B_837 8154 1149 2935 4721 6507 784CIP2B_838 8155 1150 2936 4722 6508 784CIP2B_839 8162 1151 2937 4723 6509 784CIP2B_840 8163 1152 2938 4724 6510 784CIP2B_841 8172 1153 2939 4725 6511 784CIP2B_843 8173 1154 2940 4726 6512 784CIP2B_843 8179 1155 2941 4727 6513 784CIP2B_844 8182 1156 2942 4728 6514 784CIP2B_845 8183 1157 2943 4729 6515 784CIP2B_846 8184 1158 2944 4730 6516 784CIP2B_847 8185 1159 2945 4731 6517 784CIP2B_848 8187 1160 2946 4732 6518 784CIP2B_848 <	1147	2933				
1149 2935 4721 6507 784CIP2B 838 8155 1150 2936 4722 6508 784CIP2B 839 8162 1151 2937 4723 6509 784CIP2B 840 8163 1152 2938 4724 6510 784CIP2B 841 8172 1153 2939 4725 6511 784CIP2B 842 8173 1154 2940 4726 6512 784CIP2B 844 8182 1155 2941 4727 6513 784CIP2B 844 8182 1156 2942 4728 6514 784CIP2B 845 8183 1157 2943 4729 6515 784CIP2B 846 8184 1158 2944 4730 6516 784CIP2B 847 8185 1159 2945 4731 6517 784CIP2B 848 8187 1160 2946 4732 6518 784CIP2B 849 8188 1161 2947 4733 6519 784CIP2B 850 <	1148	2934	4720			
1150		2935	4721	6507		
1151 2937 4723 6509 784CIP2B_840 8163 1152 2938 4724 6510 784CIP2B_841 8172 1153 2939 4725 6511 784CIP2B_842 8173 1154 2940 4726 6512 784CIP2B_843 8179 1155 2941 4727 6513 784CIP2B_844 8182 1156 2942 4728 6514 784CIP2B_845 8183 1157 2943 4729 6515 784CIP2B_846 8184 1158 2944 4730 6516 784CIP2B_847 8185 1159 2945 4731 6517 784CIP2B_848 8187 1160 2946 4732 6518 784CIP2B_849 8188 1161 2947 4733 6519 784CIP2B_849 8188 1161 2947 4733 6519 784CIP2B_851 8190 1162 2548 4734 6520 784CIP2B_851 <		2936	4722	6508		
1152 2938 4724 6510 784CIP2B_841 8172 1153 2939 4725 6511 784CIP2B_842 8173 1154 2940 4726 6512 784CIP2B_843 8179 1155 2941 4727 6513 784CIP2B_844 8182 1156 2942 4728 6514 784CIP2B_845 8183 1157 2943 4729 6515 784CIP2B_846 8184 1158 2944 4730 6516 784CIP2B_847 8185 1159 2945 4731 6517 784CIP2B_848 8187 1160 2946 4732 6518 784CIP2B_849 8188 1161 2947 4733 6519 784CIP2B_850 8190 1162 2948 4734 6520 784CIP2B_851 8190 1163 2949 4735 6521 784CIP2B_852 8192 1164 2950 4736 6522 784CIP2B_853 <		. 2937	4723	6509		
1154 2940 4726 6512 784CIP2B 842 8173 1155 2941 4727 6513 784CIP2B 844 8182 1156 2942 4728 6514 784CIP2B 845 8163 1157 2943 4729 6515 784CIP2B 846 8164 1158 2944 4730 6516 784CIP2B 847 8185 1159 2945 4731 6517 784CIP2B 848 8187 1160 2946 4732 6518 784CIP2B 849 8188 1161 2947 4733 6519 784CIP2B 849 8188 1161 2947 4733 6519 784CIP2B 850 8190 1162 2948 4734 6520 784CIP2B 851 8190 1163 2949 4735 6521 784CIP2B 852 8192 1164 2950 4736 6522 784CIP2B 853 8193 1165 2951 4737 6523 784CIP2B 854 8197 1166 2952 4738 6524 784CIP2B 855 8197 1167 2953 4739 6525 784CIP2B 856 8199 1168 2954 4740 6526 784CIP2B 856 8199 1169 2955 4741 6527 784CIP2B 858 8203 1170 2956 4742 6528 784CIP2B 859 8208 1171 2957 4743 6529 784CIP2B 859 8208 1172 2958 4744 6530 784CIP2B 856 8209 1173 2959 4745 6531 784CIP2B 866 8211 1174 2960 4746 6532 784CIP2B 866 8211			4724	6510		
1155 2941 4727 6513 784CIP2B 844 8179 1156 2942 4728 6514 784CIP2B 845 8183 1157 2943 4729 6515 784CIP2B 846 8184 1158 2944 4730 6516 784CIP2B 847 8185 1159 2945 4731 6517 784CIP2B 848 8187 1160 2946 4732 6518 784CIP2B 849 8188 1161 2947 4733 6519 784CIP2B 850 8190 1162 2948 4734 6520 784CIP2B 851 8190 1163 2949 4735 6521 784CIP2B 852 8192 1164 2950 4736 6522 784CIP2B 853 8193 1165 2951 4737 6523 784CIP2B 853 8193 1166 2952 4738 6524 784CIP2B 855 8197 1167 2953 4739 6525 784CIP2B 856 <			4725	6511	784CIP2B 842	8173
1156 2942 4728 6514 784CIP2B 845 8183 1157 2943 4729 6515 784CIP2B 846 8184 1158 2944 4730 6516 784CIP2B 847 8185 1159 2945 4731 6517 784CIP2B 848 8187 1160 2946 4732 6518 784CIP2B 859 8188 1161 2947 4733 6519 784CIP2B 850 8190 1162 2948 4734 6520 784CIP2B 851 8190 1163 2949 4735 6521 784CIP2B 852 8192 1164 2950 4736 6522 784CIP2B 853 8193 1165 2951 4737 6523 784CIP2B 853 8193 1166 2952 4738 6524 784CIP2B 855 8197 1167 2953 4739 6525 784CIP2B 855 8197 1167 2953 4740 6526 784CIP2B 856 <			4726	6512	784CIP2B_843	8179
1157 2943 4729 6515 784CIP2B 845 8183 1158 2944 4730 6516 784CIP2B 847 8185 1159 2945 4731 6517 784CIP2B 848 8187 1160 2946 4732 6518 784CIP2B 849 8188 1161 2947 4733 6519 784CIP2B 850 8190 1162 2948 4734 6520 784CIP2B 851 8190 1163 2949 4735 6521 784CIP2B 852 8192 1164 2950 4736 6522 784CIP2B 853 8193 1165 2951 4737 6523 784CIP2B 854 8197 1166 2952 4738 6524 784CIP2B 855 8197 1167 2953 4739 6525 784CIP2B 856 8199 1168 2954 4740 6526 <td< td=""><td></td><td></td><td></td><td></td><td>784CIP2B 844</td><td>8182</td></td<>					784CIP2B 844	8182
1158 2944 4730 6516 784CIP2B 845 8184 1159 2945 4731 6517 784CIP2B 848 8187 1160 2946 4732 6518 784CIP2B 849 8188 1161 2947 4733 6519 784CIP2B 850 8190 1162 2948 4734 6520 784CIP2B 851 8190 1163 2949 4735 6521 784CIP2B 852 8192 1164 2950 4736 6522 784CIP2B 853 8193 1165 2951 4737 6523 784CIP2B 854 8197 1166 2952 4738 6524 784CIP2B 855 8197 1166 2952 4738 6524 784CIP2B 855 8197 1167 2953 4739 6525 784CIP2B 856 8199 1168 2954 4740 6526 784CIP2B 857 8202 1169 2955 4741 6527 784CIP2B 859 <					784CIP2B_845	8183
1159 2945 4731 6517 784CIP2B 847 8185 1160 2946 4732 6518 784CIP2B 849 8188 1161 2947 4733 6519 784CIP2B 850 8190 1162 2948 4734 6520 784CIP2B 851 8190 1163 2949 4735 6521 784CIP2B 852 8192 1164 2950 4736 6522 784CIP2B 853 8193 1165 2951 4737 6523 784CIP2B 853 8193 1166 2952 4738 6524 784CIP2B 855 8197 1167 2953 4739 6525 784CIP2B 855 8197 1167 2953 4739 6525 784CIP2B 856 8199 1168 2954 4740 6526 784CIP2B 857 8202 1169 2955 4741 6527 784CIP2B 859 8208 1170 2956 4742 6528 784CIP2B 860 <					784CIP2B_846	8184
1160 2946 4732 6518 784CIP2B 848 8187 1161 2947 4733 6519 784CIP2B 849 8188 1162 2948 4734 6520 784CIP2B 851 8190 1163 2949 4735 6521 784CIP2B 852 8192 1164 2950 4736 6522 784CIP2B 853 8193 1165 2951 4737 6523 784CIP2B 854 8197 1166 2952 4738 6524 784CIP2B 855 8197 1167 2953 4739 6525 784CIP2B 856 8199 1168 2954 4740 6526 784CIP2B 857 8202 1169 2955 4741 6527 784CIP2B 858 8203 1170 2956 4742 6528 784CIP2B 859 8208 1171 2957 4743 6529 <td< td=""><td></td><td></td><td></td><td></td><td></td><td>8185</td></td<>						8185
1161 2947 4733 6519 784CIP2B 849 8188 1162 2948 4734 6520 784CIP2B 851 8190 1163 2949 4735 6521 784CIP2B 852 8192 1164 2950 4736 6522 784CIP2B 853 8193 1165 2951 4737 6523 784CIP2B 854 8197 1166 2952 4738 6524 784CIP2B 855 8197 1167 2953 4739 6525 784CIP2B 856 8199 1168 2954 4740 6526 784CIP2B 857 8202 1169 2955 4741 6527 784CIP2B 858 8203 1170 2956 4742 6528 784CIP2B 859 8208 1171 2957 4743 6529 784CIP2B 860 8209 1172 2958 4744 6530 784CIP2B 861 8211 1173 2959 4745 6531 784CIP2B 862 <						8187
1162 2948 4734 6520 784CIP2B_850 8190 1163 2949 4735 6521 784CIP2B_851 8190 1164 2950 4736 6521 784CIP2B_852 8192 1164 2950 4736 6522 784CIP2B_853 8193 1165 2951 4737 6523 784CIP2B_854 8197 1166 2952 4738 6524 784CIP2B_855 8197 1167 2953 4739 6525 784CIP2B_856 8199 1168 2954 4740 6526 784CIP2B_857 8202 1169 2955 4741 6527 784CIP2B_858 8203 1170 2956 4742 6528 784CIP2B_859 8208 1171 2957 4743 6529 784CIP2B_860 8209 1172 2958 4744 6530 784CIP2B_861 8211 1173 2959 4745 6531 784CIP2B_862 <						8188
1163 2949 4735 6521 784CIP2B_851 8190 1164 2950 4736 6522 784CIP2B_852 8192 1165 2951 4737 6523 784CIP2B_853 8193 1166 2952 4738 6524 784CIP2B_855 8197 1167 2953 4739 6525 784CIP2B_856 8199 1168 2954 4740 6526 784CIP2B_857 8202 1169 2955 4741 6527 784CIP2B_858 8203 1170 2956 4742 6528 784CIP2B_859 8208 1171 2957 4743 6529 784CIP2B_860 8209 1172 2958 4744 6530 784CIP2B_861 8211 1173 2959 4745 6531 784CIP2B_863 8214 1174 2960 4746 6532 784CIP2B_863 8217						8190
1164 2950 4736 6522 784CIP2B_852 8192 1165 2951 4737 6523 784CIP2B_853 8193 1166 2952 4738 6524 784CIP2B_854 8197 1167 2953 4739 6525 784CIP2B_856 8199 1168 2954 4740 6526 784CIP2B_857 8202 1169 2955 4741 6527 784CIP2B_858 8203 1170 2956 4742 6528 784CIP2B_859 8208 1171 2957 4743 6529 784CIP2B_860 8209 1172 2958 4744 6530 784CIP2B_861 8211 1173 2959 4745 6531 784CIP2B_862 8214 1174 2960 4746 6532 784CIP2B_863 8217						
1165 2951 4737 6523 784CIP2B_853 8193 1166 2952 4738 6524 784CIP2B_854 8197 1167 2953 4739 6525 784CIP2B_856 8197 1168 2954 4740 6526 784CIP2B_857 8202 1169 2955 4741 6527 784CIP2B_858 8203 1170 2956 4742 6528 784CIP2B_859 8208 1171 2957 4743 6529 784CIP2B_860 8209 1172 2958 4744 6530 784CIP2B_861 8211 1173 2959 4745 6531 784CIP2B_862 8214 1174 2960 4746 6532 784CIP2B_863 8217						8192
1166 2952 4738 6524 784CIP2B_854 8197 1167 2953 4739 6525 784CIP2B_855 8197 1168 2954 4740 6526 784CIP2B_856 8199 1169 2955 4741 6527 784CIP2B_857 8202 1170 2956 4742 6528 784CIP2B_859 8208 1171 2957 4743 6529 784CIP2B_860 8209 1172 2958 4744 6530 784CIP2B_861 8211 1173 2959 4745 6531 784CIP2B_862 8214 1174 2960 4746 6532 784CIP2B_863 8217						8193
1167 2953 4739 6525 784CIP2B_855 8197 1168 2954 4740 6526 784CIP2B_856 8199 1169 2955 4741 6527 784CIP2B_857 8202 1170 2956 4742 6528 784CIP2B_859 8208 1171 2957 4743 6529 784CIP2B_860 8209 1172 2958 4744 6530 784CIP2B_861 8211 1173 2959 4745 6531 784CIP2B_862 8214 1174 2960 4746 6532 784CIP2B_863 8217						
1168 2954 4740 6526 784CIP2B_856 8199 1169 2955 4741 6527 784CIP2B_857 8202 1170 2956 4742 6528 784CIP2B_859 8203 1171 2957 4743 6529 784CIP2B_860 8209 1172 2958 4744 6530 784CIP2B_861 8211 1173 2959 4745 6531 784CIP2B_862 8214 1174 2960 4746 6532 784CIP2B_863 8217						
1169 2955 4741 6527 784CIP2B_858 8202 1170 2956 4742 6528 784CIP2B_859 8208 1171 2957 4743 6529 784CIP2B_860 8209 1172 2958 4744 6530 784CIP2B_861 8211 1173 2959 4745 6531 784CIP2B_862 8214 1174 2960 4746 6532 784CIP2B_863 8217						
1170 2956 4742 6528 784CIP2B 858 8203 1171 2957 4743 6528 784CIP2B 859 8208 1172 2958 4744 6530 784CIP2B 860 8209 1173 2959 4745 6531 784CIP2B 861 8211 1174 2960 4746 6532 784CIP2B 863 8217 1175 2961 4747 6532 784CIP2B 863 8217						8202
1171 2957 4743 6529 784CIP2B 869 8208 1172 2958 4744 6530 784CIP2B 860 8209 1173 2959 4745 6530 784CIP2B 861 8211 1174 2960 4746 6531 784CIP2B 862 8214 1175 2961 4747 6532 784CIP2B 863 8217						8203
1172 2958 4744 6530 784CIP2B 860 8209 1173 2959 4745 6530 784CIP2B 861 8211 1174 2960 4746 6531 784CIP2B 862 8214 1175 2961 4746 6532 784CIP2B 863 8217						
1173 2959 4745 6531 784CIP2B 861 8211 1174 2960 4746 6532 784CIP2B 863 8217						
1174 2960 4746 6532 784CIP2B 862 8214 1175 2961 4746 6532 784CIP2B 863 8217						
1175 2967 4347 6552 784CIP2B 863 8217						
6533 784CIP2B_864 8223						
			3/3/	0333	/84C1P2B_864	8223

SEQ ID NO:	SEQ ID	SEQ ID NO:	SEO ID	I Bud and bud	
of full-	NO: of	of contig	NO:	Priority	SEQ ID
length	full-	nucleotide	of contig	docket number_	NO:in
nucleotide	length	sequence	peptide		U.S.S.N.
sequence	peptide	- Squarice	sequence	SEQ ID NO: in	09/488,725
_	sequence		aedaeuce	priority	Ì
1176	.2962	4748	6534	application	
1177	2963	4749		784CIP2B_865	8224
1178	2964		6535	784CIP2B_866	8226 ·
1179		4750	6536	784CIP2B 867	8227
	2965	4751	6537	784CIP2B 868	8229
1180	2966	4752	6538	784CIP2B 869	8232
1181	2967	4753	6539	784CIP2B 870	8236
1182	2968	4754	6540	784CIP2B 871	8239
1183	2969	4755	6541	784CIP2B_872	
1184	2970	4756	6542	784CIP2B 873	8244
1185	2971	4757	6543		8245
1186	2972	4758		784CIP2B_874	8248
1187	2973		6544	784CIP2B_875	8251
1188	2974	4759	6545	784CIP2B_876	8253
1189	d	4760	6546	784CIF2B 877	8260
	2975	4761	6547	784CIP2B 878	8262
1190	2976	4762	6548	784CIP2B 879	8268
1191	2977	4763	6549	784CIP2B 880	8270
1192	2978	4764	6550	784CIP2B 881	8272
1193	2979	4765	6551	784CIP2B 882	
1194	2980	4766	6552	784CIP2B 883	8274
1195	2981	4767	6553		8274
1196	2982	4768		784CIP2B_884	8275
1197	2983		6554	784CIP2B_885	8277
1198	2984	4769	6555	784CIP2B_886	8281
1199	2985	4770	6556	784CIP2B_887	8283
1200		4771	6557	784CIP2B 888	8289
	2986	4772	6558	784CIP2B 889	8295
1201	2987	4773	6559	784CIP2B 890	8300
1202	2988	4774	6560	784CIP2B 891	8303
1203	2989	4775	6561	784CIP2B 892	8304
1204	2990	4776	6562	784CIP2B 893	
1205	2991	4777	6563	784CIP2B 894	8305
1206	2992	4778	6564	784CIP2B_894	8309
1207	2993	4779	6565		8318
1208	2994	4780		784CIP2B_896	8319
1209	2995	4781	6566	784CIP2B_897	8321
1210	2996	4782	6567	784CIP2B_898	8322
1211	2997		6568	784CIP2B_899	8323
1212	2998	4783	6569	784CIP2B_900	8325
1213		4784	6570	784CIP2B 901	8331
	2999	4785	6571	784CIP2B 902	8332
1214	3000	4786	6572	784CIP2B 903	8333
1215	3001	4787	6573	784CIP2B 904	8335
1216	3002	4788	6574	784CIP2B 905	8336
1217	3003	4789	6575	784CIP2B 906	8337
1218	3004	4790	6576	784CIP2B 907	8340
1219	3005	4791	6577		
1220	3006	4792	6578	784CIP2B_908 784CIP2B 909	8343
1221	3007	4793	6579		8347
1222	3008	4794		784CIP2B_910	8349
1223	3009	4795	6580	784CIP2B_911	8351
1224	3010		6581	784CIP2B_912	8353
1225	3011	4796	6582	784CIP2B_913	8355
1226		4797	6583	784CIP2B_914	8361
1227	3012	4798	6584	784CIP2B_915	8365
	3013	4799	6585	784CIP2B_916	8367
1228	3014	4800	6586	784CIP2B 917	8369
1229	3015	4801	6587	784CIP2B 919	8375
1230	3016	4802	6588	784CIP2B 920	
1231	3017	4803	6589	784CIP2B 921	8387
1232	3018	4804	6590		8391
1233	3019	4805		784CIP2B_922	8393
1234	3020	4806	6591	784CIP2B_923	8393
1235	3021		6592	784CIP2B_924	8394
1236	3022	4807	6593	784CIP2B_925	8395
1237		4808	6594	784CIP2B_926	8396
-631	3023	4809	6595	784CIP2B_927	8398
					

SEQ ID NO: of full-	SEQ ID NO: of	SEQ ID NO:	SEQ ID	Priority	SEQ ID
length	full-	of contig	NO:	docket number_	NO:in
nucleotide	length	sequence	of contig	corresponding	U.S.S.N.
sequence	peptide	bequence	sequence	SEQ ID NO: in priority	09/488,725
-	sequence		Jeguence	application	
1238	3024	4810	6596	784CIP2B 928	8402
1239	3025	4811	6597	784CIP2B 929	8402
1240	3026	4812	6598	784CIP2B 930	8402
1241	3027	4813	6599	784CIP2B 931	8406
1242	3028	4814	6600	784CIP2B 932	8409
1243	3029	4815	6601	784CIP2B 933	8410
1244	3030	4816	6602	784CIP2B 934	8414
1245	3031	4817	6603	784CIP2B 935	8415
1246	3032	4818	6604	784CIP2B 936	8419
1247	3033	4819	6605	784CIP2B 937	8426
1248	3034	4820	6606	784CIP2B 938	8430
1249	3035	4821	6607	784CIP2B 939	8431
1250	3036	4822	6608	784CIP2B 940	8432
1251	3037	4823	6609	784CIP2B 941	8433
1252	3038	4824	6610	784CIP2B 942	8434
1253	3039	4825	6611	784CIP2B 943	8438
1254	3040	4826	6612	784CIP2B 944	8439
1255	3041	4827	6613	784CIP2B 945	8441
1256	3042	4828	5614	784CIP2B 946	8450
1257	3043	4829	6615	784CIP2B 947	8451
1258	3044	4830	6616	784CIP2B 948	8452
1259	3045	4831	6617	784CIP2B 949	8460
1260	3046	4832	6618	784CIP2B 950	8461 .
1261	3047	4833	6619	784CIP2B_951	8462
1262	3048	4834	6620	784CIP2B_952	8464
1263	3049	4835	6621	784CIP2B_953	8465
1264	3050	4836	6622	784CIFZB_954	8467
1265	3051	4837	6623	784CIP2B_955	8470
1266	3052	4838	6624	784CIP2B_956	8471
1267	3053	4839	6625	784CIP2B_957	8473
1269	3054	4840	6626	784CIP2B_958	8474
1270	3055	4841	6627	784CIP2B_959	8475
1271	3056	4842	6628	784CIP2B_960	8476
1272	3057	4843	6629	784CIP2B_961	8480
1272	3058	4844	6630	784CIP2B_962	8482
1274	3059 3060	4845	6631	784CIP2B_963	8482
1275	3061	4846	6632	784CIP2B_964	8486
1276	3062	4847	6633	784CIP2B_965	8488
1277	3063	4848	6634	784CIP2B_966	8492
1278	3064	4849	6635	784CIP2B_967	8494
1279	3065	4850 4851	6636	784CIP2B_968	8496
1280	3065	4851	6637	784CIP2B_969	8497
1281	3067	4853	6638	784CIP2B_970	8499
1282	3068	4854	6639	784CIP2B_971	8513
1283	3069	4855	6640	784CIP2B_972	8522
1284	3070	4856	6641 6642	784CIP2B_973	8526
1285	3071	4857	6643	784CIP2B_974	8531
1286	3072	4858	6644	784CIP2B_975	8533
1287	3073	4859	6645	784CIP2B_976	8542
1288	3074	4860	6646	784CIP2B_977	8544
1289	3075	4861	6647	784CIP2B_978	8565
1290	3076	4862	6648	784CIP2B_979	8565
1291	3077	4863	6649	784CIP2B_980	8572
		4864	6650	784CIP2B_981	8576
	3078		וורחם	784CIP2B 982	8578
1292	3078 3079				
	3079	4865	6651	784CIP2B_983	8584
1292 1293 1294	3079 3080	4865 4866	6651 6652	784CIP2B_983 784CIP2B_984	8584 8598
1292 1293	3079 3080 3081	4865 4866 4867	6651 6652 6653	784CIP2B_983 784CIP2B_984 784CIP2B_985	8584 8598 8602
1292 1293 1294 1295	3079 3080 3081 3082	4865 4866 4867 4868	6651 6652 6653 6654	784CIP2B_983 784CIP2B_984 784CIP2B_985 784CIP2B_986	8584 8598 8602 8604
1292 1293 1294 1295 1296	3079 3080 3081	4865 4866 4867	6651 6652 6653	784CIP2B_983 784CIP2B_984 784CIP2B_985	8584 8598 8602

SEQ ID NO: of full-	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
length	NO: of full-	of contig	NO:	docket number	NO:in
nucleotide	length	nucleotide sequence	of contig		U.S.S.N.
sequence	peptide	sequence	peptide	SEQ ID NO: in	09/488,72
	sequence		sequence	priority	
1300	3086	4872	6658	application	
1301	3087	4873	6659	784CIP2B_990	8640
1302	3088	4874	6660	784CIP2B_991	8643
1303	3089	4875	6661	784CIP2B_992	8645
1304	3090	4876	6662	784CIP2B_993	8650
1305	3091	4877	6663	784CIP2B_994	8651
1306	3092	4878	6664	784CIP2B_995	8654
1307	3093	4879	6665	784CIP2B_996	8655
1308	3094	4880	6666	784CIP2B_997 784CIP2B_998	8657
1309	3095	4881	6667	784CIP2B 999	8665
1310	3096	4882	5668	784CIP2B_999	8668
1311	3097	4883	6669	784CIP2B_1000	8671
1312	3098	4884	5670		8672
1313	3099	4885	6671	784CIP2B_1002 784CIP23 1003	8692
1314	3100	4886	6672		8706
1315	3101	4887	6673	784CIP23_1004	8716
1316	3102	4888	6674	784CIP2B 1005 784CIP2B 1006	8719
1317	3103	4889	6675	784CIP2B_1006 784CIP2B 1007	8743
1318	3104	4890	6676		8764
1319	3105	4891	6577	784CIP2B_1008	8764
1320	3106	4892	6678	784CIP2B 1009 784CIP2B 1010	8764
1321	3107	4893	6679		8774
1322	3108	4894	6680	784CIP2B_1011	8782
1323	3109	4895	6681	784CIP2B_1012	8796
1324	3110	4896	6682	784CIP2B_1013	8827
1325	3111	4897	6683	784CIP2B_1014 784CIP2B_1015	8842
1326	3112	4898	6684		8842
1327	3113	4899	6685	784CIP2B_1016 784CIP2B_1017	8858
1328	3114	4900	6686	784CIP2B_1017	8871
1329	3115	4901	6687	784CIP2B_1018	8921
1330	3116	4902	6688	784CIP2B 1019	8927
1331	3117	4903	6689	784CIP2B_1020 784CIP2B_1021	8942
1332	3118	4904	6690	784CIP2B_1021	8994
1333	3119	4905	6691	784CIP2B 1022	9023
1334	3120	4906	6692	784CIP2B_1023	9028
1335	3121	4907	6693	784CIP2B_1024 784CIP2B_1025	9058
1336	3122	4908	6694	784CIP2B 1026	9058
1337	3123	4909	6695	784CIP2B_1026	9079
1338	3124	4910	6696	784CIP2B 1027	9079
1339	3125	4911	6697	784CIP2B_1028	9082
1340	3126	4912	6698	784CIP2B 1030	9084
1341	3127	4913	6699	784CIP2B 1031	9093
1342	3128	4914	6700	784CIP2B 1032	9101 9103
1343	3129	4915	6701	784CIP2B 1033	
1344	3130	4916	6702	784CIP2B 1034	9105 9151
1345	3131	4917	6703	784CIP2B 1035	9161
1346	3132	4918	6704	784CIP2B 1036	9172
1347	3133	4919	6705	784CIP2B_1037	9174
1348	3134	4920	6706	784CIP2B 1038	9204
1349	3135	4921	6707	784CIP2B 1039	9234
1350	3136	4922	6708	784CIP2B_1040	9235
1351	3137	4923	6709	784CIP2B 1041	
1352	3138	4924	6710	784CIP2B_1042	9239 9256
1353	3139	4925	6711	784CIP2B 1042	
1354	3140	4926	6712	784CIP2B_1044	9276
1355	3141	4927	6713	784CIP2B_1044	9345
1356	3142	4928	6714	784CIP2B_1045 784CIP2B_1046	9379
1357	3143	4929	6715	784CIP2B_1046	9435
1358	3144	4930	6716	784CTD2B 1047	9437
1359	3145	4931	6717	784CIP2B_1048	9469
1360	3146	4932	6718	784CIP2B_1049	9500
1361	3147	4933	6719	784CIP2B_1050 784CIP2B_1051	9502
					9520

SEQ ID NO:	SEQ ID	SEQ ID NO:	LCDO TD		
of full-	NO: of	of contig	SEQ ID	Priority docket number	SEQ ID
length	full-	nucleotide	of contig	corresponding	NO:in U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	0.5.5.N. 09/488,725
sequence	peptide		sequence	priority	03/405,725
	sequence	}	•	application	
1362	3148	4934	6720	784CIP2B 1052	9541
1363	3145	4935	6721	784CIP2B 1053	9541
1364	3150	4936	6722	784CIP2B 1054	9548
1365	3151	4937	6723	784CIP2B 1055	9556
1366	3152	4938	6724	784CIP2B 1056	9556
1367	3153	4939	6725	784CIP2B 1057	9575
1368	3154	4940	6726	784CIP2B 1058	9589
1369	3155	4941	6727	784CIP2B 1059	9599
1370	3156	4942	6728	784CIP2B 1060	9602
1371	3157	4943	6729	784CIP2B 1061	9606
1372	3158	4944	6730	784CIP2B 1062	9622
1373	3159	4945	6731	784CIP2B 1063	9623
1374	3160	4946	6732	784CIP2B 1064	9646
1375	3161	4947	6733	784CIP2B 1065	9747
1376	3152	4948	6734	784CIP2B 1066	9773
1377	3163	4949	6735	784CIP2B 1067	9785
1378	3164	4950	6736	784CIP2B 1068	9801
1379	3165	1951	6737	784CIP2B 1069	9811
1380	3166	4952	6738	784CIP2B_1070	9843
1381	3167	4953	6739	784CIP2B 1071	9854
1382	3168	4954	6740	784CIP2B_1072	9854
1383	3169	4955	6741	784CIP2B_1073	9864
1384	3170	4956	6742	784CIP2B_1074	9864
1385	3171	4957	6743	784CIP2B_1075	9871
1386	3172	4958	6744	784CIP2B_1076	9879
1387	3173	4959	6745	784CIP2B_1077	9881
1388 1389	3174	4960	6746	784CIP2B_1078	9885
1390	3175	4961	6747	784CIP2B_1079	9901
1390	3175	4962	6748	784CIP2B_1080	9912
1391	3177	4963	6749	784CIP2B_1081	9916
1392	3179	4964	6750	784CIP2B_1082	9921
1394	3179	4965	6751	784CIP2B_1083	9925
1395	3181	4966	6752	784CIP2B_1084	9930
1396	3182	4967 4968	6753	784CIP2B_1085	9949
1397	3183	4969	6754	784CIP2B_1086	9951
1398	3184	4970	6755	784CIP2B_1087	9959
1399	3185	4971	6756	784CIP2B_1088	9973
1400	3186	4972	6757	784CIP2B 1089	9982
1401	3187	4973	6758 6759	784CIP2B_1090	9994
1402	3188	4974	5760	784CIP2B_1091	10021
1403	3189	4974	6761	784CIP2B_1092 784CIP2B_1094	10041
1404	3190	4976	6762	784C1P2B_1094 784C1P2B_1095	10067
1405	3191	4977	6763	784CIP2B_1095 784CIP2B_1096	10073
1406	3192	4978	6764	784CIP2B_1096 784CIP2B_1097	10112
1407	3193	4979	6765	784CIP2B_1097	10117
1408	3194	4980	6766	784CIP2B_1098 784CIP2B_1099	10132
1409	3195	4981	6767	784CIP2B 1099	10169
1410	3196	4982	6768	784CIP2B_1101	10217
1411	3197	4983	6769	784CIP2B_1101	10226
1412	3198	4984	6770	784CIP2B_1102	10232 10237
1413	3199	4985	6771	784CIP2B 1104	10279
1414	3200	4986	6772	784CIP2C 1	
1415	3201	4987	6773	784CIP2C_1	33
1416	3202	4988	6774	784CIP2C_2	271
1417	3203	4989	6775	784CIP2C_3	848
1418	3204	4990	6776	784CIP2C 5	849
1419	3205	4991	6777	784CIP2C_5	864
1420	3206	4992	6778	784CIP2C 7	953
1421	3207	4993	6779	784CIP2C_7	980
1422	3208	4994	6780	784CIP2C_8	1595
1423	3209	4995	6781	784CIP2C_9	1697
			2707	103C182C_10	1744

SEQ ID NO: of full-	SEQ ID NO: of	SEQ ID NO:	SEQ ID	Priority	SEQ ID
length	full-	of contig	NO:	docket number_	NO:in
nucleotide	length	nucleotide sequence	of contig	corresponding	U.S.S.N.
sequence	peptide	sequence	peptide	SEQ ID NO: in	09/488,72
•	sequence	1	sequence	priority	1
1424	3210	4996		application	1
1425	3211	4997	6782	784CIP2C_11	1937
1426	3212		6783	784CIP2C_12	1955
1427	3212	4998	6784	784CIP2C_13	1955
1428	3213	4999	6785	784CIP2C_14	2185
1429		5000	6786	784CIP2C 15	2889
1430	3215	5001	6787	784CIP2C 16	2901
1430	3216	5002	6788	784CIP2C 17	2902
	3217	5003	6789	784CIP2C 18	2905
1432	3218	5004	6790	784CIP2C 19	2948
1433	3219	5005	6791	784CIP2C 20	2956
1434	3220	5006	6792	784CIP2C 21	2959
1435	3221	5007	6793	784CIP2C 22	
1436	3222	5008	6794	784CIP2C 23	2965
1437	3223	5009	6795		2966
1438	3224	5010	6796	784CIP2C_24	2970
1439	3225	5011	6797	784CIP2C_25	2985
1440	3226	5012		784CIP2C_26	2987
1441	3227	5013	6798	784CIP2C_27	2993
1442	3228	5013	6799	784CIP2C_28	2993
1443	3229		6800	784CIP2C_29	3017
1444	3230	5015	6801	784CIP2C_30	3046
1445	3231	5016	6802	784CIP2C_31	3050
1446		5017	6803	784CIP2C_32	3357
1447	3232	5018	6804	784CIP2C 33	3359
1448	3233	5019	6805	784CIP2C_34	3432
1449	3234	5020	6806	784CIP2C 35	3438
	3235	5021	6807	784CIP2C 36	3439
1450	3236	5022	6808	784CIP2C 39	3463
1451	3237	5023	6809	784CIP2C_40	3466
1452	3238	5024	6810	784CIP2C 41	3466
1453	3239	5025	6911	784CIP2C 42	3467
1454	3240	5026	6912	784CIP2C 43	3468
1455	3241	5027	6813	784CIP2C 44	
1456	3242	5028	6814	784CIP2C_45	3483
1457	3243	5029	6815	784CIP2C 46	3484
1458	3244	5030	6816	784CIP2C 47	3488
1459	3245	5031	6817	784CIP2C 48	3491
1460	3246	5032	6818		3493
1461	3247	5033	6819	784CIP2C_49	3494
1462	3248	5034	6820	784CIP2C_50	3495
1463	3249	5035		784CIP2C_51	3496
1464	3250	5036	6821	784CIP2C_52	3503
1465	3251	5037	6822	784CIP2C_53	3503
1466	3252	5037	6823	784CIP2C_54	3504
1467	3253		6824	784CIP2C_55	3511
1468	3254	5039	6825	784CIP2C_56	3531
1469		5040	6826	784CIP2C_57	3536
1470	3255	5041	6827	784CIP2C_58	3546
	3256	5042	6828	784CIP2C 59	3548
1471	3257	5043	6829	784CIP2C 60	3551
1472	3258	5044	6830	784CIP2C_61	3553
1473	3259	5045	6831	784CIP2C 62	3564
1474	3260	5046	6832	784CIP2C_63	3567
1475	3261	5047	6833	784CIP2C 64	
1476	3262	5048	6834	784CIP2C 65	3572
1477	3263	5049	6835		3573
1478	3264	5050	6836	784CIP2C_66	3574
1479	3265	5051		784CIP2C_67	3583
1480	3266		6837	784CIP2C_68	3615
1481	3267	5052	6838	784CIP2C_69	3623
1482	3268	5053	6839	784CIP2C_70	3629
1483		5054	6840	784CIP2C_71	3666
1484	3269	5055	6841	784CIP2C_72	3667
1485	3270 3271	5056	6842	784CIP2C_73	3906
		5057	6843	784CIP2C 74	

SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
of full-	NO: of	of contig	NO:	docket number	NO:in
length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide	1 1 1	sequence	priority	05/400,725
1	sequence		100400000	application	
1486	3272	5058	6844	784CIP2C 75	3924
1487	3273	5059	6845	784CIP2C 76	3924
1488	3274	5060	6846	784CIP2C 77	3935
1489	3275	5061	6847	784CIP2C_77	3959
1490	3276	5062	6848	784CIP2C_78	
1491	3277	5063	6849	784CIP2C 80	3981
1492	327B	5064	6850		3989
1493	3279	<u> </u>	<u> </u>	784CIP2C_81	4295
1494		5065	6851	784CIP2C_82	4300
1495	3280	5066	6852	784CIP2C_83	4360
	3281	5067	6853	784CIP2C_84	4362
1496	3282	5068	6854	784CIP2C_85	4371
. 1497	3283	5069	6855	784CIP2C_86	4373
1498	3284	5070	6856	784CIP2C_87	4376
1499	3285	5071	6857	784CIP2C_89	4378
1500	3286	5072	6858	784C1P2C_90	4382
1501	3287	5073	6859	784CIP2C_91	4409
1502	.3288	5074	6860	784CIP2C_92	4421
1503	3289	5075	6861	784CIP2C 93	4421
1504	3290	5076	6862	784CIP2C 94	4426
1505	3291	5077	6863	784CIP2C 95	4430
1506	3292	5078	6864	784CIP2C 96	4435
1507	3293	5079	6865	784CIP2C 97	4436
1508	3294	5080	6866	784CIP2C 98	4439
1509	3295	5081	6867	784CIP2C 99	4440
1510	3296	5082	6868	784CIP2C 100	4441
1511	3297	5083	6869	784CIP2C 101	4442
1512	3298	5084	6870	784CIP2C 102	4455
1513	3299	5085	6971	784CIP2C 103	4462
1514	3300	5086	6872	784CIP2C 104	4466
1515	3301	5087	6873	784CIP2C 105	4469
1516	3302	5088	6874	784CIP2C 106	4477
1517	3303	5089	6875	784CIP2C 107	4481
1518	3304	5090	6876	784CIP2C_107	4483
1519	3305	5091	6877	784CIP2C 109	
1520	3306	5092	6878	784CIP2C_109	4484 4486
1521	3307	5093	6879	784CIP2C_110 784CIP2C 111	
1522	3308	5094	6880	784CIP2C 111	4490
1523	3309	5095	6881		4499
1524	3310	5096	6882	784CIP2C_113	4503
1525	3311	5097	6883	784CIP2C_114	4506
1526	3312	5098		784CIP2C_115	4509
1527	3313		6884	784CIP2C_116	4514
1528		5099	6885	784CIP2C_117	4516
	3314	5100	6886	784CIP2C_118	4522
1529	3315	5101	6887	784CIP2C_119	4525
1530	3316	5102	6888	784CIP2C_120	4527
1531	3317	5103	6889	784CIP2C_121	4528
1532	3318	5104	6890	784CIP2C_122	4529
1533	3319	5105	6891	784CIP2C_123	4532
1534	3320	5106	6892	784CIP2C_124	4537
1535	3321	5107	6893	784CIP2C_125	4538
1536	3322	5108	6894	784CIP2C_126	4551
1537	3323	5109	6895	784CIP2C_127	4552
1538	3324	5110	6896	784CIP2C_128	4559
1539	3325	5111	6897	784CIP2C_129	4567
1540	3326	5112	6898	784CIP2C 130	4568
1541	3327	5113	6899	784CIP2C 132	4585
1542	3328	5114	6900	784CIP2C 133	4592
1543	3329	5115	6901	784CIP2C 134	4609
1544	3330	5116	6902	784CIP2C 135	4616
1545	3331	5117	6903	784CIP2C 136	4617
1546	3332	5118	6904	784CIP2C 137	4618
1547	3333	5119	6905	784CIP2C 137	4620
				.0402620_130	7020

SEQ ID NO: of full-	SEQ ID NO: of	SEQ ID NO:	SEQ ID	Priority	SEQ ID
length	full-	of contig	NO:	docket number_	NO:in
nucleotide	length	sequence	of contig		U.S.S.N.
sequence	peptide	seddelice	peptide	SEQ ID NO: in	09/488,72
-	sequence		sequence	priority	
1548	3334	5120	6906	application	
1549	3335	5121	6907	784CIP2C_139	4624
1550	3336	5122	6908	784CIP2C_140	4632
1551	3337	5123	6909	784CIP2C_141	4634
1552	3338	5124	6910	784CIP2C_142	4638
1553	3339	5125	6911	784CIP2C_143	4639
1554	3340	5126		784CIP2C_144	4643
1555	3341	5127	6912	784CIP2C_145	4644
1556	3342	5128	6913	784CIP2C_146	4655
1557	3343	5129	6914	784CIP2C_147	4668
1558	3344		6915	784CIP2C_148	4677
1559	3345	5130	6916	784CIP2C_149	4677
1560	3345	• 5131	6917	784CIP2C_150	4677
1561	3346	5132	6918	784CIP2C_152	4682
1562		5133	6919	784C1P2C 153	4690
1563	3348	5134	6920	784CIP2C 154	4691
1564	3349	5135	6921	784CIP2C 155	4727
	3350	5136	6922	784CIP2C_156	4730
1565	3351	5137	6923	784CIP2C 157	4734
1566	3352	5138	6924	784CIP2C 158	4757
1567	3353	5139	6925	784CIP2C 159	4764
1568	3354	5140	6926	784CIP2C 160	4786
1569	3355	5141	6927	784CIP2C_161	4793
1570	3356	5142	6928	784CIP2C 162	4825
1571	3357	5143	6929	784CIP2C 163	4826
1572	3358	5144	6930	784CIP2C_164	4850
1573	3359	5145	6931	784CIP2C_165	4853
1574	3360	5146	6932	784CIP2C 166	4855
1575	3361	5147	6933	784CIP2C 167	4856
1576	3362	5148	6934	784CIP2C 168	4867
1577	3363	5149	6935	784CIP2C 169	4869
1578	3364	5150	6936	784CIP2C 170	4878
1579	3365	5151	6937	784CIP2C 171	4880
1580	3366	5152	6938	784CIP2C 172	4942
1581	3367	5153	6939	784CIP2C 173	4945
1582	3368	5154	6940	784CIP2C 174	4950
1583	3369	S155	·6941	784CIP2C 175-	4952
1584	3370	5156	6942	784CIP2C 176	4954
1585	3371	5157	6943	784CIP2C_177	
1586	3372	5158	6944	784CIP2C 178	4958
1587	3373	5159	6945	784CIP2C 179	4961
1588	3374	5160	6946	784CIP2C 180	5590
1589	3375	5161	6947	784CIP2C 181	5599
1590	3376	5162	6948	784CIP2C 182	5692
1591	3377	5163	6949		5732
1592	3378	5164	6950	784CIP2C_183 784CIP2C_184	5765
1593	3379	5165	6951	784CIP2C_184 784CIP2C_185	5771
1594	3380	5166	6952		5774
1595	3381	5167	6953	784CIP2C_186	5793
1596	3382	5168	6954	784CIP2C_187	5806
1597	3383	5169	6955	784CIP2C_188	5852
1598	3384	5170	6956	784CIP2C_189	5892
1599	3385	5171	6957	784CIP2C_190	6057
1600	3386	5172		784CIP2C_191	6061
1601	3387	5173	6958	784CIP2C_192	6109
1602	3388		6959	784CIP2C_193	6160
1603	3389	5174	6960	784CIP2C_194	6297
1604	3390	5175	6961	784CIP2C_195	6398
1605		5176	6962	784CIP2C_196	6398
1606	3391	5177	6963	784CIP2C_197	6415
1607	3392	5178	6964	784CIP2C_198	6448
	3393	5179	6965	784CIP2C 199	6469
1608	3394	5180	6966	784CIP2C_200	6476
1609	3395	5181			

SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEO ID
of full-	NO: of	of contig	NO:	docket number_	NO:in
length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide	İ	sedneuce	priority	
	sequence			application	
1610	3396	5182	6968	784CIP2C_202	6574
1611	3397	5183	6969	784CIP2C_203	6578
1612	3398	5184	6970	784CIP2C_204	6662
1613	3399	5185	6971	784CIP2C_205	6572
1614 1615	3400	5186	6972	784CIP2C_206	6691
	3401	5187	6973	784CIP2C_207	6695
1616	3402	5188	6974	784CIP2C_208	6746
1617	3403	5189	6975	784CIP2C_209	6898
1618	3404	5190	6976	784CIP2C_210	6938
1619	3405	5191	6977	784CIP2C_211	6943
1620	3406	5192	6978	784CIP2C_212	7110
1621	3407	5193	6979	784CIP2C_213	7200
1622	3408	5194	6980	784CIP2C_214	7212
1623	3409	5195	6981	784CIP2C_215	7218
1624	3410	5196	6982	784CIP2C_216	7249
1625 1626	3411	5197	6983	784CIP2C_217	7500
	3412	5198	6984	784CIP2C_218	7509
1627	3413	5199	6985	784CIP2C_219	7523
1628	3414	5200	6986	784CIP2C_220	7544
1629	3415	5201	6987	784CIP2C_221	7564
1630 1631	3416	5202	6988	784CIP2C_222	7568
1632	3417	5203	6989	784CIP2C_223	7631
1633	3418	5204	6990	784CIP2C_224	7813
1634	3419	5205	6991	784CIP2C_225	7831
1635	3420	5206	6992	784CIP2C_226	7843
1636	3421 3422	5207	6993	784CIP2C_227	7907
1637	3422	5208	6994	784CIP2C_228	7943
1638	3424	5209	6995	784CIP2C_229	8175
1639	3424	5210 5211	6996	784CIP2C_230	8216
1640	3426	5212	6997 6998	784CIP2C_231	8225
1641	3427	5212	6999	784CIP2C_232	8271
1642	3428	5214	7000	784CIP2C_233	8397
1643	3429	5215	7000	784CIP2C_234	8466
1644	3430	5216	7001	784CIP2C_235	8503
1645	3431	5217	7002	784CIP2C_236 784CIP2C_237	8953
1646	3432	5218	7004	784CIP2C_237	9106 9139
1647	3433	5219	7005	784CIP2C_238	9555
1648	3434	5220	7006	784CIP2C_239	9650
1649	3435	5221	7007	784CIP2C_240	9889
1650	3436	5222	7008	784CIP2C 241	9933
1651	3437	5223	7009	784CIP2C 243	9953
1652	3438	5224	7010	784CIP2C 244	9981
1653	3439	5225	7011	784CIP2D 1	746
1654	3440	5226	7012	784CIP2D_1	3558
1655	3441	5227	7013	784CIP2D 3	3558
1656	3442	5228	7014	784CIP2D_3	3633
1657	3443	5229	7015	784C1P2D 5	3658
1658	3444	5230	7016	784CIP2D_5	3732
1659	3445	5231	7017	784CIP2D 7	4004
1660	3446	5232	7018	784CIP2D_7	4700
1661	3447	5233	7018	784CIP2D_8 784CIP2D_9	
1662	3448	5234	7020	784CIP2D_9 784CIP2D_10	4703
1663	3449	5235	7020	784CIP2D_10 784CIP2D_11	4774
1664	3450	• 5236			4894
1665	3451	5237	7022	784CIP2D_12	4918
1666	3452	5238	7023	784CIP2D_13	5159
1667	3453		7024	784CIP2D_14	7443
1668	3453	5239	7025	784CIP2D_15	8673
1669	3454	5240	7026	784CIP2D_16	8679
1670	3456	5241	7027	784CIP2D_17	8727
1671	3457	5242	7028	784CIP2D_18	8734
40,7	J=3/	5243	7029	784CIP2D 19	8756

SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	T 0========
of full-	NO: of	of contig	NO:	docket number	SEQ ID NO:in
length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide		sequence	priority	05/400,725
1672	sequence			application	1
1673	3458	5244	7030	784CIP2D 20	8818
1674	3459	5245	7031	784CIP2D 21	8844
1675	3460	5246	7032	784CIP2D 22	8846
1676	3461	5247	7033	784CIP2D 23	8912
1677	3462	5248	7034	784CIP2D 24	8918
1678	3463	5249	7035	784CIP2D_25	8918
1679	3464 3465	5250	7036	784CIP2D_26	8941
1680	3466	5251	7037	784CIP2D_27	8941
1681	3467	5252	7038	784CIP2D_28	8951
1682		5253	7039	784CIP2D_29	8951
1683	3468 3469	, 5254	7040	784CIP2D_30	9007
1684	3470	5255	7041	784CIP2D_31	9012
1685	3470	5256	7042	784CIP2D_32	9013
1686	3472	5257	7043	784CIP2D_33	9025
1687		5258	7044	784CIP2D_34	9053
1688	3473 3474	5259	7045	784CIP2D_35	9054
1689	3474	5260	7046	784CIP2D_36	9054
1690	3476	5261	7047	784CIP2D_37	9113
1691	3476	5262	7048	784CIP2D_38	9134
1692	3478	5263	7049	784CIP2D_39	9152
1693	3479	5264	7050	784CIP2D_40	9152
1694	3480	5265	7051	784CIP2D_41	9211
1695	3481	5266	7052	784CIP2D_42	9223
1696	3482	5267	7053	784CIP2D_43	9223
1697	3483	5268	7054	784CIP2D_44	9231
1698	3484	5269 5270	7055	784CIP2D_45	9236
1699	3485	5270	7056	784CIP2D_46	9236
1700	3486	5272	7057	784CIP2D_47	9303
1701	3487	5273	7058	784CIP2D_48	9309
1702	3488	5274	7059	784CIP2D_49	9314
1703	3489	5275	7060	784CIP2D_50	9326
1704	3490	5276	7061 7062	784CIP2D_51	9339
1705	3491	5277	7062	784CIP2D_52	9348
1706	3492	5278	7063	784CIP2D_53	9376
1707	3493	5279	7065	784CIP2D 54	9382
1708	3494	5280	7066	784CIP2D_55 784CIP2D_56	9407
1709	3495	5281	7067		9414
1710	3496	5282	7068	 	9439
1711	3497	5283	7069	784CIP2D 58 784CIP2D 59	9485
1712	3498	5284	7070	784CIP2D_59	9493
1713	3499	5285	7071	784CIP2D_60	9501
1714	3500	5286	7072	784CIP2D_61 784CIP2D_62	9526 9526
1715	3501	5287	7073	784CIP2D_63	
1716	3502	5288	7074	784CIP2D 64	9551
1717	3503	5289	7075	784CIP2D 65	9557 9568
1718	3504	5290	7076	784CIP2D 66	
1719	3505	5291	7077	784CIP2D 67	9588
1720	3506	5292	7078	784CIP2D 68	9597
1721	3507	5293	7079	784CIP2D 69	9615
1722	3508	5294	7080	784CIP2D 70	9628
1723	3509	5295	7081	784CIP2D 71	9649
1724	3510	5296	7082	784CIP2D 72	9652
1725	3511	5297	7083	784CIP2D 73	9660 9662
	3512	5298	7084	784CIP2D 74	
1726		5299	7085	784CIP2D 75	9725 9746
1727	3513	7477		~-~±4D /3 [2/40
1727 1728	3513 3514	5300	7086		
1727 1728 1729		i	7086 7087	784CIP2D_76	9777
1727 1728 1729 1730	3514 3515 3516	5300	7086 7087 7088	784CIP2D_76 784CIP2D_77	9777 9787
1727 1728 1729 1730 1731	3514 3515 3516 3517	5300 5301	7087	784CIP2D_76 784CIP2D_77 784CIP2D_78	9777 9787 9790
1727 1728 1729 1730	3514 3515 3516	5300 5301 5302	7087 7088	784CIP2D_76 784CIP2D_77	9777 9787

SEQ ID NO: of full-	SEQ ID NO: of	SEQ ID NO: of contig	SEQ ID	Priority	SEQ ID
length	full-	nucleotide	of contig	docket number_ corresponding	NO:in
nucleotide	length	sequence	peptide	SEQ ID NO: in	U.S.S.N.
sequence	peptide	1	sequence	priority	09/488,72
•	sequence		20440000	application	į
1734	3520	5306	7092	784CIP2D 82	9867
1735	3521	5307	7093	784CIP2D 83	
1736	3522	5308	7094	784CIP2D 84	10010
1737	3523	5309	7095	784CIP2D 85	10011
1738	3524	5310	7096	784CIP2D 86	10057
1739	3525	5311	7097	784CIP2D 87	10085
1740	3526	5312	7098	784CIP2D 89	10139
1741	3527	5313	7099	784CIP2D 90	10133
1742	3528	5314	7100	784CIP2D 92	10165
1743	3529	5315	7101	784CIP2D 93	10173
1744	3530	5316	7102	784CIP2D 94	10173
1745	3531	5317	7103	784CIP2D 95	10273
1746	3532	5318	7104	784CIP2E 1	3121
1747	3533	5319	7105	784CIP2E 2	3628
1748	3534	5320	7106	784CIP2E 4	3673
1749	3535	5321	7107	784CIP2E 5	4018
1750	3536	5322	7108	784CIPZE 6	4467
1751	3537	5323	7109	784CIP2E 7	
1752	3538	5324	7110	784CIP2E 7	4865
1753	3539	5325	7111	784CIPZE_8	4916
1754	3540	5326	7112	784CIP2E_9	4923
1755	3541	5327	7113	784CIP2E_10	4926
1756	3542	5328	7114	784CIP2E 12	4962 4963
1757	3543	5329	7115	784CIP2E 13	4964
1758	3544	5330	7116	784CIP2E 14	4988
1759	3545	5331	7117	784CIP2E 15	5835
1760	3546	5332	7118	784CIP2E 16	7682
1761	3547	5333	7119	784CIP2E 17	7682
1762	3548	5334	7120	784CIP2E 18	7699
1763	3549	5335	7121	784CIP2E 19	7707
1764	3550	5336	7122	784CIP2E 20	7707
1765	3551	5337	7123	784CIP2E 21	7752
1766	3552	5338	7124	784CIP2E 22	8357
1767	3553	5339	7125	784CIP2E 23	9065
1768	3554	5340	7126	784CIP2E 24	9324
1769	3555	5341	7127	784CIP2F 1	2976
1770	3556	5342	7128	784CIP2F 2	3559
1771	3557	5343	7129	784CIP2F 3	4021
1772	3558	5344	7130	784CIP2F 4	4474
1773	3559	5345	7131	784CIP2F 5	4566
1774	3560	5346	7132	784CIP2F 6	4705
1775	3561	5347	7133	784CIP2F 7	4707
1776	3562	5348	7134	784CIP2F 8	4712
1777	3563	5349	7135	784CIP2F 9	5008
1778	3564	5350	7136	784CIP2F 10	5009
1779	3565	5351	7137	784CIP2F 11	5015
1780	3566	5352	7138	784CIP2F 12	5015
1781	3567	5353	7139	784CIP2F 13	7724
1782	3568	5354	7140	784CIP2F 14	7725
1783	3569	5355	7141	784CIP2F 15	8828
1784	3570	5356	7142	784CIP2F 16	8830
1785	3571	5357	7143	784CIP2F 17	9739
1786	3572	5358	7144	784CIP2F_17	9896

TRADOCS:1416247.1(%CS701!.DOC)

TABLE 7

	BLE /		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	Intovine, Marking, K=Lysine,
	to first	amino acid	L=Lcucine; M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of		S=Serine, T=Threonine, V=Valine,
l		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ſ	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence	<u></u>	\=possible nucleotide insertion)
5359	337	1131	AHLSARLSALILDEVAILPAPQNLSVLSTNMKHLLMWSPVIAPG
	i	1	ETVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITA
1	i	1	TVPYNLRVRATLGSQTS/CLEHP/VSIPLIETQPSLPDL/RMEI
1	1	1	TYPOGENIATE OF COORDINATION OF THE TOPS LPDL/RMEI
ı		ľ	TKDGFHLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSGGIP
ĺ	į.	1	VHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPL
1		1	VLALFAFVGFMLILVVVPLFVWKMGRLLQ/YLLLPRGGSSQTPW
5366			KITQF
5360	2	1115	PRVRSSGGQEDPASQQWARPRFTQPSKMRRRVIARPVGSSVRLK
ł	1		CVASGHPRPDITWMKDDQALTRPEAAEPRKKKWTLSLKNLRPED
- }	1	j	SGKYTCRVSNRAGAINATYKVDVIQRTRSKPVLTGTHPVNTTVD
•			FGGTTS FOCKUP COMENTATION OF THE POST OF T
,	{		FGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGGQKF
1 :			VVLPTGDVWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYS
	}		FRSAFLTVLPDPKPPGPPVASSSSATSLPWPVVIGIPAGAVFIL
1 1			GTLLLWLCQAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLPSL
i l	,		AALSAGPGVGLCEEHGSPAAPOHLLGPGPVAGPKLVPKLVTGHG
			TPHTYTHPPPSCQLNSSHS
5361	3	925	HEGSISSANILLDDQFQPKLTDFAMAHFRSHLEHQSCTINMTSS
			SSKHLWYMPEEYIRQGKLSIKTDVYSFGIVIMEVLTGCRVVLDD
			PKHIQLRDLLRELMEKRGLDSCLSFLDKKVPPCPRNFSAKLFCL
1 1		1	AGRCAATRAKLRPSMDEVLNTLESTQASLYFAEDPPTSLKSFRC
1			PSDI-FI-FNVDC I DVFDDFCOMBY I DESCRIPTION OF THE PROPERTY OF T
	i		PSPLFLENVPSIPVEDDESQNNNLLPSDEGLRIDRMTQKTPFEC
1	:		SQSEVMFLSLDKKPESKRNEEACNMPSSSCEESWFPKYIVPSQD
5362		4070	LRPYKVNIDPSSEAPGHSCRSRPVESSCSSKFSWDEYEQYKKE
	-	4879	SCQVEGCTRTYNSSQSIGKHMKTAHPDQYAAFKMQRKSKKGQXA
1 1			NNLNTPNNGKFVYFLPSPVNSSNPFFTSOTKANGNPACSAOLOU
1 1	1		VSPPIFPAHLASVSTPLLSSMESVINPNITSODKNEOGGMICSO
1 1	ļ		MENLPSTALPAQMEDLTKTVLPLNIDRGSDPFLSL?AESSSIDL
1 1	l	:	FPSPADSGTNSVFSQLENNTNHYSSQIEGNTNSSFLKGGNGENA
1		•	VFPSQVNVANN FSSTNAQQSAPEKVKKDRGRGQTGKERKPKHNK
	1		RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA
]]	}		ETACELLOGNEODELLA CHTI CONTAINT CORRESPONDED
	• 1	1	EIAQELLQSNGQPSLLASMILSTNAVNLQQPQQSTFNPEACFKD
!!!	1		PSFLQLLAENRS PAFLPNTFPRSGVTNFNTSVSQEGSEIIIQAL
1 1	į		ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPLLH
1	}	ĺ	TVCHPNTLLTNQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN
]	í		GLCSSSFPNSGGPSQNFTSNSSRVSVISGPONTRSSHINKKGMC
1 1	ł	ļ	ASKRRKKVAPPLIAPNASQNLVTSDLTTMGLTAKSVETDTTNIU
ļ j	1		SNVIPTCEPQSLVENLTQKLNNVNNQLFMTDVKENFKTSLESHT
]	ſ		VLAPLTLKTENGDSQMMALNSCTTSVNSDLOTSRDMVTONFRVT
,	1		LEIIKTAMNSQILEVKSGSQGAGETSQNAQINYNIQLPSVNTVQ
	1		NNKLPDSSP\FSSFISVMPTESNIPQSE\VSHKEDQIQEILEGL
ļ ,			QKLKLENDLSTPASQCVLINTSVTLTPTPVKSTADITVIQPVSE
	1	•	MINITOPHDYINIADERCONOGONICO
	t	İ	MINIQFNDKVNKPFVCQNQGCNYSAMTKDALFKHYGKIHQYTPE
j l	1	!	MILEIKKNQLKFAPFKCVVPTCTKTFTRNSNLRAHCQLVHHFTT
	I	ļ	EEMVKLKIKRPYGRKSQSENVPASRSTQVKKQLAMTEENKKESQ
1	1	1	PALELRAETONTHSNVAVIPEKOLIEKKSPDKTESSLOVITVITE
i	i	1	EQCNTNALTNTQTKGRKIRRHKKEKEEKKRKKPVSOSLEEPTPV
	į		SPYRPYRCVHQGCFAAFTIQQNLILHYQAVHKSDLPAFSAEVEE
	Į		ESEAGKESEETETKQTLKEFRCQVSDCSRIFQAITGLIQHYMKL
	1	}	HEMTPEEIESMTASVDVGKFPCDQLECKSSFTTYLNYVVHLEAD
- 1	1		HGIGLRASKTEEDGVYKCDCEGCDRIYATRSNLLRHIFNKHNDK
			HKAHI TODDDI TOCODAMOCOTATION TO TOTAL TOT
1	Ī	}	HKAHLIRPRRLTPGQENMSSKANQEKSKSKHRGTKHSRCGKEGI
ĺ	1		KMPKTKRKKKNNLENKNAKIVQIEENKPYSLKRGKHVYSIKARN
İ	I	j.	DALSECTSRFVTQYPCMIKGCTSVVTSESNIIRHYKCHKISKAR
	i	j	TSQHRNLLIVFKRCCNSOVKETSEOEGAKNDVKDSDTCVSESND
ĺ	1	1	NSRTTATVSQKEVEKNE*DEMDELTELFITKLINEDSTSVETOA
i	}	1	NTSSNVSNDFQEDNLCQSERQKASNLKRVNKEKNVSQNKKRKVE
ł	j	• 1	KAEPASAAELSSVRKEEETAVAIQTIEBHPASFDWSSFKPMGFE
l		-	VSFLKFLEESAVKQKKNTDKDHPNTGNKKGSHSNSRKNIDKTAV
1	ł	1.	TSGNHVCPCKESETENOETHINGS
			TSGNHVCPCKESETFVQFANPSQLQCSDNVKIVLDKNLKDCTEL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
}	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
}	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
İ	to first	amino acid	D-Dedcine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	ł	S=Serine, T=Threonine, V=Valine,
}		amino acid .	W=Tryptophan, Y=Tyrcsine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			VLKQLQEMKPTVSLKKLEVHSNDPDMSVMKDISIGKATGRGQY
5363	8066	703	RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP
1			PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML
1			RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS
1.	1		QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK
1			PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS
ļ			CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT
			CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR
	•		ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG
ł			PWCCEDUTCYOTTC CCCCDETDUTC PRINCED TO THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF T
1			EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT
1			DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG
		1	GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQ
			KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR
1			DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQW
}			DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN
			DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQI
			GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI
			TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP
Ĭ	İ		GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST
ł			PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV
1	i l		SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN
1		-	VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR
			PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYN
		1	ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQFVEVTDV
1 1			KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AEN
			TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVN
]			ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY
J			PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN
	i		TEVTETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTSDSGSIV
			VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH
)			LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV
			HADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV
1	j		PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKNE
	İ		GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEOHESTP
1	ſ		\LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI
1 1			TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTPGTEYVV
1 !			SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD
	ľ	•	APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD
(1	YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNS
1 1	1		ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI
(I			EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV
Į. Į			DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA
, ,			ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT
1 1			QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS
1 1			SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR
} I			ARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIORTIKP
]			DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS
1			NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP
1			RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP
į į			
ļ			QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT
1 1			SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQE
]]	J		ALSOTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT
1	i		LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVNEGLNQPT
			DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD
(ł		SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP
1 1	ł	·	HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR
]	Į.		RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ
 			ADREDSRE
5364	8066	703	RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP
]	1		PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML
<u> </u>			RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS
			301

650	I D		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	A=Alanine, C=Cvsteine, D=Aspartic haid B
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Truptophan V-Thursday V To
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence		Codon, /=possible nucleotide deletion,
		···	\=possible nucleotide insertion)
	ĺ	1	QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESH
	ł		PLAKETCFDKYTGNTYRVGDTYERPKDSMIWDCTCTGAGPGPTG
			CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGER
			CKPIAEKCFDHAAGTSYVVGETWEKPYOGWMWVDCTCLGEGGG
		}	1 TCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNIJOCICTCNCPC
			EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT
			DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG
			GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDC
			KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR
j			DNMKWCCTTONYDADOVEGEGDNA AND TO COMPANY TO CTSEGRE
-			DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQW DKOHDMGHMMRCTCYGNGBGGFWTGLAYGGLTTNEGVMYRIGDQW
1	·		DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN
ļ	l		DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQI
1	ļ		GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI
1	•		TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP
ł			GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST
ļ			PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTU
- [į		SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN
f	1		VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR
1	J.		PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLOPGYOVN
- 1	i i	į	ITIYAVEENQESTPVVIOOETTGTPRSDTVPSPPDLOEVEVEDV
1	•		KVTIMWTPPESAVTGYRVDVIPVNLPGEHGORLPI.SRNTF\ a FN
- 1	1	ı	TGLSPGVTYYFKVFAVSHGRESKPLTAOOTTKI.\DAPTNIOEIN
1	- 1		ETDSTVLVRWTPPRAQITGYRLTVGLTRRGOPROYNVGDEVEV
j	i		PERNEQPASEYTVSLVAIKGNOESPKATGVFTTLOPGSSIDDVN
- !		i	TEVTETTIVITWTPAPRIGFKLGVRPSOGGEAPREVTSDSGSTV
1	ì	,	VSGLTPGVEYVYTIQVLRDGOERDAP\IVNK\VVTPI.GDDTNI U
			LEANPDTGVLTYSWERSTTPDITGYRITTTPTNGQQGNSLEEVV
			HADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV
i	i	ľ	PPPTDLRFTM/ILGPDTMRVTW\APPPSIDLTMFLVRYSPVKNE
- 1	1	1	GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEQHESTP
Į	· •	j	\LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI
Ī	ŀ	f	TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTPGTEYVV
	l l	ì	SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD
- 1	1)	APAVTURYUR I TYGETTOCH COLORDON TO THE TOTAL I SWD
- 1	ŀ	J	APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD
1	1		YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNS
- 1	i	1	ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI
}			EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV
1			DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA
1		Į.	BLQGLRPGSEYTVSVVALHDDMESOPLIGTOSTAIDADTDIVET
1	Ì	}	QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS
1	J	i	SVVVSGLMVATKYEVSVYALKDTLTSR PAOGVAPPTI PARKEDDDD
[ì	AKVIDATETTITISWRTKTETITGFOVDAVPANGOTPIOPTIVE
1	1	ļ.	DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTATAARS
j	1	1 .	NURFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPPEUUDDD
}	1	i -	RPGVTEATITGLEPGTEYTIYVIALKNNOKSEPLIGRKKTDFID
ĺ	1	Į '	QLVTLPHPNLHGPEILDVPSTVOKTPFVTHPGYDTGNGTOL DOW
]		1	SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYDDNNGOF
1	ļ) ·	ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLOFRVPGTST8AT
)]:	LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVNEGLNQPT
		1 :	DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD
ĺ]	1 :	SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP
1		1 i	HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR
1		1;	RPGGEPSPECTTGOGVNOVGODUSCO
1	1	15	RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ ADREDSRE
365	8066		
1	1		RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP
ļ		1 1	PSWRRQPPGGIRRDFSRRLRREANLVATCI, PVRASI, DHPI, NIMI.
	1	1 1	GPGPGLLLLAVLCLGTAVPSTGASKSKROAOOMVOPOSDVAVS
1		1 4	15KPGCYDNGKHYQINQOWBRTYLGNALVCTCYGGSRGENCESK
i			TENERMODOVIII
	}] *	EAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS
		1 0	PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS TIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT KPIAEKCFDHAAGTSYVVGETWEKPYQGWMWVDCTCLGEGSGR

÷.
÷.
÷
::-

SEQ	Predicted	Predicted end	l hari
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	1 1	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1 40.	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	1	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
- [residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
•	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	acquence	_	\=possible nucleotide insertion)
			ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG
	1	}	EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT
i			DECUTIVE ICHOL A TRACCIONAL A CHECK CONTROL OF THE
i	1	1	DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG
]	j	1	GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQ
	i	1	KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR
1	}	}	DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQW
	l	1	DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN
Ī	1		DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDOCODSETGTFYOT
ı	ł	l	GDSWEKYVHGVRYQCYCYGRGIGEWHCOPLOTYPSSSGPVEVFI
j			TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP
Ì		1	GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST
i	ł	ł	PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV
Į]		SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN
1			VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR
f			PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYN
1			ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQFVEVTDV
1	1		VVTTMWTDDECAUTOUTUNETED FOR THE TOTAL OF THE
	1		KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AEN
1	1		TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVN
}]		ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY
			PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN
ı	}		TEVTETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTSDSGSIV
1	1 .		VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH
	[LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV
1	1 1		HADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV
J.	J [PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKNE
			GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEOHESTP
	1		LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TDT
1 1	j j		TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTPGTEYVV
i l			SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD
1	l j		APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD
1 .	j j		YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNS
1	.		ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI
1 1	i		EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV
1 1	!		DVDSTYTAMESDOCOUSDYDUMYGGDDDSCTOTY DD2 DD DD DD DD DD DD DD DD DD DD DD DD
1 1	1		DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA
1 [ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT
1 1			QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS
1			SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR
1 1			ARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP
	•		DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS
]]	1		NLRFLATTPNSLLVSWQPPRARITGY11KYEKPGSPPREVVPRP
			RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP
			QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIOLPGT
1		ļ	SCOOPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQE
1 1			ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT
[LTGLTRGATYNI IVEALKDQQRHKVREEVVTVGNSVNEGLNOPT
; !		ļ	DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD
]	1		SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP
		į	HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR
1		Ì	RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ
	I		ADREDSRE
5366	8066	703	RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP
1	1		PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML
1			REPERCELLIANT OF CHANDERGY CYCEROS CONTROL CONTROL
1			RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS
1 1	1	I	QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK
]]		J	PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS
1	Į.	l	CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT
1		1	CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR
1	Ì	}	ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG
1	1	i	EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT
1	1		DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG
L		1	GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQ
			The state of the s

SEQ	Predicted	Predicted end	l Amino d d
ID	beginning	nucleotide	Amino acid segment containing signal peptide
.NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ł	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
į.	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
j	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
ŀ	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion,
ļ	Bequence		\≈possible nucleotide insertion)
ľ	1	1	KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR
	ľ		DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDOW
Í		· ·	DKQHDMGHMMRCTCVGNGRGEWTCIAYSOLRDOCIVDDTTVNVN
ļ.	•		DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTEYQT
1	ł	1	GDSWEKYVHGVRYQCYCYGRGIGEWHCOPLOTYPSSSGPVEVET
İ			TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP
į			GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST
	1	· ·	PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV
		ĺ	SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN
Ì	1	i	VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR
1	1		PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYN
			ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQFVEVTDV
1	j .		KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AEN
			TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVN
	ı		ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY
	[]		PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN
ŀ	i I		TEVTETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTSDSGSIV
ł			VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH
	1		LEANPOTGVLTVSWERSTTPDITGYRITTTPTMGQQGNSLEEVV
j			IIADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV
1	1		PPPTDLRFIN/ILGPDTMRVIW\APPPSIDLTNFLVRYSPVKNE
			GRMLOSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEQHESTP
			\LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI
í	1		TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTPGTEYVV
]		SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPISLLI\SWD
1	1 1		APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD
	!		YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNS
			ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI
	. [EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV
1	<u> </u>		DVDS1KIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA
	1 1		ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT
	l i		QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS
1	}		SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR
			ARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP
1	l l		DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS
	[1	NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGS?PREVVPRP
1			RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP
1	1	i	QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT
			SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQE
1	J	J	ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT
] ;		ļ	LTGLTRGATYNI IVEALKDQQRHKVREEVVTVGNSVNEGLNQPT
1			DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD
			SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP
	1	ł	HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR
1 1		Ì	RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ
	ł	1	ADREDSRE
5367	235	3591	KKILNMLCKKNIVIEYLADILYEYLYGFCFSGIKKYLIIHVLRL
]]	1	_	ILELWMTRLLLEKSVSLQTQYLLLIVKILSWFPGKEMRHHLQIM
1			EVMMRKQDS/RIVGNGSEQQLQKELADVLMDPPMDDQPGEKELV
j		İ	KRSQLDGEGDGPLSNQLSASSTINPVPLVGLQKPEMSLPVKPGQ
1 [[1	GDSEASSPFTPVADEDSVVFSKLTYLGCASVNAPRSEVEALRMM
1 1			SILRSQCQISLDVTLSVPNVSEGIVRLLDPQTNTEIANYPIYKI
, 1	}	į	LFCVRGHDGTPESDCFAFTESHYNAELFRIHVFRCEIQEAVSRI
	1		LYSEATA ERREAKOTRI CATA A DOTTO DE LA CONTROL DE LA CONTRO
	1		LYSFATAFRRSAKOTPLSATAAPQTPDSDIFTFSVSLEIKEDDG
1 1	J		KGYFSAVPKDKDRQCFKLRQGIDKKIVIYVQQTTNKELAIERCF
ļ [GLLLSPGKDVRNSDMHLLDLESMGKSSDGKSYVITGSWNPKSPH
; l			FQVVNEETPKDKVLFMTTAVDLVITEVQEPVRFLLETKVRVCSP
1		ľ	NERLFWPFSKRSTTENFFLKLKQIKQRERKNNTDTLYEVVCLBS
]]	ESERERRKTTASPSVRLPQSGSQSSVIPSPPEDDEEEDNDEPLL
1	ł	1	SGSGDVSKECAEKILETWGELLSKWHLNLNVRPKQLSSLVRNGV
			PEALRGEVWQLLAGCHNNDHLVEKYRILITKESPQDSAITRDIN

SEO	Predicted	Predicted end	Amino poid comment
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
)	amino acid	residue of	S-Sarine, T. Thursday, K-Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
ţ	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotice deletion,
	sequence	ļ	\=possible nucleotide insertion)
1			RTFPAHDYFKDTGGDGQDSLYKICKAYSVYDEEIGYCQGQSFLA
i			AVLLLHMPEEQAFSVLVKIMFDYGLRELFKQNFEDLHCKFYQLE
1	(ĺ	RLMQEYIPDLYNHFLDISLEAHMYASQWFLTLFTAKFPLYMVFH
1	Ĭ	ĺ	IIDLLLCEGISVIFNVALGLLKTSKDDLLITDFEGALKFFRVQL
	1		PKRYRSEENAKKLMELACNMKISQKKLKKYEKEYHTMREQQAQQ
J	1	l	EDPIERFERENRRLQEANMRLEQENDDLAHELVTSKIALRKDLD
1	İ		NAEEKADALNKELLMTKQKLIDAEEEKRRLEEESAHLKKMCRRE
ĺ	(LDKAESEIKKNSSIIGDYKQICSQLSERLEKQQTANKVEIEKIR
ļ			QKVDDCERCREFFNKEGRVKGISSTKEVLDEDTDEEKETLKNQL
1	Ì		REMELELAQTKL\QLVEAECKIQD\LEHPF*GLPFNE\VQAA\K
L			KTWFNRTLSSIKTATGVQGKETC
5368	573	2014	GAAAGAADPRRGSLGGRTMLDFAIFAVTFLLALVGAVLYLYPAS
1			RQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLHERYGPVVS
1	ł	Ì	FWFGRRLVVSLGTVDVLKQHINPNKTLD/LF*NHAEVIIKVSIW
1			WWQCE*KP\QRKKLYENGVTDSLKSNFALLLKLPEELLDKWLSY
			PETQH\VPLSQHMLGFAMKSVTQMVMGSTFEDDQEVIRFQKNHG
			TVWSEIGKGFLDGSLDKNMTRKKQYEDALMQLESVLRNIIKERK
			GRNFSQHIFIDSLVQGNLNDQQILEDSMIFSLASCIITAKLCTW
1			AIWFLTTSEEVQKKLYEEINQVFGNGPVTPEKIEQLRYCQHVLC
			ETVRTAKLTPVSAQLQDIEGKIDRFIIPRETLVLYALGVVLQDP
1	1		NTWPSPHKFDPDRFDDELVMKTFSSLGFSGTQECPELRFAYMVT
1	[TVLLSVLVKRLHLLSVEGQVIETKYELVTSSREEAWITVSKRY
5369	1	6622	PRSLCFSLWAEAAVLADGGLRRRRRLLRGTMSASFVPNGASLED
}	İ		CHCNLFCLADLTGIKWKKYVWQGPTSAPILFPVTEEDPILSSFS
1	J		RCLKADVLG/VWRRDQRPERRE\L*IFWGGEDP\VLLTLFTMTY
			QKKKMECGRMDFPMNAVLCFSKAVHNLLERCLMNRNFVRIGKWF
1			VKPYEKDEKPINKSEHLSCSFTFFLHGDSNVCTSVEINQHQPVY
1			LLSEEHITLAQQSNSPFQVILCPFGLNGTLTGQAFKMSDSATKK
1 :	1		LIGEWKQFYPISCCLKEMSEEKQEDMDWEDDSLAAVEVLVAGVR
			MIYPACFVLVPQSDIPTPSPVGSTHCSSSCLGVHQVPASTRDPA
1]		MSSVTLTPPTSPEEVQTVDPQSVQKWVKFSSVSDGFNSDSTSHH
			GGKIPRKLANHVVDRVWQECNMNRAQNKRKYSASSGGLCEEATA
			AKVASWDFVEATQRTNCSCLRHKNLKSRNAGQQGQAPSLGQQQQ
			ILPKHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A
]	, ,		SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTEMANSPQ
	i		PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMPTPDPLVPSKPM
			EDRIDSLSQSFPPQYQEAVEPTVYVGTAVNLEEDEANIAWKYYK
			FPKKKDVEFLPPQLPSDKFKDDPVGPFGQESVTSVTELMVQCKK
]]			PLKVSDELVQQYQIKNQCLSAIASDAEQEPKIDPYAFVEGDEEF
1			LFPDKKDRQNSEREAGKKHKVEDGTSSVTVLSHEEDAMSLFSPS
			IKQDAPRPTSHARPPSTSLIYDSDLAVSYTDLDNLFNSDEDELT
			PGSKRSANGSDDKASCKBSKTGNLDPLSCISTADLHKMYPTPPS
1			LEQHIMGFSPMNMNNKEYGSMDTTPGGTVLEGNSSSIGAOFKIE
			VDEGFCSPKPSEIKDFSYVYKPENCQILVGCSMFAPLKTLPSQY
1			LPLIKLPEECIYRQSWTVGKLELLSSGPSMPPIKEGDGSNMDQE
			YGTAYTPQTHTSCGMPPSSAPPSNSGAGILPSPSTPRFPTPRTP
	1		RTPRTPRGAGGPASAQGSVKYENSDLYSPASTPSTCRPLNSVEP
(1		ATVPSIPEAHSLYVNLILSESVMNLFKDCNSDSCCICVCNMNIK
1 1			GADVGVYIPDPTQEAQYRCTCGFSAVMNRKFGNNSGLFFEDELD
, j	j		IIGRNTDCGKEAEKRFEALRATSAEHVNGGLKESEKLSDDLILL
]	1		LQDQCTNLFSPFGAADQDPFPKSGVISNWVRVEERDCCNDCYLA
1 1	1		LEHGRQFMDNMSGGKVDEALVKSSCLHPWSKRNDVSMQCSQDIL
1			RMLLSLQPVLQDAIQKKRTVRPWGVQGPLTWQQFHKMAGRGSYG
1	1		
1	ŀ		TDESPEPLPIPTFLLGYDYDYLVLSPFALPYWERLMLEPYGSQR DIAYVVLCPENEALLNGAKSFFRDLTATYESCRLGOHRPVSRLL
1	j		
	1	, i	TDGIMRVGSTASKKLSEKLVAEWFSQAADGNNEAFSKLKLYAQV
	l	l	CRYDLGPYLASLPLDSSLLSQPNLVAPTSQSLITPPQMINTGNA
1 1	į		NTPSATLASAASSTMTVTSGVAISTSVATANSTLTTASTSSSS
1. 1	İ		SNLNSGVSSNKLPSFPPFGSMNSNAAGSMSTQANTVQSGQLGGQ
	[QTSALQTAGISGESSSLPTQPHPDVSESTMDRDKVGIPTDGDSH
L			AVTYPPAIVVYIIDPFTYENTDESTNSSSVWTLGLLRCFLEMVQ

SEQ	Predicted	Predicted end	Dmino agid gogment containing
ΔI	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	1	\=possible nucleotide insertion)
			TLPPHIKSTVSVQIIPCQYLLQPVKHEDREIYPQHLKSLAFSAF
			TQCRRPLPTSTNVKTLTGFGPGLAMETALRSPDRPECIRLYAPP
1	1	Į.	FILAPVKDKQTELGETFGEAGQKYNVLFVGYCLSHDQRWILASC
1	1	j ·	TDL.YGELLETCIINIDUDNDADDKYGGADDWGGCLSHDQRWILASC
		1	TDLYGELLETCIINIDVPNRARRKKSSARKFGLQKLWEWCLGLV QMSSLPWRVVIGRLGRIGHGELKDWSCLLSRRNLQSLSKRLKDM
ĺ			CRMCGISAADSPSILSACLVAMEPQGSFVIMPDSVSTGSVFGRS
1	ľ	1	TTLNMQTSQLNTPQDTSCTHILVFPTSASVQVASATYTTENLDL
		1	AFNPNNDGADGMGIFDLLDTGDDLDPDIINILPASPTGSPVHSP
			GSHYPHGGDAGKGQSTDRLLSTEPHEEVPNILQQPLALGYFVST
ł		1	AKAGPLPDWFWSACPQAQYQCPLFLKASLHLHVPSVQSDELLHS
\		1	KHSHPLDSNQTSDVLRFVLEQYNALSWLTCDPATQDRRSCLPIH
		{	FVVLNQLYNFIMNML
5370	1226	716	
}		1 .20	RWSRKLELRRAAQATESRPPQSQEMHPPTGKEVHALKRLRDSAN
1	1]	ANDVETVQQLLEDGADPCAADDKGRTALHFASCNGNDQIVQLLL
	1		DHGADPNORDGLGNTPLHLAACTNHVPVITTLLRGGARVDALDR
1	1		AGRTPLHLAKSKLNILQEGHAQCLKAVR/HGGEADHPYAEGVSG
ı	1		APRAT*AARCSGVFPSPSRWLGSAPWSRSSCTIWSLPLHEAKCR
1	1		AVRPLSSAAQGSAPSSSSCCTVSTSLALAESLSLFRACTSLPVG GCISWL
5371	1331	167	IAAMLWKLLLRSQSCRLCSFRKMRSPPKYRPFLACFTYTTDKQS
-			SKENTRTVEKLYKCSVDIRKIRR*KDGYF*RMKPMLKKLRI/F
ſ	1		LOELGADETAVASILERCPEAIVCSPTAVNTQRKLWQLVCKNEE
 	(ELIKLIEQFPESFFTIKDQENQKLNVQFFQELGLKNVVISRLLT
1			AA DNIGHNDYEKNYOMUR I OEGY DIGGERINGEN TO THE TENT OF
}	[AAPNVFHNPVEKNKOMVRILQESYLDVGGSEANMKVWLLKILSQ NPFILLNSPTAIKETLEFLQEQGFTSFEILQLLSKLKGFLFQLC
			PRSIQNSISFSKNAFKCTDHDLKQLVLKCPALLYYSVPVLEERM
1			QGLLREGISIAQIRETPMVLELTPQIVQYRIRKLNSSGYRIKDG
	1		HLANLNGSKKEFEANFGKIQAKKVRPLFNPVAPLNVEE
5372	51	857	SPGAQFLWAAPDMPDPLFSAVQGKDEILHKALCFCPWLGKGGME
1			PLRLLILLFVTELSGAHNTTVFQGVAGQSLQVSCPYDSMKHWGR
]	ŀ		RKAWCRQLGEKGPCQRVVSTHNLWLLSFLRRWNGSTAITDDTLG
1 1	[GTLTITLRNLQPHDAGLYQCQSLHGSEADTLRKVLVEVLADPLD
1			HRDAGDLWFPG\DLRASRMPMWSTASPGASWKEKSPSHPLPSFS
1 1			SWPASFSSRF*QPAPSGLQPGMDRSQGHIHPVNWTVAMTQGISS
L. 1	ì	j	KLCQG KLCQG
5373	2814	346	VKKTKSIFNSAMQEMEVYVENIRRKFGVFNYSPFRTPYTPNSQY
1 1			QMLLDPTNPSAGTAKIDKQEKVKLNFDMTASPKILMSKPVLSGG
			TGRRISLSDMPRSPMSTNSSVHTGSDVEQDAEKKATSSHFSASE
1 !			ESMDFLDKSTASPASTKTGQAGSLSGSPKPFSPQLSAPITTKTD
1 1	1		KTSTTGSILNLNLDRSKAEMDLKELSESVQQQSTPVPLISPKRQ
	1		IRSRFQLNLDKTIESCKAQLGINEISEDVYTAVEHSDSEDSEKS
))	i J		DSSDSEYISDDEQKS*GTSQEDTEDKEGCQMDKEPSAVKKKPKP
] }	1		TNPVEIKEELKSTSPASEKADPGAVKDKASPEPEKDFSGKAKPS
1 [1	i	PHPIKDKLKGKDETDSPTVHLGLDSDSE\NELVIDLGEDHSGRE
1	Į		GRKNKKEPKEPSPKQDVVGKTPPSTTVGSHSPPETPVLTRSSAO
1 1	ł	Į.	TSAAGATATTSTSSTVTVTAPAPAATGSPVKKQRPLLPKE\TAP
1 1	ļ	j	AVQRSCGTSSTVQQKEITQSPSTSTITLVTSTOSSPLVTSSGSM
} I	j		STLVSSVNGDLPIGTASADVAADIAKYTSKL\MDAIKGTM\TET
1		Į.	YNDLSKN\TTWKAQLAEDSQGLRIEIEKLOWLHOOEL\SEMKHN
į į	i	1	LELTMAEMRQSWEQERDRLIAEVKKOLELEKOOAVDETKKKOWC
,	ł	1	ANFKKEAIFYCCWNTSYCDYPCQ\QAHWPEH\MKSCTOSATAPO
	1		\QEADAE\VNTETLNKSSQGSSSSTOSAPSETASA\SKEKETSA
1	1		EKSKESGSTLDLSGSRETPSSILLGSNOGSDHSR\SNKSSWSSS
			DEKRGS\TRSDHN/TPSTQHGRSLLPGKESRAGTPFLGTSK
5374	2814	346	VKKTKSIFNSAMQEMEVYVENIRRKFGVFNYSPFRTPYTPNSOV
1 1		j	QMLLDPTNPSAGTAKIDKQEKVKLNFDMTASPKILMSKPVLSGG
1			TGRRISLSDMPRSPMSTNSSVHTGSDVEQDAEKKATSSHFSASE
1		1	ESMDFLDKSTASPASTKTGQAGSLSGSPKPFSPQLSAPITTKTD
] [1	KTSTTGSILNLNLDRSKAEMDLKELSESVOOOSTPVPLISPKRO
1	1	1	IRSRFQLNLDKTIESCKAQLGINEISEDVYTAVEHSDSEDSEKS
<u> </u>		1	DSSDSEYISDDEQKS*GTSQEDTEDKEGCOMDKEPSAVKKKPKP
		~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	- CHANGE CHANGE AF

SEO

Deginning nucleotide location corresponding continue c	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
NO: nucleotide corresponding to first of first amino acid residue of smino acid residue of smino acid sequence		•	1	(A=Alapine C=Custoine D=Assertion
Cocation Corresponding	NO:			Glutamic Agid F-Phonelalanian G. G.
corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence service of amino acid sequence service of amino acid sequence service of amino acid sequence service of amino acid sequence service of amino acid sequence service of amino acid sequence service of amino acid sequence service of amino acid sequence service of amino acid sequence service of amino acid sequence service of amino acid sequence service of amino acid sequence service of amino acid sequence service of amino acid sequence service of amino acid sequence service of amino acid sequence service of amino acid sequence service of amino acid sequence sequence service of amino acid sequence sequenc		•		Gideanic Acid, Fernenylatanine, GeGlycine,
amino acid residue of amino acid residue of amino acid sequence Securine, T=Threonine, V=Vydaine, W=Tryptophan, X=Tytrosine, X=Duknown, *=Stop Codon, /=possible muclectide deletion SEGURACY SEGURACY TARMENT VETTERRENTUCKS*VPGSFWD SEGURACY TARMENT VETTERRENTUCKS*VPGSFWD SEGURACY TARMENT VETTERRENTUCKS*VPGSFWD SEGURACY TARMENT VETTERRENTUCKS*VPGSFWD OVXTICLDVANSSERPTFVETVETVETVETPROPORTHEOLOGIACHESIS EELLISGADIKVGIGPGSVCTTEKETVGVATPULSANVECNDAA HOLKOHIISDGCGCGCOPDUARAFAGAALKELSERTTFITVTOO VMPIFSEAC SSTOP 2009 664 CASGTTLRFLPDLPPLKREMINGLISVLLAPRESTLKERSEDGLTEXY FPKODVETTIRDLIGETSTCTVVAGALKELSERTTFITVTOO VMPIFSEAC SSTOPSSKATYSGVYSVUTTANNOTVOTEPHANVLCS*VPGSFMD VPGWGCVFLIYKLFTLWOMPS*VLLAPRESTLKERSEVDLTER SSTOPSSKATYSGVYSVUTTANNOTVOTEPHANVLCS*VPGSFMD VPGWGCVFLIYKLFTLWOMPS*VLDASSILVAEPKSELTTANT RITSLUCMGEFAGORPOCLEHARENGVTGSFWD VPGWGCVFLIYKLFTLWOMPS*VLDASSILVAEPKSELTTANT RITSLUCMGEFAGORPOCLEHARENGVTGSFWD VPGWGCVFLIYKLFTLWOMPS*VLDASSILVAEPKSELTTANT RITSLUCMGFAGORPOCLEHARENGVTGSFWD VPGWGCVFLIYKLFTLWOMPS*VLDASSILVAEPKSELTTANT RITSLUCMGFAGORPOCLEHARENGVTGSFWD VPGWGCVFLIYKLFTLWOMPS*VLDASSILVAEPKSELTTANT RITSLUCMGFAGORPOCLEHARENGVTGSFWD VPGWGCVFLIYKLFTLWOMPS*VLDASSILVAEPKSELTSTRITTINVTGO VRYLTCLWAMPSSENVENGVKRFPGWTINAGHVVTGSFWD VRYLTCLWAMPSSENVENGVKRFPGWTINAGHVVTGSFWD VRYLTCLWAMPSSENVENGVKRFPGWTINAGHVVTGSFWD VRYLTCLWAMPSSENVENGVKRFPGWTINAGHVVTGSFWD VRYLTCLWAMPSSENVENGVKRFPGWTINAGHVVTGSFWD VRYLTCLWAMPSSENVENGVKRFPGWTINAGHVVTGSFWD VRYTCCHGCAUGAGAAASSPGGSAAGWCCSVLDGAAGACTUSCUTSSCVS SOPSSNRAAPODELGGGSSSSESGVKPGAAAGASSSONAPHL SGRALADAAAASSPGGSAAGWCCSVLDASPGGGCTOP VRRYTCCHGCAUGAGAAAASSPGGSAAGWCCSVLDAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	Ī	N Company of the Comp		nantscidine, laisoleucine, Kabysine,
amino acid residue of amino acid sequence S-Serine, T-Threodino, V-Valina, acid sequence Sequence SPSFRONKOTYSOVPILANMOTYGFERMAVICES VVESTPO VPOMCOTILINE, TILKERGILLISUELPASILLORE SERVICES VPOMCOTILINE, TILKERGILLISUELPASILLORE SERVICES VPOMCOTILINE, TILKERGILLISUELPASILLORE SERVICES VPOMCOTILINE, TILKERGILLISUELPASILLORE SERVICES VPOMCOTILINE, TILKERGILLISUELPASILLORE SERVICES SPSFRONKOTYSOVPILANMOTYGFERMAVICES VVESTPOM VPOMCOTILINE, TILKERGILLISUELPASILLORE SERVICES VPOMCOTILINE, THE SERVICE SERVICES SERVICES SERVICES BELLEROKKYKLFYGESS-I.MAM KEXAGOVARTASEGKTUEV PERCHET SERVICES TENDENCH SERVICES SERVICES SERVICES SPONGOTILLISUEL SERVICES SERVI			1	L=Leucine, M=Methionine, N=Asparagine,
residue of amino acid sequence		1		P=Proline, Q=Glutamine, R=Arginine,
sequence Codon, /-possible nucleotide deletion, Sequence Seprence Nucleotide insertion Sequence Seprence Nucleotide insertion Sequence Seprence Nucleotide insertion Veposcible nucleotide insertion Veposcible nucleotide insertion Veposcible nucleotide insertion Veposcible nucleotide insertion Veposcible nucleotide insertion Veposcible nucleotide insertion Veposcible nucleotide insertion Veposcible nucleotide insertion Veposcible nucleotide insertion Veposcible nucleotide insertion Veposcible nucleotide insertion Veposcible nucleotide insertion Set insertion insertion Set insertion insertion Veposcible nucleotide insertion Veposcible nucleotide insertion Set insertion insertion Veposcible nucleotide insertion Veposcible nucle				S=Serine, T=Threonine, V=Valine,
sequence Codon, /-possible nucleotide deletion,		1		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Sequence Apossible nucleotide insertion		1	sequence	Codon, /=possible nucleotide deletion.
SSS-FRINKCYTSGVF11AANNUTVGTPENAKULCKS-VPGESPAN VOOMCCVELIVKEPTLAKKMILLSULDASILUKERSLEFTAWH KHYSLUVMGEFAGGNPDCLEHLAASSCTGSSDFEGLEGILEAFI OVKYLCLDVANGSEFFUEFEVKOWKRFPGUTTMAGNUVTGENV EELLISGADIIKVG1GPGSVCTTRKKTGVGYPGLSAVMECADAA HGLKGHI1SDGGGCGCGDVAKAFGGGDPWHAGHGESGGG ELTERDGKKYKLFYGMSS-Y-\AM\KKXAGGVAEYRASEGKTVEV PKGDVEHTIRGHGGISTGTTVVAAAKKLEISPTTSIVTOO VAPIFSSAC 5379 664 GASGTTLRFLDDLPGLKKREATSRRRALKPRGRIJVMTSCLPAL RFIATFELSAMPHINDNOKLDFKOVLLRPKRSTLKSRSEVDLTR SSSFRNSKGTYSGVF11AANNUTVSTEEMAKULCSTPAL RFIATFELSAMPHINDNOKLDFKOVLLRPKRSTLKSRSEVDLTR SSSFRNSKGTYSGVF11AANNUTVSTEEMAKULCSTPAL RFIATFELSAMPHINDNOKLDFKOVLLRPKRSTLKSRSEVDLTR SSSFRNSKGTYSGVF11AANNUTVSTEEMAKULCSTPAL RFIATFELSAMPHINDNOKLDFKOVLLRPKRSTLKSRSEVDLTR SSSFRNSKGTYSGVF11AANNUTVSTEEMAKULCSLGALLASHLOKE SSSTANSKGTYSGVF11AANNUTVSTEEMAKULCSLGALLASHLOKE RFIATFELSAMPHINDNOKLDFKOVLLRPKRSTLKSRSEVDLTR SSSFRNSKGTYSGVF11AANNUTVSTEEMAKULCSLGALLASHLOKE SSSTANSKGTYSGVF11AANNUTVSTEEMAKULCSLGALLASHLOKE RFIATFELSAMPHINDNOKLDFKOVLLRPKRSTLKSRSEVDLTA RRINGTAKTELTAKTOVATATATATATATATATATATATATATATATATATATA		sequence	1	\=possible nucleotide insertion)
VOMCCUPILYKLPTILKRKULLUSVILPASIUVAREFSELTANI KHYSIVUMQREFAGONPOLENIALASSICTSSIPPOLOGIULFAIP OVKYICLDVANGYSEHFUEVKUVKREFOULTIMAGNUVTUSVIL EELILGSADII IKWGIOPSSVETRIKKTGVOYPOLGSAVMECADA HOLKSHI ISDGGCSCFGUVKAFGAGADEVMIGALAGHESSITVEV PEKGDVEHTIRDILGGIRSTCTYVGARKLKELSRRTTFIRVTOOV OVPIPSEAC 379 664 OASGTTIRFLDDLPQLKREATSRRALKFERRILVLMTSCLPAL FIRATELSAANIHODVKLDERKOVLLREKKSTLKERSEVDLTR SFS RRASKQTYSOVPI LAAMMUTVOTFERAKVLCKS - VPOESTU WERGOVETILKRIPLANIHODVKLDERKOVLLREKKSTLKERSEVDLTR SFS RRASKQTYSOVPI LAAMMUTVOTFERAKVLCKS - VPOESTU WERGOVETILKRIPLANIHODVKLDERKOVLLREKKSTLKERSEVDLTR SFS RRASKQTYSOVPI LAAMMUTVOTFERAKVLCKS - VPOESTU WERGOVETILKRIPLANIHODSSTUSDERGLEGULANIHON WERGOVETILKRIPLANIHONSSTUDEN SONDERGEVDLEGULANIHON WERGOVETILKRIPLANIHONSSTUDEN SONDERGEVDLEGULANIHON WERGOVETILKRIPLANIHONSSTUDEN SONDERGEVDLEGULANIHON WEYLICLDVANGYSHEVHERINGSSTUDENGLANIHON EELILGGADI IKWGI GEPSUVTHERKETOVEV VILGANIHOON RUKYICLDVANGYSHEVHEN SONDERGETVELEV FERGOVERVILLYGMSS - I AMM KKYAGGGAREVEGETVELEV PRODUMENTAMUK KYAGGGAREVERSTUDENGSTUDEN GELIGEROKKYKLEVINGSS - I AMM KYAGGGAREVEGETVELEV PPKGDVEHTIRDILGGIRSTCTYVGAAKLKELSRRTFFIRVTOQ VEPLFERSON PERAGGERGRAAAARSFGGSAAGMRECFSVLDERGGTVBSCVS SOPSSNRAAPOBELGGRGSSSSSESKIPCEARRIGGTVBLYSGSSONSP RLPRRTVESHINGSTEMODEVOLLANIHORGUTESTILVSEL SGRRLSLGERSGGAAAGGSLDMRGCTCSSLEYPSVSSPOSSP RLPRRTVESHINGSKALUKKALIRGAAPPERPEPROFREGULANOKII HARDIVERSHIVENSHIVALKKALIRGAAPPERPEPROFREGULANOKII HARDIVERSHIVENSHIVALKKALIRGAAPPERPEPROFREGULANOKII HARDIVERSHIVENSHIVALKKALIRGAAPPERPEPROFREGULANOKII HARDIVERSHIPPTUSHINGHANIHON VILKUSVALUKSUR SELKIT KISPLARCKYTI EEPIHSAGGRESGAAGGSLANGKOTOSSONAH WERDHTYYAMKULSKKALIRGAAPPERPEPROFREGULSSONAH BELLETT KISPLARCKYTI EEPHHSAGGRESGAARGATMSSON SOPSSIRAAPOBELGGGSSSSSESONCCARRGCTSSISCHA BELKIT KISPLARCKYTI EEPHHSAGGRESGAATAARSONGSONGERSTUSSONAH BELKIT KISPLARCKYTI EEPHHSAGGRESGAARGATMSSON SOPSSIRAAPOBELGGGGSSSSSESONCCARRGCTSSISCHA BELKIT KISPLARCKYTI EEPHHSAGGRESGAATAARSONGSONAH BELKIT BERGORDAAARSONAH TILKTUSTAANIH BELKIT BERGORDAAARSONAH TILKTUSTAANIH BELKIT BERGORDAAARSON				SFSFRNSKOTYSGVPI I AANMOTVGTFEMAKVLCKS*VDGGEMD
HYSLIVOMOEPAGON PDCLEHLANSSTOSPEGLEG LIEATP OVKYICLDVANYSEHVEYKOVREPEGOTTMAGNIVYCENV EBILISGADI IKVGIGGSVCTTRKITGVGYPGLSAVWEGDAA HOLKGHI 13 BGGCSCPGDVAKAFQAGDPWILAGGHAGHESGG ELIERDOKKYKLFYGMSS 1 \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	1		1	VPOMGCVFLIYKI,FTI,KWKMI,I,I,SVI,I,DACTI,WAEVEGI EMALITI
GVKYICLDVANGYSEHFVEFVKDVRRFPORTIMGROWYGENV EBLILGSOAL IKVGIGGGSUCTTAKKTGVOFDLSAVMECADA HOLKGHI ISDGGCSCPODVAKAFGAGAPFVMLGGHLAGHESGG ELIERDCKKYKLFYGNSS *I LWM KKYAGGAPFVMLGGHLAGHESGG ELIERDCKKYKLFYGNSS *I LWM KKYAGGAFASEGGKTUV PFKGDVEHTIRDILGGIRSTCTYVGAAKLKELSRRTTFIRVTOO VPHFSSEC 5379 664 CASGTTLRFLPDLPOLEKREATSRNRALKFRGELVLWTSCLPAL RIATRILGAHPHDMDVLCHFSOLVLLFRKSELSKRSEPDLTR SFSFRNSKOTYSGVFIIAANNDTVGTFEMAKVLCKS *VPGSFMD VPOMGCVFIITKGLTLKMEMLLSVLLPASITLKSRSEPDLTR SFSFRNSKOTYSGVFIIAANNDTVGTFEMAKVLCKS *VPGSFMD VPOMGCVFIITKGLTKLAGTHAGAPTKAGAPTWAMGVVTGENV KHYSLVOWGEFAGONPOLCHHAASSGTGSSDFEGLBGILGAIP GOVKYICLDVANGYSEHFVEWVDVRKFRFPATMGVVYGENV KHYSLVOWGEFAGONPOLCHHAASSGTGSSDFEGLBGILGAIP GOVKYICLDVANGYSEHFVEWVDVRKFRFPATMGVVYGENV KHYSLVOWGEFAGONPOLCHHAASSGTGSSDFEGLBGILGAIP GOVKYICLDVANGYSEHFVEWVDVRKFRFPATMGVVYGENV RELLESGADIIKVGIGPGSVCTTFKKTGVGYPGLSAVMECADA HOLKGHIISDGGSCSCPODVARFARGAADFYMMGVVYGENV FERLESGADIIKVGIGPGSVCTTFKKTGVGYPGLSAVMECADA HOLKGHIISDGGSCSCPODVARFARGAADFYMGAVASEAGACTVEV PFKGDVERFIIRDLGGIGSTGTVGVGAALKELSGLAGHSSGCV VNPIFSBAC 2050 FERRAGGAERGRANAARSPGGSAAGWECFSVLDEAGACTWSSCVS SOPSSNRAAPODELGGIGSSSSSSGNCFCALRGILSSIS HLGME SFIVYTCEGFCAVADLGLARDFYLEADOCHOOTSGOARPHI SGRKLSLGERSGGGLAAGGSLDMORGCICPSLPYSPVSSPOSSP RLPRFPTVENSHVSITGMOCYOLMOYTLKDGSGYAVVLA NENDDYTYAMKVLSKKLIKQAAFFRRPPFRGTFPAFGGCTOP ROPT \COUNTY COUNTY THE COUNTY COUNTY THE COUNTY COUNTY REDDYTYAMKVLSKKLIKOAAFFRRPPFRGTFPAFGGCTOP ROPT \COUNTY COUNTY THE COUNTY COUNTY COUNTY COUNTY ROPT \COUNTY COUNTY COUNTY COUNTY COUNTY COUNTY REDDYTYAMCHOOT THE COUNTY COUNTY COUNTY COUNTY REDDYT COUNTY COUNTY COUNTY COUNTY COUNTY COUNTY REDDYT COUNTY COUNTY COUNTY COUNTY COUNTY COUNTY REDDYT COUNTY COUNTY COUNTY COUNTY COUNTY REDDYT COUNTY COUNTY COUNTY COUNTY COUNTY REDDYT COUNTY COUNTY COUNTY COUNTY REDDYT COUNTY COUNTY COUNTY REDDYT COUNTY COUNTY COUNTY REDDYT COUNTY COUNTY COUNTY REDDYT COUNTY COUNTY COUNTY REDDYT COUNTY REDDY COUNTY COUNTY REDDY COUNTY REDDY COUNTY COUNTY COUNTY REDDY COUNTY REDDATE COUNTY REDDY COUNTY REDDY COUNTY REDDY COUNTY REDDY COUNTY R	Į.	ì	i	KHYSI VOMOEFACONDOG EULA A CCCEGGGDDEGA DOTA DA
ERLILISGADI IKVGIGGGSVCTTRKITGVGYPQLSAVMEGADAM HOLKGHI 13 BGGGSCPGDVAKFORGADFMAGHESEGG ELIERDCKKYKLFYGNS* 1 \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	1		i	OUVATOL DAY MONGDIA DE LE CONTRACTOR DE LA CONTRACTOR DE
HOLKOHIISDGGCSCPODVAKAFGAGADFYMLGGKLAGHSESGG ELIERDCKKYKLFYGMSS 1 (AM) KKYAGGVAKASGAGTUMYTE SEGATUMY PFKGDVBHTTRDILGGIRSTCTYVGAAKIKELSRRTTPIRVTOO VMPIFSEAC FRIATPRILAMPHDMDVLKJEKSCKSTENRALKPRGGLULMYTSCLPAL RITATPRILAMPHDMDVLKJEKSCKSTENRALKPRGGLULMYTSCLPAL RITATPRILAMPHDMDVLKJEKSCLVLKSSEVDLTR SYSPRNSKOTYSGVPIIAANNDTVGTFEMARVLCKS 1 VDSSFMD VVOMCCVFILIVKALTILKMENLLSVLLPAS INSTALKSRSEVDLTR SYSPRNSKOTYSGVPIIAANNDTVGTFEMARVLCKS 1 VDSSFMD VVOMCCVFILIVKALTILKMENLLSVLLPAS INSTALKSRSEVDLTR SYSPRNSKOTYSGVPIIAANNDTVGTFEMARVLCKS 1 VDSSFMD VVOMCCVFILIVKALTSVLTAVETTAKTOKY POLGAVMERODDA HOLKOHIISDGGCSCPODVAKAFGAGADFYMNIAGRIVYTGGMV KIYSLUVMOSSEMFVEVKVDVRKPRPOHTIMAGRIVYTGGMV EELLISGADIIKVGIGGGSCPODVAKAFGAGADFYMNIAGRIVYTGGMV PKINTALIGGGCSCPODVAKAFGAGADFYMNIAGRIVYTGGAV WARTISBAC 5380 2 2050 FRAGGARGRRANARSPOGSAAGMECPSULDEAGACTHSSCVS SOPSSNRAAPODELGGRGSSSSSSOKPCRALRGLESS LIHLGME SSIVYTECSPCAVDIGLARDFILEAMOGSVALAGHESGARPHL SCRILSLQERSOGGLAAGGSLDMNRKGLOPSLPYSFVS SOQSSI RIPRRPTVESHNSJTOMOCVOLNOYTLINGEPLATOROGVANA VMEMDNTYYAMKULSKKLIROAAFPRPPPDRGTGRAFGGCIOP ROPT \COVYGLA LIKKLUBHVAV KLUTVI\ DDNREDHIMM P\ELIVNIGGPVMENPTLIKLESDAARSYNOTHERAMPGGCIOP ROPT \COVYGLA LIKKLUBHVAV KLUTVI\ DDNREDHIMM P\ELIVNIGGPVMENPTLIKLESDAARSYNOTHERAMPGGCIOP RAPSELSFTKITSCKALDVAMMVTILCTPRICHTHAN HADIKRSHLUKGEDHIK KIDDRYSV MERKGDALAGNITVOTPA PAPSELSFTKITSCKALDVAMMVTILCTPRICHTHAN LIHWATHRIGAZELPEDDNCTIVE VTFETERSVRITSLIKTVOPI KLHBWYTRIGAZELPEDDNCTIVE VTFETERSVRITSLIKTVOPI LIKKTMIRKRSFCNPPEGGRREGEDSAAGMECPSVLIDEAGACTMSSCVS PEPPRTDBALCTYFTONTOWATERSTAND PRAGGARGKRAAARSPGGSRAGMECPSVLIDEAGACTMSSCVS SOPSSNRAAPDDELGRGSSSSESKOKCRALRGISSISTHOMM SFILVYTECEPCCAVDIGLARDRFLEADOGSVPLITNSGAAPHIL SGRKLSLQERSGGGAGAGGSLOMMRGCCICSPPPOETHTHSOFP ROPPTEDALCTYFTONTOWATERSTAND PRAGGARGKRAAARSPGGSRAGMETCSPPSVLISSAAPHIL SGRKLSLQERSGGGAGAGGAGAMETCPSVLIDEAGACTMSSCVS SOPSSNRAAPDDELGRGRASSSESKOKCRAKRGSISSISTHOMM CLIKKKINGALEPDOPOLAGAAPRPRPPPERPPGGCTCGCCPPPOETH ROPPTEDALICATURAL RATEGRATICATURAL RATEGRACH PROMPTENSISTAND SAARVENTAMARVILIKANDIA RATEGRACH PRAGGARGRAARASPGGGRAGAGGRATARLESTA		}	1,	QVKIICEDVANGISEHFVEFVKDVKKRFPQHTIMAGNVVTGEMV
ELIERDOKKYKLFYGNSS*I\AM\KRYAGGVASYRASEGKTVEV PENGOVENTIFOLIGGIGSTOTYOGANIKERTTFIEVTOQ VMPIFSEAC 5379 664 QAGGTTERPLDEDOLKREGATSRNEALKPRGELVLMYSCLEAL RFIATFELSAMPHIDMOVELDFKOVLLEASILVAEKSESEDUTR SFSFRINSKGTYGGYFIAAMDTVGTFEMAKUKCS*POSEMD VOMGCOFFLYKLFTLKMEMLLLSVLLPASILVAEKSELETAVH KRYSLUQWGEFAGONPOLLEHAAASSGTOSEDLGOLLEAIP OVKYICLDVANGYSEHFVEFVKDVRKFPOHTIMAGNVVTGEMV EELILGAGDI KVG1GFGGVCTTYRKTGVGYLGAMMCADAH HOLKGHIISDGGCSCFDVARAFGAGADFVMLGGMLAGKHSESGG ELIERDOKKYKLFYGMSS*I\AM\KKYAGGVAAGAMGAGHASGGG ELIERDOKKYKLFYGMSS*I\AM\KKYAGGVAAGAMGAGHASGGG ELIERDOKKYKLFYGMSS*I\AM\KKYAGGVAAGAMGAGHASGGG ELIERDOKKYKLFYGMSS*I\AM\KKYAGGVAAGAMGAGHASGGG FFKGDWHTTADILGGIRSTCTTYGAAKLKELSERTTFIRVTOQ VMPIFSEAC 2050 FSRAGGREGRRAAARSPGGSAAGMECFSVLDEAGACTMSSCVS SOPSSNRAAPODELGGRGGSSSSSKOPCPCARAGLSSLSIHLGME SFIVVTECEPGCAVDLGLARDRFLEADOGSVPLDTSGSQARPHL SGRKLSLGERSGGGLAAGGSLBOMNGRCICSBYPVSSPOSSP RLPREPTVESH-WSITGMQDCVOLMOYTLKDEIGKGSYGVVVLA YMEMDHYYAMAVLSKKLILDRAAFFREPBAGGCTP ROPI\SQCVYQEIA\ILKKLDHPMVV\KUVSVL\DDPHEDHLYMV P\ELIVAGGVEWPTIKKLESDARFYFGOLLAGFTHPGGCTD ROPI\SQCVYQEIA\ILKKLDHPMVV\KUVSVL\DDPHEDHLYMV F\ELIVAGGSVEWPTIKKLESDARFYFGOLLAGFTHPGGCTD RHAPESLSETKETSGAADUMAGVTICYFOFPHMESTRI LUKTHIRRRSFONPFEGGRREERSLSABANLLTKRFTRECGSL SELKT*KISPLPACCKV"* FERPFSGCRESVKHIPSLATV LUKTHIRRRSFONPFEGGRREERSLSABANLLTKRFTRECGSL SELKT*KISPLPACCKV"* FERPFSGCRESVKHIPSLATV LUKTHIRRRSFONPFEGGRREERSLSABANLLTKRFTRECGSL SELKT*KISPLPACCKV"* FERPFSGCRESVKHIPSLATV LUKTHIRRRSFONPFEGGRREERSLSABANLLTKRFTRECGSL SELKT*KISPLPACCKV"* FERPFSGCRESVKHIPSLATV LUKTHIRRRSFONPFEGGRREERSLSABANLLTKRFTRECGSL SELKT*KISPLPACCKV"* FERPFSGCRESVKHIPSLATV LUKTHIRRRSFONPFEGGRREERSLSABANLLTKRFTRECGSL SELKT*KISPLADVANJAKVLISKKLILTGAAFPROFTPEPFHHTHPSC SPEPPATOBALCYBTGTTAMPLOQUVALAVATLEPPILYSTVB PULVGAPGSHRAAARSPGGSAAGGREFSVLDEAGACTMSSCVS SPESNRAAPODELGRGRESSESSCKCCEALAGSLSISHHLOME SPIVVTECEPCAVDLGLARDRPLEADOGSVPLDTSGSOARPHL GGRRASLCLERSPETVESHTENDERPPILYSHPSCHIPSCHIPSCHIPSCHIPSC LUKTHIRRRSFONPFEGGRREGGSRAGGRRETABAGGTSLSHLINTVTTPP MAPPELSLEFTKKFSKALDVAMAVAVVLVACTPP PMAPPELSLEFTKKFSKADLAVAMAVA	1	ľ	ł'	EREILSGADIIKVGIGPGSVCTTRKKTGVGYPQLSAVMECADAA
PFKGDVEHTIRDILGGIRSTCTYVGANKLKELSRRITTPIRVTOQ WPFIESES 375 2009 664 QASGTTLRPLPDLPQLKRREATSRNRALKFEGRILVLMTSCLDAL RF1ATPILASMHDINDVKLDFROVLLRPRSTLKSRSEVDLTR SFSFRNSKGTYSGVPITAANMUTVSTERMAKVLCKS VPOSFEM VPOMSCVFLTYLETPILKWRLLLSVLLIPASILVAEKFSLFTAVH KHYSLVQMGEFAGONPDCLEHLAASSGTGSSDFGOLBOILEAI GUKNICLJOVANNYSEHPVERVDVKKRFDAFMLGONTGEMV EELILSGADIIKVGIGFGSVCTTRKKTGVGYPOLSAMECDADA HGLKGHIISDGGCSCPDDVAKAFGGAGAPFMLGGMALGGHSESGG ELIRDGKKYKLFVGMSS*I\AM\KKVAGGVAEVRASEGKTVEV PPKGDVEHTIRDILGGIRSTCTYVGAAKLKELSRRITFIRVTQG VPFIFSEAC SOPSSNRAAPODELGGRGSSSSESGKPCRALEGISSLSTHLAME SGRKLSLQBRSGOSLAAGGSLDMNGRCICPSLDPYSPVSSPQSED RLPRRPTVESHAVSITMOMDCVOLNOVTLADDREDHGKSSYVVLA VNEMDNTYYAMKVLSKKKLIROAAFPRRPPPPBFRTRPAPGOTOM P\ELVNOGEVMEVPTLKPLSEDOARFYFODLIKGIEVHVGKII HADIIKRSKLLUGSDENH ILADPTVSENEDBICKGSSTVVELA VNEMDNTYYAMKVLSKKKLIROAAFPRRPPPPBFRTRPAPGOTOM P\ELVNOGEVMEVPTLKPLSEDOARFYFODLIKGIEVHVGKII HADIIKRSLLUGSDENH ILADPTVSENEDBICKGSTVVELA KLHBWTRHIGASPLJSEBDANCTLVEVTEREBENVRHI SILATV ILLVKTMIRKRSGNAPPSGAAMERSLSAAFGHLINKRPTECESL SELKT*KISPLPACKVT*EPHPSGCGNAPFHLINKRTFECSSI SELKT*KISPLPACKVT*EPHPSGCGNAPFHLINGRAP PEPPRTBALLOYETGHTENDLOVLTHWOTFLEFELSTUM DDLVGARGSHPCHLITALLRIVGSTM PSRAGGAERGRAAARSPGGSAAMERSPGULGAGACTMSSCVS SOPSSURAAPODELGGRGSSSSESGKPCRALRGISSLSIHGME SFILVYTECEPGCAVDILGLARRDREAGGSPTSFRSCVS SOPSSURAAPODELGGRGSSSSESGKPCRALRGISSLSIHGME SFILVYTECEPGCAVDILGLARRDREAGGSPTSFRSCVS SOPSSURAAPODELGGRGSSSSESGAMPPFRGTSRAPGGCIO RGPI (RQVYQGIA) ILKKLDHRVVV\KLIVGAPFPRFRGTSRAPGGCIO RGPI (RQVYQGIA) ILKKLDHRVVVKLIVGAPFPRFRGTSRAPGGCIO RGPI (RQVYQGIA) ILKKLDHRVVVKLIVGAPFPRFRGTSRAPGGCIO RGPI (RQVYQGIA) ILKKLDHRVVVKLIVGAPFPRFRGTSRAPGGCIO RGPI (RQVYQGIA) ILKKLDHRVVVKLIVGAPFPRFRGTSRAPGGCIO RGPI (RQVYQGIA) ILKKLDHRVVVKLIVGAPFPLKTRSCVS SOPSSURAAPODELGGRGSSSSSESGKPCRALRGISSLSIHVTVGTA FMAPSELLSFRKLFSGKALDWAMQVTILYCVFRG*CPPPMERIM CLHSKKKSQALEFPDQPDIAABCKLIVCVFVRSVSVHTPSLATV ILKKTMIKRSFCNPFFGGSRAERSLSAPGHLLTKKPTRGESI SELKT*KTSPLAPACCVT*FFPHPSGCGRAVKAPLTVFRCESI SELKT*KTSPLAPACCVT*FFPHPSGCGRAPSVHTPSLATVUTAS VMSPRDARRSPDGGRGGAGRRSVLRGFCNNSLAFPTKERPD DIPMSEL	}	j	J	HGLKGH11SDGGCSCPGDVAKAFGAGADFVMLGGMLAGHSESGG
S379 2009 664 QAGGTTERPLPDLPQLKRREATSRNRALKPEGRIJVLMTSCLPAL RFIATPELSAMPHIONOVKLDFREDVLERPESTLKES,SEVDLTER SPSPRNSKQTYSGVPI I ARAMOTVOTE THE VIVLCES * POPSFMD VPOMGCYFLIYKLFTLKWRILLSVILPASILVAEKFSLFTNVH KHYSLVQWGPFAGOMPDCLEHLAPASIGNFEDLESO ILEAIP OVKYICLDVANGYSSHPVERVKDVEKRPPOHTIMAGUVVTGEMV EELILSGADII KVGIGGEGSUGCTTRKKTOVDISAVMEKADAA HGLKGHI ISDGCSCPGDVAKAFGAGADPVMLGOKLAGHSESGG ELIERDGKKYKLPYGWASS* 1'AM\KKYAGGVAPTASEGKTVEV VPKSGVSHTIRDILGGIRSTCTYVGAAKKELSRRTFIRVTQQ VPKSGVSHTIRDILGGIRSTCTYVGAAKKELSRRTFIRVTQQ SQFSSNRAAPODELGGGGSSSSESGKPCRAIKGLSSILHLGME SGRILSLQBRSGGGLAAGGSLDMMSRCICPSLPYSVSPGSSP RLPRRFVTSHAVSITGMODCVQLMQYTLGKKSYGVVVKLA YNENDRTYYAMKULSKKKLIRQAAFPREPPRGTRAPGGCIOP RGF1\EQVYQEIA\ILKKLDHRVV\KLUHPVVLOVULSKKSYGVVVKLA YNENDRTYYAMKULSKKKLIRQAAFPREPPRGTRAPGGCIOP RGF1\EQVYQEIA\ILKKLDHRVV\KLUHPVVL\ADDNEDHLYMV F\ELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIEYLHYOKII H\RGIKFRSHLUNGSBGHIKJADFVSNERGALLSINTVGTFA FMAPESLSSTKKIFSGKALDVAMGVTLICFVFG*CPMDERIM LUKTMIRRSFGNPFEGGRRESSSSDADLLKNPTVGTFA FMAPESLSSTKRIFSGKALDVAMGVTLICFVFG*CPMDERIM LUKTMIRRSFSGNPFEGGRRESSSSDADLLKSPTSTUPET KLHHWYTRIGASPLPSEDDARTLEVFTSTKLIPSGVALDLKMPTECGSL SELKT*KISPLPACKVT*EPHPSGCRPSGCMPFFLHTHSQPR *PEPPRTDEALCPYFTSTRCAAPLLOVETSPFLYKDFLSTSWL PDLVGAPGSHCFLNIALLRYNSHTM 5381 2 2050 59SSNRAAPQDELGGRSSSSESOKPCRALRGLSSI-HILGME SGRKLSLGERSGGGAGAGGSLDMMGRCICPSLTPSTVSPPLSSSCA SGRSKLSLGERSGGSGAGGEFSVLDEAGACTMSSCVS SQPSSNRAAPQDELGGRGSSSSESOKPCRALRGLSSI-HILGME SGRKLSLGERSGGGAAGGSLDMMGRCICPSLTPSTVSPPLSSG RLPRFTVYSHVSTINGMOPCVOLNOYTIKEDIGKGSYOVVKLA YNENDHTYYAMKULSKKKLIRQAAFPRPPPRGTRAPGGCIOP RGF1\NOVYGCAPCSCALAGLGSLAHMAGRCICPSLTPSTVSPPLGGRSSVSSOKYCAL YNENDHTYYAMKULSKKKLIRQAAFPRPPPRGTRAPGGCIOP RGF1\NOVYGCAPCHVPTLKPLSSEDARFYPPRGTRAPGGCIOP RGF1\NOVYGCAPCHLINTLANDHVNYKLUDDHDISHLYW F\SLLVYGCGPVGEVPTLKPLSSEDARFYPPRGTRAPGGCIOP RGF1\NOVYGCAPCHLINTLANDHVNYKLUDDHDISHLYW F\SLLVYGCGPCAAPCHLANDHVNYKLUDDHDISHLYW F\SLLVYGCGPCAAPCHLANDHVNYKLUDDHDISHLYW F\SLLVYGCGPCAAPCHLANDHVNYKLUDDHDISHLYN LYMYMIRRSFROMPFEGGRRSVLRGFCANSLAFPTKERPD OLINSKTKARSFROMPFEGGRRSVLRGFCANSLAFPTKERPD VMSPRDA			ł	ELIERDGKKYKLFYGMSS*I\AM\KKYAGGVAEYRASEGKTVEV
S379 2009 664 QAGGTTERPLPDLPQLKRREATSRNRALKPEGRIJVLMTSCLPAL RFIATPELSAMPHIONOVKLDFREDVLERPESTLKES,SEVDLTER SPSPRNSKQTYSGVPI I ARAMOTVOTE THE VIVLCES * POPSFMD VPOMGCYFLIYKLFTLKWRILLSVILPASILVAEKFSLFTNVH KHYSLVQWGPFAGOMPDCLEHLAPASIGNFEDLESO ILEAIP OVKYICLDVANGYSSHPVERVKDVEKRPPOHTIMAGUVVTGEMV EELILSGADII KVGIGGEGSUGCTTRKKTOVDISAVMEKADAA HGLKGHI ISDGCSCPGDVAKAFGAGADPVMLGOKLAGHSESGG ELIERDGKKYKLPYGWASS* 1'AM\KKYAGGVAPTASEGKTVEV VPKSGVSHTIRDILGGIRSTCTYVGAAKKELSRRTFIRVTQQ VPKSGVSHTIRDILGGIRSTCTYVGAAKKELSRRTFIRVTQQ SQFSSNRAAPODELGGGGSSSSESGKPCRAIKGLSSILHLGME SGRILSLQBRSGGGLAAGGSLDMMSRCICPSLPYSVSPGSSP RLPRRFVTSHAVSITGMODCVQLMQYTLGKKSYGVVVKLA YNENDRTYYAMKULSKKKLIRQAAFPREPPRGTRAPGGCIOP RGF1\EQVYQEIA\ILKKLDHRVV\KLUHPVVLOVULSKKSYGVVVKLA YNENDRTYYAMKULSKKKLIRQAAFPREPPRGTRAPGGCIOP RGF1\EQVYQEIA\ILKKLDHRVV\KLUHPVVL\ADDNEDHLYMV F\ELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIEYLHYOKII H\RGIKFRSHLUNGSBGHIKJADFVSNERGALLSINTVGTFA FMAPESLSSTKKIFSGKALDVAMGVTLICFVFG*CPMDERIM LUKTMIRRSFGNPFEGGRRESSSSDADLLKNPTVGTFA FMAPESLSSTKRIFSGKALDVAMGVTLICFVFG*CPMDERIM LUKTMIRRSFSGNPFEGGRRESSSSDADLLKSPTSTUPET KLHHWYTRIGASPLPSEDDARTLEVFTSTKLIPSGVALDLKMPTECGSL SELKT*KISPLPACKVT*EPHPSGCRPSGCMPFFLHTHSQPR *PEPPRTDEALCPYFTSTRCAAPLLOVETSPFLYKDFLSTSWL PDLVGAPGSHCFLNIALLRYNSHTM 5381 2 2050 59SSNRAAPQDELGGRSSSSESOKPCRALRGLSSI-HILGME SGRKLSLGERSGGGAGAGGSLDMMGRCICPSLTPSTVSPPLSSSCA SGRSKLSLGERSGGSGAGGEFSVLDEAGACTMSSCVS SQPSSNRAAPQDELGGRGSSSSESOKPCRALRGLSSI-HILGME SGRKLSLGERSGGGAAGGSLDMMGRCICPSLTPSTVSPPLSSG RLPRFTVYSHVSTINGMOPCVOLNOYTIKEDIGKGSYOVVKLA YNENDHTYYAMKULSKKKLIRQAAFPRPPPRGTRAPGGCIOP RGF1\NOVYGCAPCSCALAGLGSLAHMAGRCICPSLTPSTVSPPLGGRSSVSSOKYCAL YNENDHTYYAMKULSKKKLIRQAAFPRPPPRGTRAPGGCIOP RGF1\NOVYGCAPCHVPTLKPLSSEDARFYPPRGTRAPGGCIOP RGF1\NOVYGCAPCHLINTLANDHVNYKLUDDHDISHLYW F\SLLVYGCGPVGEVPTLKPLSSEDARFYPPRGTRAPGGCIOP RGF1\NOVYGCAPCHLINTLANDHVNYKLUDDHDISHLYW F\SLLVYGCGPCAAPCHLANDHVNYKLUDDHDISHLYW F\SLLVYGCGPCAAPCHLANDHVNYKLUDDHDISHLYW F\SLLVYGCGPCAAPCHLANDHVNYKLUDDHDISHLYN LYMYMIRRSFROMPFEGGRRSVLRGFCANSLAFPTKERPD OLINSKTKARSFROMPFEGGRRSVLRGFCANSLAFPTKERPD VMSPRDA	1	í	{	PFKGDVEHTIRDILGGIRSTCTYVGAAKLKELSRRTTFIRVTQO
RPIATPELGAMHIDMUNKLUPROVLERSKENTEKSRSEVDLTR SFS FRANSKOTYSGVPITAANMITVOTEEMAKULCKS VPOSEMD VPOMGCUTLI YRLETILKKRUKUKULLISULLIPAS ILVAEKESLFTAVH VROMGCUTLI YRLETILKKRUKUKULLISULLIPAS ILVAEKESLFTAVH KITSLUOMGEFAGONPOCLEHLAASSTOSSPEOLOTILEAIP OVKYITCLDVANOYSEHPEVEVUVKKREPOHTIMAGNUVTOEMV EELILISGADI IKVGIGGGSUCTTRKKTGVEYPOLSAMECADAA HOLKGHI ISDGGCSCPDOVAKAFGGAGDFVMLGGMLAGISESGG ELIBROKKYKLFYGMSS *I\AM\KKVAGGVAEVRASEGKTVEV PPKODVETITIDILGGITESTCTYVOAKAKTGAGADFVMLGGMLAGISESGG ELIBROKKYKLFYGMSS *I\AM\KKVAGGVAEVRASEGKTVEV VNPIFSEAC 50PSSNRAAPODELGGGSSSSSESGKPCREALKGISSISHLGME SFIVVTECTEPGCAVDIGLIANDEP LEADGGACTMSSCVS SOPSSNRAAPODELGGGSSSSSESGKPCREALKGISSISHLGME SSRIVLSLOBERGGAUDILANDEP LEADGGACTMSSCVS SOPSSNRAAPODELGGGSSSSSESGKPCREALKGISSISHLGME SSRIVLSLOBERGAVALLANDEP LEADGACTMSSCVS ANDRONTYYAMKULSKKKLIRQAAFPREPPPRGTRAPGGCIOP REPT-VECTOR LANDEN VAN STANDER VAN STA		L)	VNPIFSEAC
RFIATPRLESAMPHIDNOVKLDFKOVLLFKRSTLKSRSEVDLTR SPSPRNSKOVTYSGVPII AANNOTVOTEMVLKCKS VPOSFMD VPOMGCYFLIYKLFTLKWKILLSVILPASILVAEKSLFTAVH KHYSLOVMOGFAGONPDCEHLAASSTOPFOLLSOTLEAIP OVKYICLDVANGYSEHPVERVEVKDVKKFPOHTIMAGWLAGHESEGG ELIKROGKYKLFYGMSS 'I'AM\KKVAGARPYAGSAMCADAA HGLKGHII SDGGGSCPGDVAKAFGAGADFYMLGGMLAGHESEGG ELIKROGKYKLFYGMSS 'I'AM\KKVAGARPYABSEGKTVEV PPKODVEHTIRDILGGIRSTCTYVGAAKLKELSRRTTFIRVTQO VMPIPSEG 5380 2 2050 FSRAGGAERGRAAARSPGGGAAGMECFSVLDEAGACTVESCVS SOPSSNRAAPODELOGRESSSESQKPCEALRGLSSLSILLGME SFIVVTECEPCCAVDLGLARDFPLEADGGVPLDTSGSQARPHL SCRILLSLQERSQGGAAAGGSLDMMGCICPSLPYSEVSSPOSSP RLPRRPTYDSH-WSITMODCVCULNGYTLEKGKSYGVVKLA XMENDATTYAMKVLSKKKLIRQAAFPREPPRGTRAFGGCIOP RGPI\GCVGLATLKKKLIRQAAFPREPPRGTRAFGGCIOP RGPI\GCVGLATLKKKLIRQAAFPREPPRGTRAFGGCIOP RGPI\GCVGLATLKKKLIRQAAFPREPPRGTRAFGGCIOP RGPI\GCVGLATLKKKLIRQAAFPREPPRGTRAFGGCIOP RGPI\GCVGLATLKKKLIRQAAFPREPPRGTRAFGGCIOP RGPI\GCVGLATLKKKLIRQAAFPREPPRGTRAFGGCIOP RGPI\GCVGLATLKKKLIRQAAFPREPPRGTRAFGGCIOP RGPI\GCVGLATLKKLUSDEDHIKLDEDHOLITUKOPTGFACPROBERIM CLHSKIKSGALEPPODPDIAEDLKDLITUKOPPEGSCTPHDERIM CLHSKIKSGALEPPODPDIAEDLKDLITUKKPPTECESSI SELKT-KISPLPACKVT-EPPHSGCRSGKOPPFHITHSLATV ILVKTMIRKRSFGNPPEGGRERESSLSAPILHKOPPSRIVVPEI KLHBWTRRGAEPLPSEDENCTLUEVTEEEVENSVKHIPSLATV ILVKTMIRKRSFGNPPEGGRABERSLSAPILHKKOPPSRIVVPEI PSPRAGGAERGRAAAARSPGGAAGMECPSVLDEAGACTMSSCVS SOPSSNRAAPODELGGGGSSSSESOKPCEALRGLISSLHILGMS FIVVTECEPCCAVDIGLAARPPDLEADLCHVKOPTLEPFLSTSWL PDLWGAPGSHCFLINIALLRYNSHTM SGRKLSLGERSQGSLAAGGSLDMMGRCICFELPYSPSSPOGSP RLPRRFTVESHHWSITGMODCVOLNOYTIKDEIGKGSYGVVVKLA VNSNDHTYYAKVLSKKLLIRQAAFPRPPPRGTRAPAGGCIOP RGPI\GVGVGVGVFTLXPLSCDAARFPRPPRFGTRBAPGGCIOP RGPI\GVGVGVGVFTLXPLSCDAARFPRPPRGTRBAPGGCIOP RGPI\GVGVGVGVFTLXPLSCDAARFPRPPRFTTSTAVTTD PMAPESLAGTKYT-REPRSULADELKOTT, LEDGTGKGSYGVVVKLA VNSNDHTYAKKULAURDHONVKLUNDENDKLILVJDENDKLILVJDE SELKT-KISPLACKCYT-REPRSULADROKMYTLYCFVFO-CPFMDERIM CLHSKKKSGALEPDOPOLDLADLKDLI TRMLDKNPESRIVVPEI SELKT-KISPLACKCYT-REPRSULADROKMYTLYCFVFO-CPFMDERIM CLHSKKKSGALEPDOPOLDLKALARNSHTM GARGSQCDAPALGEARVKGFDLPRKTERSLSHAPPTKERPPD DINSELSHL	5379	2009	664	QASGTTLRPLPDLPOLKRREATSRNRALKPRGRI,VLMTSCL.DAI.
SFSPRINSKOTYSQVPITAANINDTVGTFEMAKVLKS-VVPGSFWD VPOMGCVPLTYKIFTLKKKMILLSVIKKSPTAVH KIYSLVQWGEFAGQNPDCLEHLAASSGTGSBFPGUEGOTLEAIP OVKYICLDVANGYSERFVEVKUVDYRFDVITMAGMVVTGEMV EELILGGADIIKWGIGPGSVCTTRKKTGVGYPOLSAVMECADAA HGLKGHIISDGGCSCPGDVARAFGAGPVMLGGMLAGKESEGG ELIERDGKKYKLFYGMS-Y-LAM\KKYAGGVAEVRASEGKTVEV PPKGDVPHTIRDILGGIRSTCTYVGAAKKRELGRITFITRVTQQ VMPTFSEAC 2 2050 PSRAGARGRAAARSPGGSAAGWECPSVLDEAGACTMSSCVS SQPSSNRAAPQOELGGRGSSSSSSGKPCEARIGLSSLSIHLGME SFIVVTECEPGCAVDLGLARDRFLEADGGCVPJDTGGSQARPHL SGRILSLGERSGGGLAAGGSLDMNGRCICPSLPYSPVSSPOSSP RLPRRPTVESHLVSITGMQDCVQLNQYTLKDEIGKGSYGVVKLA VNEMDNTYYAMKULSKKLLTRAAFPPRGTTRPPGGCIQP RGPI\ECVYQEIA\TLKKLDHPNV\KLVEVL\DDPNEDHLYMV F\ELVNGGVPMSVPTILKJLSEDQARFPPRGTTRPPGGCIQP RGPI\ECVYQEIA\TLKKLDHPNV\KLVEVL\DDPNEDHLYMV F\ELVNGGVPMSVPTILKJLSEDQARFPGGSTQPFAUTHSQPR FMAPESLSETRRIFSGRALDVAMMGTULVSVFG-CPFMDERIM CLHSKIKSQALBFPDQPDIAEDLKDLTTRNDANDESRIVVPEI KLHPWTRIGASPLDSEDENCTIVEVTLYVFG-CPFDMGRIM CLHSKIKSQALBFPDQPDIAEDLKDLTTRNDANDESRIVVPEI KLHPWTRIGASPLDSEDENCTIVEVTLYVFG-CPFDMGRIM CLHSKIKSGALBFPDQFDIAEDLKDLTTRNDANDESRIVVPEI KLHPWTRIGASPLDSEDENCTIVEVTLYVFG-CPFDMGRIM CLHSKIKSGALBFPDQGSAAGWECPSVLDEAGACTMSSCVS SQPSSNRAAPQDELIGGRGSSSSESGKPCEALRGISSLSIHLGGE SELKT-K-KISPLPACKTV-FEPPPBGCROPPPLHTHSQPR *PEPPRTDRALCPVETGRTCARPLLQVLGWGTPLPFPLSTSNL DDLVGAAGSHPCFINIALLEXYNSHTM. 5381 2 2050 PSRAGAGERGRAAAARSPGGSAAGWECPSVLDEAGACTMSSCVS SQPSSNRAAPQDELIGGRGSSSSESGKYCEALRGISSLSIHLING SGRKLSLGERSGGLAAGGSLDMNGCCICSBJFSPSSSPQSSP RLPRRPTVSSHHVSTINGDCVOLNGVTLKDEIGRGSSVOVKLA NNENDNTYYAMKULSKKLIRQAAFPRRPPPBGTSPPSSPQSSP RLPRRPTVSSHHVSTINGDCVOLNGVTLKDEIGRGSSVOVKLA NNENDNTYYAMKULSKKLIRQAAFPRRPPPBGTBALGYDVILL H\RDINFRSSHUPPBGRACHSTAAPBGGCIQP KGGIL\GCVYQEIA ILKKLDHNTVV,KIVSUL\DDPNNEHLIYW F\SLUVGGPVEEVTLKPJSEGGARGFSSAALLSTVTQTPA FMAPESLSSTRKIPSGRAENSLAFOLLSVYRIDESSLAFIHLGOR **PEPPRTBBALCPPCTGRGRGRRESSLAFIHLGNTVGTPA FMAPESLSSTRKIPSGRAENSLAFOLLSVYRIDESSAAL **CLHSKKKSQALEFPGDPATAGRGRGRGRGRAGGATAGRGRTWKALFRINGUNG **CHISKKKSQALEFPGDPATAGRGRGRGRGRGRAGGATHAGATYCTYPECSL SGLKT**KISPLDACKYT**PEPPBGGRPESSVGG **CHINGATAGATYCTYPATA	1 .	ł	}	RFIATPRLSAMPHIDNDVKLDFKDVLLRPKRSTLKSPSFVDLTR
VPOMGCVFLIYKIFTLKKKMILISVLIPASILIVAEKISLIFTAVH KHYSLVOWOGFRAGONPOLUBILANSISSDFPOLEOILEAIP OVKYICLDVANGYSEHFVERVKDVRRRFPORTIMAGNVYTGEMV BELLISGADIIKUG JOGGSCCPGUNAKAFGAGAPFVMLGCMLAGHSESGG ELIERDGKKYKLFYGMS* T\M\KKYAGGVARVARSEGKTVEV VNPISEAC SOPSNRAPGDELGGRSSTSSSESGKPCEALRGLSLSIFTIRTOQ VNPIFSEAC SOPSNRAPGDELGGRSSSSSSSGKPCEALRGLSLSIFTLGME SORKLSLQERSGGLAAGGSLDMNGRCICPSLPYSPVSSPOSSP RLPRRPTVESHAVSITUMDECUGALARDRILEANINLEDIGKSSYSVVKLA VNEMDNYYAMKULSKKLIRQAAFPRRPPPRGTRPAPGGCIQP RGPI\EQVYQEIA\LKKLDHPMV\KUPL\LDDENGARPHL H\RDIKFSRLVGSGLAAGGSLDMNGRCICPSLPYSPVSSPOSSP RLPRRPTVESHAVSITUMDECUGARPRIEDHLYMV F\ELVNGGPVMEVPILKBLSEDDARFYFODLIKGIFYLHYOKII H\RDIKFSRLVGSGBGAGGSLDNNGRCICPSLPYSPVSSPOSSP RGPI\EQVYQEIA\LKKLDHPMV\KUPL\LDDENGARPHLYOKII H\RDIKFSRLLVGSGBGIKTADPGVSTAVELVL\LDDENGARPHLYOKII H\RDIKFSRLLVGSGBGIKTADPGVSTAVELVL\LDDENGARPHCUPLITAVELICANINLESICKSYVVKLA KLHPWVTRIGASPLPSEDRCCILVEVTEEVERNSVKHIPSLATV LLVKTMIRRRSFGRPFSGSREERSLSAPGNLLTKKPTRECESL SELKT*KISPLPACKVYT*EFPENSCWOPPFLHITHSQPR *PEPPRTDEALCPYETTORTCMAPLLQVLMWGTPLPFPLSTSWL LLVKTMIRRRSFGRPFSGSREERSLSAPGNLLTKKPTRECESL SELKT*KISPLPACKVYT*EFPENSCWOPPFLHITHSQPR *PEPPRTDEALCPYETTORTCMAPLLQVLMWGTPLPFPLSTSWL SGRKLSLGERSGGSLAAGGSLDMNGRCICPSLPYSPVSSPOSSP RLPRRPTVSSHHVSITUMQDCVQLAQVTLKDEIGKSYGVVKLA YNEMDTYTYAMKVISKKLIRQAAFPRRPPRGTRAPGGCIQP SGRFSLGRRSGGSSSSSCKORCEALRCLSSLSIHLGM SFIVVTECEPGCAVDLCLARDRPLEADQGVPPLDTGSQAAPHL SGRKLSLGRRSGGSSSSSCKORCEARCLSSLSIHLGM SGRKLSLGRRSGGSSSSSCKORCEARCLSSLSIHLGM SFIVVTECEPGCAVDLCLARDRPLEADQGVPPLDTGSQAAPHLINGNISHTM F\ELVNQGPVWEYTLXPLSEDQARFYFODLIKGEYHPOWENGAN SGRKLSLGRRSGGSSSSSCKORPEARCLSSLSIHLGM SFIVVTECEPGCAVDLCLARDRPLEADQGVPPLDTGSQAAPHUND KLHPWTRIGAEPLPSEDBNCTLVEVTEEVERNUTGTA FMAPESLSETRK IPSGKALDWAMGVTLYCFVFG*CPPMDERIM CLHSKKKSQALFFDOPD TABELKDITHKNTRECSL SELKT*KISPLDACKVT*FFFPBGCRSGSOPDALFSTWYPEI KLHPWTRIGAEPLPSEDBNCTLVEVTEEVERNLITKTGTRECSL SELKT*KISPLDACKVT*FFFPBGGRRSGSSSSACHUPPETLITARDPPSCHITTSOP YNDSPRDAARRSPDORGGRRGG	}	1		SESERNSKOTYSGVPTTAANMDTVQTEEMAKUI QUOLINGGOODIR
KHYSLVOWOSFAGONPDCLEHLASSGTOSDFDOLGOILEND OVKYICLDVANGYSERPFEVEWDUKTORPOUTIMAGNVVTCEMV EELILSGADIIKWGIGPGSVCTTRKKTGWGYPOLSAVMECADAA HOLKGHIISDGGCSCPGDVAKAFGAGOVMALGMAAGRESGGG ELIERDGKKYKLFYGMS*TLAM\KKYAGGVAEYRASECKTVEW PYKGDVEHTIRDILGGIRSTCTYVGAAKLKELSRRTFIRVTQQ VMPIFSEAC 5380 2 2050 PSEAGGREGRAAAARSPGGSAAGMSCPSVLDEAGACTMSSCVS SOPSSNRAAPQDELGGRGSSSSSSKPCCHARGLSLSIHLGME SFIVVTECEPGCAVDLGIARDRPLEADGSEVPJUDTGSGARPHL SGRILSLGERSGGGLAAGGSLDMMGGIC OFSLPYSVSSPSSSPOSSP RLPRRPTVESHHVSITGMODCVQLNQYTLKDEIGKGSYGVVKLA YNENDNTYYAMKVLSKKLLTROAAFPPPRGTTRPAPGGIQP RGPI\EQVYQEIA\ILKKLLPHWV\KLVEVL\DDPNEDHLYMV F\ELVNGGOVMEVPTILKPLSEDDARFYFQDLIKGISTHYOFTIA H\RDIKPSNLLVGBOGHIKTADPGVSNFFKGSDALLSNTVGTPA FMAPESLSETRKIFSGRALDVWAMGTURVFVSFGCFGDERIM CLHSKIKSQALFPPOPDIAEDLKDLITRMDKNPSSRIVVPET KLHBWUTRGAPIPSEDENCTILVETVFVSFG-TPOPDERIM CLHSKIKSQALFPPOPDIAEDLKDLITRMDKNPSSRIVVPET KLHBWUTRGAPIPSEDSCRIFTSVFSGWOPPPLHTHSOPR *PEPPRTDBALCPYETGRTCMAPLLQVLWWGTPLPFPLSTSWL DDLVGAPGSHPCFINIALLRYNSHTM SGRKLSLGERSGGGLAAGGSLDMMGCCCTSLFFFSVSSPSSPOSSP REARGRESGRAAARSDEGGSAAGWCCPSVLDEAGACTMSSCVS SOPSSNRAAPQDELGGRGSSSSESGXPCEALRSLSLSIHLGGE SFIVVTECEPGCAVDLOLARDFPLEDOQSVPLDTGSGGARPHL SGRKLSLGERSGGGLAAGGSLDMMGCCCTSLFFFSVSSPOSSP RLPRRPTVSSHHVSITMODCVOLANGVTLKDEIGGGSSVOVKLA YNSDDNTYYAMKVLSKKKLIRQAAFPREPPBGSARPHLYGKII H\RDIKPSHLVSEDGGIKKLADPGVVERSGSJALLSVNTVGTPA FMAPESLSETKKIFSGKALDVWAMGVTLXCFVFG CPPMDERIM CLHSKIKSQALFFDQDIAELDKUTLKKPPTRECGSL SGELT*KTSPLADACKVT*EFPHPSGCRPCCNDPLHYGKII H\RDIKPSHLVSEDGGIKKLADPGVVERSGSJALLSVNTVGTPA FMAPESLSETKKIFSGKALDVWAMGVTLXCFVFG*CPPMDERIM CLHSKIKSQALFFDQDIAELDKUTLKKPPTRECGSL SELKT*KTSPLADACKVT*EFPHPSGCRPCCNDPPLHTHSOPR FMAPESLSETKKIFSGKALDVWAMGVTLXCFVFG*CPPMDERIM CLHSKIKSQALFFDQDIAELDKUTLTKCPTRECGSL SELKT*KTSPLADACKVT*EFPHPSGCRPCCNDPPLHTHSOPR FMAPESLSETKKIFSGKALDVAMGVTLXCFVFG*CPPMDERIM CLHSKKSQALFFDQDAAFFVFQLIAGRAFTYCTVPE CHIPSTITURGSGAPFFFGRREERSCARSALPTRECGSDALLSKTRYTGCPP TLIVATMIRKRSFGMPFFGSREERSLSGADALLTKKPPTRECGSL SELKT*KTSPLADACKVT*EFPHPSGCRPCCNDPLTTKTRPTCCBL SELKT*KTSPLADACKVT*FFFFFTBGFBFBCFTFDPDDRE TLYATMIRKRSFGMPFFGGRREERSC		1	1	VPOMECUEL TYPE ETT PUPPLET TO THE PROPERTY OF
OVKYICLDVANGYSERFVERVOVRKERPGOHTIMAGNIVITGEMY EELLISGADIIKUGIGPGSVCTIRKKTGVGYPOLSAVBECDDAA HOLKGHIISDGGCSCGDDVARAFAKAGAGAPFWILGGMLAGHSESGG ELIEEDGKKYKLEPGMS* 1'\AM, KKYAGGVABYWASEGKTVEV PPKGDVEHTIDDLIGGIRSTCTYVGAAKLKELSRRTTFIRVTQQ VNPIFSEAC 2 2050 PSRAGGAERGRAAARSPGGSAAGWECPSVLDEAGACTWSSCVS SQPSSNRAAPQDELGGRGSSSSSSQKPCRAARGKSSLSIHLGME SSIVVYTECEPGCAVDLGLARDRPLEADCQEVPLDTSGSQARPHI- SGRKLSLQERSQGLAAGGSLDMMGRCICTSLPYSPVSSPQSSP RLPRRPFVESHHVSITGMDCVCJNQVTLKDEIGGKSYGVVKLA YNDENDTYYAMKVLSKKLIRQAAFPRPPPRGTRPAPGGCIQP RGPI'EQVYQEIA'LIKKLDHPNVLKIPUL'NDDPBHLHYW F\ELVNQGPVMEVPTLKPLSEDQARFYFODLIKGTEYLHYOKII H\RDIKFSNLLVSGENGHIK KIADFAVERKSGDALLSTTVGTPA FMAPESLSETRKIFSGKALDWAMGVTLYCFVVGG'CPMDBERIM CLHSKIKSQALEFPDOPDIAGDLUTRHLDKNPESRIVVPEI KLHDWYTRHGASPLPSEDBNCTLVEVTEEEVENSVKHIPSLAVT ILVXTMIRKRSFGNPFBGGRREERSLSAPQHILTKKPTRECESL SELKT'K KISPLPACCKVT'EPPHPSGCRPSCWOPPFHTHSQPR *PEPPRTDBALCPYBTGRTCWAPLLQVLMWVGTPLPPPLSTSWI- PDLWGAPGSHFCFLANLALRNSGYGRALBGLSSISHLGWE SFIVVTECEPGCAVDLGLARDRPPLEADCGSVEDAGACTMSSCVS SQPSSNRAAPQDELGGGRSSSSESGKREALGASSISHLGWE SFIVVTECEPGCAVDLGLARDRPPLEADCGSVDLTGSGSARPHL SGRRLSIGERSGGGLAAGGSLDMWSCCICPLBYPSPVSSPOSSP RLPRRPTVSSHHWSTTGMODCVOLNOYTLKDEIGKGSYGVWLA YNENDMTYYAMKVLSKKLIRQAAFPRPPPPBTPBGGCTQP RGPI'EOVYOCIA'LLKKLLDPNVV\KLVEVLDDPMEDRIM H\RDIKPSNLLYGEDGHIK TLDBTGVSNEFKGSDALLGNTWGTA FMAPESLSSTRKIFSGKALDWAMGVTLXCFVG*CPFMBERIM CLHSKIKSQALEFPDQPDIAEDLUKIKTPTGPAFGCIQP RGPI'EOVYOCIA'LLKKLDPNVV\KLVEVLDDPMEDRILMY F\ELVNCGPVMEVPTLKPLSEDQARFYFOLLKGIEVHTYGKII H\RDIKPSNLLYGEDGHIKTADFFSRFFORSPERIVVPEI KLHFWYTRIGASPLDENGTHVVVKLTPCFSCPPHTHTSQPR *PEPPRTDBALCPYBTGRTGAADGLUKTFTEEDEUNSWHIPSLATV ILVKTMIRRSSGGBFFGSSREERSAAGAMGTTLKCFTPG*CPPBPGFERIM CLHSKIKSQALEFPDQPDIAEDLUKTERSVMFFRCESL SELKT*KISPLPACCKVT*EFFBPSGCRPSGWOPPFHTHTSQPR *PEPPRTDBALCPYBTGRTGAADLUKTFTEEDEUNSWHIPSLATV ILVKTMIRRSSGMFFGSSREERSAAGAMGTLTKCFTFECEDISTWU- PEPPRTDBALCPYBTGRTGAADLUKTFTEEDEUNSWHIPSLATV ILVKTMIRRSSGMFFGSSREERSAAGAMGHTLTTSTRPTTGPPPLTTGFDRDRE LTADSUDGFILKFLSAGWGGOLPRSKTCFGANSLAFTFLKEPD DIFMSELSHLIVUNDRAGAHFTLTTSRPPTTGPPLPTTGFDRDRE LTADSUDGFILKFLSA	1	1	1	VI VIII TOUR TURNING TOUR TOUR TOUR TOUR TOUR TOUR TOUR TOUR
EELLISGADIIKWGIGPGSUCTTRKKTGUGYPQLSAVMECADAA HGLKKHIISDGGGSCGDUNAKAFGAGADFYMLGGMLGHGSEGG ELIERDGKKYKLFYGMS\$*I\AM\KKYAGGVAFYRASGKTVEV PFKGDVGFHTIRDILGGIRSTCTYVGAAKLKELSRITTFIRVTQQ VMPIFSEAC 2 2050 PSRAGGAERGRAAARSPGGSAGMECPSULDEAGACTMSSCVS SOPSSNRAAPQDELGGRGSSSSESQKPCRAIRGLSSLSIHLGME SFIVVTECEPGCAVDLGLARDRPHEADGGDYDLDTGSGQARPHL SGRKLSLQERSQGGLAAGGSLDMMGRCICFSLPYSPVSSPQSSF RLPRRPTVERHWSTIGMDGUNQYTLKDEIGKGSYGVVKLA YMENDNIYYAMKULSKKLIRGADFRPPPRGTAPAGGCIOP RGPI\EOVYQEIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV F\ELVNGCPYMEVPTIKULSEDQAFYPQDLIKGIEYLHYOKII H\RDIKFSNLLVGEDGHIKLADFGVSNEFKGSDALLSNTVGTFA FMAPESLSETRKIFSGKALDWAMGVTLVCFVFG*CFFMDERIM CLHSKIKSQALEFPDQPDIAEDLIDLITTMLDKNEPSRIVVPEI ILVKTMYRKRSFGNPFEGSRREESLSAPGNLLIKKRPTRECESL SELKT*KISPLPACCKVT*EPFHPSGCRPSCWOPPFLHTHSOPR *PEPPRTDBALCFYBTGTCARPLYLWVEVEEVRSVKHIPSLATV ILVKTMYRKRSFGNPFEGSRREESLSAPGNLLIKKPTRECESL SELKT*KISPLPACCKVT*EPFHPSGCRPSCWOPPFLHTHSOPR *PEPPRTDBALCFYBTGTCARPLYLWWFOTELPFPLSTSML PDLVGARGSHFGFLNIALLRYNSITM PSRAGGREGGAAARSPGGSAAGMECPSVLDEAGACTMSSCVS SOPSSNRAAPODELGRGSSSESQKPCBALRGLSSLSIHLGME SFIVVTECEPGCAVDLLALARRPLEADGGVPLDTGSGQARPHL SGRKLSLGERSGGGLAAGGSLDMAGFTRPPPRGTTRSPGCVG RGPI\EOVYGETA\ILKKLDHPNVV\KLVEVLDDFNEDHLYMV IFFLEVMSPGLLVGGGHIKTADFGVSNFFKGSDALLSNTVGTDA RMPBESLSTRRIFTGSKALDVMAGFPRPPPRFGTTRPGGCIOP RGPI\EOVYGETA\ILKKLDHPNVV\KLVEVLDDFNEDHLYMV IH\RDIKRSSGDALSGTRTRAGPGGCIOP RGPI\EOVYGETA\ILKKLDHPNVV\KLVEVLDDFNEDHLYMV IH\RDIKRSSGDAFSGRSALDVANFFKGSDALLSNTVGTDA EKAPPVTERBREFGSRREESHSAFGNLLTKKFRECESL SELKT*KISPLBACCKVT*EPFHPSGCRPSCWOPPFLHTHSGOPR *PEPPFTDBALCPYTGRTCMAPLITVLFVTGEVENSVHIPSLATV ILVKTMIRKRSFGBPFGSRALDVAMGPTROPPFLSTSML PDLVGAPGSHFFFTINALLLYNNSHTM CLHSKLKSQALEFPDQDPDLAEDLKDLITRMLDKAPPSRIVVPEI SELKT*KISPLBACCKVT*EPFHPSGCRPSCWOPPFLHTHSGOPR *PEPPFTDBALCPYTGRTCMAPLLDVLWVGTTLPPFLSTSML PDLVGAPGSHFFFTINALLYNNSHTM GARGSGODAPALDGERBFGGSRAGGPARGEMTGARLPFLHTULGS VFMILLILVYNDSAGAAHFYLHTSPSRPHTGPPLPPTSTSML PDLVGAPGSHFFGTNALLRYNNSHTM AGAPKARDPLRIPRETWINNSAHLITSKAPFREPERFEPP DIFNSELSHLIVDDRHAGAIVCTVPLKWRTYGLSRHMWKKL KKYTKPLEVUNDFVALLSAGRVGGCANSSLEPFLERPFO PROFRER	1	}]	ONE VIOLENCE PUR NOVE PROPERTY OF THE PROPERTY
HOLKGHIISDGCSCPGDVAKFAGRAGAPFMLGMLAGHSESGG ELIERDGKKKKLFYGMS* 1\AM, KKYAGGVAFYMAGGKAYHASEGKTYEV PPKGDVEHTIRDILGGIRSTCTYVGAAKLKELSRRTTFIRVTQQ VNPIFSEAC 5360 2 2050 FSRAGGAERGRAAAARSPGGSAAGWECPSVLDEAGACTMSSCVS SOPSSNRAAFQDELGGRGSSSSSSSQKPCEALRGLSSLSIHLGME SSIVVYTECPGCAVUDGLARDRYPLEADCOGVPLDTGSGAAPHL SGRKLSLQERSQGLAAGGSLDMMGRCICSPLYSPSVSSPOSSP RLPRRPTVESHHVSTTGMDCVOLONOTILKDEIGGSVGVVKLA YNDENDTYYAMKVLSKKLLIRQAAFPRPPPPRTRAPGGCIQP RGPI\EQVYQEIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV F\ELVNQGPVMEVPTIKPLSEDQAFFFFQDLIKGISTHYGKTI H\RGIFRSNLLVEBOHIKIADFGVSNEFKGBDALLSHTVGTPA FMAFESISETRKIFSKALDVMAGVTLYCFVFGG-CFPMDERIM CLHSKIKSQALEFPDQPDIAEDLKDLITMIDNNPESRIVVPEI KLHBWYTRHGAZPLSEBENCTLYVEFEVENSVKHTPSLATV ILVKTMIRKSFGNPPEGSREGSLBAPGNLITKRPTRECESL SELKT*KISPLPACCKVY*EPPBEGGRSGVSQVPPFHTHSOPR *PEPPRTDRALCYYETGRTCMAPLLQVLMWGTPLPFFLSTSML DDLWGAPGSHFFFINIALIRNSHIM 5381 2 2050 PSRAGGRERGRAAARSPGGSAAGMECPSVLDEAGACTMSSCVS SOPSSNRAAPQDELGGRGSSSSESQKPCRALRGLSSLSIHLGME SFIVVTCECRPGCAVDLGLARRPFLAGGGVPLDTSGQAPHH SGRKLSGREGGBAAGGSLDMNGRCICPSLPYSPVSSPOSSP RLPRRPTVSSHHVSITAMODCVOLNYLMBEIKGKSYGVVKLA YNSMDNTYVAMKVLSKKKLIRQAAFPRRPPPRGTRPAFGGCIQP RGPI\EQVYQEIA\TLKKLDHNVV\KLDEVLVLDPDHEDHLYMV F\ELVNGGPVMSVPTLKPLSEDGARFFFFDLIKGIETHHYQKIL H\RDIKRSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTGTDA FMAPESLSTRKIFSGKALDVMAGAFFFFDLIKGIETHHYQKIT H\RDIKRSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTGTDA GLISKIKSQALEFPDQPDIAEDLKVLVLVFVFG-CFPMDERIM CLHSKIKSQALEFPDQPDIAEDLKVLLVLVLVDPENEDHLYMV KLHPWTRIGASPLPSEBDENCTLVTEGVFG-OFPMDERIM CLHSKIKSGALEFPTGRTGATALDVLWWGTFLEPFLSTSML KLHPWTRIGASPLPSEBDENCTLVTEGEVENSWHIPSLATV ILVKTMIRKSFGNFFGSRRERSLSAPGNLTKKPTRECESL SELKT*KISPLDACCKVT*EPFBGCRSCOPPFLHTHSOPR *PPPPREALCPYTGRTGATALDVLWWGTFLEPFSLSTRG SGRAGGODPATALGERGEWGGPFRAGMYTARLFFRIMIVLGS VFMILLILVYMDSAGAAHFYLHTSFSPRTGPD,PTGTDRDE LTADSVODDFILDKLSAGAVGGDFRAGAPRGGMYTARLFFRIMIVLGS VFMILLILVYMDSAGAAHFYLHTSFSPRTGPD,PTGTDRDE LTADSVODDFILDKLSAGAVGGPGRAGAPRGGMYTARRFTLMFUNGS TUNSPLAHHTUNDSALLTFINKFWRRYGLSBESNIMV KARAPVEDGARLGARGGPGRAGARSLAPPTEGRFFAG TUNSPLAHHTUNGABALTFINKFWRRYGLSBESHMKVKL KKYTKFLEVUNDFVALISABA			[UVKIICLDVANGYSEHFVEFVKDVRKRFPQHTIMAGNVVTGEMV
BELIEROKKYKLPYGMS:1/M/KKYAGGVAPYRASEGKYVEV PYKGDVEHTIRDILGGIRSTCTYVGAMKKELSRRTTFIRVTQQ	1	l	1	ELLILSGADI I KVGIGPGSVCTTRKKTGVGYPQLSAVMECADAA
BELIEROKKYKLPYGMS:1/M/KKYAGGVAPYRASEGKYVEV PYKGDVEHTIRDILGGIRSTCTYVGAMKKELSRRTTFIRVTQQ	1		İ	HGLKGHIISDGGCSCPGDVAKAFGAGADFVMLGGMLAGHSESGG
PPKGDVEHTIADLIGGIRSTCTYVGAAKLKELSRRTTFIRVTQQ VNPIPSEAC SOPSNRAAPQDELGGRGSASAGWECPSVLDEAGACTMSSCVS SOPSNRAAPQDELGGRGSSSSESQKPCAARGISSLSIHLGME SFIVVTECEPCAVDLGLARDRPLEADGGVPUDTGGSQAPHL SGRKLSLQERSQGSLAAGGSLDMINGRCICPSLPYSPVSSPQSSF RLPRRPTVESHIVSITMODCVQLNQYTLKDEIGGKGSVGVVKLA YNENDNTYYAMKVLSKKKLIRQAAFPREPPRGTEPAPGGCIOP RGP1'EQVYQEIA'ILKKLDHPNVV\KLVEVL\DDPKEDHLYMV F\ELVNGCPVMEVPTLKPLSEDQARPYFQDLIKGIEYLHYOKII H\RDIKPSNLLVGBDGHIKIADFGVSNEFKSDALLSINTGTFA FMAPESLSETRKIFSGKALDVWAMGVTLYCVFG*CPFMERIM CLHSKIKSQALEPPDQPDIAEDLKDLITMLDKNPESRIVVPEI HWYTRHGAEPLESEDDARCTLVEVTEEEVENSVKHIPSLATV ILVXTMIRKRSFGNPFEGSRREGRSJAAGNLLTKKPPTRECESL SELKT*KISPLPACKXVT*BPPFPSGCRESKGMOPPPHHTISQPR *PEPPRTDBALCPYETGRTCWAPLLQVLMWVGTPLPPFPSTSWL PDLVGAPGSHFCLNIALLRYNSHTM. SGRKLSLQERSQGSLAAGGSSSSESGXPCEALRGLSSLSIHLGME SFIVVTECEPGCAVDLGLAARPAPLEADGGVPLDTGGSARPHL SGRKLSLQERSQGSLAAGGSSASSESGXPCEALRGLSSLSIHLGME SFIVVTECEPGCAVDLGLAARPAPLEADGGVPLDTGGSARPHL SGRKLSLQERSQGSLAAGGSSASSESGXPCEALRGLSSLSTLIKGME SFIVVTECEPGCAVDLGLAARPAPLEADGGVPLDTGGSARPHL SGRKLSLQERSQGSLAAGGSSASSESGXPCEALRGLSSLSTLIKGME PEPPRTVESHHVSITGMGDCVOLMYYTLKDEIGKSSYGVVKLA YNEMDNTYVAMKVLSKKKLIRQAAPPRRPPRGTRPAPGGCIOP RGPI'EQVYQEIA\ILKKLDHPNVV\KLVEVL\DDPNEDBLYMV F\ELVNGGFWBYPTIKPLSEDQARFFRQDLIKSIEVLHYQKII H\RDIKPSNLLVGEDGHIKIADFGVSNFKSDALLSNTVGTFA FMAPESLSETRKIFSGKALDWAMGVTLYCFVG*CPFMDERIM CLHSKIKSQALEFPDQPDIAEDLKDLITRHDKNPESRIVVPEI KLHFWVTRIGABPLFSBEDENCLUVTSTEPVENSVHIJPSLATV ILVXTMIRKRSFGNPFGGSRREERSLSAPGNLLTKKPTRECESL SELKT*KISPLPACCKVT*EFFHDSGRCGOPPFLHTHSQPR *PEPPRTDBALCPYSTGRTCWAPLLQVLMWGTT-LFPFLSTSWL PDLVGAPGSHFCFLNIALLRYNSHTM CLHSKIKSGQDDAPALGARBYREFERGPARGRWTKARLFRLWLVLGS VFMILLIIVYWDSAGAAHFYLHTSFSRPHOPPLPPPPEGRDRE VFMIDDLAGABSSHFCFLNIALLRYNSHTM CHAPACKARAPCHARACH PDLVGAPGSHFCFLNIALLRYNSHTM SPRDARRSPDQGRQAARRSVLRGFCANSSLAFPTKERFFD DIVNSELSBLIVDDRHGAIVCYVPKVACTNMKWWILJSGSLLH RGAPYADDURFILGAFRWGNYDKASGRHIMKWKL KKYTKELFVRDFFVRLISAPRSKFELBERF/P PORFTERFFD DIPNSELSBLIVDDRHGAIVCYVPKACTNMKWWIVJLSGSLLH RGAPYADDLRIFERFUNDASALFFFNEYFERFO DIPNSKLSSHIMKWKL KKYTKPLFVRDFFVRLISAPRSFERFINFOYLLTKKLSFH		Ì	1	ELIERDGKKYKLFYGMSS*I\AM\KKYAGGVAEYRASEGKTVEV
VNPIFSEAC 2 2050 PSRAGGAERGRAAARS PGGSAAGWECPSVLDEAGRCTMSSCVS SOPSSNRAA PODELGGRGSSSSESQKPCEALRGLSLSIHLGME SFIVVTECEPGCAVDLGLARDR PLEADGGVPLDTSGSQARPHL SGRKLSLQERSQGSLAAGGSLDMNGRCICPSLPYSPVSSPOSS PLPRRPTVESHWSITMODCVQLNQYTLKDEIGKGSGVVKLA VNENDNTYYAMKVLSKKLIRDAF PRRPPPRGTRPAPGGGIQP RGP1\EQVYQEIA\ILKKLDHPNVV\KLUEVL\DDPNEDHLYMV F\ELVNCOPVMEVPTLKPLSEDQARFYFQDLIKGIETYLHYOKTI H\RDIKPSNLLVGEDGHIKTAPFGVSNEFKGDALLSNTVGTFA FMAPESLSETKKIFSGKALDVWAMGYTLYCFVFG*CFFMDERIM CLHSKKISQALEPFDQPDIAEDLKDLITMIDLKNPESRIVVPEI KLHPWVTRHGAEPLPSEDGNCTLVEVTBEEVENSVKHIPSLATV ILVKTMIKRSFGNPFEGGRREGRSLAAGGULTKRPTRECESL SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR *PEPPRTDEALCPYETGRTCWAPLLQVLWWGTFLPFFLSTSKL PDLWGAPGSHFCFLNIALLRYNSHTM 2 2050 PSRAGGAERGRAAARSFGGSAAGWECPSJLGGLSLSISHIGME SFIVVTECEPGCAVDLGLARDRPLEADGGCVPLDTSGSQARPHL GGRKLSLQERSQGSLAAGGSLDMNGRCICPSLPYSEVSSPQSEP RLPRRPTVESHHVSITGMQDCVJNQYTLKDEIGKGSSYGVVKLA YNENDNTYYAMKVLSKKKLIRQAFPRRPPRGTRPAPGGCIQP RGPI\EQVYGEIA\ILKKLDHENVV\KLVEUL\DDPNEDHLYMV F\ELVNGGPWEVPTLKPLSEDQARFYFDDLIKGIEXLYHYGKII H\RDIKPSNLLUCEDGHIKLIDAFGVSNFFKGSDALLSNTVGTPA FMAPESLSETRKIFSGKALDWAMGVTLYCFVG*CFFFDERIM CLHSKIKSQALEPPDQPDIAEDLKDLITMIDKNPESRITVVEPI KLHPWVTRIGABPLESDENCTLVEVTEEVENSVKHIPSLATV ILVKTMIRKRSFGNPFGGSRRERSLSAPGNLITKKPTRECSL SELKT*KISPLPACCKVT*EFPHPSGCRPSCWOPPIHTHSQPR *PEPPRTDBALCPYETGRTCWAPLLQVLWWGTPLPFFLSTSWL PLIVAGRGSCQDAPALQEAEVRGFERSQAPRARMTKARLFRLWLVGS VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPFPEDRDRE 1 1536 203 GARGSQQDAPALQEAEVRGFERSQAPRRENTKARLFRLWLVGS VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPEGDRDRE \$ VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPEGDRDRE \$ VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPEGDRDRE \$ VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTFGBRDRE \$ VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTFGBRDRE \$ VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTFGBRDRE \$ VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTFGBRDRE \$ VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTFGBRDRE \$ VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTFGBRDRE \$ VFMILLIIVYWDSAGAHFYLHTSFSRPHTGPPLPTFGBRDRE \$ VFMILLIIVYWDSAGAHFYLHTSFSRPHTGPPLPTFGBRDRE \$ VFMILLIIVYBDSAGAHFYLHTSFSRPHTGPPLPTFGBRDRE \$ VFMIL	-	ł	1	PFKGDVEHTIRDILGGIRSTCTYVGAAKLKELSRRTTFIRVTOO
5380 2 2050 PSRAGGAERGRAAARSPGGSAAGWECPSVLDEAGACTMSSCVS SOPSSNRAAPQDELGGGSSSSESGKPCALKGISSIS IHLGME SFIVVTECEPSCAVDLGLARDRPLEADGGVVPLDTGGSQAPPHL SGRKLSLQERSOGGLAAGGSLDMIGGCLOPSLPYSPVSSPOSSP RLPRRPTVESHHVSITMODDCUAQYTLKDEIGKGSVGVVKL YNENDNTYYAKKULSKKKLIRQAAFPRRPPPRGTRPAPGGCIQP RGPI\EQVYQEIA\IIKKLDHPNVV\KLIVEVL\DDPNEDHLYMV NEWDNTYYAKKULSKKKLIRQAAFPRRPPPRGTRPAPGGCIQP RGPI\EQVYQEIA\IIKKLDHPNVV\KLIVEVL\DDPNEDHLYMV H\RDIKPSNLLVGEDGHIKTADPGVSNEFKGSDALLSNTVGTPA H\RDIKPSNLLVGEDGHIKTADPGVSNEFKGSDALLSNTVGTPA H\RDIKPSNLLVGEDGHIKTADPGVSNEFKGSDALLSNTVGTPA CLHSKIKSQALEPPDQPDIAEDLKDLITTMLDKNPESRIVVPEI KLHPWVTRHGAEPLPSEDENCTLVEVTEEVENSVKHIPSLATV ILVKTMTRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESL SELKT*KISPLPACCKVT*EPPHPSGCTRPSCWQPPFLHTISQPR *PEPPRTDEALCPETGRTCWAPLLQVLWWGTPLPPPLSTSWL PDLWGAPGSHFCEINIALLRYNSHTM PSRAGGAERGRAAARSFGGSAAGWECPSVLDEAGACTMSSCVS SQPSSNRAAPQDELGGRGSSSSESGKPCEALRGISSLSIHLIGME SFIVVTECEPGCAVDLGLARDRPLEADGGVPFLDTSGSQARPHL SGRKLSQERSGGLAAGGSLDMIGRCICPSLYSPVSSPOSP REPRPTVESHHVSITGMODCVQLMQYTLKDEIGKGSYGVVKLA YNENDNTYYAMKVLSKKKLIRQAAFPRRPPPPGTRPAPGGCIQP RGPI\EQVYQEIA\IIKKLDHRVV\KLVEVL\DDDNEDHLYMV F\ELVNQGPVMEVPTLKPLSEDQARFYFDQLIKGIEVLHYQKII H\RDIKSPNLLVGEOCHIKIADFGVSNFFKGSDALLSNTVGTPA FMAPESLSFTRKIFSGKALDVMAMGVTLYCVFG*CPFMDERIM CLHSKIKSQALEFPDQPDIAEDLKOLITRMLDKNPESRIVVPEI KLHPWVTRIGAEPLPSEDENCTLIVEVTEEVENSVKHIPSLATV ILVKTMIRKRSFGNFFGSRREERSLSAPGNLLTKKPTRECESL SELKT*KISPLBACCKVT*EPPHPSGCRPSGWOPPIHTHSQPR *PEPPRTDEALCPYETGRTCWAPLLQVLWWGTPLPFPLSTSWL DLVGAAGSHFCFLNIALLRYNSHTM SELXTKSJSJSPRSKPELNSAPHKSQPRSVRG YDWSPRDARRSPDQGRQAERRSVLRGFCANSSLAPPTKERPFD DIPNSELSHLIVDDRHGAIYTHTSFSRPHTGPPLPTPGBRDRE VTMILLIIVYMDSAGAAHFYLHTSFSRPHTGPPLPTPGBRDRE VTMSPRDARRSPDQGRQAERRSVLRGFCANSSLAPPTKERPFD DIPNSELSHLIVDDRHGAIYTCYVPKVACTNMKRVMIVLSGSLLH RGAPYRDPIRIPREBLIVINDSSAHLTFNKRVMCKLSRHLMKVYLL KKYTKELFVRDFFVRLISAPKSEPENPICYLLDFFKLAPFMEH KKYTKELFVRDFFVRLISAPRSKFEELNES/F PQVRRHAAAV]	
SOPSSNRAPQDELGGGGSSSESGKPCBALRGLSSLSIHLGME SFIVVTECEPGCAVDLGLANDFLEADAGGEVPLDTSGGARPHL SGRKLSLQERSGGGLAAGGSLDMNGRCICPSLPYSPVSSPSSP RLPRRPTVESHHVSITGMQCVQLNQYTLKDEIGKGSYGVVKLA VNENDNTYYAMKVLSKKLIRQAAFPRRPPPPBGTRPAPGGCIQP RGP1\GQVYQEIA\ILKKLDHPNVYKLVEVL\DDPEDGLLYMV F\ELLVNQGPVMEVPTLKPLSEDQARFYFQDLIKSIEVLHVOKII H\RDIKFSNLLVGEDGHIKTADFGVSNEFKGSDALLSNTVGTPA FMAPPSLSETKIFSGKALDVMAMGVTLYCFVF6*CFFMDERIM CLHSKIKSQALEPFDQPDIAEDLKDLTTRHDKNPESRIVVPEI KLHPWVTRHGAEPLPSEDENGTLVEVTEEVENSVKHIPSLATV ILVXTMIRKRSFGNPFEGSRREERSLSAPGNLTLKKPTRECESL SELKT*KISPLPACCKVT*EPPHSSGCGFGCWGPPFLHTHSQPR *PEPPPTDEALCPYETGRTCAPLLQVLWWGTPLPFPLSTSWL PDLVGAPGSHFCFLNIALLRYNSHTM 5381 2 2050 PSRAGGAERGRAAAARSPGGSAAGWECFSVLDEAGGACTMSCCVS SQPSSNRAAPQDELGGGGSSSSESQKPCEALRGLSSLSIHLGME SFIVVTECEPGCAVDLGLARDFRLEADGGSVPLDTSGSQARPHL SGRRLSLQERSGGLAAGGSLDMNGRCICPSLPYSPVSSPQSSP RLPRRPTVESHHVSITGMQDCVQLNQYTLKDEIGKGSYGVVKLA YNENDNTYYAMKVLSKKKLTRQAFFPRPPPRGTSRPGGCIQP RGPI\GQVYGEIA\ILKKLDRAPFYPPPRFPPPRGTSRPGGCIQP RGPI\CQVYGEIA\ILKKLDRAPFYPPPPTDLIKGIEYLHYQKII H\RDIKSMLLVGEDGHIKLTGEVSNEFKGSDALLSNTVGTPA FMAPESLSFTRKIFSGKALDVMAMGVTLYCFVFG*CPFMDERIM CLHSKIKSQALEFPDQPDIAEDLKDLITRNDINTGTPA FMAPESLSFTRKIFSGKALDVMAMGVTLYCFVFG*CPFMDERIM CLHSKIKSQALEFPDQPDIAEDLKDLITRNDINTGTPA FMAPESLSFTRKIFSGKALDVMAMGVTLYCFVFG*CPFMDERIM CLHSKIKSQALEFPDQPDIAEDLKDLITRNDINTGTPA FMAPESLSFTRKIFSGKALDVMAMGVTLYCFVFG*CPFMDERIM CLHSKIKSQALEFPDQPDIAEDLKDLITRNDINTGTPA FMAPESLSFTRKIFSGKALDVMAMGVTLYCFVFFCCBPFDCRE KLHPWVTRHGABFLPSGEDRCTLIVEVTEEEVENSVGHIBSLATV ILVKTMTRKRSFGNPFFGSRREERSLSAPGNLLTKKPTRECSSL SELKT*KISPLPACKVT*FEPPGGCRPSCMOPPPLHTHSQRR *PEPPPTDEALCPFTCTCMPALLQVMWGTPLPFPLSTSWL DLVGAFGSHPCFLNIALLRYNSHTM SGRRSQQDAPALQEABVRGPERKQDPPRHTHSQRR *PEPPPTDEALCPFTCNTCMPALLRYNSHTM ILVKTMTRKSFGNPFFGSRREERSLSAPGNLLTKKPTRECSSL SELKT*KISPLPACKVT*FEPPGGCRPSCGDPPPLGGBREE VPMSPLDAARSPDQGRQAERRSVLRGFCANSSLAFPTKERPFD DLVGAFGSHPCFLNIALLRYNSHTM KKKYTLFLFVDDPFVRLISAFRSKFELENEEF/*PQURRHAAAAV KWKYLFLFVDDPFVRLISAFRSKFELENEEF/*PQURRHAAAAN RQPHQPARLGARGLEPRIPGVARATNEFGLARAAAN	5380	2	2050	PSRAGGAERGRAAAARSPCGSAAGWECDSVIDEAGACTMCCCVC
SFIVVTECEPGCAVDLGLARDRELEADGCEVPLDTSGSQARPHIL SGRKLSLQERSGGGLAAGGSLDAMGRCICPSLPYSPVSSPSSPSRLPRRFYESHIVSITGMODCVQLNQYTLKDEIGKGSYGVVKLA YNENDNTYYAMKULSKKLIRQAAFPRPPPRGTRAPGGCIOP RGP1\EQVYQEIA\1LKKLIRQAAFPRPPPRGTRAPGGCIOP RGP1\EQVYQEIA\1LKKLIRQAAFPRPPPRGTRAPGGCIOP RGP1\EQVYQEIA\1LKKLIRQAAFPRPPPRGTRAPGGCIOP RGP1\EQVYQEIA\1LKKLIRQAAFPROPULKGIEVLHYOKII H\RDIKPSNLIVGEDGHIKJDGVSNEFKSGDALLSTVGTPA FMAPESLSETRKIFSGKALDVWAMGVTLYCFVFG*CPFMDERIM CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPPI KLHPWVTRHGAEPLPSSDEDROTLIVEVTEEVEEVENSVKHIPSLATV ILVXTMIRKRSFGNPFEGSRREESSLSAPGNLLTKKPTRSCESL SELKT*KISPLAACKVTV*EPHPSGCRPSCWOPPFLHTHSQPR *PEPPRTDEALCPYETGRTCWAPLLQVLWWGTPLPFPLSTSNL PDLVGARGSHFCFLNIALLKYNSHTM *PEPPRTDEALCPYETGRTCWAPLLQVLWWGTPLPFPLSTSNL PDLVGARGGAERGRAAARSPGGSAAGWECPSVLDEAGACTMSSCVS SQPSSNRAAPQDELGGGSSSSSSGNCEALRGLSSLSIHLGME SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL SGRKLSLQERSQGLAAGGSIDNNGRCICPSLPYSFVSSPQSSP RLPRRPTVESHHVSITIMQDCVOLNOYTLKDEIGKGSYGVVKLA YNERDNTYYAMKVLSKKKLIRQAAFPRRPPPRFTRAPGGCIQP RGP1\EQVYQEIA\1LKKLDHPNVV\KLVEVL\DDDREDHLYMV F\ELVNGGPVMEVPTLKKPLSEDDARFYFQDLIKKGIEYLHYQKII H\RDIKRSNLLVGEDGHIKIADFGVSUNDEFRGSDALLSNTVGTPA FMAPESLSETRKIFSGKALDVWAMGVTLYCFVFG*CPFMDERIM CLHSKIKSQALEFFDQDPLAKIDLITRKUDENPSRIVVPDI KLHPWVTRHGAEPLPSGDERCTLVEVTEEEVENSVKHIPSLATV ILVKTMIRKRSFGNPFEGSRREERSLAAGNLLTKRPTRECBSL SELKT*KISPLPACKVT*EFFPHSGCRPSCMOPPPLHTHSQPR *PEPPPRTDEALCPTGRTCWAPLLQVJWWGTPLPFPLSTSWL DLUGARGSHFCTINIALLYNSHTM. 5382 1536 203 GARGSQQDAPALQEAEVRGPERAQPARGRMTKARLFRLWLVLGS VFMILLITVYBDSAGAAHFYLLTTSFSRPTGGPPAFGSMESVGG YDWSPRDARRSPDQGRQAERRSVLRGFCANSSLAPPTKERPD DIPNSELSHLIVVDDRHGALYCTVVRVACTNWKRWIVLSGSLLH RGAPYRDPLRIPREWHNASAHLTFNKFWRRYGKLSRHIMKVKL KKYTKELFVUDPFVKLISAFRSKFELENEEF/*PQVRRAHAAAN RQPHQPARLGARGLEPREPQDVRAFAFRFFORPFORPTMERP	1	İ	l	SOPSSNRAAPODELGGPGSSSSPGOVDGRALDGLGGLGGLGAU
SGRKLSLQERSOGGLAAGGSLDMNGRCICPSLPYSPVSSPOSSP RLPRPTVESHIVSTIGMODOVQLNQYTLKDEIGKGSYGVVKLA YNENDNTYYAMKVLSKKKLIRQAAFPRRPPPRGTRPAPGGCIQP RGPI\EQVYQEIA\ILKKLDHPUVV\KLVEVL\DDPNEDHLYMV F\ELVNQQPVMEVPTIKKLBENQVAPYFQDLIKGISYTUHYOKII H\RDIKPSNLLVGBDGHIKIADFGVSNEFKGSDALLSNTVGTPA FMAPESLSETRXIFSGKALDVWAMGVTLYCFVFG*CFFMDERIM CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI KLHBWVTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLARV ILVXTMIRKRSFGNPFEGSREFSLSAGFNLLTKKPTRECESL SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQFR *PEPPRTDEALCPYETGRTCWAPLUQVLWWOTPLFFFLSTSWL PDLVGAPGSHCFINIALLRYNSHTM 5381 2 2050 PSRAGGAERGRAAARSPGGSAAGMECPSVLDEAGACTMSCCVS SQPSSNRAPADDELGGRGSSSESQKPCEALRGLSSLSIHLGME SFIVVTECEPGCAVDLGLARDRPLEADGGEVPLDTSGSQARPHL SGRKLSLQERSQGGLAAGGSLDMNGRCICPSLPYSFVSSPQSSP RLPRPTVESHWSITGMOVOLNOVYTLKDEIGKGSYGVVKLA YNENDNTYYAMKVLSKKKLIRQAAFPRRPPPRGTRPAPGGCIQP RGPI\EQVYQEIA\ILKKLDHFNVV\KLVEVL\DDPNEDHLYMV F\SLVNOGPVWEVPTLKFLSEQARFYFQDLIKGIEFLHYQKII H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGTPA FMAPESLSETRKIFSGKALDVAMGVTLYCFVFG*CPFMDERIM CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI KLHPWVTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV ILVXTMIRKRSFGMPFEGSRERSLSAGFMLITKKPTRECESL SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR *PEPPRIDEALCCYTT*EFPHPSGCRPSCWQPPFLHTHSQPR *PEPPRIDEALCCYTT*EFFTCAPAPLLQVLWWWGTPLPFFLSTSWL PDLVGAPGSHFCFLINIALLRYNSHTM. 5382 1536 203 GARGSQDAPALQEABVRGPERQPRAGRMTKARLFFILWLUGS VFMILLIIVYWDSAGAAHFYLHTSPSRPHTGPPPPTGPDRORE LTADSDVDEFLDKKLSAGVKQSDLPRKETEQPPPRGSMEESVG YDWSPRDARRSPDQGRQAERSVLGGFCANSSLAFFTKERFPD DIPNSLSHHIVJODRHGAIYCYDVENACTNMKYMIVLSGSLLH RGAPYRDPLRIPPROPLYBELDRINKVKL KKYTKFLFVRDPFVRLISAFRSKELENEEF/*PQVRRAHAAAV ROPHQPARLGARGLFRRPQVYSAFNFICYLLDBHTESKLAPFNEH	1	ļ		SETIMPECED COANDICT ADDRESS ENDODED DECOCO PONT
RLPRPPTVESHIVSTITEMODCVQLINQYTLKDEIGKGSYGVVKIA, YNENDNTYYMAKULSKKLIRQAAFPRPPRGTRPAFGGCIQP RGPI\EQVYQEIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMW F\ELVNQGPVMEVPTIKPLSEDQARFYFQDLIKGIEYLHYOKII H\RDIKPSDILJVGBDGHIADFGYSDALFYFQDLIKGIEYLHYOKII H\RDIKPSDILJVGBDGHIADFGYSDALFYFQDLIKGIEYLHYOKII H\RDIKPSDILJVGBDGHIADFGYSDALFYFQDLIKGIEYLHYOKII H\RDIKPSDILJVGBDGHIADFGYSDALFYFQDLIKGIEYLHYOKII KLHPWYTRHGAEPLFSEDARTLVEVTBEEVENSVKHIPSLATV ILVKTMIRKRSFGNFFGGSRRERFLSAAPGNLLTKKPTRECESL SELKT*KISPLPACCKVY*EFPHFSGCRPSCMPPFHTHSOPR *PEPPRTDEALCPYBTGRTCMAPLLQVLWWVGTPLPFPLSTSWL PDLVGAPGSFFCFLNIALLRYNSHTM 5381 2 2050 PSRAGGREGRAAAARFSGSAAGWECFSVLDEAGACTMSSCVS SQPSSNRAAPQDELGGRGSSSSESKPCCBALBGLSSLSHLKME SFIVYTECEPGCAVDLGLARDRPLEADGGVPLDTSGSQAPHL SGRKLSLQERSQGGLAAGGSLDMNGRCICPSLPYSPVSSPQSSP RLPRPPTVESHVSITGMQDCVQLNQYTLKDEIGKSSYGVVKIA YNENDNTYYAMKVLSKKKLIRQAAFPRRPPRGTSTAPFGGCTOP RGFI\EQYYGEIA\ILKKLDHENVV\KLVEVL\DDPNEDHLYMV F\ELIVNGSPVMEVPTLKSEDQAAFYPDDLIKGIEYLHYQKII H\RDIKPSNLLVGEDGHIKIADFGVSNFFKGSDALLSNTVGTPA FMAPESLSETRKIFSGKALDWAMMVTLYCFVFG*CPPMDERIM CLHSKIKSQALEFFDQPIAEDLKDLITMDKNYPSRIVVPEI KLHPWVTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIFSLATV ILVKTMIRKRSFGNFFEGSRERERSLSAPGNLLTKKPTRECESL SELKT*KISPLPACCKVT*EFFHBGGRPSCWQPFFLITHSOPR *PEPPRTDEALCPYETGRTCWAPLLQVLWWWGTPLPFFLSTSWL PDLVGAFGSHFCFLINIALTWISHTM. 5382 1536 203 GARGSQQDAPALQEAEVGPERAQPARGMTKARLFRLWLVLGS VFMILLIUVWDSAGAHFYLHTSFSRPHTGPPLPTFCOPDRDRE LTADSDVDEFLDKELSSAVGSDLPRKETGPPAPBGRESVKG YDWSPRDARRSPDQGRQAERSSLRGFCANSSLAFPYKERFPD DIFNSLSHILJUDDRHGAIYCYVPKVACTNWKRWMIVLSGSLLH RGAPYRDPLRIPREHVINASAHLTFINKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVPRRAHAAAV ROPHQPARACRAGLRENDRYGVFANFICLAPPTNEH		1	1	SCRVI CLOED COCCE AN COCCE PROGRAM OF THE PROGRAM O
YNENDNTYYAMKUJSKKKLIRQAAFPRRPPPRGCTIQP RGP1\GVYQEIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV F\ELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIEYLHYQKII H\RDIKFSNLLVGEDGHIKTADFGVSNFFKGSDALLISNTYGTFA FMAPESLSETRKIFSGKALDWAMGVTLYCFYFG-CPFMDERIM CLHSKIKSQALFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI KLHPWVTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV ILVXTMIRKRSGNPLPSGSRREERSLGAPGNLITKKPTRECESL SELKT*KISPLPACCKVT*FFPHPSGCRPSCWQPPFLHTHSQPR *PEPPRTDEALCPYEFTGTWAPLLQVLWWVGTPLPFPLSTSWL PDLVGAPGSHFCFLNIALLRYNSHTM SGLKT*KISPLPACCKVT*FFPHPSGCRPSCWQPPFLHTHSQPR *PEPPRTDEALCPYEFTGTWAPLLQVLWWVGTPLPFPLSTSWL PDLVGAPGSHFCFLNIALLRYNSHTM SQPSSNRAAPQDELGGGSSSESGVPCEALRGISSLEIHLGME SFIVVTECEPGCAVDLGLARDRPLEADQEVPLDTSGQARPHL SGRKLSLQERSQGGLAAGGSLDNNGCCLCESLPYSPVSSPQSSP RLPRRPTVSSHWSTISMQDCVQLNQVTLKDEIGKGSVGVVKLA YNEMDNTYYAMKVLSKKKLIRQAAFPRRPPPPRGTRPAPGGCIQP RGPI\EQVYQEIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV F\ELVNGGPVMEVPTLKPLSEDQARFYFQDLIKGIEYLHYQKII H\RDIKPSNLLVGEDGHIKIADFGVSNEFKKSDALLSNTVGTPA FMAPESLSETKKIFSGKALDVWAMGVTLYCFVFG*CPPMDERIM CLHSKIKSQALEFPDQPDIAEDLKDLITRNLDKNPESRIVVGFI KLHPWVTRHGAEPLFSEDENCTILVEVTEEPVENSVKHIPSLATV ILVKTMIRKRSFGNPFEGSREERSLSAPGNLITKKPTRECESL SELKT*KISPLPACKVT*EFPHPSGCRPSCWQPPFLHTHSQPR *PEPPRTDEALCPYETGGTCWAPLLQVUWWGTPLPFPLSTSWL LUKTMIRKRSFGNPFEGSRREERSLSAPGNLITKKPTRECESL SELKT*KISPLPACKVT*EFPHPSGCRPSCWQPPFLHTHSQPR *PEPPRTDEALCPYETGGTCWAPLLQVUWWGTPLPFPLSTSWL PDLVGAPGSHPCFLNIALLRYNSHTM. SGRAGGQDAPALQEABVRGGERAQPARGMTKARLFRLMULGS VFMILLILVYWDSAGAAHFYLHTSFRPHTGPPLPTPGPDRDRE LTADSDVDEFLDKELSAGVKQSDLPRKETEQPPAPGSMEESVRG YDWSPRDARRSPDQGRQQAERSVLRGFCANSLAFFTKREPFD DIPNSELSHLIVDDRIGATVCYVPKVACTNWKRWIULSGSLH RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFELENEEF/PQVQRAHAAAV RGOPHQPARLGARGLPWPQV VSFAMFIOVLLDHISKLAFPNEH	1		}	DI DE DE DE LE CONTROL DE LA C
RGPI\EQVYQEIA\ILKKLDHPNVV\KIJEVL\DDPNEDHLYMV F\ELVNQGPVMEVPTIKPLSEDQARFYFQDLIKGIEYLHYQKII H\RDIKPSNLLVGEDGHIKTADFGVSNEFKGSDALLSNTVGTFA FMAPESLSETRKIFSGKALDVWAMGVTLYCFVFG*CPFMDERIM CLHSKIKSQALEFPDGHIADLKDLITRMLDKNPSRIVVPEI KLHPWVTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV ILVKTMIRKRSFGNPFEGSREESSLSAPGHLITKKPTRECESL SELKT*KISPLPACCKUT*EPPHSGCRESCMPSCMCPPPLHTHSQPR *PEPPRTDEALCPYETGRTCWAPLLQVLWWVGTPLPFPLSTSWL PDLVGAPGSHFCFLNIALLRYNSHTM PSRAGGAERGRAAAARSPGGSSAAGWECPSVLDEAGACTMSSCVS SQPSSNRAPQDDELGGRGSSSESQKPCEALRGLSSLSIHLGME SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL SGRKLSLQERSGGGLAAGGSLDNNGRCICPSLPYSPYSSPQSSP RLPRRPTVESHHVSITGMQDCVQLNQVTLKDEIGKGSYGVVKLA YNENDNTYYAMKVLSKKKLIRQAAFPRRPPPRGTRPAPGGCIQP RGPI\EQVYQEIA\ILKKLDHPNVV\KIVEVL\DDPNEDHLYMV F\ELVNQGPVWEVPTLKPLSEDQARFYFQDLIKGIEYLHYQKII H\RDIKPSNLLVGEDGHIKILADFGVSNEFKGSDALLSNTVGTPA FMAPESLSETRKIFSGKALDVWAMGVYLYCFVFG*CPFMDERIM CLHSKIKSQALEFFDQDPIAEDLKDLITRMLDKMPESRIVVPEI KLHPWVTRHGAEPLJSEDENCTLVEVTEEEVENSVKHIPSLATV ILVKTMIRKRSFGNPFEGSREERSLSAPGNLLTKKETRECESL SELKT*KISPLPACKVT*EFPHSGCRPSCWOPPFLHTHSQPR *PEPPRTDEALCPYETGRTCWAPLLQVIWWGTPLPFPLSTSWL DLVGAPGSHFCFLNIALLRYNSHTM 5382 1536 203 GARGSQQDAPALQEABVRGPERAQPARGRMTKARLFRLWLVLGS VFMILLITVMDSAGAATVLHTSFSSP RPHGPPLPTFOPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRG YDWSPRDARRSPDQGRQQAERSVLRGFCANSLAFPTKERPFD DIFNSELSHLIVDDRIGATVCVVPKVACTNMKPRWILLSGSLH RGAPYRPPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRKFELNEEF,F PQWRRAHAAAV RQPHQPARLGARGLPRWQV VSFAMFIOVLLDHITSKLAPFNEH			ļ ·	RLPRRPTVESHHVSITGMQDCVQLNQYTLKDEIGKGSYGVVKLA
F\ELVNQGPVMEVPTIKPLESDQAFFYFQDLIKGIEYLHYQKII H\RPILKPESNLLVGEBQAFFYFQDLIKGIEYHHYQKII FMAPESLSETRKIFSGKALDVWAMGVTIYCFVFG*CPFMDERIM CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNFESRIVVPEI KLHPWTYRHGASPLPSEDCRTLTVEVTEEVENSVKHIPSLATV ILVXTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESL SELKT*KISPLPACCKVT*EFPHSGCRPSCWQPFFLHTHSQPR *PEPPRTDEALCPYETGRTCWAPLLQVIMWVGTPLPFPLSTSWL PDLWGAPGSHFCFLNIALLRYNSHTM 5381 2 2050 FSRAGGAERGRAAARSPGGSAAGWECPSVLDEAGACTMSSCVS SQPSSNRAAPQDELGGRGSSSSESGKPCEALRGLSSLSIHLGME SFIVVTECEPGCAVDLGLARDRPLEADOQEVPLDTSGSQARPHL SGRKLSLGERSGGGLAAGGSLDMMGRCICPSLPYSPVSSPQSSP RLPRRPTVESHHVSITGMQDCVQLNQYTLKDEIGKGSVGVVKLA YNENDNTYYAMKVLSKKKLIRQAAFPRRPPPPRGTRPAPGGCIOP RGF1\EQVYQEIA\LKKLDHRNVV\KIVEVL\DPDPMEDHLYMV F\ELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIEYLHYQKII H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGTPA FMAPESLSETRKIFSGKALDVWAMGVTLYCFVFG*CPFMDERIM CLHSKIKSQALEFDQPDIAEDLKDLITRMLDKNFESRIVVPEI KLHPWTTRHGASPLSPEGSRREERSLSAPGNLIKKRFTRECESL SELKT*KISPLBACCKVT*EFPHSGCRPSCWQPPFLHTHSQPR *PEPPRTDEALCPYETGRTCWAPLLQVLWWGTPLPFPLSTSWL ILVKTMIRKRSFGNFFGSRREERSLSAPGNLIKKRFTRECESL SELKT*KISPLBACCKVT*EFPHSGCRPSCWQPPFLHTHSQPR *PEPPRTDEALCPYETGRTCWAPLLQVLWWGTPLPFPLSTSWL DDLVGAPGSHFCFLNIALLRYNSHTM 5382 1536 203 GARGSQDAPALQEABVRGPERAQPARGRMTKARLPRIMLVLGS VFMILLILVYMDSAGAAHFYLHTSPSR PHTGPPLPTPGPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRG YDWSPRDARRSPDQGRQQAERSVLRGFCANSLAFFTKERPFD DIFNSELSHLIVDDRIGATCVYDFXACTNMRKWITULSGSLH RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFLENEEF;F PQVRRAHAAAV RQDPHQPARLGARGLPRPQV VSFAMFIQVLLDHTSKLAFFNEH	{		Í	YNENDNTYYAMKVLSKKKLIRQAAFPRRPPPRGTRPAPGGCIQP
H\RDIKPSRILIVGEDGHIKIADFGVSNEFKGSDALLSNTVGTFA FMAPSESSETRKIFSGKALDVWAMGVTLYCFVFG*CPFMDERIM CLHSKIKSQALEPPDQPDIAEDLKDLITRMLDKNPESRIVVPEI KLHPWYTRIGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV ILVXTMIRKRSFGNPFEGSRREGRSLGAPGNLLTKKPTRECESL SELKT*KISPLPACCKVT*EPPHPSGCRPSCWGPFFHTHSOPR *PEPPRTDEALCPYETGRTCAPLLQVLWWGTPLPFPLSTSWL PDLVGAPGSHFCFLNIALLRYNSHTM 5381 2 2050 PSRAGGAERGRAAARSPGGSAAGWECPSVLDEAGACTMSSCVS SQPSSNRAAPQDELGGRGSSSESSESKPCEALRGLSSLSIHLGME SFIVVTECEPGCAVDLGLARRPPLEADGQSVPLDTSGSQARPHL SGRKLSLQERSQGGLAAGGSLDMNGRCICFSLPYSFVSSPOSSP RLPRRPTVESHHVSITGMQDCVQLMQYTLKDEIGKGSYGVVKLA YNEMDNITYAMKVLSKKLIRQAAFPRRPPBPGGRPAPGGCIQP RGPI\EQVYQEIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV F\ELVNGGPVMSVPTLKPLSEQQARFYFGDLIKGIEVLHYQKII H\RDIKPSNLLVGEFBUNDFILKSDLALLSNTVGTPA FMAPESLSETRKIFSGKALDVWAMGVTLYCFVFG*CPFMDERIM CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI KLHPWVTHGABPPLPSGEDENCTLVEVTEEEVENSVKHIPSLATV ILVXTMIRKRSFGNPFGSRREERSLSAPGNLLTKKPTRECESL SELKT*KISPLPSCCKVT*EFPHPSGCRPSCWGPPFLHTHSQPR *PEPPRTDEALCPYETGTCVAPPLLQVLWWGTPLPFPLSTSWL PDLVGAPGSHPCFLNIALLRYNSHTM. 5382 1536 203 GARGSQQDAPALQEAEVRGGERAQPARGRMTKARLFRLWLVLGS VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRG YDWSPRDARRSPDQGRQQAERSVLRGFCANSSLAFFTKERPFD DIFNSELSHLIYUDBHGAIVCYVYKACTNMKRWITVLSGSLH RGAPYRDPLRI PREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTSKLAPFNEH	1 1		ļ	RGPI\EQVYQEIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV
H\RDIKPSRILIVGEDGHIKIADFGVSNEFKGSDALLSNTVGTFA FMAPSESSETRKIFSGKALDVWAMGVTLYCFVFG*CPFMDERIM CLHSKIKSQALEPPDQPDIAEDLKDLITRMLDKNPESRIVVPEI KLHPWYTRIGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV ILVXTMIRKRSFGNPFEGSRREGRSLGAPGNLLTKKPTRECESL SELKT*KISPLPACCKVT*EPPHPSGCRPSCWGPFFHTHSOPR *PEPPRTDEALCPYETGRTCAPLLQVLWWGTPLPFPLSTSWL PDLVGAPGSHFCFLNIALLRYNSHTM 5381 2 2050 PSRAGGAERGRAAARSPGGSAAGWECPSVLDEAGACTMSSCVS SQPSSNRAAPQDELGGRGSSSESSESKPCEALRGLSSLSIHLGME SFIVVTECEPGCAVDLGLARRPPLEADGQSVPLDTSGSQARPHL SGRKLSLQERSQGGLAAGGSLDMNGRCICFSLPYSFVSSPOSSP RLPRRPTVESHHVSITGMQDCVQLMQYTLKDEIGKGSYGVVKLA YNEMDNITYAMKVLSKKLIRQAAFPRRPPBPGGRPAPGGCIQP RGPI\EQVYQEIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV F\ELVNGGPVMSVPTLKPLSEQQARFYFGDLIKGIEVLHYQKII H\RDIKPSNLLVGEFBUNDFILKSDLALLSNTVGTPA FMAPESLSETRKIFSGKALDVWAMGVTLYCFVFG*CPFMDERIM CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI KLHPWVTHGABPPLPSGEDENCTLVEVTEEEVENSVKHIPSLATV ILVXTMIRKRSFGNPFGSRREERSLSAPGNLLTKKPTRECESL SELKT*KISPLPSCCKVT*EFPHPSGCRPSCWGPPFLHTHSQPR *PEPPRTDEALCPYETGTCVAPPLLQVLWWGTPLPFPLSTSWL PDLVGAPGSHPCFLNIALLRYNSHTM. 5382 1536 203 GARGSQQDAPALQEAEVRGGERAQPARGRMTKARLFRLWLVLGS VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRG YDWSPRDARRSPDQGRQQAERSVLRGFCANSSLAFFTKERPFD DIFNSELSHLIYUDBHGAIVCYVYKACTNMKRWITVLSGSLH RGAPYRDPLRI PREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTSKLAPFNEH	1	•		F\ELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIEYLHYOKII
FMAPESLSETRKIPSGKALDWAMGVTLYCFVFG+CPFMDERIM CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI KLHPWVTRIGAZEILPSEDENCTLVEVTEEEVENSVKHIPSLATV ILVKTMIRKRSFCNPFEGSRREFSLSAPGNLLTKKPTRECESL SELKT*KISPLPACCKVT*EFPHPSGCRPSCWOPFPHTHTSOPR *PEPPRTDEALCPYETGRTCWAPLLQVLWWGTPLPFPLSTSWL PDLVGAPGSHFCFLNIALLRYNSHTM 5381 2 2050 PSRAGGAERGRAAARSPGGSAAGWECPSVUDEAGACTMSSCVS SQPSSNRAAPQDELGGGSSSSESOKPCEALRGLSSLSIHLGME SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL SGRKLSLQERSGGBLANGGCLOFSLPYSPVSSPQSSP RLPRRPTVESHHVSITGMQDCVOLNGYTLKDEISKGSYGVVMLA YNEMDNTYYAMKVLSKKKLIRQAAFPRRPPPRGTRPAPGGCIQP RGPI\EQVYQCIA\ILKKLDHPNVV\KLVEVL\DDDNEDHLYMV F\ELVNCGOPVMEVPHXLSBCDARFYFQDLIKGIEVLHYQKII H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGTPA FMAPESLSETRKIFSGKALDVAMMGVTLVCFVFG*CFFMDERIM CLHSKIKSQALEFPDQILADLKDLITRMLDKNPESRIVVPEI KLHPWVTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV ILVKTMIRKRSFGNPFEGSREERSLSAPGNLLTKKFTRECESL SELKT*KISPLBACCTW*T*EFPHPSGCRPSCWOPPFLHTHSOPR *PEPPRTDEALCPYETGRTCWAPLLQVLWWVGTPLPFPLSTSWL PDLVGAPGSHFCFLNIALLRYNSHTM GARGSQQDAPALQEAEVRGPERAQPARGMTKARLFRLWLVLGS VFMILLILVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRG YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD DIFNSELSHLIVDDRHGATYCYVPKVACTNNKRVMTUNLSGSLIH RGAPYRDPLRI PREHVHNASAHLTFNKFWRRYGKLSRHMKVKL KKYTKFLFVRDPFVRLISAFRSKFELEBEF*PFVFKERPFD	ĺ		l	H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGTPA
CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVUPEI KLHPWVTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV ILVKTMIRKRSFGNPFEGSRREERSLSAPGNLITKRPTRECESL SELKT*KISPLPACCKVT*EPPHPSGCRPSCWQPPPHHTHSQPR *PEPPTDEALCPYETGRTCWAPLLQVLWWVGTPLPPPLSTSWL PDLWGAPGSHFCFLNIALLRYNSHTM 2 2050 PSRAGGAERGRAAARSPGGSAAGWECPSVLDEAGACTMSSCVS SQPSSNRAAPQDELGGRGSSSSESQKPCEALRGLSSLSIHLGME SFIVVTECEPGCAVDLGLARDRPLEADQGEVPLDTSGSQARPHL SGRKLSLGERSQGGLAAGGSLDNNGRCICPSLPYSPVSSPQSSP RLPRRPTVESHHVSITGMQDCVQLNQYTLKDEIGKGSYGVVKLA YNENDNTYYAMKVLSKKKLIRQAAFPPRPPPRGTRPAPGGCIQP RGPI'EQVYQEIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV F\ELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIEYLHYQKII H\RDIKPSNLLVGEDGHIKIADPGVSNEFKGSDALLSNTVGTPA FMAPESLSETRKIFSGKALDWAMGVTLYCFVFG*CPFMDERIM CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI KLHPWVTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV ILVKTMIRKRSFGNFFEGSRREERSLSAPGRLLTKKPTRECESL SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR *PPEPPRTDEALCPYETGRTCWAPLLQVLWWGTPLFFFLSTSWL PDLVGAPGSHFCFLNIALLRYNSHTM. 5382 1536 203 GARGSQDAPALQEAEVRGPERAQPARGRMTKARLFRLWLVLGS VPMILLITVYMDSAGAAHFYLHTSPSRPHTGPPLPTPGPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRG YDMSPRDARRSPDQGRQQARRSSVLRGFCANSSLAFPTKERPFD DIFNSELSHLIVDDRHGAIYCYVPKVACTMKKYMIVLSGSLLH RGAPYRDPLRIPREPVRILSAPRSKFELENEEF/*PQVRRAHAAAV KKYYKFLFVRDPFVRILSAPRSKFELENEEF/*PQVRRAHAAAV	}			FMAPESLSETRKIFSGKALDVWAMGVTLYCFVFG*CPFMDFPTM
KLHPWTRIGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV ILVKTMIRKRSFGNPFEGSRERSLSAPGNLLTKKPTRECESL SELKT*KISFLPACCKVT*ETPHPSGCRPSCWQPPFLHTHSQPR *PEPPRTDEALCPYETGRTCKAPLLQVLWWVGTPLPFPLSTSWL PDLVGAPGSHFCFLNIALLRYNSHTM 2 2050 PSRAGGAERGRAAARSPGGSAAGWECPSVLDEAGACTMSSCVS SQPSSNRAAPQDELGGRGSSSSESQKPCEALRGLSSLSIHLGME SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL GGRKLSLQERSGGLAAGGSLDMNGRCLCPSLPYSPVSSPQSSP RLPRRPTVESHHVSITGMQDCVQLNQYTLKDEIGKGSYGVVKLA YNEMDNTYYAMKVLSKKKLTRQAAFPRRPPPRGTRPAPGGCIQP RGP1'LGVYQEIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV F\ELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIEYLHYQKII H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGTPA FMAPESLSETRKIFSGKALDVWAMGVTLYCFVFG*CPFMDERIM CLHSKIKSQALEFFDQPDIAEDLKDLITRMLDKNFESRIVVPEI KLHPWTRIGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV ILVKTMIRKRSFGNFFEGSREERSLSAPGNLUTKKPTRECESL SELKT*KISPLPACCKVT*EFFPBSGCRPSCWOPPFLHTHSQPR *PEPPRTDEALCPYETGRTCWAPLLQVLWWVGTPLPFPLSTSWL PDLVGAPGSHFCFLNIALLRYNSHTM. 5382 1536 203 GARGSQQDAPALQEABVRGGPERAQPARGRMTKARLFRLWLVLGS VFMILLILVYWDSAGAAHYLHTSFSRPHTGPPLPTPGPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETGPPLPTPGPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETGPPLPTPGFDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETGPPLPTPGFDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETGPPLPTFGFDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETGPPLPTFGFDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETGPPLPTFGFDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETGPPLPTFKERPFD DIFNSELSHLIVDDRHGAIYCYVPKVACTNWKRWIVLSGSLLH RGAPYRDPLRIPPEHVHNASAHLTFNKFWRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFELENEEF/F-PQVURRAHAAAN ROPHQPARLGARGLPRWPQ\VSFANFICYLLDPHTEKLAPFNEH			ļ	CLHSKIKSOALEFPDOPDIAFDI.KDI.TTPMI.DKNDECDIMDET
ILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESL SELKT*KISPLPACCKVT*EFPPHSGCRPSCWQPPFLHTHSQPR *PEPPRTDEALCYSTGRTCWAPLLQVLWWVGTPLPFPLSTWL PDLVGAPGSHFCFLNIALLRYNSHTM 2 2050 PSRAGGAERGRAAARSPGGSAAGWECPSVLDEAGACTMSSCVS SQPSSNRAAPQDELGGRGSSSESQKPCEALRGLSSLSIHLGME SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL SGRKLSLQERSQGGLAAGGSLDMNGRCICPSLPYSPVSSPQSSP RLPRRPTVESHVSITGMQDCVQLNQYTLKEDIGKGSYGVVKLA YNERDNTYYAMKVLSKKKLIRQAAFPRRPPPPRGTRPAPGGCIQP RGPI\EQVYQEIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV F\ELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIEYLHYQKII H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGTPA FMAPESLSETRKIFSGKALDVWAMGVTLVCFVFG*CPFMDERIM CLHSKIKSQALEFPDQDIAEDLKDLITRMLDKNPESRIVVPEI KLHPWVTRHGAEPLFSEDENCTLVEVTEEEVENSVKHISSLATV ILVKTMIRRRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESL SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR *PPPPRTIDEALCPYETGRTCWAPLLQVLWWVGTPLPFFLSTSWL DDLVGAPGSHFCFLNIALLRYNSHTM. 5382 1536 203 GARGSQQDAPALQEABVRGPERAQPARGRWTKARLFRLWLVLGS VFMILLIIVYWDSAGAAHFYLHTSFRPHTGPPLPTPGPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETTQPPAPGSMEESVRG VFMSLLIIVYDDRHGAIYCYYPKVACTNWKRWIVLSGSLH RGAPYRDPLRIPREDRFLISPERVHISAFRSKFELENEEF/*PQVRRAHAAAV KYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAANV KYTKFLFVRDPFARLISAFRSKFELENEEF/*PQVRRAHAANV ROPHQPARLGARGLPRWPQ\VSFANFIQYLLDHTEKLAPFNEH	1 1			KI.HPWVTRHGAEDI.DCEDENCTI VEVTERRIVENCIPVIEDO A PORT
SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR *PEPPRTDEALCPYETGRTCWAPLLQVLWWGTPLPFPLSTSWL PDLVGAPGSHFCFLNIALLRYNSHTM PSRAGGAERGRAAARSPGGSAAGWECPSVLDEAGACTMSSCVS SQPSSNRAAPQDELGGRGSSSSESGKPCEALRGLSSLSIHLGME SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL SGRKLSLQERSQGLAAGGSLDMNGRCICPSLPYSPVSSPQSSP RLPRRPTVESHHVSITIGMQDCVQLNQYTLKDEIGKGSYGVVKLA YNENDNTYYAMKVLSKKKLIRQAAFPRRPPPRGTRPAPGGCIQP RGPI\EQVYQGIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV F\ELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIEYLHYQKII H\RDIKPSNLLVGEDGHIKIADFGVSNBFKGSDALLSNTVGTPA FMAPESLSETTKIFSGKALDWAMGVTLYCFVFG*CPFMDERIM CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI KLHFWVTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV ILVXTMIRKRSFGNPFEGSRREBRSLSAPGNLLTKKPTRECESL SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPFFLHTHSQPR *PEPPRTDEALCPYETGRTCWAPLLQVLWWVGTPLPFFLSTSWL PDLVGAPGSHFCFLNIALLRYNSHTM 5382 1536 203 GARGSQQDAPALQEABVRGPERAQPARGRMTKARLFRLWLVLGS VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMESVRG YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD DIPNSELSHLIVDDRHGAIVCYVPKVACTNWKRVMIVLSGSLLH RGAPYRDPLRIPREHVNNSAAHLTENKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAPRSKFELENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLDLDHTSKLAPFNSH	1 1		J	TLVYPMIDVDCCONDEPCCEDEEDCLGARGY A BUSINESS
*PEPPRTDEALCPYETGRTCWAPLLQVLWWVGTPLPFPLSTSWL PDLVGAPGSHPCFLNIALLRYNSHTM PSRAGGAERGRAAAARSPGGSAAGWECPSVLDEAGACTMSSCVS SQPSSNRAAPQDELGGRGSSSSESQKPCEALRGLSSLSHLGME SFIVVTECEPGCAVDLGLARDRPLEADGGEVPLDTSGSQARPHL SGRKLSLQERSQGGLAMGRCLCPSLPYSPVSSPQSSP RLPRRPTVESHIVSITGMQDCVQLNQYTLKDEIGKGSYGVVKLA YNENDNTYYAMKVLSKKKLIRQAAFPRRPPPRGTRPAPGGCIQP RGPI\EQVYQEIA\ILKKLDHENVV\KLVEVL\DDPNEDHLYMV F\ELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIEYLHYQKII H\RDIKPSNLUGEDCHIKIADFGVSNEFKGSDALLSNTVGTPA FMAPESLSETRKIFSGKALDWAMGVTLYCFVFG*CPFMDERIM CLHSKIKSQALEFPDOPDIAEDLKDLITRMLDKNPESRIVVPEI KLHPWTRHGAEPLBSEDENCTLVEVTEEEVENSVKHIPSLATV ILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESL SELKT*KISPLPACCKVT*EFPHPSGCRPSCWOPPFLHTHSQPR *PEPPRTDEALCPYETGRTCWAPPLQVTWWVCTPLPFFLSTSWL PDLVGAPGSHFCFLNIALLRYNSHTM. 5382 1536 203 GARGSQQDAPALQEAEVRGPERAQPARGRMTKARLFRLWLVLGS VPMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRG VPMSPRDARRSPDQGRQQAERRSVLRGCFCANSSLAFPTKERPFD DIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLSGSLLH RGAPYRDPLRIPREHVHNASAHLTFMKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAPRSKFELENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLDHTSKLAPFNEH				CEL VELVICEN DE COMME DESMES DE SAPGNELTRAPTRECESE
PDLVGAPGSHFCFLNIAL_RYNSHTM PSRAGGAERGRAAARSPGGSAGGWECPSVLDEAGACTMSSCVS SQPSSNRAAPQDELGGRGSSSESQKPCEALRGLSSLSIHLGME SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL SGRKLSLQERSQGGLAAGGSLDMNGRCICPSLPYSPVSSPQSSP RLPRRPTVESHHVSITGMQDCVQLNQYTLKDEIGKGSYGVVKLA YNENDNTYYAMKVLSKKKLIRQAAFPRPPPRGTRPAPGGCIQP RGPT\EQVYQEIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV F\ELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIEYLHYQKII H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGTPA FMAPESLSETRKIFSGKALDVWAMGVTLYCFVFG*CPFMDERIM CLHSKIKSQALEFPDQPPDIAEDLKDLITRMLDKNPESRIVVPEI KLHPWVTRHGAEPLPSEDENCTLVEVTEEVENSVKHIPSLATV ILVKTMIRKRSFGNPFEGSREERSLSAPGNLLTKKPTRECESL SELKT*KISPLPACCKVT*EFPHPSGCPSCWQPPFLHTHSQPR *PPEPPRIDEALCPYETGRTCWAPJLQVLWWVGTPLPFPLSTSWL PDLVGAPGSHFCFLNIALLRYNSHTM 5382 1536 203 GARGSQQDAPALQEAEVRGPERAQPARGRMTKARLFRLWLVLGS VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTTGPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRG YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFFTKERPFD DIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLSGSLLH RGAPYRDPLRIPREHVHNASAHLTFNKFWRYGKLSRHLMKVKL KKYTKFLFVRDFFVRLISAFRSKFELENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIOYLLDPHTSKLAPFNSH	1 1			SEBAT* KISPLPACCKVT* EPPHPSGCRPSCWQPPFLHTHSQPR
PSRAGGAERGRAAARSPGGSAAGWECPSVLDEAGACTMSSCVS SQPSSNRAAPQDELGGRGSSSESQKPCEALRGLSSLSIHLGME SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL SGRKLSLQERSQGGLAAGGSLDMNGRCICPSLPYSPVSSPQSSP RLPRRPTVESHHVSITGMQDCVQLNQYTLKDEIGKGSYGVVKLA YNENDNTYYAMKVLSKKKLIRQAAFPRRPPPRGTRPAPGGCIQP RGPI\EQVYQEIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV F\ELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIEVLHYQKII H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGTPA FMAPESLSETRKIFSGKALDVWAMGVTLVCFVFG*CPFMDERIM CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI KLHFWYTRHGABPLFSEDENCTLVEVTEEEVENSVKHIPSLATV ILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESL SELKT*KISPLFACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR *PPPPTDEALCPYETGRTCWAPLLQVLWWVGTPLPFPLSTSWL PDLVGAPGGSHFCFLNIALLRYNSHTM. 5382 1536 203 GARGSQQDAPALQEAEVRGPERAQPARGRMTKARLFRLWLVLGS VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETQPPAPGSMEESVRG YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD DIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLSGSLLH RGAPYRDPLRIPREHVINASAHLTFRKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTSKLAPFNEH]			*PEPPRIDEALCPXETGRTCWAPLLQVLWWVGTPLPFPLSTSWL
SQPSSINAARARAKSESSAKEVELTSULEKGASTAKEVELTSULEKGATTMSSCVS SQPSSINAAPQDELGGRGSSSSESQKPCEALRGLSSLSIHLGME SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL SGRKLSLQERSQGGLAAGGSLDMMGRCICPSLPYSPVSSPQSSP RLPRRPTVESHHVSITGMQDCVQLNQYTLKDELGKGSYGVVKLA YNENDITYYAMKVLSKKKLIRQAAFPRRPPPRGTRPAFGGCIQP RGPI\EQVYQEIA\ILKKLDHPNVV\KLVEVL\DDPMEDHLYMV F\ELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIEYLHYQKII H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGTPA FMAPESLSETRKIFSGKALDVWAMGVTLYCFVFG*CPFMDERIM CLHSKIKSQALEFPDQPDIAEDLKDLITTMLDKNPESRIVVPEI KLHPWVTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV ILVKTMIRKRSFGNFFEGSRREERSLSAPGNLLTKKPTRECESL SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR *PSPPTTDEALCPYETGRTCWAPLLQVLWWVGTPLPFPLSTSWL PDLVGAPGSHFCFLNIALLRYNSHTM. 5382 1536 203 GARGSQQDAPALQEABVRGPERAQPARGRMTKARLFRLWLVLGS VFMILLIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRG YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD DIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLSGSLLH RGAPYRDPLRIPREHVHNASAHLTFRKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTSKLAPFNEH	6202			
SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL SGRKLSLQERSQGGLAAGGSLDMMGRCICPSLPYSPVSSPQSSP RLPRPTVESHHVSITGMQDCVQLNQYTLKDEIGKGSYGVVKLA YNENDNTYYAMKVLSKKKLIRQAAFPRRPPPRGTRPAPGGCIQP RGPI\EQVYQEIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV F\ELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIEYLHYQKII H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGTPA FMAPESLSETRKIFSGKALDVWAMGVTLYCFVFG*CPFMDERIM CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI KHHPWTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV ILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESL SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR *PPFPRTDEALCPYETGRTCWAPLLQVLWWVGTPLPFPLSTSWL PDLVGAPGSHFCFLNIALLRYNSHTM. 5382 1536 203 GARGSQQDAPALQEAEVRGPERAQPARGRWTKARLFRLWLVLGS VPMILLIVYWDSAGAAHFYLHTSFSPHTGPPLPTPGPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRG YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD DIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLSGSLLH RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLDPHTSKLAPFNEH	3301	· 4	2050	PSKAGGAERGRAAAARSPGGSAAGWECPSVLDEAGACTMSSCVS
SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL SGRKLSLQERSQGGLAAGGSLDMMGRCICPSLPYSPVSSPQSSP RLPRPTVESHHVSITGMQDCVQLNQYTLKDEIGKGSYGVVKLA YNENDNTYYAMKVLSKKKLIRQAAFPRRPPPRGTRPAPGGCIQP RGPI\EQVYQEIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV F\ELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIEYLHYQKII H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGTPA FMAPESLSETRKIFSGKALDVWAMGVTLYCFVFG*CPFMDERIM CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI KHHPWTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV ILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESL SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR *PPFPRTDEALCPYETGRTCWAPLLQVLWWVGTPLPFPLSTSWL PDLVGAPGSHFCFLNIALLRYNSHTM. 5382 1536 203 GARGSQQDAPALQEAEVRGPERAQPARGRWTKARLFRLWLVLGS VPMILLIVYWDSAGAAHFYLHTSFSPHTGPPLPTPGPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRG YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD DIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLSGSLLH RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLDPHTSKLAPFNEH] }	· •		SQPSSNRAAPQDELGGRGSSSSESQKPCEALRGLSSLSIHLGME
SGRKLSLQERSQGLAAGGSLDMNGRCICPSLPYSPVSSPQSSP RLPRRPTVESHHVSITGMQDCVQLNQYTLKDEIGKGSYGVVKLA YNENDNTYYAMKVLSKKKLIRQAAFPRRPPPRGTRPAPGGCIQP RGPI\EQVYQEIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV F\ELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIEYLHYQKII H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGTPA FMAPESLSETRKIFSGKALDVWAMGYTLYCFVFG*CPFMDERIM CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI KKHPWTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV ILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESL SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR *PBFPRTDEALCPYETGRTCWAPLLQVLWWVGTPLPFPLSTSWL PDLVGAPGSHFCFLNIALLRYNSHTM. 5382 1536 203 GARGSQQDAPALQEABVRGPERAQPARGMTKARLFRLWLVLGS VFMILLIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRG YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFFTKERPFD DIPNSELSHLIVDDRHGAIYCTVPKVACTNWKRVMIVLSGSLLH RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKLL KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTSKLAPFNEH		ı		SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSOARPHL
RLPRRPTVESHHVSITGMQDCVQLNQYTLKDEIGKGSYGVVKLA YNENDNTYYAMKVLSKKKLIRQAAFPRRPPPRGTRPAPGGCIQP RGPI\EQVYQEIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV F\ELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIEYLHYQKII H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGTPA FMAPESLSETRKIFSGKALDVMAMGVTLYCFVFG*CPFMDERIM CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI KLHPWVTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV ILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESL SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR *PEPPRTDEALCPYETGRTCWAPLLQVLWWVGTPLPFPLSTSWL PDLVGAPGSHFCFLNIALLRYNSHTM. 5382 1536 203 GARGSQQDAPALQEABVRGPERAQPARGRMTKARLFRLWLVLGS VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRG YDWSPRDARRSPDQGRQQAERSVLRGFCANSSLAFFTKERPFD DIPNSELSHLIVDDRHGAIYCTVPKVACTNWKRVMIVLSGSLLH RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFBLENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTSKLAPFNEH	1			SGRKLSLQERSQGGLAAGGSLDMNGRCICPSLPYSPVSSPOSSP
YNENDNTYYAMKVLSKKKLIRQAAFPRRPPPRGTRPAPGGCIQP RGPI\EQVYQEIA\ILKKLDHPNVV\KLVEVL\DDPMEDHLYMV F\ELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIEYLHYQKII H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGTPA FMAPESLSETRKIFSGKALDVWAMGVTLYCFVFG*CPFMDERIM CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI KLHPWVTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV ILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESL SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR *PEPPRTDEALCPYETGRTCWAPLLQVLWWVGTPLPFPLSTSWL PDLVGAPGSHFCFLNIALLRYNSHTM. 5382 1536 203 GARGSQQDAPALQEABVRGPERAQPARGRMTKARLFRLWLVLGS VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRG YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD DIPNSELSHLIVDDRHGAIYCYVPKVACTMKRVMIVLSGSLLH RGAPFYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQVILDPHTEKLAPFNEH	·			RLPRRPTVESHHVS ITGMODCYOLNOVTLKDE TOKGEVOLDER A
RGPI\EQVYQEIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV F\ELVNQGPYMEVPTLKPLSEDQARFYFQDLIKGIEYLHYQKII H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGTPA FMAPESLSETRKIFSGKALDVWAMGVTLYCFVFG*CPFMDERIM CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI KLHPWVTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV ILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESL SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR *PEPPRTDEALCPYETGRTCWAPLLQVLWWVGTPLPFFLSTSWL PDLVGAPGSHFCFLNIALLRYNSHTM 5382 1536 203 GARGSQQDAPALQEABVRGPERAQPARGRMTKARLFRLWLVLGS VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRG YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD DIPNSELSHLIVDDRHGAIYCYVPKVACTNNKRVMIVLSGSLLH RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTEKLAPFNEH	1 1	į		YNENDNTYYAMKVI.SKKKI.TROAA PRODURDROCTORA POGGTOR
F\ELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIEYLHYQKII H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGTPA FMAPESLSETRKIFSGKALDVWAMGVTLYCFVFG*CPFMDERIM CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI KLHPWVTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV ILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESL SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR *PEPPRTDEALCPYETGRTCWAPLLQVLWWVGTPLPFPLSTSWL PDLVGAPGSHFCFLNIALLRYNSHTM. 5382 1536 203 GARGSQQDAPALQEABVRGPERAQPARGRMTKARLFRLWLVLGS VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRG YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD DIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLSGSLLH RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTEKLAPFNEH	1 1	ł		RGPT EOVYOFIA TIKKI DUDMAN EKKEPEKGI KEMPGGCIQP
H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGTPA FMAPESLSETRKIFSGKALDVWAMGVTLYCFVFG*CPFMDERIM CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI KLHPWVTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV ILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESL SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR *PEPPRTDEALCPYETGRTCWAPLLQVLWWVGTPLPFFLSTSWL PDLVGAPGSHFCFLNIALLRYNSHTM. 5382 1536 203 GARGSQQDAPALQEAEVRGPERAQPARGRMTKARLFRLWLVLGS VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRG YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD DIPNSELSHLIVVDDRHGAIYCYVPKVACTNWKRVMIVLSGSLLH RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQVLLDPHTEKLAPFNEH]]	•		E/EI MOCDIMENDOLKEL ORDC
FMAPESLSETRKIFSGKALDVWAMGVTLYCFVFG*CPFMDERIM CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI KLHPWVTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV ILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESL SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR *PEPPRTDEALCPYETGRTCWAPLLQVLWWVGTPLPFFLSTSWL PDLVGAPGSHFCFLNIALLRYNSHTM. 5382 1536 203 GARGSQQDAPALQEAEVRGPERAQPARGRMTKARLFFLWLVLGS VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRG YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD DIPNSELSHLIVVDDRHGAIYCYVPKVACTNWKRVMIVLSGSLLH RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQVLLDPHTEKLAPFNEH	1	1		L ADDINGS VINE OF TEXT DESCRIPTION OF THE PROPERTY OF THE PROP
CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI KLHPWYTHGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV ILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESL SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR *PEPPRTDEALCPYETGRTCWAPLLQVLWWVGTPLPFPLSTSWL PDLVGAPGSHFCFLNIALLRYNSHTM. 5382 1536 203 GARGSQQDAPALQEAEVRGPERAQPARGRMTKARLFRLWLVLGS VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRG YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD DIPNSELSHLIVDDRHGAIYCYVPKVACTMKRVMIVLSGSLLH RGAPFYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTEKLAPFNEH	1	į		n\kulkpsnllvgedghikiaDfgvsnefkgsdallsnTvgTpA
KLHPWVTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV ILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESL SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR *PEPPRIDEALCPYETGRTCWAPLLQVLWWVGTPLPFPLSTSWL PDLVGAPGSHFCFLNIALLRYNSHTM. 5382 1536 203 GARGSQQDAPALQEABVRGPERAQPARGRMTKARLFRLWLVLGS VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRG YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD DIPNSELSHLIVDDRHGAIYCYVPKVACTMKRYWIVLSGSLLH RGAPFYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTEKLAPFNEH] 1			FMAPESLSETRKIFSGKALDVWAMGVTLYCFVFG*CPFMDERIM
KLHPWVTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV ILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESL SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR *PEPPRIDEALCPYETGRTCWAPLLQVLWWVGTPLPFPLSTSWL PDLVGAPGSHFCFLNIALLRYNSHTM. 5382 1536 203 GARGSQQDAPALQEABVRGPERAQPARGRMTKARLFRLWLVLGS VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRG YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD DIPNSELSHLIVDDRHGAIYCYVPKVACTMKRYWIVLSGSLLH RGAPFYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTEKLAPFNEH	1 1	ľ	i	CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI
ILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESL SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR *PEPPRTDEALCPYETGRTCWAPLLQVLWWVGTPLPFPLSTSWL PDLVGAPGSHFCFLNIALLRYNSHTM 5382 1536 203 GARGSQQDAPALQEABVRGPERAQPARGRMTKARLFFLWLVLGS VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRG YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD DIPNSELSHLIVDDRHGAIYCYVPKVACTNNKRVMIVLSGSLLH RGAFYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTEKLAPFNEH	1	ļ.		KLHPWVTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPSI.ATV
SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR *PEPPRTDEALCPYETGRTCWAPLLQVLWWVGTPLPFPLSTSWL PDLVGAPGSHFCFLNIALLRYNSHTM 5382 1536 203 GARGSQQDAPALQEABVRGPERAQPARGRMTKARLFRLWLVLGS VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMBESVRG YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD DIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRYMIVLSGSLLH RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTEKLAPFNEH	1	1		ILVKTMIRKRSFGNPFEGSRREPRSI.SADGMIJ.TKKDTDBCDer
*PEPPRTDEALCPYETGRTCWAPLLQVLWWVGTPLPFPLSTSWL PDLVGAPGSHFCFLNIALLRYNSHTM 5382 1536 203 GARGSQQDAPALQEABVRGPERAQPARGRMTKARLFRLWLVLGS VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTFGPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRG YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD DIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLSGSLLH RGABYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTEKLAPFNEH	1	i	l	SELKT*KISPLPACCKVT*EFPHDGGCDDGCWODDGTUTUGGG
PDLVGAPGSHFCFLNIALLRYNSHTM. 5382 1536 203 GARGSQQDAPALQEABVRGPERAQPARGRMTKARLFRLWLVLGS VFMILLIIVYWDSAGAAHFYLHTSFSR PHTGPPLPTFGPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMBESVRG YDWSPRDARRSPDQGRQQAERSVLRGFCANSSLAFPTKERPFD DIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLSGSLLH RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKLL KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTSKLAPFNEH	, 1	1		*PEPDRTDEAL COVETCOTOMART TOTAL MURICIPAL PORT
GARGSQQDAPALQEABVRGPERAQPARGRMTKARLFRLWLVLGS VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRG YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD DIPNSELSHLIVDDRHGAIYCYVPKVACTMMKRYMIVLSGSLLH RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTSKLAPFNEH	1 1		ĺ	
VFMILLIIVYMDSAGAAHFYLHTSFSR PHTGPPLPTPGPDRDRE LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRG YDDSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD DIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRYMIVLSGSLLH RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTEKLAPFNEH	5382	1536	202	
LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRG YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD DIPNSELSHLIVDDRHGAIYCYVPKVACTNNKRVMIVLSGSLLH RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTSKLAPFNEH		1330	203	GARGSQQDAPALQEABVRGPERAQPARGRMTKARLFRLWLVLGS
YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFFTKERPFD DIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLSGSLLH RGAFYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTSKLAPFNEH	1	1	ſ	VFM1LL1IVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRE
YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFFTKERPFD DIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLSGSLLH RGAFYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTSKLAPFNEH	1 1	1	1	LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRG
DIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLSGSLLH RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTEKLAPFNEH	j	Į		YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD
RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTEKLAPFNEH	1	{	(DIPNSELSHLIVDDRHGAIYCYVPKVACTNWKPVMTVI.SGGTTU
KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTEKLAPFNEH	1			RGAPYRDPLR I PREHVHNASAHI TENKEMBUCKI COLI MOTO
RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTEKLAPFNEH		l	ļ	KKYTKELEVEDENDI I CARROUPET ENGER (+ NOTER
WRQVYRLCHPCQIDYDFVGKLETLDEDAAQLLQLLQVDLAAPLP	1 1	İ	1	POPUODADI CARCI PRINCALISATISKI FELENEEF/*POVRRAHAAAV
WKQVYRLCHPCQIDYDFVGKLETLDEDAAQLLQLLQVDLAAPLP	1	j	1	ROPHQPARLGARGUPRWPQ\VSFANFIQYLLDPHTEKLAPFNEH
	<u> </u>			WKQVIKLCHPCQIDYDFVGKLETLDEDAAQLLQLLQVDLAAPLP

SEQ	Predicted	Predicted end	Amino
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalarine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
İ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
į.	sequence	=====================================	\=possible nucleotide insertion)
			PELECTORECONTROL
Í	ĺ	[PELPGTGPPSSWEEDWFAKIPLAWRQQLYKLYEADFVLFGYPKP ENLLRD
5383	45	5250	
	1	1 2230	VERLLGCRNSKRTWRMLISKNMPWRRLQGISFGMYSAEELKKLS
	1		VKSITNPRYLDSLGNPSANGLYDLALGPADSKEVCSTCVQDFSN
İ			CSGHLGHIELPLTVYNPLLFDKLYLLLRGSCLNCHMLTCPRAVI
	1		HLLLCQLRVLEVGALQAVYELERILSRFLEENADPSASEIREEL
1			EQYTTEIVQNNLLGSQGAHVKNVCESKSKLIALFWKAHMNAKRC
1)		PHCKTGRSVVRKEHNSKLTITFPAMVHRTAGQKDSEPLGIEEAQ
			IGKRGYLTPTSAREHLSALWKNEGFFLNYLFSGMDDDGMESRFN
			PSVFFLDFLVVPPSRSRPVSRLGDQMFTNGQTVNLQAVMKDVVL
1	ì		IRKLLALMAQEQKLPEEVATPTTDEEKDSLIAIDRSPLSTLPGQ
1	1		SLIDKLYNIWIRLQSHVNIVFDSEMDKLMMDKYPGIRQILEKKE
			GLFRKHMMGKRVDYAARSVICPDMYINTNEIGIPMVFATKLTYP
1			QPVTPWNVQELRQAVINGPNVHPGASMVINEDGSRTALSAVDMT
ŀ			QREAVAKQLLTPATGAPKPQGTKIVCRHVKNGDILLLNRQPTLH
1			RPSIQAHRARILPEEKVLRLHYANCKAYNADPDGDEMNAHFPQS
}			ELGRAEAYVLACTDQQYLVPKDGQPLAGLIQDHMVSGASMTTRG
1	l		CFFTREHYMELVYRGLTDKVGRVKLLSPSILKPFPLWTGKQVVS
			TLLINIIPEDHIPLNLSGKAKITGKAWVKETPRSVPGFNPDSMC
	l		ESQVIIREGELLCGVLDKAHYGSSAYGLVHCCYEIYGGETSGKV
			LTCLARLFTAYLQLYRGFTLGVEDILVKPKADVKRQRIIEESTH
			CGPQAVRAALNLPEAASYDEVRGKWQDAHLGKDQRDFNMIDLKF
			KEEVNHYSNEINKACMPFGLHRQFPENTLQLMVQSGAKGSTVNT
1			MQISCILGQIELEGRSTPLMASGKSLPCFEPYEFTPRAGGFVTG
1 1	l		RFLTGIKPPEFFFHCMAGREGLVDTAVKTSRSGYLQRCIIKHLE
1 1			GLVVQYDLTVRDSDGSVVQFLYGEDGLDIPKTQFLQPKQFPFLA
1			SNYEVIMKSQHLHEVLSRADPKKALHHFRAIKKWQSKHPNTLLR
1			RGAFLSYSQKIQEAVKALKLESENRNGR/RPWDS/G/RMLRMWY
1 6	1		ELDEESRRKYQKKAAACPDPSLSVWRPDIYFASVSETFETKVDD
}			YSQEWAAQTEKSYEKSELSLDRLRTLLQL\KWQRSLCEPGEAVG
	į		LLAAQSIGEPSTQMTLNTFHFAGRGEMNVTLGIPRLREILMVAS
1 1			ANIKTPMMSVPVLNTKKALKRVKSLKKQLTRVCLGEVLQKIDVQ
]]			ESFCMEEKQNKFQVYQLRFQFLPHAYYQQEKCLRPEDILRFMET
1 1	i		RFFKLLMESIKKKNNKASAFRNVNTRRATORDLDNAGELGRSRG
1 1			EQEGDEEEGHIVDAEAEEGDADASDAKRKEKQEEEVDYESEEE
1			EEREGEENDDEDMQEERNPHREGARKTQEQDEEVGL/GH*GGPV
]	i		PSRPPDAAPETHPQPGAPGA\EAMERRVQAVREIHPFIDDYQYD
1 1	i		TEESLWCQVTVKLPLMKINFDMSSLVVSLAHGAVIYATKGITRC
1	}		LINETTNNKNEKELVLNTEGINLPELFKYAEVLDLRRLYSNDIH
1 1			AIANTYGIEAALRVIEKEIKDVFAVYGIAVDPRHLSLVADYMCF
1			EGVYKPLNRFGIRSNSSPLQQMTFETSFQFLKQATMLGSHDELR
5384	196	886	SPSACLVVGKVVRGGTGLFELKQPLR
		000	QSCGQRLPTVL+L+GPPGSCPCILSLF\PGRPHALPEIRPYINI
1			TILKGDKGDPGPMGLPGYMGREGPQGEPGPQGSKGDKGEMGSPG
			APCQKRFFAFSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMAT
1 1			GQFAAPLRGIYFFSLNVHSWNYKETYVHIMHNQKEAVILYAQPS
1 1	ľ	{	ERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITF
5385	326	700	SGHLIKAEDD
	320	799	LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM
1			SPTFRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A
1 1			VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ
5386	326	700	SDGERKAYVRLAPDYDALVVATKIGIT
5555	320	799	LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM
1			SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A
[[1		VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ
-5383-1-			SDGERKAYVRLAPDYDALVVATKIGIT
5387	2	2117	FVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWATA
]		ŀ	SDDLVFPGFFELVVRVLWWIGILTLYLMHRGKLDCAGGALLSSY
[j	.	LIVLMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL
[ļ	Ì	ALFFPEMVWASLGAAWVADGVQCDRTVVNGIIATVVVSWIIIAA
LL			TVVSIIIVFDPLGGKMAPYSSAGPSHLDSHDSSQLLNGLKTAAT

SEO	Predicted	T 50-232	
ID		Predicted end	
NO:	beginning	nucleotide	(A=Alanine, C=Cvsteine, D=Aspartic Asia D
1 140:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
- 1	corresponding	to first	L-Lenging M Mathieutine, Kanysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
į	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of		S=Serine, T=Threonine, V=Valine,
		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown *~Cro-
	amino acid	sequence	Codon, /=possible nucleotide deletion
 	sequence	ł	\=possible nucleotide insertion)
1			SVWETRIKLLCCCIGKDDHTRVAFSSTAELFSTYFSDTDLVPSD
1		i	TAAGLALLHOOODNIDNNOTRIONETRICHERSTYFSDTDLVPSD
- [ſ		IAAGLALLHQQQDNIRNNQEPAQVVCHAPGSSQEADLDAELKNC
ì	ł		HHYMQFAAAAYGWPLYIYRNPLTGLCRIGGDCCRSKNPQTMT/M
i	1	1	VGGDQLQL/CTSAPILHTHRAAVOGLHPROLPWTPFTFLDFLUA
į	İ	1 .	LIDHKKESVVAVRGTMSLODVLTDLSAESEVLDVECEVODDI 311
ł	1	j.	KGISQAARYVYQRLINDGILSQAFSIAPEYRLVIVGHSLGGGAA
			ALLATMVRAAYPQVRCYAFSPPRGLWSKALQEYSQSFIVSLVLG
ł	1	ſ	KDVIPRLSVTNLEDLKRRILRVVAHCNKPKYKILLHGLWYELFG
		•	CNEWNI DEEL DOCUMENT CONTROLL CONTROLLER CON
j	1	į	GNPNNLPTELDGGDQEVLTQPLLGEQSLLTRWSPAYSFSSDSPL
	1	1	DSSPKYPPLYPPGRIIHLQEEGASGRFGCCSAAHYSAKWSHEAE
1	1	!	FSKILIGPKMLTDHMPDILMRALDSVVSDRAACVSCPAOGVSSV
5388			DVA
2388	1569	753	TADGGAGGGGRRQAGVRRHYLYPFTGGYRRRAACQAERPAARS
1			KDTDLAAYQKGNLGVQLRNMAQETNHSQVPMLCSTGCGFYGNPR
}	1		TNGMCSVCYKEHLQRQNSSNGRISPPVQCTDGSVPEAQSALDST
	1		SSCHOPERICHOELL CROSS SAGRISPPYQCTDGSVPEAQSALDST
	1 :		SSSMQPSPVSNQSLLSESVASSQLDSTSVDKAVPETEDVQASVS
į	1	•	DTAQQPSEEQSKSLE\NRNKKRIAVSCAGRKWDLLGLNAGVEMF
1	1		TVVYTVTQMYTIALTITKQMLKNFVFQQEFKSFGSFHQQLLEYK
5389	7.550		TEEHLOTKN
3383	1569	753	TADGGAGGGRRQAGVRRHYLYPFTGGYRRRAACQAERPAARS
			KDTDLAAYQKGNLGVQLRNMAQETNHSQVPMLCSTGCGFYGNPR
Ì	1 !		TNGMCSVCYKEHLQRQNSSNGRISPPVQCTDGSVPEAQSALDST
l l			SSSMQPSPVSNQSLLSESVASSQLDSTSVDKAVPETEDVQASVS
	1		DTACORGEROGY TO ASSOCIATE TO AS
	1		DTAQQPSEEQSKSLE\NRNKKRIAVSCAGRKWDLLGLNAGVEMF
]]		TVVYTVTQMYTIALTITKQMLKNFVFQQEFKSFGSFHQQLLEYK
5390	217		ILERLOTKN
2330	21'	1332	EDPRKLMEDKMWSECEGPEMSLVCLTDFQAHAREQLSKSTRDFI
1	1		EGGADDSITRDDNIAAFKRIRLRPRYLRDVSEVDTRTTIQGEEI
1	1 1		SAPICIAPTGFHCLVWPDGEMSTARAAQAA\GICYITSTFASCS
1	1 1		LEDIVIAAPEGLRWFQLYVHPDLQLNKQLIQRVESLGFKALVIT
1	1		LOTPYCGNERHOTPNOLERNI WILLIAM CONTROL OF THE LOTPYCGNERHOTPNOLERNI WILLIAM CONTROL OF THE LOTPY CONTROL OF THE LOT
	1		LDTPVCGNRRHDIRNQLRRNLTLTDLQSPKKGNAIPYFQMTPIS
ł	l l		TSLCWNDLSWFQSITRLPIILKGILTKEDAELAVKHNVQGIIVS
1.	ł J	•	NHGGRQLDEVLASIDALTEVVAAVKGKIEVYLDGGVRTGNDVLK
			ALALGAKCIFLGDAILWALASKGEHGVKEVINII.TMEEUTCMA\
5391			LIGCESVAEINENLVOFSEL
1 2222 1	1	1292	VKKAAGRSRGPPTAGGQRCEEAPGTVMERRLGVRAWVKENRGSF
1		i	VEEVCINAL WINDEQUARYMEVGGPNTRKDYHTEEGEEVEVOLDODM
1 1	.	j	VLRVLEQGKHRDVVIRQGEIFLLPARVPHSPQRFANTVGLVVER
1 1	1		RRLETELDGLRYYVGDTMDVLFEKWFYCKDLGTQLAPIIQEFFS
1 1	!	}	SEQYRTGKPIPDQLLKEPPFPLSTRSIMEPMSLDAWLDSHHREI.
1 1	·	· ·	OAGTELSI-FEDTVETOUTANGOCO
	:	İ	QAGTPLSLFGDTYETQVIAYGQGSSEGLRQNVDVWLWQLEGSSV
1 1	1		VINGGREESLGPWMDSLLVLSWGPSY\AW\EPTOGGVALGUT\O
] [DVACKKSPWGEPSCHGLKAATGVPSTI,FVPSI,DMMcDcDtlvt GV
1	ſ	i	*CRCVPHRPAHCCHPPSCPSOPRCHAPGPAAADULLUOTOPTTA
1-222-1	··		PVLPGGLPPAPLLPIPLSLOTOCSTSTPRRPSTKAG
5392	1	1623	IRGSNAQKVVGASGSGGAGPQPDPAGPGGVPALAAAVLGACEPR
1		•	CAAPCPLPALSRCRGAGSRGSRGGRGAAGSGDAAAAAEWIRKGS
1 1	- 1	1	FIHKPAHGWLHPDARVLGPGVSYVVRYMGCIEVLRSMRSLDFNT
1 1	1	Į.	PTOUTER THE HEALTS TO SOME STATE OF THE STAT
1 [i	{	RTQVTREAINRLHEAVPGVRGSWKKKAPNKALASVLGKSNLRFA
1	· · · · · · · · · · · · · · · · · · ·	1	GMS181H1STDGLSLSVPATROVIANHHMPS1SFASGGDTDMTD
1	1		IVAIVAKDPINQRACHILECCEGL\AOSIISTVCOAFFI.BEVOV
j 1	1	1	LASPPKVALPPERLAGPEESAWGDEEDSLEHNVVNSTDGKEDDI
, 1	- 1	1	GGLVDSRLALTQPCALTALDQGPSPSLRDACSLPWDVGSTGTAP
1 1	J		PGDGYVQADARGPPDHEEHLYVNTQGLDAPEPEDSPKKDLFDMR
}	1		PFEDALKI-HECSVA ACUTA DI DI DICINA DI DICINA DI DI DICINA DI DI
[1	1	PFEDALKLHECSVAAGVTAAPLPLEDQWPSPPTRAPVAPTEEQ
	i		TROEFWINGRMSRRAAERMLRADGDFLVRDGVTNPGOVULTCMU
]	ļ		AGGERHALLVDPEGVVRTKDVLFESISHLIDHHLONGOPTVAAR
5393			SELHDRGVVSREP
-3,73	2	982	GGDSAGMTMETQMSQNVCPRNLWLLQPLTVLLLLASADSQAAAP
L		· ·	PKAVLKLEPPWINVLQ\EDSVTLTCQGAPQP/ERSDSIQWFHNG
			THE TELEGOAT OF A PROPOSED HANG

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence	Ì	\=possible nucleotide insertion)
J			\NLIPTHTQPS\YRFKANNN\DSGEYTCQTGQTSL\SDPVHLTV
1	1		LSEWLVLQTPHLEFQEGETIMLRCHS\WRDKP\LVKVTFFONGK
1		Î	SQKFSHLDPTFSIPQANHSHSGDYHCTGNIGYTLFSSKPVTITV
1	}	}	QVPSMGSSSPMGIIVAVVIATAVAAIVAAVVALIYCRKKRISAN
]	ļ	STDPVKAAQFEPPGRQMIAIRKRQLEETNNDYETADGGYMTLNP
			RAPTDDDKNIYLTLPPNDHVNSNN
5394	2	982	GGDSAGMTMETQMSQNVCPRNLWLLQPLTVLLLLASADSQAAAP
ł	i		PKAVLKLEPPWINVLQ\EDSVTLTCQGAPOP/ERSDSIOWFHNG
			\NLIPTHTQPS\YRFKANNN\DSGEYTCOTGOTSL\SDPVHLTV
1.			LSEWLVLQTPHLEFQEGETIMLRCHS\WRDKP\LVKVTFFONGK
ì	1		SQKFSHLDPTFSIPQANHSHSGDYHCTGNIGYTLFSSKPVTITV
1	1		QVPSMGSSSPMGIIVAVVIATAVAAIVAAVVALIYCRKKRISAN
1]		STDPVKAAQFEPPGRQMIAIRKRQLEETNNDYETADGGYMTLNP
			RAPTDDDKNIYLTLPPNDHVNSNN
5395	3135	531	RASDAKNQEGLLNTRRKSTDSVPISKSTLSRSLSLQASDFDGAS
1			SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKKOTTK
1			KPTETPPVKETQQEPDEESLVPSGENLASETKTESAKTEGPSPA
	l		LLEETPLEPAAGPKAACPLDSESVEGVVPPASGGGRVONSPPVG
1	i		RKTLPLTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS
1			SWDNQQENPPPTKKIGKKPVAKMPLRRPKMKKTPEKLDNTPASP
1			PRSPAEPNDIPIAKGTYTFDIDKWDDPNFNPFSSTSKMQESPKL
ł			PQQSYNFDPDTCDESVDPFKTSSKTPSSPSKSPASFEIPASAME
}			ANGVDGDGLNKPAKKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP
			TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD
1			YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD
			DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFEETE
1	j		ALVNTAAKNOHPVPRGLAPNOESHLOVPEKSSOKELEAMGLGTP
			SEAIEITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN
			PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ PDLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMRKIVAE
1			YEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADLNSVEK
			\SLADLFRRYEKMKEVLEGFRKNEEVLKRCAQEYLSRVKKEEQR
		į.	YQALKVHA\EEKLDRANAE\IAQVRGKAQQEQAAHQASLAERSS
1 1			CRV\DALERTLEQKNKEIBELTKICDELIAKMGKS
5396	3135	531	RASDAKNQEGLLNTRRKSTDSVPISKSTLSRSLSLQASDFDGAS
1			SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKKQTTK
1	ĺ		KPTETPPVKETQQEPDEESLVPSGENLASETKTESAKTEGPSPA
1 1		1	LLEETPLEPAAGPKAACPLDSESVEGVVPPASGGGRVQNSPPVG
] -	· .		RKTLPLTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS
1 1	. [SWDNQQENPPPTKKIGKKPVAKMPLRRPKMKKTPEKLDNTPASP
1 1	Ì		PRSPAEPNDIPIAKGTYTFDIDKWDDPNFNPFSSTSKMQESPKL
[i		ļ	PQQSYNFDPDTCDESVDPFKTSSKTPSSPSKSPASFEIPASAME
}			ANGVDGDGLNKPAKKKKTPLKTDTFRVKKSPKRSPLSDPPSOD?
]	ſ	[TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKOD
1	ł	ł	YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPOD
]]	ł	Į	DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFRETE
J I	•	1	ALVNTAAKNQHPVPRGLAFNQESHLQVPEKSSQKELEAMGLGTP
) i	ĺ	1	SEAIBITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN
, <u>1</u>			PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFOO
1 1	}	1	PDLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMRKIVAE
j			YEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADLNSVEK
j (İ	ł	\SLADLFRRYEKMKEVLEGFRKNEEVLKRCAOEYLSRVKKEEOR
]			YQALKVHA\EEKLDRANAE\IAQVRGKAQQEQAAHQASLAERSS
5397			CRV\DALERTLEQKNKEIEELTKICDELIAKMGKS
339/	3135	531	RASDAKNQEGLLNTRRKSTDSVPISKSTLSRSLSLQASDFDGAS
		1	SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKKOTTK
] }			KPTETPPVKETQQEPDEESLVPSGENLASETKTESAKTEGPSPA
		ł	LLEETPLEPAAGPKAACPLDSESVEGVVPPASGGGRVQNSPPVG
	1		RKTLPLTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS
}	}	1	SWDNQQENPPPTKKIGKKPVAKMPLRRPKMKKTPEKLDNTPASP
L			PRSPAEPNDIPIAKGTYTFDIDKWDDPNFNPFSSTSKMQESPKL

SEO	Predicted	I produce	
ID	beginning	Predicted end	
NO:	nucleotide	nucleotide location	I Managarane, Calvateine, Dalamartic haid a
i	location		Gracamic Acia, F=Phenvlalanine G_Cluster
]	corresponding	corresponding	""" " " " " " " " "
	to first	to first	L=Leucine, M=Methionine, N=Acnaration
- 1	amino acid	amino acid	P=Proline, O=Glutamine D=A~~i=i==
ļ	residue of	residue of	S=Serine, T=Threonine, V=Valine
1	amino acid	amino acid	W=Tryptophan, Y=Tvrosine Y=Unknown + Gt
l	sequence	sequence	(COUCH, /=possible bucleofide dolories
	Jodgeonee	<u> </u>	\=possible nucleotide insertion\
1			PQQSYNFDPDTCDESVDPFKTSSKTPSSDSVCDACEETDAGGE
- 1			ANG VOGOGUNKPAKKKTPI,KTDTPDVVVCDVDCDI CDDDCC
- 1	İ		IFAGIPEIPPVISAVVHATDEEKIAVTNOKUTOMTUDI III DIIO
	1	ľ	1 - Y- ODDS F VNE I ALSSETERI JOYRNG VETEVMENTORGE
ļ	1	1	DESPERAÇÃO LIMEDISOES PVESSOVOM SECONDO COCCODO DO COCCODO DO COCCODO DO COCCODO DO COCCODO DO COCCODO DO COCCODO DO COCCODO DO COCCODO DO COCCODO DO COCCODO DO COCCODO DO COCCODO DO COCCODO DO COCCODO DO COCCODO DO COCCO
1	1	}	1 ****** AAANQAP V PKGLAPNOESHLOVDEK CCOKET DAMAT CER
ĺ	1	1	OBSTRUCT TAPEGSTASADALLSRLAHDVST CCAT DVI EDDI ADGI
1	ļ		FELFAQALQREAAHPTDVSISKTALYSRIGTARVEVDAGII FOO
		ĺ	POLIDSALQIARAETITKEREVSEWKDKVERCDDEVMEMDVIVID
1	İ		TEXTIAUMIEDEQREKSVS\HOTVOOT,VT,FKFOX\TARTAYOTTE
	1		1 CHAPTERKITCHIKEVLEGERKNEEVIKPCAOPVICEURICE
1	İ		1 TANKANA (BEKEDRANAE) IAOVRGKA OOROA A BOA CE A BOA CE
5398			CK VDADERIDEUKNKEIKELTKICDELIANMERE
3336	56	5426	SGEVCRMESNFNQEGVPRPSYVFSADDIAPDGETNEDGTVIDE
	1		I THE SUVAPNI DANSEESKI) VI.OVCI.DIDDDTOCTURE DODG
	1		1 1000X1 VVDAEPUCILGRESEKSSG\OM\ AOVECERDODE CELE
1]		A SVEET SOCIMES / AKDPI'KCORKI'LELASCI'LINGCAMAMAGO COM
İ			THE TAXABLE PROPERTY OF THE PR
1	i i		DELASKSALLKQIKEVTVHNDSDDTI.VGSI.TNSI.NICEPPPGTI
1	j l		I DIEGENENSIKESVWVSFFEIVNRVIVDI.EUDUCCUROUS
			I MANAGED ANGEST INDIOMIONS DERKEYABITAT CIANOCAS DE
1	1		ADMINASSASIBLETVALLOIEDSEMSRUTDUGET.GT.COT.ACCED
1	1 1		THRIUNEGERERETGNINTSLLTTERCTNULVNCEVCVDOOTTE
i			1 PRESKLIBIT/QSPFNGKGKICMIVNI SOCVI AVDERT NET 1500
1	1 1		ATAXAVCVPDILMSSOEKLFGPVKSSODVSI DOMONOVITA NAMED
1	1)		AT TOWERS DEDUMEDED LIVE ELENA EFTED AGETY I DEDT DE
-	i · .		**DECKMAP ISHEEKRKLLDLIEDLKKKI, TNEVVEVI OF DEVICE
1	{ }		1 PATAGETATINGOREADERETTIONERETTERMARDET ATTEMPT TO
	l i		TOT RESEARCH CATEVETEE ATACLEL VENOTER AVERS
1	[1 TALKEEDKKRENESDSLIOELETSNKKITTONODIVELINITES 1
1 1			REDITINE FONLKSHMENT FKCNDKADTSSI. TAMENT TONERSONS
1 1			FKDSKSKICSSKKKVNENELOODEPPAKKGGTHNGGATDDDOVW
			OBVRENIAGIOUIRVLOENNEGIRARII. TRITORITA EN I
i i	1		1 DANGIVE QUEDSUSEKKNITUSKEVOOTOSMUDTA TARELINGE
1 1	ļ		DAWYS DE ATMALS NOTETATES ITNNUSOTET MUTEUT DET DOT
1 1	i		DSVSQISNIDLENERDESNGSEEDNEPNTOLDELGNDVI VEVOX
1 1	l.		NEIRIQEPHRENSPHSSIEAIWEECKETVKASCVVCUOTERV DO
1 1	j		VIEWDOME VKGYKDENNRLKEKEHKNODDIJ.KEVETI TOOL VAN
1 1			1 DVERTV ADDVQIOHVVEGKRATSET.TOCVTCVVAVIVOI TOTA - 1
1	· ·		I TANTERSHOAKLEUDILEKESTIT.KI.PONI VEPORIT OROTING I
} }	1		ADDINANTED KTYKEET LOPLANT ODWKHIT OF KEEPER MAD OR ADDING
	l l		~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
1 1	1	ł	QKEVSVMRDEDKLLRIKINELEKKKNQCSQELDMKQR\TIQQLK
1	j		EQUINVAVERALUUYERACKDI.NVKEKT TEDMOMUT EDOROMOT.
1 1	İ		BUDGET BAKUSEVERLATELDRWRVECNDI.FTENMODENTER 1
1 1	ł		THE TO A LOCAL TRADUCTURE OF THE PROPERTY OF T
))	1		SNIRNAEMAKYAEDRERFFKOONEMETT. TAOL TEKDEDI OKUDD
			ERDQUVAALEIQUKALISSNVOKDNEIEOLKRIIGDTEVIDTO
1 1		Į	TO THE RELIGIOUS DESCRIPTION OF THE PROPERTY O
	}	İ	SIENDOSIRFPRPEDEIOFTPLOPNKMAVKHPGCTTPDVITVYTDV (
		1	AKAKASNEMEEDLVKCENKKNATPRTNI.KRPISDDDNGGUVVDG
1	1	ł	AVALAPSSKETYSLRSOASIIGVNLATKKKEGTLOVEGDELOVG
].	j	PSILQSKAKKIIETMSSSKLSNVRASKENUSODYDAVDVI VEGD
5399	705	220	ISSPIDISGQVILMDOKMKESDHOIIKRRI.RTKTAV
1		230	GPRMAKFLSQDQ INEYKECFSLYDKOORGK I KATDI MYAMDOLO
			ASPIPGEVQRHLOTHGIDGNGELDFSTFT.TIMHMOTKOEDDKKE
ĺ	Í		ADDROVED VERKING YVMASDLRSKI.TSI (SEKI.TUKEV) DDI EDE
5400	931		ADIEPIGKVKIDEFIHKITSYLDGTV
j		248	SHCSSGMEIPPTNYPASRAALVAQNYINYQQGTPHRVFEVQKVK
1	•	1	PASHEDI PGRGHKYRLKFAVEEIIOKOVKVNCTARVI VDCTCOR
			TAPEVNFTFEGETGKNPDEEDNTFYQRLKSMKEPLEAQNI\PDN

5406	279	2732	RWRTYNVEGPLTFMDVAIEFCLEEWQCLDTAQQNLYRNVMLENY
E406			PINVNNNYEHRHTSHLGHAVLPSNARGPILSRSTSTGSAASSGS NSSASSEQGLLGRSPPTRPVPGHRSERAIRTQPKQLIVDDLKGS LKEDLTQHKFICEQCGKCKCGECTAPRTLPSCLACNRQCLCSAE SMVEYGTCMCL\VKGIFYHCSNDDEGDSYSDNPCSCSQSHCCSR YLCMGAMSLFLPCLLCYPPAKGCLKLCRRCYDWIHRPGCRCKNS NTVYCKLESCPSRGQGKPS
5405	2199	1220 .	QNSRSLHMDPQNQHGSGSSLVVIQQPSLDSRPRLDYEREIQPTA ILSLDQIKAIRGSNEYTEGPSVVKRPAPRTAPRQEKHERTHEII
			LYARPNKIKKLT\AKDFADIPNLRRLDFTGNLIEDIEDGTFSKL SLVEELSLAENQLLKLPVLPPKLTLFNAKYNKIKSRGIKANAFK KLNNLTFLYLDHNALESVPLNLPESLRVIHLQFNNIASITDDTF CKANDTSYIRDRIEEIRLEGNPIVLGKHPNSFICLKRLPIGSYF
5404	187	1111	LPVTLIFAKMKTLQSTLLLLLLVPLIKPAPPTQQDSRIIYDYGT DNFEBSIFSQDYEDKYLDGKNIKEKETVIIPNEKSLQLQKDEAI TPLPPKKENDEMPTCLLCVCLSGSVYCEEVDIDAVPPLPKESAY
		,	MNYEPMGRALRYYYQRGILAKVEGQRLVYQFKEMPKDLIYINDE DPSSSIESSDPSLSSSATSNRNQTSRSRVSSSPGVKGGATTVLK PGNSKAAKPKDPVEVAQPSEVLRTVQPTQSFYPTQLFRTVHVVQ PVQAVPEGEAARTSTMQDETLNSSVQSIR\TIQAPTQVPVVVSP RNQQ\LHTVTLQTVPLTTVIASTDPSAGTGSQKFILQAIPSSQP MTVLKENVMLQSQKAGSPPSIVLGPARV\QQVLTSNVQTICNGT VSV\ASSPSFS\ATAPVVTLFLGSSQLVAHPPGTVITSVIKTQ ETKTLTQEVEKKESEDHLKENTEKTEQQPQPYVMVVSSSNGFTS QVAMKQNELLEPNSF
5403	3445	1563	GECFIMAAVVQQNDLVFEFASNVMEDERQLGDPAIFPAVIVEHV PGADILNSYAGLACVEEPNDMITESSLDVAEEEIIDDDDDDITL TVEASCHDGDETIETIBAAEALLNMDSPGPMLDEKRINNNIFSS PEDDMVVAPVTHVSVTLDGIPEVMETQQVQEKYADSPGASSPEQ PKRKKGRKTKPPRPDSPATTPNISVKKKNKDGKGNTIYLWEFLL ALLQDKATCPKYIKWTQREKGIFKLVDSKPVSRLWRKHKNKP\D
			PGNSKAAKPKDPVEVAQPSEVLRTVQPTQSPYPTQLFRTVHVVQ PVQAVPEGEAARTSTMQDETLNSSVQSIR\TIQAPTQVPVVVSP RNQQ\LHTVTLQTVPLTTVIASTDPSAGTGSQKFILQAIPSSQP MTVLKENVMLQSQKAGSPPSIVLGPARV\QQVLTSNVQTICNGT VSV\ASSPSFS\ATAPVVTLFLLGSSQLVAHPPGTVITSVIKTQ ETKTLTQEVEKKESEDHLKENTEKTEQQPQPYVMVVSSSNGFTS QVAMKQNELLEPNSF
			PGADILNSYAGLACVEEPNDMITESSLDVAEEEIIDDDDDDITL TVEASCHDGDETIETIEAAEALLNMDSPGPMLDEKRINNNIFSS PEDDMVVAPVTHVSVTLDGIPEVMETQQVQEKYADSPGASSPEQ PKRKKGRKTKPPRPDSPATTPNISVKKKNKDGKGNTIYLWEFLL ALLQDKATCPKYIKWTQREKGIFKLVDSKPVSRLWRKHKNKP\D MYEPMGRALRYYYQRGILAKVEGQRLVYQFKEMPKDLIYINDE DPSSSIESSDPSLSSSATSNRNQTSRSRVSSSPGVKGGATTVLK
5402	3445	1563	HIHKKKSQQVFASPSKHPMDSKGEESKISYPNIFFMIDSF\EE\ VFSDMTVGKGEMVCVELVASDKTNTFQGVIFQGSIRYEALKKVY DNRVSVAARMAQK\MSFGFSKYSNMEF\VR\MKGPQGKGHAEMA VSRVSTGDTSPCGTEEDSSPASPMHERVTSFSTPPTPERNNRPA FFSPSLKRKVPRNRIAEMKKSHSANDSEEFFREDDGGADLHNAT NLRSRSLSGTGRSLVGSWLKLNRADGNFLLYAHLTYVTLPLHRI LTDILEVRQKPILMT GECFIMAAVVQQNDLVFEFASNVMEDERQLGDPAIFPAVIVEHV
5401	3	1360	TGWSYGPTTSLAFLAPRDFPFPPKLLIHPQAVVRLSCGAGSMGS QAAAEWRNWASWEGSSSLSGCSMGCFKDDRIVFWTWMFSTYFME KWAPRQDDMLFYVRRKLAYSGSESGADGRKAAEPEVEVEVYRRD SKKLPGLGDPDIDWEESVCLNLILQKLDYMVTCAVCTRADGGDI
			FGNVSPEMTLVLHLAWVACGYIIWQNSTEDTWYKMVKIQTVKQV QRNDDFIELDYTILLHNIASQEIIPWQMQVLWHPQYGTKVKHNS RLPKEVQLE
	amino acid sequence	sequence	Codon, /=possible nucleotide deletion, /=possible nucleotide insertion)
	amino acid residue of	residue of amino acid	S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	corresponding to first	to first amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
NO:	beginning nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid. E=
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine
	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine
	residue of	residue of amino acid	S=Serine, T=Threonine, V=Valine
]	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
L	sequence	Sequence	Codon, /=possible nucleotide deletion, -possible nucleotide insertion)
			RNLVFLG/IIAVSKPDLITCLEQEKEPWEPMRRHEMVAKPPVMC
			SHFTQDFWPEQHIKDPFQKATLRRYKNCEHKNVHLKKDHKSVDE
ļ	1		CKVHRGGYNGFNQCLPATQSKIFLFDKCVKAFHKFSNSNPHKIS
			HTEKKLFKCKECGKSFCMLSHLAOHKIIHTRVNFCKCEKCGKAF
1		}	NCPSIITKHKRINTGEKPYTCEECGKVFNWSSRLTTHKKNVTDV
1	ĺ		KLYKCEECGKAFNKSSILTTHKIIRTGEKFYKCKECAKAFNOSS
1	}	}	NLTEHKKIHPGEKPYKCEECGKAFNWPSTLTKHKRIHTGEKPYT
			CEECGKAFNQFSNLTTHKRIHTA\EKFYKCTECGEAFSRS\SNL TKHKEIHTEKKPYKCEECGKAFKWSSKLTEHKLTHTGEKPYKCE
j			KCGKAFNCPSIITKHNRINTGEKPYTCEECGKVFNWSSRLTTHK
1		[KNYTRYKLYKCEECGKAFNKSSILTTHKKIHIEKKFYKCEECGK
ļ			AFKWSSKLTEHKITHTGEK?YKCEECGKAFNHFSILTKHKBTUT
			GEKPYKCEECGKAFTQSSNLTTHKKIHTGEKFYKCEECGKAFTO
1	1		SSNLTTHKKIHTGGKPYKCEECGKAFNOFSTLTKHKITHTFFKD
			YKCEECGKAFKWSSTLTKHKIIHTGEKPYKCEECG\KAFKLSST
			LSTHKIIHTGEKPYKCEKCGKAFNRPSNLIEHKKIHTGEQPYKC EECGKAFNYSSHLNTHKRIHTKEQPYKCKECGKAFNQYSNLTTH
			NKIHTGEKLYKPEDVTVILTTPQTFSNIK
5407	3	659	RPRRRQSSCCTGWLAGWLLRAAPRFCRRTETDMEQGKGLAVLIL
1			ALLELQGTLAQSIKGNHLVKVYDYOEDGSVLLTCDAFAKNITUD
1	ļ		KDGKM1GFLTEDKKKWNLGSNAKDPRGMYOCKGSONKSKPLOVV
l			YEMCQNCIELNAATISGFLFAEIVSIFDLAVGVVFIAGTGMEED
5408	2745	6128	QS\RASDKQTLLP\NDPAPTQPLKDPRKMTQYSHLQGN\QLRRN
			QGSKGTCHPQAQQPWDEGVWQEAPSQSEPWGQSQEPPTMPQRLP HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL
			APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF
			STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP
			REPTOLDIGGPWFPHYDFERSCWVRAISOEDOLATCWOAFUCCE
			VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGI.SNI.GNTCEM
1			NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCVGD
			LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSQELLAFL
	1		LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRPDPFNFLSLPLPMDSYMHL
1	İ		EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL
1 1			LAEVHGSNIKNFPQDNQKVRLSVSGFLCAFEIPVPVSDTSAGGD
1 1			TQTDFSSSPSTNEMFTLTTNGDLPRPTFIPNGMDNCGDCCTEV
1			NETNGMVNGHMPSLPDSPFTGYIIAVHRKMMRTELVELGGOVND
1 1	ļ		PSLFGMPLIVPCTVHTRKKDLYDAVWIQVSRLASPLPPQEASNH
1 1		j	AQDCDDSMGYQYPFTLRVVQKDGNSCAWCPWYRFCRGCKIDCGE
i			DRAFIGNAYIAVDWHPTALHLRYQTSQERVVDEHESVEQSRRAQ VEPINLDSCLRAFTSEEELGENEMYYCSKCKTHCLATKKLDLWR
1			LPPILIIHLKRPQFVNGRWIKSQKIVKFPRESFDPSAFLVPRDP
1	1		ALCOHKPLTPQGDELSEPRILAREVKKVDAOSSAGERDVILLEVE
1 (PSSLSANIISSPKGSPSSSRKSGTSCPSSKNSSPNSSPRTICES
j i			KGRLRLPQIGSKNKLSSSKENLDASKENGAGOICET.ADAT.GDGu
1	l		VLGGSQPELVTPQDHEVALANGFLYEHEACGNGCGNGVSNGOLG
1 1		i	NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK
<u> </u>			TDGKKMADTSSMDEDFESDY\EKYCVLQ
5409	2745	6128	QGSKGTCHPQAQQPWDEGVWQEAPSQSEPWGQSQEPPTMPQRLP
į	ļ	İ	HARQHTPLPLGSADYRRVVSVRPOGPHRDPKDSRDAAKPEOGSL
1	1	1	APRPVPASRGGKTLCKGYROAPPGPPAOFORPTCSASDDWAGDE
1 1	j	1	STPCPGGAVREDTYPVGTOGVPSLALAOGGPOGSWRET.FWZGMD
			RLPTDLDIGGPWFPHYDFERSCWVRAISOEDOLATCWOAEHCGE
j l		l l	VKNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGISNIGNTORM
]			NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSQELLAFL
1		}	LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS
]]			IVVDLFHGQLRSQVKCKTCGHISVRFDPPNFLSI.PLPMDSVMHI.
İ			EITVIKLDGTTPVRYGLRLNMDEKYTGLKKOLSDLCGLNSEOTI.
<u> </u>			LAEVHGSNIKNFPQDNQKVRLSVSGFLCAFEIPVPVSPISASSP

SEQ	Predicted	Predicted end	Amino soid comments
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	U-Wistiding T Tarkerylatanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid		P=Proline, Q=Glutamine, R=Arginine,
ŀ	residue of	residue of	S=Serine, T=Threonine, V=Valine,
	I .	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
į.	amine acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
•	1		TQTDFSSSPSTNEMFTLTTNGDLPRPIFIPNGMPNTVVPCGTEK
· }	1	1	NFTNGMVNGHMPSLPDSPFTGYIIAVHRKMMRTELYFLSSOKND
ľ	1	} ·	PSLFGMPLIVPCTVHTRKKDLYDAVWIQVSRLASPLPPQEASNH
[1	1	AQDCDDSMGYQYPFTLRVVQKDGNSCAWCPWYRFCRGCKIDCGE
1	ļ	1	DRAFIGNAYIAVDWHPTALHLRYQTSQERVVDEHESVEQSRRAQ
		1	VEPINLDSCLRAFTSEEELGENEMYYCSKCKTHCLATKKLDLWR
j		į	LPPILIIHLKRFQFVNGRWIKSQKIVKFPRESFDPSAFLVPRDP
1	1	{	ALCOHKPLTPQGDELSEPRILAREVKKVDAQSSAGEEDVLLSKS
i	1 .		PSCI.SANTICS PROGRESS PROGRESS CONTROL OF THE PROGRESS OF THE
1			PSSLSANIISSPKGSPSSSRKSGTSCPSSKNSSPNSSPRTLGRS
	1		KGRLRLPQIGSKNKLSSSKENLDASKENGAGQICELADALSRGH
[1	VLGGSQPELVTPQDHEVALANGFLYEHEACGNGCGNGYSNGQLG
l		l	NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN
Ī			PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK
5410	 		TDGKKMADTSSMDEDFESDY\EKYCVLQ
3413	2	710	LRFPGQARHVWLAARMQAPHKEHLYKLLVIGDLGVGKTSIIKRY
İ	1		VHQNFSSHYRATIGVDFALKVLHWDPETVVRLQLWDIAGQERFG
}	<u> </u>		NMTRVYYREAMGAFIVFDVTRPATFEAVAKWKNDLDSKLSLPNG
1			KPVSVVLLANKCDQGKDVLMNNGLKMDOFCKEHGFVGWFETSAK
	}		ENINIDEASRCLVKHILANECDLMESIEPDVVKPHLTSTKVASC
L			SG\CAKILVGTFAGVW
5411	1302	289	TGPAAAGRRKALGSFGKPSPVTGLRAARRRTRPSAPAAPSVGC
	1		GKRRESDAGAGGERASVRTGSGRRGGRTMAGDSEQTLQNHQQ?N
			GGEFFLIGVSGGTASGKSSVCAKIVQLLGQNEVDYRQKQVVILS
			QDSFYRVLTSEQKAKALKGQFNFDHPDAFDNELILKTLKEITEG
1	1 1		KTVQIPVYDFVSHSRKEETVTVYPADVVLFEGILAFYSQER/IR
	l i		DLFQMKLFVDTDADTRLSRRVLKDISERGRDLEQILSSSTLRFV
	[KPA\FEEFCLPPK\KYADVIIPR\GADN\RVPINLIVQHIQ\DI
	j		LNGGPS\NRQTNGCLNGYTPSRKRQASESSSRPH
5412	3180	313	QGISNFFHKEANFWFEVSGYLISPLRSPFVDPALEWSLMASPWN
	}		KMEGESSRFEIHTPVSDKKKKKCSIHKERPQKHSHEIFRDSSLV
			NEQSQITRRKKRKKDFQHLISSPLKKSRICDETANATSTLKKRK
			KRRYSALEVDEBAGVTVVLVDKENINNTPKHFRKDVDVVCVDMS
	}		IEQKLPRK\PKTDKFQVLAKSH\AHKSEALHSKVREKKNKKHQR
}	1		VANCHECORA DEEL DOCUMENTO DE LA CONTRACTOR DE LA CONTRACT
ł	1		KAASWESQRA\RDTLPQSEFPTQEESWLSVGPGGEITELP\ASA
			HKNKSKKKKKSSNREYET\LAMPEGSQAGREAGTDMQESQPTV
1 1	1		GLDDETPQLLGPTHKKKSKKKKKKKKKNHQEFESLAMPEGSQVGS
j j	ļ <u></u>		EVGADMQES\RPAVGLHGETAGIPAPAYKNKSKKKKKKSNHQEF
	ţ		EAVAMPESLESAYPEGSQVGSEVGTVEGSTALKGFKESNSTKKK
1	1	• .	SKKRKLTSVKRARVSGDDFSVPSKNSESTLFDSVEGDGAMMEEG
			VKSRPRQKKTQACLASKHVQEAPRLEPANEEHNVETAEDSEIRY
1 1	j		LSADSGDADDSDADLGSAVKQLQEFIPNIKDRATSTIKRMYRDD
1			LERFKEFKAQGVAIKFGKFSVKENKQLEKNVEDFLALTGIESAD
			KLLYTDRYPEEKSVITNLKRRYSFRLHIG\RNIARPWKLIYYRA
1 1			KKMFDVNNYKGRYSEGDTEKLKMYHSLLGNDWKTIGEMVARRSL
1 1			SVALKFSQISSQRNRGAWSKSETRKLIKAVEEVILKKMSPQELK
		l	EVDSKLQENPESCLSIVREKLYKGISWVEVEAKVQTRNWMQCKS
1 1	i		KWTEILTKRMTNGRRIYYGMNALRAKVSLIERLYEINVEDTNET
1		ļ	DWEDLASAIGDVPPSYVQTKFSRLKAVYVPFWQKKTFPEIIDYI.
1 1			YETTLPLLKEKLEKMMEKKGTKIQTPAAPKQVFPFRDIFYYEDD
		ĺ	SEGGGHRKRKRRPRRHAWFTPVIPVLWEAKAGWII
5413	3753	1304	RFPAGVAPRRAMANVSKKVSWSGRDRDDEEAAPLLRRTARPGGG
1		ļ	TPLLNGAGPGAARQSPRSALFRVGHMSSVKLDDELLEP\DMDPP
			HPFPKEIPHNEKLLSLKYESLDYDNSENQLFLEEERRINHTAFR
1	1		TVEIKRWVICALIGILTGLVACFIDIVVENLAGLKYRVIKGNID
[[1		KFTEKGGLSFSLLLWATLNAAFVLVGSVIVAFIEPVAAGSGIPQ
1	ł		IKCFLNGVKIPHVVRLKTLVIKVSGVILSVVGGLAVGKEGPMIH
1			SCEVIAGESCOCRETELEDERY BOY BOY BOY
1	İ		SGSVIAAGISQGRSTSLKRDFKIFEYLRRDTEKRDFVSAGAAAG
1	1		VSAAFGAPVGGVLFSLEEGASFWNQFLTWRIFFASMISTFTLNF
1	1	1	VLSIYHGNMWDLSSPGLINFGRFDSEKMAYTIHEIPVFIAMGVV
[GGVLGAVFNALNYWLTMFRIRYIHRPCLQVIEAVLVAAVTATVA
·			FVLIYSSRDCQPLQGGSMSYPLQLFCADGEYNSMAAAFFNTPEK

SEQ Predicted on aucleotide location orresponding company of the beginning of succession of the sum of the first amino acid acid acid acid acid acid acid acid					
Dogsinning moticotide location location				Predicted end	1 Amino acid com
Mo: nucleotide location corresponding to first amino acid areadou of amino acid sequence Leucine, Mambehionine, Manghaire, Leucine, Mambehionine, Manghaire, Leucine, Mambehionine, Manghaire, Leucine, Mambehionine, Manghaire, Leucine, Mambehionine, Manghaire, Leucine, Mambehionine, Manghaire, Leucine, Mambehionine, Manghaire, Leucine, Mambehionine, Manghaire, Leucine, Mambehionine, Manghaire, Leucine, Mambehionine, Manghaire, Leucine, Mambehionine, Manghaire, Leucine, Mambehionine, Manghaire, Leucine, Manghaire, Manghaire, Leucine, Manghaire, Manghaire, Leucine, Manghaire, Manghaire, Leucine, Manghaire, Manghaire, Leucine, Manghaire, Manghaire, Leucine, Manghaire, Manghaire, Leucine, Manghaire, Manghaire, Leucine, Manghaire, Manghaire, Leucine, Manghaire, Manghaire, Leucine, Manghaire, Manghaire, Leucine, Manghaire, Manghaire, Leucine, Manghaire, Manghaire, Leucine, Manghaire, Manghaire, Manghaire, Leucine, Manghaire, Manghaire, Leucine, Manghaire, Manghaire, Leucine, Manghaire, Manghaire, Manghaire, Leucine, Manghaire, Manghaire, Leucine, Manghaire, Manghaire, Manghaire, Leucine, Manghaire, Manghaire, Leucine, Manghaire, Manghaire, Leucine, Manghaire, Manghaire, Leucine, Manghaire, Manghaire, Leucine, Manghaire, Manghaire, Leucine, Manghaire, Manghaire, Leucine, Manghaire, Manghaire, Leucine, Manghaire, Manghaire, Leucine, Manghaire, Manghaire, Leucine, Manghaire, Manghaire, Leucine, Manghaire, Manghaire, Leucine, Manghaire, Manghaire, Leucine, Manghaire, Manghaire, Leucine, Manghaire, Leucine, Manghaire, Manghaire, Leucine, Manghaire, Leucine, Manghaire, Leucine, Manghaire, Leucine, Manghaire, Leucine, Manghaire, Leucine, Manghaire, Leucine, Manghaire, Leucine, Manghaire, Leucine, Manghaire, Leucine, Manghaire, Leucine, Manghaire, Leucine, Manghaire, Leucine, Manghaire, Leucine, Manghaire, Leucine, Manghaire, Leucine, Manghaire, Leucine, Manghaire, Leucine, Manghaire, Leucine, Mangha		ID	beginning	nucientida	
Cocresponding to first anine acid acid acid acid acid acid acid acid		NO:			I MATCHELLING. CELVSTRING DENOMALE: - x · 1 -
corresponding to first amino acid samino acid samino acid sequence		1			Giucamic Acid, F=Phenvlalaning C Cl
Corresponding to first amino acid senion acid should be provided to first amino acid senion acid senion acid senion acid senion acid senion acid sequence se		1		corresponding	H=Histiding T-Yeal-withthe, G=Glycine,
to first amino acid residue of amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid sequence sequenc			corresponding	to first	
amino acid eraidue of amino acid sequence control the control of amino acid sequence control the control of amino acid sequence control of amino acid sequence control of amino acid sequence control of amino acid sequence control of amino acid sequence control of amino acid sequence control of amino acid sequence control of amino acid sequence control of amino acid sequence control of amino acid sequence control of amino acid sequence control of amino acid sequence control of amino acid sequence control of amino acid sequence control of acid		i	to first		Labeline, Mamethionine, NaAsparagine
residue of amino acid sequence		ì			F=PiOiine, O=Giutamine D=hraini-
amino acid sequence Sequence				residue of	S=Serine, T=Threenine, W. W-1:
amino acid sequence Codom. /=possible Netsible deletion \[\] \[amino acid	Walling, Vavaline,
Sequence Substitution The Nucleotide Insertion		}	amino acid		""" 1 ypcophan, Y=Tyrosine, X=Unknown, *=Stop
STUDIEST OF THE STATE OF THE ST		1		seductics	codon, /=possible nucleotide deletion
SVVSLPHDPRSYNPETIGLEFILVYFFIAGWYGIAVBAGHQUAD SULFAAMGHA SOLSISISINICHAA HADDEKKAHAGAAGLGUTV BMTLGLAVIMMAAGAWTYGFI HMULMTAKIVGDVF EUGHAN HOLGSVYFLIMEAPVTSSILTARWYSTPYTGERREKWYDIV DUSSTIASHNAFFVVSHADTOPARIGGILHSGOLIVERREKWYDIV FVERSHIGSVORGRIKDROHADYFFPYTOGATICHREKWYDIV FVERSHIGSVORGRIKDROHADYFFPYTOGATICHREKWYDIV FVERSHIGSVORGRIKDROHADYFFPYTOGATICHREKWYDIV SEFPHINSPYTYPOGATIPACYFFPYTOGATICHRUNODDROWG LEFPHINSPYTYPOGATIPACYFFPYTOGATICHRUNODDROWG GOVASAWDRAFFSPLLSPTSRVFRTSPRCOSTETTGRRERAPY GOVASAWDRAFFSPLLSPTSRVFRTSPRCOSTETTGRRERAPY GOVASAWDRAFFSPLLSPTSRVFRTSPRCOSTETTGRRERAPY GOVASAWDRAFTSPLLSPTSRVFRTSPRCOGARGTSPR AGAPROHGEVRHERPSSARMTITTGOCLAPRGOGARGTSPR AGAPROHGEVRHERPSSARMTITTGOCLAPRGOGARGTSPR AGAPROHGEVRHERPSSARMTITTGOCLAPRGOGARGTSPR REYNICHCOLAPROHADYTAGHTSPRUTTSP		ļ	sedifetice		\=possible nucleotide incertion\
SATIA STORE STATE AND STATE ST			_		SVVSLEHDPDGSVNDI TI OT DTV VIII
SATIA STORE STATE AND STATE ST		1	1	1	CITECHNORY
INCLOSOP PILMERAPYTSISTIARE MAST PYTCHERREKYGYLY DYSSDYSNING PVYENDINA REMOTE PYTCHERREKYGYLY DYSSDYSNING PVYENDINA REMOTE PARTICLES IN SODERSCITUD PVENDINA REMOTE PARTICLES STREWETS PRECOST IN SODERSCITUD LISPRING PYTCH PRESIDENCE PRESIDENCY STREET REMOTE PROPERTY PROPERTY OF THE PARTICLE PROPERTY PROPE		1	j .	}	SDD:GAVWGRD:GISLSYLTGAATWADDGKVALMGAAAAA GOTTE
DUSSTANDING FVVEHABLE PUTCHERSE KYGIV DUSSTANDING FVVEHABLE PUTCHERSE KYGIV FVERSING STORM FOR THE STATE OF		ì	ŀ	1	TWILD DI VINNEATSNVTYGFPTMINT,MTAKTNCDVETEGT 1771
FVERSINGLY (VERNEL DEPROPRED IN SODERECTED FVERSINGLY (VERRIELLED PROPRED IN SODERECTED LOFFMRISE) PTTY/PORAL PROPERLY SILVS (DEPROPRED VERY OF THE PROPERLY		1	l e	1	HIOLOSVPFLHWEAPVTSHSLTAPEIMSTRUMSTRUMSTRUMSTRUMSTRUMSTRUMSTRUMSTRU
S414 2130 390 GVASAMBRALE PULLSPANDEN PROVENT PRAIGENE PROPENT PROVINCE CONTROL OF THE PROVENT PROVENT PROVENT PROVINCE PROVENT PROVINCE PROVINC			ŀ	1	DVI.SDID CHUNCEDING TO TOTAL VIOLETTIC DE LE CONTRE LE VIOLETTE DE LE VIOLETTE DE LE VIOLET
S414 2130 390 GVASAMBRALE PULLSPANDEN PROVENT PRAIGENE PROPENT PROVINCE CONTROL OF THE PROVENT PROVENT PROVENT PROVINCE PROVENT PROVINCE PROVINC			1	Į.	DVISDIASNANGFPVVEHADDTQPARLQGLILRSQLIVLLKHKV
5414 2130 390 GVASANDERJEDSTENSVERTSPERCYSTETNERBERUPS GVASANDERJESSPLISFTSEVERTSPERCYSTETNERBERUPS RAGARENHORVERHERPSSARMTETTSCCLAREGOCOPHISTES RESPERTERGOCSASPACLY CESALIVAUCTIMILMYMDRETV AGVLPDIEDFFMIGDSSGLIOTVEISSYMVLAVFGYLGDRYM REYLENCGS INFENILTURSSFIPGERSWYLLAVFGYLGDRYM REYLENCGS INFENILTURSSFIPGERSWYLLAVFGYLGDRYM REYLENCGS INFENILTURSSFIPGERSWYLLAVFGYLGDRYM REYLENCGS INFENILTURSSFIPGERSWYLLAVFGYLGDRYM REYLENCGS INFENILTURSSFIPGERSWYLLAFGLYGGRAY REYLENCGS INFENILTURSSFIPGERSWYLLAFGLYGGRAY REYLENGERSPERTSPHISTAGRAFGYLGSHLPPL MITSWADLERALRYPFGLGVAVALLLFLVVREPFGRAVERHSDLPPL MITSWADLERALRYPFGLGVAVALLLFLVVREPFGRAVERHSDLPPL MITSWADLERALRYPFGLGVAVALLLFLVVREPFGRAVERHSDLPPL MITSWADLERALRYPFGLGVAVALLLFLVVREPFGRAVERHSDLPPL SERVLLGETFPCLEGDSSSSISLIFOLTGVALGVER SERVLLGETFPCLEGDSSSSISLIFOLTGVALGVER SERVLLGETFPCLEGDSSSSISLIFOLTGVALGVER SERVLLGETFPCLEGDFALGYSTAGARGA AGSPYLIGLISDRIRRNWPDFSLSEFFALGYSLACAFGALGG AGSPYLIGLISDRIRRNWPDFSLSEFFALGYSLACAFGALGG AGSPYLIGLISDRIRRNWPDFSLSEFFALGYSLACAFGALGG AGSPYLIGHERMAVADALITAVITURSMKGTGAMARNIGSLIPPSATR RICHLINKARANSLIESLES LISSGNKARGLQBHS ISVOLDSSIS STLENTSKEPSVCKERALP ISESSFALLSDSDSSSKILPE EPABLEPQOAFRRANTLSHFPIECGEPGPARGSSPGGRUM RYNEVSTETPHERWOFSSCHANHLGDSGGTVAVARRISKROOI FL RVATPOKACDSSRYRDVSELGSLIPPRSPLEPVCESDFGOPPE EKKRTSRELRELWGKALLQCILLARRISKROLGASENDLINKR RYNEVSTETPHERWOFSSCHANHLGDSGGTVAVARRISKROOI FL RVATPOKACDSSRYRDVSELGSLIPPRSPLEPVCESDFGOPPEPE EKKRTSRELRELWGKALLQCILLARRISKROLGASENDLINKR LKLDVSETTPCLKEVTTVMEMILSTFGRSKIKEDMEKSHASVOO GVEVRIHINGERWKFLAGGFURVERKORGASENDLINKR LKLDVSETTPCLKEVTTVMEMILSTFGRSKIKEDMEKSHASVOO GVEVRIHINGERWKFLAGGFURVERKORGASENDERGERS VENGULFARRISKROMALTILLEERSALLQTVEERPR ASGPLGFVARVEDMIT FLOGTGVT VKRVALGAMBLINKR ASGPLGFVARVEDMIT FLOGTGVT VKRVALGAMBLINKR LETIVUPFIKSTLENLISSESKIKOMALTILLEERSALLQTVEERPR ASGPLGFVARVEDMIT FLOGTGVT VKRVALGAMBLINKR LETIVUPFIKSTLENLISSESKIKOMALTILLEERSALLQTVEERPR ASSONDINGCVRNITIKALIOKREKRSVENCOR PETTSGGGGTWTOTESTES LSSSNODNINGCVRNITIKALIOKREKRSVENCOR PETTSGGGGTWTOTESTES LSSSNODNINGCVRNITIKALIOKREKRSVENCOR PETTSGGGGTTVOTENTI		1	Į.	J	1 TARCHICGO VORKERLANDER DAY PREPERTOR AND THE CONTRACTOR OF THE C
S414 2130 390 GVASAWARALFSELLSTSAVRTSPERCYSTETURRERARVPS QWCSVLOGKLPVSGRTSLACVES ILLSPASSERKUTVGGTGAR AGABRENDERVERREPSSARARWITTIGGCLAPRGCOCPEGTESP RSPRSRTRRGCSASPACLP/CRSALIVAULCYIN.LWMDRETV AGVLPDIEGDFMIGDSSSGLIOTVFISSWILAPVEGYLOGDYN RSYLLWCGGTAFWSLUTLGSSFIFGEHSWLLLUTRGLUGUGEASY STIAPTILADLEVADQRSRWLSIFFFALGSGLATVASKVKD MAGDDHWALRVTPGLGVVAVLLLELVVREPPRGAVERHSULPPL NSTSWAADLRALRNEPFY-ISSLGFTAVGSLGAVTAGSKVKD MAGDDHWALRVTPGLGVVAVLLLELVVREPPRGAVERHSULPPL NSTSWAADLRALRANSPFJ-USSLGFTAVGSLGAVAGSKVKD AGROWHALRVTPGLGVVAVLLLELVVREPPRGAVERHSULPPL NSTSWAADLRALRANSPFJ-USSLGFTAVGSLGAVAGAG SREUHSNPRAPDPLVCATGLGSAPFI-ISCAGRAVGSLAVATYIF IFIGETILSMMARVADILLYVVI PTERSTARAFQTVLSHLLGD AASFYLIGLISDRLRNWAPPSILLSFRALGFSTULGARGSIVATYIF IFIGETILSMMARVADILLYVVI PTERSTARAFQTVLSHLLGD AASFYLIGLISDRLRNWAPPSILLSSEDGLACRGSIVATYIF IFIGETILSMMARVADILLYVVI PTERSTARAFQTVLSHLLGD AASFYLIGLISDRLRNWAPPSILLSSEDGLACRGSIVATYIF IFIGETILSMMARVADILLYVVI PTERSTARAFQTVLSHLLGD AASFYLIGLISDRLRNWAPPSILLSSEDGLACRGSILPSATTF ILIDHANKARSSLITESISSESILSRGNNARGLOCHNE IS VIDLOSSIS STLENTSKEPSVCKKALP ISESSFYLLOSSEDLASSINGSEN SERVEN STLENTSKEPSVCKKALP ISESSFYLLOSSEDLASSINGSEN SEVGRKIM RYHSVSTETPHERKDESKANHLLOGGGTPPVRTRRSKROOTISL RYHSVSTETPHERKDESKANHLLOGGGTPPVRTRRSKROOTISL RYHSVSTETPHERKDESKANHLLOGGGTPPVRTRRSKROOTISL RYHSVSTETPHERKDESKANHLLOGGGTPPVRTRRSKROOTISL RYHSVSTETPHERKDESKANHLOGGGTPPVRTRRSKROOTISL RYHSVSTETPHERKDESKANHLOGGGTPPVRTRRSKROOTISL RYHSVSTETPHERKDESKANHLOGGGTPPVRTRRSKROOTISLOGG GVV_RHINGGETWELAGDELLHUNG PTS GLOGGLINTRIKASSLLOGG GVV_RHINGGETWELAGDELLHUNG PTS GLOGGLINTRIKASSLLOGG GVV_RHINGGETWELAGDELLHUNG PTS GLOGGLINTRIKASSLLOGG GVV_RHINGGETWELAGDELLHUNG PTS GLOGGLINTRIKASSLLOGG GVV_RHINGGETWELAGDELLHUNG PTS GLOGGLINTRIKASSLLOGGENG VGCCQCLSFLUGGLINTRIKANGENGANDLAGGLINTRIKASSLLOGGENGANG ASSPEDEFOTOPETY ASSPEDEFOTOPETY IS RYBORDARGENGANGENGANG RICCAMARVENGANGANGANGANGANGANGANGANGANGANGANGANGAN		Į.	1		LOGETIMPSPYTVPQEASLPRVFKT.FRAT.GT.DUI.TATIONIDNO.TEG
GNASADDRAFFS PLISTTS AVERTS PERCYSTETORR DRAFFS GNASADDRAFFS PLISTS AVERTS PERCYSTETORR DRAFFS GNASADDRAFFS PRIST AS ARMITET TO CLARECO PROTTER AGAAPRDHOK VRHERP SSARMITET TO CLARECO PROTTER AGAAPRDHOK VRHERP SSARMITET TO CLARECO PROTTER AGVILDED FRICTS STARMITET VERSION TO AVERT AVERT AND AVERT AVERT AND AVERT AND AVERT AVERT AVERT AND AVERT AVERT AND AVER AND AVERT AND AVER AVER AND AVERT AND AVERT AND AVERT AND AVERT AND AVERT AND AVER AVER AND AVERT AND AVERT AND AVERT AND AVERT AND AVER AND AVERT AND AVER AND AVERT AND AVER AND AVER AND AVER AND AVER AND AVER				1	LVTRKDLARYRLGKEGLEGI.GT
OMCSVLOGKLIP VSGRTS LACVES ILLSPASSPRAVGI VGGTGAR AGAAPRDHEKVERREPS SAGRWITSTEGGLARGOCOPROTEST REPRESTRANCES AGRACIA (CASALIVALUCY INLIMYMBRETY AGVALPD LEGOFFRIEDSSGLIOTVEISSYMVLAUCY INLIMYMBRETY AVVLPD LEGOFFRIEDSSGLIOTVEISSYMVLAUCY INLIMYMBRETY AVVLPD LEGOFFRIEDSSGLIOTVEISSYMVLAUCY INLIMYMBRETY AVVLPD LEGOFFRIEDSSGLIOTVEISSYMVLAUCY INLIMYMBRETY AVVLPD LEGOFFRIEDSSGLIOTVEISSYMVLAUCY INLIMYMBRETY AVVLPD LEGOFFRIEDSSGLIOTVEISSYMVLAUCY INLIMYMBRETY AVVLPD LEGOFFRIEDSSGLIOTVEISSYMVLAUCY INLIMYMBRETY AVVLPD LEGOFFRIEDSSGLIOTVEISSYMVLAUCY INLIMYMBRETY AVVLPD LEGOFFRIEDSSGLIOTVEISSYMVLAUCH LEGOFFRIEDSPIL BERNVLOETT PCLEGOSCOSSELI PET PLOUGACE VALLE BERNVLOETT PCLEGOSCOSSELI PET PLOUGACE VALLE GRANDER PLOUGATEL STANDARD LACKS IN AVVI INCIDENTAL PLOUGATION AND AVERAGE AGRETICAL PROPERTY AND AVAILABLE AND AVAILABLE AGRETICAL PLOUGATION AND AVAILABLE BERLEDGRAND AND AVAILAB		j 5414	2130	390	CVACAMDDALECTIVE
AGASPHIGHEVERRIPSESARRITETTGOCLAPRGCORPGTESP REPRESTERGCSASPACLE/CRSALIVAULCYIN.LWHENETV AOVEDIEGP FINGESSESCILOTVESSEMULAUVECYIN.LWHENETV AOVEDIEGP FINGESSESCILOTVESSEMULAUVECYIN.LWHENETV REVILMCGGTAFWSLUTLGSSFIPGEHSWLLLLTRGLUGGGENAS REVILMCGGTAFWSLUTLGSSFIPGEHSWLLLLTRGLUGGGENASKYKD MGDWHMALRVTPGLGVVAVLLLELVVREPPRGAVERHSDLPPL MTSWAADLRALARNEPYL-SSLOFTAVGSLGVIAGSKYKD MGDWHMALRVTPGLGVVAVLLLELVVREPPRGAVERHSDLPPL RERVVLGETT PCLPGDSCSSSDSLIFGLITCLTGVUGLGWEI SREWLHSNPRAPPLVLATGLGSAPPLFISLAGCARGSIVATYIF IFIGETILLSMWAAVADILLYVUT PTRRSTARAPGIVLSHLLJGD AOSPYLIGLISDRIRRWBPSSLSEPFALOFSLACAPVGALGG AAFLGTAHLB ISPLRCLEFERGUEHHLIGBMKGTGOMAARNIGSELPSANTY IFIGETALLSMWAAVADILLYVUT PTRRSTARAPGIVLSHLLJGD AOSPYLIGLISDRIRRWBPSSLSEPFALOSSENLSE EPRALEPPOGAPRRAWITLSHEN FERGEPOLAMCSSELPSANTY ISPLRCLEFERGUEHHLIGBMKGTGOMAARNIGSELPSANTY REVENDEN SENGEN STEINSRONLAGGUES INFONTANTY ISPLRCLEFERGUEHHLIGBMKGTGOMAARNIGSELPSANTY RYHSVSTETPHERKDFSKANHLIGDSGTPVKTRRISKROOJIL RYHSVSTETPHERKDFSKANHLIGDSGTPVKTRRISKROOJIL RYHSVSTETPHERKDFSKANHLIGDSGTPVKTRRISKROOJIL RYHSVSTETPHERKDFSKANHLIGDSGTPVKTRRISKROOJIL RYHSVSTETPHERKDFSKANHLIGDSGTPVKTRRISKROOJIL RYHSVSTETPHERKDFSKANHLIGDSGTPVKTRRISKROOJIL RYHSVSTETPHERKDFSKANHLIGDSGTPVKTRRISKROOJIL RYHSVSTETPHERKDFSKANHLIGDSGTPVKTRRISKROOJIL RYHSVSTETPHERKDFSKANHLIGDSGTPVKTRRISKROOJIL RYHSVSTETPHERKDFSKANHLIGSGGTPVKTRRISKROOJILORG GVV.RIHIRGETWKFLAEDFHLIKIGPPSKOPKRVIFYKELKKOIT SOORALLILDGATFPHPTFYFAGLGAGGLSINNIIKAKSLLDOD GVV.RIHIRGETWKFLAEDFHLIKIGPPSKOPKRVIFYKELKKOIT SOORALLILDGATFPHPTFYFAGLGAGGLSINNIIKAKSLLDOD VGVCQGLSFVAGILLLIHMSEBEAFGUEHVENDITALVGHEN LETTUPTIKSKLERIJUKSHLIGHTEN TIRVVERDITARLGKOVTRPDM ASSPERIFETOPEPPIN ASSPLAGATEN TIRVERMSTANDHLIFTEN TIRVVERDITARLGKOVTRPDM VLOEBILIDSSPLSBNORMBLKKTNSSIRKONLOKAVEVETV VLOEBILIDSSPLSBNORMBLKKTNSSIRKONLOKAVEVETV VLOEBILIDSSPLSBNORMBLKKTNSSIRKONLOKAVEVETV VLOEBILIDSSPLSBNORMBLKKTNSSIRKONLOKAVEVETV VLOEBILIDSSPLSBNORMBLKKTNSSIRKONLOKAVEVETV VLOEBILIDSSPLSBNORMBLKSTRINGSCKADAVOVOTROMMOUS AKSSINDONAGINGTANTALTERSVANDILLIKT NILLSENSSIDDNROCHNILTRATHLITTALTERSVANDILLDKO AT		ļ	1	1	OVASANDRALP SPLLSPTSRVFRTSPPRCVSTETGRRDRARVPS
RSPRENTERGCSASPACLIP/CRSALIVCYINILIAMBRETV ROYLDDIEOFFNIGOSSGLIOTVFISSYMULAPVECYLORNYM RYIMCGIAFWSLUTHOSSFIGENILLITRGLUGGESY STIAPTLIADLFVAPORSRMISIFYPATPUSGLGYIAGSKYM MAGDHMANLAVTGLGUVAVLLIFLITULUGGESY STIAPTLIADLFVAPORSRMISIFYPATPUSGLGYIAGSKYM MAGDHMANLAVTGLGUVAVLLIFLITULUGUGESY STIAPTLIADLFVAPORSRMISIFYPATPUSGLGYIAGSKYM MAGDHMANLAVTGLGUVAVLLIFLITULUGUGESY SRERHSNPRADPLVCATGLIGSAPFLFISLACARGSIVATYIF IPIGETLISNNAVAVDILLIAVVI PITALLACAFVUGUEVEI SRERHSNPRADPLVCATGLIGSAPFLFISLACARGSIVATYIF IPIGETLISNNAVAVDILLIAVVI PITALLACAFVGALGG AASISYLIGLISNRIERNMPPSFISEFRALQFSIMCCAFVGALGG AASISYLIGLISNRIERNMPPSFISEFRALQFSIMCCAFVGALGG AASISYLIGLISNRIERNMPPSFISEFRALQFSIMCCAFVGALGG AASISYLIGLISNRIERNMPPSFISEFRALQFSIMCACAPVGALGG AASISYLIGLISNRIERNMPPSFISEFRALQFSIMCACAPVGALGG AASISYLIGLISNRIERNMPPSFISEFRALQFSIMCACAPVGALGG AASISYLIGLISNRIERNMPPSFISEFRALQFSIMCACAPVGALGG AASISYLIGLISNRIERNMPPSFISEFRALQFSIMCACAPVGALGG AASISYLIGLISNRIERNMPPSFISEFRALQFSIMCACAPVGALGG AASISYLIGLISNRIERNMPPSFISEFRALQFSIMCACAPVGALGG AASISYLIGLISNRIERNMPPSFISEFRALQFSIMCACAPVGALGG IISPICARTUNIAMAGESTEVARAGELOFSSATAFT RICHMINAKARSLITESLESILERGRUKARGOLGHISISVDDISSLS STLENNTKERPSVCEKERLPISESSFKLLGSSEDILGSBLSDSESHLEE BERALEPOQAFFRRANTLIGHFPIECGSPPOGRAGGGGGVGANA RYHNSTETPHERMSPSSILERUPSFISEFLERIPSFICOPPPE EKKRTSRELRELRELRENGFPISEGLOGTSPVCECAGFOPPE EKKRTSRELRELRELRELRENGFPISEGLOGTSVARAGENDLLINKR LELDYBEITPHFSACLGAGOLGININIKARSAVO GVP\RHIMRGEIWRFLAGGTHIKHGFPISKOCPROVYKELLKOLT SQHARLILDLARTFTPHFSACLGAGOLGININIKARGAVO GVP\RHIMRGEIWRFLAGGTHIKHGFPISKOCPROVYKELLKOLT SQHARLILDLARTFTPHFSACLGAGOLGININIKARGAVO GVP\RHIMRGEIWRFLAGGTHIKHGFPISKOCPROVYKELLKOLT SQHARLILDLARTFTPHFYSACLGAGOLGININIKARGAVO GVP\RHIMRGEIWRFLAGGTHIKHGFPISKOCPROVYKELLKOLT SQHARLILDLARTFTPHFYSACLGAGOLGININIKARGAVOPPHY LLKGULGAARGAVENGULGARGAVENGULGANGANA ASSOREPEGTOPPPTGO SAPARAFTSSMGSIRINGHAGAGLUFFTTSGAGLGAUCHAGAGA AKSOREPEGTOPPTGO FRENCHLEGART THE STANCHLARGAVENTHARAGAUCHAGAGAGANATULARGAVENTHARAGAUCHAGAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA		1	1	j	QWC5VLQGKLPVSGRTSLACVRSTLT.SDDSSDDVKGTVGGTGS
ASPASATIRACEASPACIP/CRSALIVAULCY INLINIMENT ACULD LEGIFATIONS SEGICTOVE IS SYMILAPURGUS TO THE ACULD THE STATE OF THE STAT		l	İ		AGAAPRDHGRVRHRRPSSARRMTPTTGOGLARBGGGGRAGE
RYLINGGIAFWSLITYLGSSTIGGENENLLLTREILVGGEASY STIAPTLIADLEVADORSEMISTYPATPVOSGIGYIAGSKYRD MAGDHHAMLEVTFGLVOVAVLLIPLYEVEPROADERISDLPPL NETSWAADLEALARNESFVLSSIGFTAVAFVTGSLALWAPAFLL RSRVVLGGTFPCLPGBCSSSDGLTGLTCHTOVLOGUEVEI SRRUEHSNNPRADPLVCATGLIGSAPFLETSLACARGS IVATYTF IFIGETLISNNARIVADILLIVVU FIRSTAEAPGVUKGLEVEI SRRUEHSNNPRADPLVCATGLIGSAPFLETSLACARGS IVATYTF IFIGETLISNNARIVADILLIVVU FIRSTAEAPGVUKGLEVEI AGSSYLIGLISNRERWAPSFLSEFTALOFSLM-CAFVGALGG AAFLGTHHU AGSSYLIGLISNRERWAPSFLSEFTALOFSLM-CAFVGALGG AAFLGTHHU AGSSYLIGLISNRERWAPSFLSEFTALOFSLM-CAFVGALGG AAFLGTHHU AGSSYLIGLISNRERWAPSFLSEFTALOFSLM-CAFVGALGG AAFLGTHHU AGSSYLIGLISNRERWAPSFLSEFTALOFSLM-CAFVGALGG AAFLGTHHU AGSSYLIGLISNRERWAPSFLSEFTALOFSLM-CAFVGALGG AAFLGTHHU AGSSYLIGLISNRERWAPSFLSEFTALOFSLM-CAFVGALGG AAFLGTHHU AGSSYLIGLISNRERWAPSFLSEFTALOFSLM-CAFVGALGGE ITSPLKTLEFPERKKNERSTSSESTLERGRVAR-GLOPHS INVOLDSILS STLENTS KEPSVCKERELPI ISESS FKLLGSSEDLISDSSLESHLEE BPABLEPQOAFRRANTLISHFILGSGTPVXTRHSWRQOIFL RVATPOKACOSSRYEDYSELLELPER PLEPVCCCGGFOPPE EKKTTSGELRELRUMGKAILOGILLERMEKENGKLOASENDLINKR RVHSVSTETPHERKKNEPSKANLLGGSTPVXTRHSWRQOIFL RVATPOKACOSSRYEDYSELLELPER PLEPVCCCGGFOPPE EKKTTSGELRELRELWGKAILOGISCTPVXTRHSWRQOIFL RVATPOKACOSSRYEDYSELLELPER PLEPVCCCGGFOPPE EKKTTSGELRELRELWGKAILOGISCTPVXTRHSWRQOIFL RVATPOKACOSSRYEDYSERVENGKAILOGISCRENGLINKR GVPVRHIRGGETWRILGERGVTVAKENFDMEKLERSVERTHSWRQOIFLING SOHALLILLOATFFTIPTFSACIGAGCISLVTNIKARSAVO GVPVRHIRGGETWRILLAGGTHLKHGFFSKOPPKDVYKELLKOIT SOHALLILLOATFFTIPTFSACIGAGCISLVTNIKARSAVO GVPVRHIRGGETWRILLOATFTTPTFSACIGAGCISLVTNIKARSAVO GVPVRHIRGGETWRILLOATFTTPTFSACIGAGCISLVTNIKARSAVO GVPVRHIRGGETWRILLOATFTTPTFSACIGAGCISLVTNIKARSAVO ASSPLEFERINGERGETVALTERGETSTATATTRICHTPTTVALTHETRERLEGERATMOTIVETER ASSPCEPECTOPPTGO TUDGINGT TEXTLANGASSIRICH TRANGOLIDATORY GONGDYG SVAPAPTTSSMGGS IRISPLSGTITTVTWSSMIHOHIEROM ALALKRIKELEGOVRTI THARGSVTTETISTVTWSSMIHOHIEROM ALALKRIKELEGOVRTI THARGSSCCIDANAVGTLVERMENGOVSVTE AALALKRIKELEGOVRTI THARGSSCCIDANAVGTLVERMENGOVSVTE AALALKRIKELEGOVRTI THARGSSCCIDANAVGTLVERMENGOVSVTE AALALKRIKELEGOVRTI THARGSSCCID			}	}	RSPRSPTPPGCSASPACIA (ODSPICE TO THE TOTAL RGCQGPRGTRSP
RYLINGGIAFWSLITYLGSSTIGGENENLLLTREILVGGEASY STIAPTLIADLEVADORSEMISTYPATPVOSGIGYIAGSKYRD MAGDHHAMLEVTFGLVOVAVLLIPLYEVEPROADERISDLPPL NETSWAADLEALARNESFVLSSIGFTAVAFVTGSLALWAPAFLL RSRVVLGGTFPCLPGBCSSSDGLTGLTCHTOVLOGUEVEI SRRUEHSNNPRADPLVCATGLIGSAPFLETSLACARGS IVATYTF IFIGETLISNNARIVADILLIVVU FIRSTAEAPGVUKGLEVEI SRRUEHSNNPRADPLVCATGLIGSAPFLETSLACARGS IVATYTF IFIGETLISNNARIVADILLIVVU FIRSTAEAPGVUKGLEVEI AGSSYLIGLISNRERWAPSFLSEFTALOFSLM-CAFVGALGG AAFLGTHHU AGSSYLIGLISNRERWAPSFLSEFTALOFSLM-CAFVGALGG AAFLGTHHU AGSSYLIGLISNRERWAPSFLSEFTALOFSLM-CAFVGALGG AAFLGTHHU AGSSYLIGLISNRERWAPSFLSEFTALOFSLM-CAFVGALGG AAFLGTHHU AGSSYLIGLISNRERWAPSFLSEFTALOFSLM-CAFVGALGG AAFLGTHHU AGSSYLIGLISNRERWAPSFLSEFTALOFSLM-CAFVGALGG AAFLGTHHU AGSSYLIGLISNRERWAPSFLSEFTALOFSLM-CAFVGALGG AAFLGTHHU AGSSYLIGLISNRERWAPSFLSEFTALOFSLM-CAFVGALGGE ITSPLKTLEFPERKKNERSTSSESTLERGRVAR-GLOPHS INVOLDSILS STLENTS KEPSVCKERELPI ISESS FKLLGSSEDLISDSSLESHLEE BPABLEPQOAFRRANTLISHFILGSGTPVXTRHSWRQOIFL RVATPOKACOSSRYEDYSELLELPER PLEPVCCCGGFOPPE EKKTTSGELRELRUMGKAILOGILLERMEKENGKLOASENDLINKR RVHSVSTETPHERKKNEPSKANLLGGSTPVXTRHSWRQOIFL RVATPOKACOSSRYEDYSELLELPER PLEPVCCCGGFOPPE EKKTTSGELRELRELWGKAILOGISCTPVXTRHSWRQOIFL RVATPOKACOSSRYEDYSELLELPER PLEPVCCCGGFOPPE EKKTTSGELRELRELWGKAILOGISCTPVXTRHSWRQOIFL RVATPOKACOSSRYEDYSERVENGKAILOGISCRENGLINKR GVPVRHIRGGETWRILGERGVTVAKENFDMEKLERSVERTHSWRQOIFLING SOHALLILLOATFFTIPTFSACIGAGCISLVTNIKARSAVO GVPVRHIRGGETWRILLAGGTHLKHGFFSKOPPKDVYKELLKOIT SOHALLILLOATFFTIPTFSACIGAGCISLVTNIKARSAVO GVPVRHIRGGETWRILLOATFTTPTFSACIGAGCISLVTNIKARSAVO GVPVRHIRGGETWRILLOATFTTPTFSACIGAGCISLVTNIKARSAVO GVPVRHIRGGETWRILLOATFTTPTFSACIGAGCISLVTNIKARSAVO ASSPLEFERINGERGETVALTERGETSTATATTRICHTPTTVALTHETRERLEGERATMOTIVETER ASSPCEPECTOPPTGO TUDGINGT TEXTLANGASSIRICH TRANGOLIDATORY GONGDYG SVAPAPTTSSMGGS IRISPLSGTITTVTWSSMIHOHIEROM ALALKRIKELEGOVRTI THARGSVTTETISTVTWSSMIHOHIEROM ALALKRIKELEGOVRTI THARGSSCCIDANAVGTLVERMENGOVSVTE AALALKRIKELEGOVRTI THARGSSCCIDANAVGTLVERMENGOVSVTE AALALKRIKELEGOVRTI THARGSSCCIDANAVGTLVERMENGOVSVTE AALALKRIKELEGOVRTI THARGSSCCID			1	ì	ACUI DE LEGENARIE
STIAPTLIADLFVADORSSMUSIFYPAIPVOSCIGEASY MAGDMHWALKVTEGLCVVAVLLLFLVVREPPRAVERISDLPPL NTSWADLRALARNESFVJSSLGFTAVAPVTGSLAKAPAPLL RSRVVLGETPFCLPGDSCSSDSLIFGLITCLTGVLGVGLGVEI SREMERSNPRAPPLVCATGLISSAFFLFLSLACARSCSIVATYIF IFIGETLLSNIWAIVADILLYVVIPTRESTARAFOTULSHLIGD ASSPYLIGLISDRIRNIWPSFLSEFRALOFSLM_CAFVCALGG AASPYLIGLISDRIRNIWPSFLSEFRALOFSLM_CAFVCALGG AASPYLIGLISDRIRNIWPSFLSEFRALOFSLM_CAFVCALGG AAFLGTAHLH 1PPKKRLECKHLITTIV NOGGATIFEEVOKLRPRINGRENEL ILSPLRCLFEEKOKEHIHIGEMKOTSOMAARHIGSELPFSATEF RLDALMKAARSLTSTEISFILSKENKARGLGBHSISVDLDSSLS STLSINTSKEPSVCEKRALPISESFILSKENKARGLGBHSISVDLDSSLS STLSINTSKEPSVCEKRALPISESFILSKENKARGLGBHSISVDLDSSLS STLSINTSKEPSVCEKRALPISESFILSKENKARGLGBHSISVDLDSSLS STLSINTSKEPSVCEKRALPISESFILSKENKOKLGASENDLLINKR RYHSVSTETPHEK MFDESKANHLGOGTPVKTRRHSWRQOIFL RVATPCKACDSSRVEDYSELGELPPRSPLEEVCEDGPGPPBE EKKRTSRELRELWGKALLQGILLKHRENDKLGASENDLLINKR LKLDYEEITPCLKEVTTVWEKHNSTEGRSKIKFDMEUMSAVGO GVPKRHRRGEHKFLEEGFHLKHGFFSKOKPCHDPYKELLKOLT SQOBALLIDLGRTFFTHEYTSAGLGAGGLSLYNILKAYSLLDGS VGVCGLSFVAGILLHIMSEERSFKOKQOFKDDYFKELKKOLT SQOBALLIDLGRTFFTHEYTSAGLGAGGLSLYNILKAYSLLDGS VGVCGLSFVAGILLHIMSEERSFKOKQOFKDDYFKELKKOLT SQOBALLIDLGRTFFTHEYTSAGLGAGGLSLYNILKAYSLLDGS VGVCGLSFVAGILLHIMSEERSFKOKGOFKDDYFKELKKOLT SQOBALLIDLGRTFFTHEYTSAGLGAGGLSLYNILKAYSLLDGS VGVCGLSFVAGILLHIMSEERSFKOKGOFKDDYFELKKOLT SQOBALLIDLGRTFFTHEYTSAGLGAGGLSLYNILKAYSLLDGS VGVCGLSFVAGILLHIMSEERSFKOKGOFKDDYFELKKOLT LETTUPFIKSTLPRIGLINGBERVARDFHLOKAYSLUCHERNOLT ASSPERDENCYPPPITGLOKKTURGENGATMOMTGGEF RIGSLEATIEKLLSSEKKKAMALILERSALLGVVCHELRRSA ASSDERBEDDINGCOFNILLASGVTTSTIGGGGIMTSTES LSSSNSDDINGCOFNILLASGVTTSTIGGGGIMTSTES SANGAGENNINDIVVYHRGSRSCKDANVSTLVERNINGSCR SVAPAPTTSSMGSSTRHBPLSSGISTPTVVNSPHILDHIREOM ATALKKRIKELEBGOVTTSJLFSVCSTTIPLVLOKTSCHEKOLVSOLKORAA SQINVCGYRKSVSAGNAGGLGSGRANGTHENVOLGNOLTAG RIGGERSFERCHERNINGER RENAWGABENNINDIVVYHRGSRSCKDANVSTLVERNINGSVTT ANLGWERDERACRSVENGUNGSVTTSLKKRITTLEGGTHENDENT KLKELLGAGGRSVENGUNGSVTTSLKERITTHREEMT KLKELLGAGGRSVENGUNGVTSTRTSLIGGTLAGGGPR PSAKYTREAGGGTSUMGUNGSTRTTSLIGECTHATUSGUNGAAV NAVRTADOTSSTITSSLERGSLOCHT		1	[i	I AGVERDIEUFFNIGUSSSGITOTVFTCCVMMT ADMOCKT CONTO
SILEYTLI LAUDYWALGERSMUSITYPATEVGGLGYLAGSLYKE MAGDWHWALRYTEGLOVAVILLETVAREPPROAUERISDLPPL NPTSWADLERALARNSFVISSLGFTAVAPYTOSLALWAPAPLL RSVVLGETPECLPGSCSSDSLI FGLITCLTGYLGYGLGVEL SRRUKHSNPRADPLVCATGLIGSAPFLFLSLACARGSIVATYIF FIGETLISNWALVADILLYVYT FREYARAFQIVISHLED AGSPYLIGLISDRLRRNWPPSFLSEFRALGFELM.CAFVGALGG AFLGTTAHLH 15PLRCLISDRLRRNWPPSFLSEFRALGFELM.CAFVGALGG AFLGTTAHLH 11SPLRCLPBEKQRHILITEM WEGATIFEEVQKLRFRNEQRENEL 11SPLRCLPBEKQRHILITEM WEGATIFEEVQKLRFRNEQRENEL 11SPLRCLPBEKQRHILITEM WEGATIFEEVQKLRFRNEQRENEL 11SPLRCLPBEKQRHILITEM WEGATIFEEVQKLRFRNEQRENEL 11SPLRCLPBEKQRHILITEM WEGATIFEEVQKLRFRNEQRENEL 11SPLRCLPBEKQRHILITEM WEGATIFEEVQKLRFRNEQRENEL 11SPLRCLPBEKQRHILITEM WEGATIFEEVQKLRFRNEQRENEL 11SPLRCLPBEKQRHILITEM WEGATIFEEVQKLRFNEQRENEL REALESPOOAFRRARNTLSHPFIECPD POPLARGS PGVSQKLM RYHSVSTETTHERKFFESKANHLGDGGTPVTRRHSWRQOITL RVATPOCKACDS SERVEYSLGIGLIPSPLEVCEC-DEPOPPDE EKKRTSRELRELWQKALLOGILLRREKENQXLQASENDLLIKR LKLDYSEITPCLKEVTTVWEKMISTREKIKFMDREMHSANG GVP.RHHRGEIWKFLASCFHLKWOPPSKQVEROPY YEGLLKQLT VGYCQGLSFVAGILLLHMSEBEAFRUKKFLMEMGRIGANG GVP.RHHRGEIWKFLASCFHLKWOPPSKQVEROPY KELLKQLT VGYCQGLSFVAGILLLHMSEBEAFRUKKFLMEMGRAYPHDIMF ASGPFLGFVARVFBMIFLQTSVITIVAVALSLLGSHKKPLILQHEN 11LOIOMYOLSRLLHDHRIDLYMHEEBIESIGSLYNILKAYSLLDOS VGYCQGLISFVAGILLHMSEBEAFRUKKFLMENGINGVERWH VLOEELISDSSLISNORMMUKLKRISSLRKONLDLLEGOLVANG RIGSLBATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRS AKSGREFPECTQPEPTOD KSQLFCFMGGRAGDILSGDDDEGNDFYFVETPGYQLDLDFLK YVDDICKGNTIKENINGKRKBVSVEPFRITSGQGINTSTES LSSNSDDNKQCPPFLIARSQVTSTPISKPPPLETSGQGINTSTES LSSNSDDNKQCPPFLIARSQVTSTPISKPPPLETSGQGINTSTES LSSNSDDNKCCPPFLIARSQVTSTPISKPPPLETSGGGRAMMOTFGEF RRPRLASFGGGTISSJESFVCNNVYSPHILQHIREMENT KKKRELBEGVGTTSJLSFVCSGNAPAGICGJORSCEASSEIREMGE RSVANGAEEMNNDIVVYHGSRSCKDAVGTLVERRNCGVSVTE ANLGWTEABACHTURCTSTVALVAGERGVADITSTKIRSIGGRANTEMVIVKER VEMHDRCAGRSVEMCDAVSTGGCCSVDVTVCSPKECASRGVITEAVSQVEAAV NAVRITADDITSTILLGCOVLETTSTILESCTINTCLSTLDKO TSIQTVETRIVAUGERGVKDINSTKTRISIGGTLLSGLADQUAD BANKTREGGGGCSVDVTVCSPKECASRGVITEANGQVLAAV NAVRITADDITSTILLGCOVLCTTSTT.		ł	į	1	TRAILINGGIAFWSLVTLGSSFTDGFUGWLLLLINDGLUGWGDDG
NPTSWADLRALANDSFYLSSLOFTAVAPPROSLAMPAPHIL RERVVLGETPFCLPGDSCSSDSLIFGLITCLIGVLGUGLGUEI RERVVLGETPFCLPGDSCSSDSLIFGLITCLIGVLGUGLGUEI RERVVLGETPFCLPGDSCSSDSLIFGLITCLIGVLGUGLGUEI RERVVLGETPLCLAFURCATGLIGSAFLFLSLCARGESTVATYIF IFIGETLLISNWAIVADILLYVUTPTRESTARAPQIVLSHLLGD ASSPYLIGLISDRIRNWPSFLSEFRALQFSHL.CAPVGALGG AAFLGTAHLH 1			1		STIAPTLIADLEVADORSDMICTEVENTOUGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
RRVVLGETPPCLPGBCSSSBSLIFGLITCLIGVLGGGLEVEI SRRUKHSNPRADPLVCATGLIGSAPFIFTSLACARGSIVATYTE IFIGETLISNNWALVADILLYVYTERSTARAFQIVISHLIGD AGSYLIGLISDRLRNWPPSFLSEFRALGFSLM.CAFVGALGG AAFLGTHALH 1PPKTKLELGKH\LTTLT\NOBCATTEEVQKLRPRNEQRENEL 1SPLRCHPERGKKEHTHIGEMKOTSOMBARIGSEDPSATTF RLDMLKKKARSLTESLESILSRGNKARGLGHBISTVDLDSSLS STLSNTSKEPSVCEKRALPTISESFFLLGSSBDLSDSESHLEE BPAPLSPQOAFRRANTISHFPIECPPOPARRSSPGVSGKLM RYHSVSTETPHERKDFSKANHLGDSGGTPVXTRRHSWRQOTIL RVATPGGKACDSSRFEVDYSLIGGLIVEPPOPARRSSPGVSGKLM RYHSVSTETPHERKDFSKANHLGDSGGTPVXTRRHSWRQOTIL RVATPGGKACDSSRFEVDYSLIGGLIVEPSLEVCECDPFOPPDE EKKRTSRELRELWQKAILQDILLIRNEKENOKLGASENDLLING LKLDYSETTPLEKVTTVWEKMISPSLEVCECDPFOPPDE EKKRTSRELRELWQKAILQDILLIRNEKENOKLGASENDLLING LKLDYSETTPLEVTYWEKMISPSLEVCHOPFOPPDE EKKRTSRELRELWGKAILDGILLIGNERSKIKFDMERMSAVQO GVP\RHRRGEINKFLAEGFHLKNGPPSKQDRDVPYKELLKQLT VGYCQGLSFVAGILLILMSBEBAFRALKFLMEDMGIRKGVRPDM ILIQIGMYOLSRLIHDVHRDLINHLEBELIGFBLYAAPMFLTMF ASQPFLGFVARVFUMIFLQGTEVTEVALSLILGSHKFLLQHEN LETIVDFIKSTLPHGLVGMEKTINQVFEMDIKGUQAVEVSTH VLQEBLIDSSPLSNDGMEMELEKTNSSLRKONLDLLGOLQVANG RIGSLEATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRRS AKSDREPECTOPPFTOD KSQLFCFMGGKAGDILSGDDDEGOKDFFFVETFYGYQDLDLIPELK YVDDIGKONTIKENINGKRKFUSPPERTTSGQQGIWTSTES LSSNSDDNKQCPMFLIARSQVTSTPISKPPPLETSLPFITIP ERNOLPPS SPQLFWHILVTKTLETTRRLEGGRATMOMTGGEF RPRILASFGGMGTISSLPSFVUSNMPAHKQLQNNYQONDDYG SYAPAPTTSMGSTRHSPLSSGISTPVINNYPHHLOHIREGM ATALKRIKELBEQVRTTPULOVINSDSCRASSEIREMGEC RSVANGAEEMNNDIVVYHEGSRSCKDAAVGTLVERENCGVSVTE AALGGWMEAAKELBEQVRTTSPLJOVGSCRASSEIREMGEC RSVANGAEEMNNDIVVYHEGSRSCKDAAVGTLVERENCGVSVTE AALGGWMEAAKELBEQVRTNSVGISCOPECKNKVVGEFLERMENT KLKGELQAAGSRKWDKATMAQPLVPSKVVEAVVQTRQOMVGSH MCLUDTCCTSVETNSWGISCOPECKNKVVGEFLEMMWIVKER VERHORCAGRSVEMCDKSVSVESVCECTGSNTEASVGQVEAAV NAVRTADQDTSTILLGCOCSVDVTVCSFKECASRGVNTEAVSQVEAAV NAVRTADQDTSTILLGCOLGVDVTYCSFKECASRGVNTEAVSQVEAAV NAVRTADQDTSTILLGCOLGVDVTYCSFKECASRGVNTEAVSQVEAAV NAVRTADQDTSTILLGCOLGVDVTYCSFKECASRGVNTEAVSQVEAAV NAVRTADQDTSTILLGCOLGVDVTYCSFKECASRGVNTEAVSQVEAAV NAVRTADDOTSTILLGCOLGVDVTTATATLIESCTNTCLSTLDKOLG			1	ł	MAGDWWWAI DYEDGE GUILDING THAT PVGSGLGYIAGSKVKD
RRVVLGETPPCLPGBCSSSBSLIFGLITCLIGVLGGGLEVEI SRRUKHSNPRADPLVCATGLIGSAPFIFTSLACARGSIVATYTE IFIGETLISNNWALVADILLYVYTERSTARAFQIVISHLIGD AGSYLIGLISDRLRNWPPSFLSEFRALGFSLM.CAFVGALGG AAFLGTHALH 1PPKTKLELGKH\LTTLT\NOBCATTEEVQKLRPRNEQRENEL 1SPLRCHPERGKKEHTHIGEMKOTSOMBARIGSEDPSATTF RLDMLKKKARSLTESLESILSRGNKARGLGHBISTVDLDSSLS STLSNTSKEPSVCEKRALPTISESFFLLGSSBDLSDSESHLEE BPAPLSPQOAFRRANTISHFPIECPPOPARRSSPGVSGKLM RYHSVSTETPHERKDFSKANHLGDSGGTPVXTRRHSWRQOTIL RVATPGGKACDSSRFEVDYSLIGGLIVEPPOPARRSSPGVSGKLM RYHSVSTETPHERKDFSKANHLGDSGGTPVXTRRHSWRQOTIL RVATPGGKACDSSRFEVDYSLIGGLIVEPSLEVCECDPFOPPDE EKKRTSRELRELWQKAILQDILLIRNEKENOKLGASENDLLING LKLDYSETTPLEKVTTVWEKMISPSLEVCECDPFOPPDE EKKRTSRELRELWQKAILQDILLIRNEKENOKLGASENDLLING LKLDYSETTPLEVTYWEKMISPSLEVCHOPFOPPDE EKKRTSRELRELWGKAILDGILLIGNERSKIKFDMERMSAVQO GVP\RHRRGEINKFLAEGFHLKNGPPSKQDRDVPYKELLKQLT VGYCQGLSFVAGILLILMSBEBAFRALKFLMEDMGIRKGVRPDM ILIQIGMYOLSRLIHDVHRDLINHLEBELIGFBLYAAPMFLTMF ASQPFLGFVARVFUMIFLQGTEVTEVALSLILGSHKFLLQHEN LETIVDFIKSTLPHGLVGMEKTINQVFEMDIKGUQAVEVSTH VLQEBLIDSSPLSNDGMEMELEKTNSSLRKONLDLLGOLQVANG RIGSLEATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRRS AKSDREPECTOPPFTOD KSQLFCFMGGKAGDILSGDDDEGOKDFFFVETFYGYQDLDLIPELK YVDDIGKONTIKENINGKRKFUSPPERTTSGQQGIWTSTES LSSNSDDNKQCPMFLIARSQVTSTPISKPPPLETSLPFITIP ERNOLPPS SPQLFWHILVTKTLETTRRLEGGRATMOMTGGEF RPRILASFGGMGTISSLPSFVUSNMPAHKQLQNNYQONDDYG SYAPAPTTSMGSTRHSPLSSGISTPVINNYPHHLOHIREGM ATALKRIKELBEQVRTTPULOVINSDSCRASSEIREMGEC RSVANGAEEMNNDIVVYHEGSRSCKDAAVGTLVERENCGVSVTE AALGGWMEAAKELBEQVRTTSPLJOVGSCRASSEIREMGEC RSVANGAEEMNNDIVVYHEGSRSCKDAAVGTLVERENCGVSVTE AALGGWMEAAKELBEQVRTNSVGISCOPECKNKVVGEFLERMENT KLKGELQAAGSRKWDKATMAQPLVPSKVVEAVVQTRQOMVGSH MCLUDTCCTSVETNSWGISCOPECKNKVVGEFLEMMWIVKER VERHORCAGRSVEMCDKSVSVESVCECTGSNTEASVGQVEAAV NAVRTADQDTSTILLGCOCSVDVTVCSFKECASRGVNTEAVSQVEAAV NAVRTADQDTSTILLGCOLGVDVTYCSFKECASRGVNTEAVSQVEAAV NAVRTADQDTSTILLGCOLGVDVTYCSFKECASRGVNTEAVSQVEAAV NAVRTADQDTSTILLGCOLGVDVTYCSFKECASRGVNTEAVSQVEAAV NAVRTADQDTSTILLGCOLGVDVTYCSFKECASRGVNTEAVSQVEAAV NAVRTADDOTSTILLGCOLGVDVTTATATLIESCTNTCLSTLDKOLG					MODERATION OF THE PERCENTAGE OF
SRRIKHSNPRADPLVCATGLISSPIFITSLACARGSIVATYTY IFIGETLISMWAATVADILLYVUI PYRKTARAPQIVLISHLEDD ASSYLIGLISBURJRRNWPPSFLSEFRALGFSLMCAFVGALGG AAFLGTAHLH IPIGETLISMWAATVADILLYVUI PYRKTARAPQIVLISHLEDD AASPULIGLISBURJRRNWPPSFLSEFRALGFSLMCAFVGALGG AAFLGTAHLH ISPLRCLPEKQNEHIHIGENKQTSQNAARMIGSELPPSATGF RLDMLKNKAKRSLTESLESILSGNKAARGLOBHISVDLDSSLS STLSNTSKEPSVCEKRALPISSSSYKLIGSSEDLSVDLDSSLS STLSNTSKEPSVCEKRALPISSSSYKLIGSSEDLSVDLDSSLS STLSNTSKEPSVCEKRALPISSSSYKLIGSSEDLSVDLSSUSSHLPE EPAPLSPQOAFRRANTLSHTPIECQEPPOPARGSPGVSQNKLM RYHSVSTETPHEKKDPESKANHLGDSGGTPVKTRRHSWRQOIFL RVATPQKACDSSRYEDVSELGLDPRSPLEPVCEDGPFGPPE EKKRTSRELRELWGKAILQOILLEMKEKENGKLQASENDLLMKR LKLDYBEITPCLKEVTTVWEKMLSTFORSKIKEDMEKMHSAVGQ GVPNLHRGGINKFLAEQFHLKHGFFSKQQPKOVPYKELIKQLT SQOHAILIDLGRTFFTHYFSGAGGAGLSLYNILKAYSLIDGS VGCQGLSFVAGILLHHNSEERARMLKFLHFMFMGLRKGYRPDM INQUISMLINDYHDLYNHLBEHEIGPSLVAAPMFITMF ASGPPLGFVARVFDMIFTGGTEVIFKVALSLIGSHKPLILQHEN LETTUPFIKSTLPHIGLVOMSKTINOVFENDIAKQLQAYEVEYH VLQEELIDSSPLSDNQRNDKLEKTNOSERKONLOLASEVEYH VLQEELIDSSPLSDNQRNDKLEKTNOSERKOLOLAVEVEYH VLQEELIDSSPLSDNQRNDKLEKTNOSERKOLOLAVEVEYH VLQEELIDSSPLSDNQRNDKLEKTNSSLRKONLDLLEGLQVANG AKPSDREPECTQPEPTGD SQUEATIEKLISSESKLKQAMLTLELERSALLQTVEELRRRS AKPSDREPECTQPEPTGD SQUEATIEKLISSESKLKGAMLTLELERSALLQTVEELRRRS AKPSDREPECTQPEPTGD SQUEATIEKLISSESKLKGAMLTLELERSALLQTVEELRRS AKPSDREPECTQPEPTGD SQUEATIEKLISSESKLKGAMLTLELERSALLQTVEELRRS AKPSDREPECTQPEPTGD SQUEATIEKLISSESKLKGAMLTLELERSALLGTVEELRRS AKPSDREPECTQPEPTGD SQUEATIEKLISSESKLKGAMLTLELERSALLGTVEELRRS AKPSDREPECTQPEPTGD SQUEATIEKLISSESKLKGAMLTLELERSALLGTVEELRRS AKPSDREPECTQPEPTGD SQUEATIEKLISSESKLKGAMLTLELERSALLGTVEELRRS AKPSDREPECTQPEPTGD SQUEATIEKLISSESKLKGAMLTLELGRANGTHERGAM AKPSDREPECTQPEPTGD SQUEATIEKLISSESKLKGAMLTLEVOLGHTHREMT KLKQELGAAGSRKVDKATHAGQLUSGGCLYTDYNDHLUGHTREMT KLKQELGAAGSRKVDKATHAGQLUSGGCLYTDYNDHLUGHTHREMT KLKQELGAAGSRKVDKATHAGQLUSGCCCONSUTALANGUSVTE ALLGWMTEDAKEILEGQCTTESTUKTVTREVERHOGGVENHULVKRR VEMHBRCAGRSVENCDKSVSVEVSVCETGSNTEESVMDLTLLKT NINLKEVES IGCGCCSVDUTVCSPRECASRGGUTALANGUTARR RSVGVGDDVGGSLENPQDQALGMMT			ľ	•	I ME ISWWALDRALARNESEV SSLCETAVA DUTCOL AT LIBERT DE
SARIMSHPADDIVATGILGSAPFIETSLACARGSIVATYIF IFIGETLLSMWAVADILLYVIPTRRSTARAFQIVLISHLIGD AGSPYLIGLISDERRRWPSFISEFRALQFSLM_CAFVGALGG AAFLGTAHLH ISPLRCLPEKQNEHIHIGEMKQTSQMARMIGSELPSATRF RLDMLKNKARRSLTESLESILSGNKARGLOBHSISVDLDSSLS STLSNTSKEPSVCEKEALPISESSFKLIGSEDLSSDSSSHLPE BPAFLSPQOAFRRANTLSHTPIECQEPPOPARGSPOYSQNKLM RYMSVSTETPHEWKDPESKANHLGDSGTPVKTRRHSWRQOIFL RVATPQKACDSSSYRDYSELEDPRSPLEPVCESOPPOPPAGSPOYSQNKLM RYMSVSTETPHEWKDPESKANHLGDSGTPVKTRRHSWRQOIFL RVATPQKACDSSSTRDYSELEDPRSPLEPVCESOPPOPPAGE EKKRTSRELRELWQKALLQUILLIMMEKENGKLQASENDLLINKR LKLDYSEITPCLKEVTTVWEKMLSTPGRSKIKFDMSRWHSANGQ GVP\RHRREEINKFLAGPHLWHGPSKQDFKDVYKELLKGUT SQOBALLIDGRTFFTHPYFSAQLGAGQLSLYNILKAYSLLDOG VGVQGLSFVAGILLIMMSEERKIKFIMFMGRIKGYRPDM IILQIGMYQLSKILLIMDYRDLYNHLEBHEIGPSLYAAPWFLTMF ASQPFLGFVARVEMDHFLQGTSKWALLTSLEGSKLKDLULGUKNGL LETTUPFIKSTLPNLGLVQMEKTINQVFEWDLIKKQLQAYEVEYH VLQEELIDSSPLSDNQRMCKLEKTNSSLIRGNLDLLEQLQVANG RIQSLEATTEKLLSSESKLKQAMLTLELERSALLQTVEELRRS AKPSDREPSCTQPEPTGD SSQLFFWGGKRGDILSGDDKECKDPYFVETPYGYQLDLDFLK YVDDIQKGNTIKRLNICKRRPSVPCPEPRTTSQQGIWTSTES LSSNSDDNKQCPMFLIARSQVTSTPJRSPPPLETSLPFLTIP ENROLPPSPQLFKHNLHVIKTLMTRRRLEGERATMOMTGGF RRPHLASFGGMSTTSSLPSVGSGNNDPARHOLONGYGGNDYG SVAPAPATTSSMGSI SHBSLSSTFVTNNSWHLDHIREOM ATALKRIKELEEQVRTIPVLQVKISVLOBEKROLVSQLKNORAA SQINVCGYRKSYSSGAMSAGLGSTFVTNNSWHLDHIREOM ATALKRIKELEEQVRTIPVLQVKISVLOBEKROLVSQLKNORAA SQINVCGYRKSYSSGAMSAGLGSTFVTNNSWHLDHIREOM ATALKRIKELEEQVRTIPVLQVKISVLOBEKROLVSQLKNORAA SQINVCGYRKSYSSGAMSAGLGSTFVTNNSWHLDHIREOM ATALKRIKELEEQVRTIPVLQVKISVLOBEKROLVSQUKNORAA SQINVCGYRKSYSSGAMSAGLGCFGETTVHNSWHLDHIREOM ATALKRIKELEEQVRTIPVLOVKISVLOBEKROLVSQUFETHDREMT KLKGELQAAGSRKVDKAMAQPLVFSKVVARVQTEDAWVGSH MULDTJCVCGTVETNSYGISCQPECKNKVVARVQFELPMWIST VKER VEMBGRCAGRSVENCKSVSVSVSVCTGSNTEESVINDLILLKT NINLKEVRS ICCGGOSCOSVDVTVCSPECASRVTEAVSQUFEAV MAVPRTADQDTSTDLEQVGCFTINTTATLIESCTNTCLSTLDKO TSTQTVETTRVAVGRGGVEOINSSTKTRS IGGGTLGTUTGLTLASR RSVGVGDDVVGSSLERPPGOQALGMMTALDSTURGLTVALGR			1	1	ASK VIGGTPPCLPGDSCSSSDST.TECLTCUTCUTCUTCUTCUTCUTCUTCUTCUTCUTCUTCUTCUT
ASSYLIGLISBERRENWPSILSERRALOFSLMLCAFVGALGG ASFYLIGLISBERRENWPSILSERRALOFSLMLCAFVGALGG AAFLGTHHIH 1PPKYKLEJOKH\LITLT\NOEQATIFEEVQXLRFRNEQRENEL 1ISPLRCLPEKQKEHIHIGENKOTSQNAAENIGSELPPSATKF RLDMLKNKAKRSLTESLESILSGKKARGLOBHISVDLDISSLS STLSNTSKEPSVCEKEALPISESSYKLLGSSEDLSJDSSSHLPE BPAPLSPQOAFRRANTLSHTPIECOEPPPBRGSPGVSQRKLM RYHSVSTETPHEWRDFSKANHLGDSGGTPVWTRRHSWRQQIFL RVATPOKACDSSRYEDVSELGELPPRSPLEPVCEOPPGPPPE EKKTSRELRELWQKAILQQILLLEMREKENGKLQASENDLLMKR LKLDYEEITPCLKEVTTWEKNLSTFGRSKIKEPMERWHSAVGQ GVP\RHHRGEIMFLAEQFHLKHGPPSKQDPKDVPVKELLKQDT SQOHALIDLGMFTFTPHPYFSAGLAGGGLSLYNILKAYSLLDQE VGYCQGLSFVAGILLIHMSEEBAFKMLKFLMFDMGLRKQYRPDM IILQIOMYQLSRLLDYHRDLYNHLEBIGSSLYAAPWFLTMF ASQPPLGFVARVFDMIFLQGTEVIFKVALSLLGSHKPLILQHEN LETIVDPIHSTLPNLGLUQMSKTINQVFBDIAKQLQAYEVEYH VLQEELIDSSPLSDNQRMCMLKEXTNSSLRKONLDLLEQLQVANG RIGSLBATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRRS AKPSDREPECTQPEPTGD SSQLBFTEKKLSSESKLKQAMLTLELERSALLQTVEELRRRS AKPSDREPECTQPEPTGD KSQLFFWGGKAGDILSGDQDKEOKDPYFVETPYGYQLDLDFLK YVDDIQKGNTIKKINIOKRKRSPVPCPFPRTTISGQGITMSTES LSSNSDDNKQCPMFLLARSQVTSTISKPPPDLBTSLPPLTIP ENRQLPPSPQLPKNHLHVTYTLMETERRLEGERATMOMTPGEP RRPRLAFGGGMGTTSSLPSFVGSONHPAKRQLONGYQGNDDYS SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNNSPHLQHIREOM AIALKRLKELBEQVRTIPVLQVKISVLOEKROLVSQLKNORAA SQINVCGVRKSYSSAGNASGLEGLSRARRSGGELY IDTEEEME TVEGSTGRIKFFROL\TAMQALECKIODSSCEASSELRENGEC BSVAVGAEENNHDVVYHKGSRSCLSRARRSGGELY IDTEEEME TVEGSTGRIKFFROL\TAMQALECKIODSSCEASSELRENGEC BSVAVGAEENNHDVVYHKGSRSCLORAVGTLVERMWTVVKRR VEMBCAGRSVENCDKSVSVEVSVCETGSNTEESVADLILLKT NINLKEVRS ICCGEOSVDTVCSPCCARGVNTEAVSQVEAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETRTVAVGRGRVEGINSSTKRTSIGVGTLUSGRIFGPR PSAVXTKEGSVGGINNDNTVLQLKMRTIAGGPPCJVVGLTASR RSVGVGDDPVGSSLERPPGPQARLMMTALAGDTVFLAGTGGFLOR			1	í	SRRLRHSNPRADPLYCATCLICGARELECTOR
AAFLGTAHLE 5415 693 2986 IPPKTKLELQKH\LTIT\NGGATIFEEVGKLEPRNEQRENEL ISPKRKLELGKKH\LTIT\NGGATIFEEVGKLEPRNEQRENEL ISPKRCLEBEKQKEHHIGEMGOTSGMAAENIGSELPSATKF RLDMLKNKAKRSLTSLES ILSRGNKARGLGHSISVDLDSSLS STLENTSKEPSVCEKEALPISESSFKLIGSSEDLSSDSSHLDE EPAPLSPOOAFRRANTLSHFFIECGE;POPARGSGSVGNKIM RYHSVSTETPHEKDFESKANHLGDSGGTPVKTRRISWRQOIFL RVATPQGACOSSSRYEDYSELPPRSPLEPVGEOPPGPPBE EKKRTSRELRELWGKAILQOILLLRMEKENGKLQASENDLINKR LKLDYEBITPCLKEVTTVWEKHSTPGRSKIKFDHEKMHSAVGQ GVP\RHHIGEIWKFLAEQFHLKRQFPSKQCPKOVPYKELLKGLT SQQHAILIDLGRTFPTHPYFSAQLGAGGLSINTIKAYSLLDOS VGICQGLSFVAGILLHMSEERMKLKEIMSGKAPVTMFLKGLT SQQHAILIDLGRTFPTHPYFSAQLGAGGLSINTIKAYSLLDOS VGICQGLSFVAGILLHMSEERMKLKEIMSGKRYPTMFLTMF ASGPFLGFVARVFDMIFLGGTEVFRVALSKLIGSKKPLILKQLT SQQHAILIDLGRTFPTHPYFSAQLGAGGLSINTIKAYSLLDOS VGICQGLSFVAGILLHMSERFKMLKEIMSMGKRCYRDM IILQIGMYGLSRLHHDYHRDLYNHLEBHIGPSLYAAPWFLTMF ASGPFLGFVARVFDMIFLGGTEVFRVALSKLIGSKKPLILQOL LETTVDFIKSTLPNLGLVGMEKTINOVFEMDIAKQLQAVEVEYH VLQEELIDSSPLSDNORMDKLEKTMSSIRKÖNLDLLEGLQVANG RIGSLEATIEKLLSSESKLKQMLTLELERSALGTVEELERRS AKPSDREPECTOPEPTGD 4074 KSQLFCFWGGKAGDILSGDOKEOKDPYFVETPYGYQLDLDFLK YVDDIQKGMTIKRLNIOKRKRSVDCPPRTTSGQQGIWTSTES LSSNSDNKQCPNFLIARSJCSTFPITNVSPMLOHTREGM ALKEKLESGVOCHNFLIARSJCSTFPITNVSPMLOHTREGM ATALKRLKELEBQVETTPVLOVKTSVLGEERGULVSGLKNORNA SGINVCGVKRSYSGNNSGLGNARRSGELYIDYEEEME TVEGSTORI KEFROL TADMQALECKIQDSSCASSELERNGEC RSVAVGABENNMDIVVYHRGSRSKCNDAAVGTLUEMRNCGVSVTE AMLGVMTEADKEIELQQTTISKKEKTYRLEVQLRETTHIBREMT KLKGELGAAGSRKVDKATMAQPLVFEKVVEAVVOTROMVGSH MDLUDTCVGTSVETNSVGISCOPECKNKVVGBLPHNWNITVKER VEMHBCCAGRSVEMCDKSVSVEVSVECTGSNTEESVNDLTLLKT NINKEVRS IGGCDCSVDVTVCCSPECKNKVVGBLPHNWNITVKER VEMHBCCAGRSVEMCDKSVSVEVSVECTGSNTEESVNDLTLLKT NINKEVRS IGGCDCSVDVTVCSPECARGRWTEAVSQVEAAV MAVPRTADODTSTDLEQVKGTNTEATALLESCTNTCLSTLDKQ TSTQTVETRTVAVGEGRKKINSTKTRSIGWTLLSKRGGFDR PSAVKTKESGYGGIN INDSTAURSIGNON LTETLESKRENTENSTENDENT	- 1		!	1	IFIGETI I CMM TITE TO THE LIBERT AND
AAFLGTAHLE 5415 693 2986 IPPKTKLELQKH\LTIT\NGGATIFEEVGKLEPRNEQRENEL ISPKRKLELGKKH\LTIT\NGGATIFEEVGKLEPRNEQRENEL ISPKRCLEBEKQKEHHIGEMGOTSGMAAENIGSELPSATKF RLDMLKNKAKRSLTSLES ILSRGNKARGLGHSISVDLDSSLS STLENTSKEPSVCEKEALPISESSFKLIGSSEDLSSDSSHLDE EPAPLSPOOAFRRANTLSHFFIECGE;POPARGSGSVGNKIM RYHSVSTETPHEKDFESKANHLGDSGGTPVKTRRISWRQOIFL RVATPQGACOSSSRYEDYSELPPRSPLEPVGEOPPGPPBE EKKRTSRELRELWGKAILQOILLLRMEKENGKLQASENDLINKR LKLDYEBITPCLKEVTTVWEKHSTPGRSKIKFDHEKMHSAVGQ GVP\RHHIGEIWKFLAEQFHLKRQFPSKQCPKOVPYKELLKGLT SQQHAILIDLGRTFPTHPYFSAQLGAGGLSINTIKAYSLLDOS VGICQGLSFVAGILLHMSEERMKLKEIMSGKAPVTMFLKGLT SQQHAILIDLGRTFPTHPYFSAQLGAGGLSINTIKAYSLLDOS VGICQGLSFVAGILLHMSEERMKLKEIMSGKRYPTMFLTMF ASGPFLGFVARVFDMIFLGGTEVFRVALSKLIGSKKPLILKQLT SQQHAILIDLGRTFPTHPYFSAQLGAGGLSINTIKAYSLLDOS VGICQGLSFVAGILLHMSERFKMLKEIMSMGKRCYRDM IILQIGMYGLSRLHHDYHRDLYNHLEBHIGPSLYAAPWFLTMF ASGPFLGFVARVFDMIFLGGTEVFRVALSKLIGSKKPLILQOL LETTVDFIKSTLPNLGLVGMEKTINOVFEMDIAKQLQAVEVEYH VLQEELIDSSPLSDNORMDKLEKTMSSIRKÖNLDLLEGLQVANG RIGSLEATIEKLLSSESKLKQMLTLELERSALGTVEELERRS AKPSDREPECTOPEPTGD 4074 KSQLFCFWGGKAGDILSGDOKEOKDPYFVETPYGYQLDLDFLK YVDDIQKGMTIKRLNIOKRKRSVDCPPRTTSGQQGIWTSTES LSSNSDNKQCPNFLIARSJCSTFPITNVSPMLOHTREGM ALKEKLESGVOCHNFLIARSJCSTFPITNVSPMLOHTREGM ATALKRLKELEBQVETTPVLOVKTSVLGEERGULVSGLKNORNA SGINVCGVKRSYSGNNSGLGNARRSGELYIDYEEEME TVEGSTORI KEFROL TADMQALECKIQDSSCASSELERNGEC RSVAVGABENNMDIVVYHRGSRSKCNDAAVGTLUEMRNCGVSVTE AMLGVMTEADKEIELQQTTISKKEKTYRLEVQLRETTHIBREMT KLKGELGAAGSRKVDKATMAQPLVFEKVVEAVVOTROMVGSH MDLUDTCVGTSVETNSVGISCOPECKNKVVGBLPHNWNITVKER VEMHBCCAGRSVEMCDKSVSVEVSVECTGSNTEESVNDLTLLKT NINKEVRS IGGCDCSVDVTVCCSPECKNKVVGBLPHNWNITVKER VEMHBCCAGRSVEMCDKSVSVEVSVECTGSNTEESVNDLTLLKT NINKEVRS IGGCDCSVDVTVCSPECARGRWTEAVSQVEAAV MAVPRTADODTSTDLEQVKGTNTEATALLESCTNTCLSTLDKQ TSTQTVETRTVAVGEGRKKINSTKTRSIGWTLLSKRGGFDR PSAVKTKESGYGGIN INDSTAURSIGNON LTETLESKRENTENSTENDENT			1	l	TETGET BESMINWALVADILLYVVI PTRRSTAEAFQIVLSHLLGD
1986 1PPKTKLELÇKH\LTTLT\NQEQATIFEEVQKLRPRNEQRENEL IISPLRCLFEEKQKEHLHIGEMKQTSQMAAENIGSELPPSATRF RLDMLKNKAKRSLTESIESITSKGMAAENIGSELPPSATRF RLDMLKNKAKRSLTESIESITSKGMAAENIGSELPPSATRF RLDMLKNKAKRSLTESIESITSKGMAAENIGSELPPSATRF RLDMLKNKAKRSLTESIESITSKGMAAENIGSELPPSATRF RLDMLKNKAKRSLTESIESITSKGMAAENIGSELPPSATRF RLDMLKNKAKRSLTESIESITSKGMAAENIQSELSDLSDESSHLDE EPAPLSPOQAFRRANTLSHFPIECQEPPGPAGSPSVSQRKLM RYHSVSTETPHEKKDFFSKAKHLGDSGGTVEVTRRIKSWRQOIFL RVATPQIACDSSRYEDYSELGELPPSPDLEVCEDGPGPPPE EKKRTSRELREHUWKALLQOILLLRMEKENQKAPAGOILLLRMEKENQKAPAGOILLLRMEKENQKARDHEN LKLDYEEITPCLKEVITVWEKMLSTPGRSKIKFDMEKHSAVGQ GVEVRHURGEIWKFLAEQFHLKHQFFSKQPKDVEYVELLKQLT SQUHALLIDIGRTFPTHPYFSAQLGAGQUSIVNILKAYSLDDGE VGYCQGISFVAGILLHMSEEBEAFKMLKFLMEDMELRKQYRDDM IILQIGMYQUSRILHDYHRDINLEEHEIGESLYAAPWFLIMF ASQPFLGFVARVEDMIFLQGTEVIFKVALSLIGSHKPLILQHEN LETIVDFIKSTLPNLGLVQMERTINQVFFMDLAKGLQAYEVEYH VLQEELIDSSPLSDMRRMDKLEKTMSSLRKQNLDLLEGLQVANG RIQSLEATIEKLLSSESKKQAMLTLELERSALLQTVEELRRS AKPSDREPECTOPPEPTGD 5416 27 4074 KSQLFCFWGKAGDLISGDODKEQNDFYFVETPYGYQLDDFLK YVDDICKGMTIKKUCFPRITSGQGIMTSTES LSSNSDDNKQCPNLIARSQVTSTPISKPPPPLETSIPPLITIP ENNQLPPPSPQLPKINLHVTKILMETRRILEGEATMOMTPGGF RPRRLASFGGMGTTSSLBSFVGNHPDAKIQLOMGYQGMGDVG SYAPAAPTTSSMGSIRISPLSSGISTPVTNVSPMHLQHIREOM AIALKRLKELEEQVRTIPVLQVKISVLGEKROLVSQLKNGRAA SQINVCGYKRSYSAGNSGLEOLSRARRSGGIIYIDYEEEME TVEGSTGRIKEFGELYDIQUKKSTLOGSCCRASSLRENGEC RSVAVGAEENNMDIVVHRGSRCKDAWGTLVEMRNCGVSVTE AMLGWMTEADKEIELQQCTIESLKEKIYRLEVQLRETTHDREMT KLKQELQAAGSRKKVDKAATMAQPLVESKVVEAVQTLEMRNCGVSVTE AMLGWTEADAGRIKKOURATARQPLVESKEVAVEAVQTRDAMVGSH MDLVDTCVGTSVETNSVGISCQFCKNKVVGPQLTPDMVGSH MDLVDTCVGTSVETNSVGISCQFCKNKVVGPQLTPDMVGSH MDLVDTCVGTSVETNSVGISCQFCKNKVVGPQLTPDMVGSH VEMPCAGRSVEMCDKSVSVEVSVCETGSNTESSVNDLILLKT NINLKEWRS IGGGCSDDVTCHRATTLESCTNTCLSTLDKQ TSTOTVETRTVAVGGGRVKDINSSTKTRSIGWTTLASGGGPDR PSAVKTRESGVGQIINDMNUTLARGRINGDHYIERIOKLLARGG			f	ĺ	AGSETHIGHTSDRERRNWPPSFLSEFRALOFSIM-CAPICAL CO
1 IPPKTKLEJOKH\LITUT\NOEOATI FEVOKLEFRNEQRENEL 1 ISPLRCLIFEEKOKEHHIIGEKOTSOMAAENIGSELPFSATEF RLDMLKNKAKRSLTESLES ILSKONKARGLORIS ISVUDLOSSIS STLSTIKEFSVEKERALPISESS FILIGSSEDLSSISSISHIPE EPAPLSPOOAFERRANTLSHFFIECOE POPAGSGOTOSORILM RYHSVSTETPHERKDFSKANHLGDSGGTPVKTRRHSWRQOIFL RVAMPOKACOSSSRYEDVSSELGEIPPRSPLEVVCEGGFEPPPE EKKTSRELRELWOKAILQOILLLRMEKENOKIQASENDLINKR LKLDYEEITPCLKEVTTVMEKMISTEGRSKIKFDMEKMHSANGQ GVP\RHRIGEIMKFLAEOFIRKPFSKORDVPYKELLKOLT SQOHALLIDLGFTFPTHPYFSAQLGRGQISLYNILKATSLIDQE VGYCQCLISFVAGILLHMSEEBAFKMLKEIMFDMELRGYRPDM 1ILQIGMYQLSRILHDYHRDLNHLEEHBIGISLYAAPWEITIMF ASGPFLIGFVARVEDMIFLQGTEVIFKVALSLLGSHKPLILCHEN 1ILQIGMYQLSRILHDYHRDLNHLEEHBIGISLYAAPWEITIMF ASGPFLIGFVARVEDMIFLGGTEVIFKVALSLLGSHKPLILCHEN LETIVDFIKSTIENLGLVOMETINOVFFBMLJKGLOAVEVEYH VLQEELIDSSPLSDNGRMCKLEKTNSSLRKONLDLLEQLGVANG RIOSLEATIEKLLSSESKIKQAMLTLEEBRSALLQTVEETRRR AKPSDREPECTOPEPTGD 5416 27 4074 KSQLFCFWGGKAGDLISGDODKEOKDPYFVETPVGYQLDLDFLK YVDDICKGMTIKKLINICKREKPSVPCPPPRTTSGQQGIWTSTES LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPDLETSLPFLTIP ENROLPPPSPQLPKINLHVTKILMERRELEGERATMOMTPGGF RRPRLASFGGMGTTSSLPSFVGSONHPPAKIGLONGYGGNGDYG SYAPAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIRBOM ATALKRIKELBENGVTIFPULVSTVIFVGEKRRULVSQLKNORNA SQINVCGYRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEME TVEQSTORIKEFROL\TAMMQALBCKTODSSCEASSELEENGEC RSVANGAEENNNDIVVYHRGSRCKDANGGTLVSQVTVE AMLGVMTEADKEIELOOTIESLKEKTYRLEVOLRETTHDREMT KLKQELQAAGSKKVDKATMAQDVLYSVIEWENGCGVSVTVE AMLGVMTEADKEIELOOTIESLKEKTYRLEVOLRETTHDREMT KLKQELQAAGSKKVDKATMAQDVLYSVERSCKCDRAVGTLVKROM VEMHDRCAGRSVENCDKSVSVEVSVCETSINTESSVNDLTLLKT NLNKLEVRS ISCGCSVDVTVSPCEFCSNTEVSTESVNDLTLLKT NLNKLEVRS ISCGCSVDVTVSPCEFCSNTESSVNDLTLLKAT NLNKLEVRS ISCGCSVDVTVSPCEFCSNTESSVNDLTLLKAT NLNKLEVRS ISCGCSCDVTVTVSPKETSIGWTTLISCTNTCLSTLDKO TSTGTVETRTVAVGGGRVKDINSSTKTRS IGVGTLLSGRGGDR PSAVKTKESGVGGININDNYLVCKNRTIACGPOLTVCLITASR RSVCVGDDPVGSSLENDPQADAGMMIGDHYTERIOKLAROG TLLAEMYSELAEAFGPBHSGMSMINSOLLSTERISMVANG EN	ŀ	E41E			1 Mari DO I MILIM
RLDMLKNRAKRSLTESLESILSRGKARACIQHSISYDJDASLS STLSNTSKEPSVCEKEALPISSESSKLLGSSEDLSDASSESHLPE BPAPLSPOOAPRRRANTLSFPIECCEPPOPARGSPCVSQRKIM RYHSVSTETPHERKIPFEKANHLGDSGGTPVKTRHSWRQOIFL RVATPOKACDSSRYEDVSELGELPPRSPLEFVCDCPPGPPPE EKRRTSREIRELWCKALIGLILLERMEKENOKLOASENDLLINKR LKLDYBEITPCLKEVTTVWEKMLSTPGRSKIKFDMEKMHSAVGQ GVP\RHINGERIWKFLAEDGLILLHRMEKENFOKLOASENDLLINKR LKLDYBEITPCLKEVTTVWEKMLSTPGRSKIKFDMEKMHSAVGQ GVP\RHINGERIWKFLAEDGLINKHGPPSKQOPKDVPYKELLKOLT SOOHALLIDLGRTFPTHPYFSAQLGAGGLSLYNILKAYSLLDGS VGYCQGLSFVAGILLHMSEEBAFKMLKFLMFDMGLRKOYRPDM IILCIOMYOLSRLHDVHRIEBEIGFSLYAAPWFLTMF ASGPPLGFVARVFPMIFLQGTEVIFKVALSLLGSHKPLILQHEN LETTVDFIKSTLPNLGLVOKKTINQVFEMDIJAKQLQAYEVEYH VLQEELIDSSPLSDNQRMDKLEKTNSLSKKONDLLEDLQVANG RIQSLEATIEKLISSESKLKQAMLTLELERSALLQTVEELRRS AKPSDREPECTQPEPTGD **SQLFFFWGGKAGDILSGDQDKEOKDPFYFETPYGYQLDLDFLK* YVDDIQKGMTIKKLINQKRKSVPVPCPEPRTTSGQGGIWTSTES* LSSSMSDDNKQCPNFLIARSQVTSTEISKPPPPLETSLPFLTIP ENRQLPPPSPGLEKHNLHVYKTLMETRRLEGBRATMOMTPGBF RRPRLASFGGMGTTSSLDSFVGSGNINPARHOLONGYGGMDYG SYAPAAPTTSSMGSSIKHSPLSSGISTPYTNVSPMHLQHIRBQM AIALKRLKELBEQVRTIPLVKISVLOEKRGLUSOLKNORAA SQINVCGVRKRSYSAGNASQLEOLSRARRSGGELYIDVEBEME TVEGSTGRIKGERGVTANDVKISVLOEKRGLUSOLKNORAA SQINVCGVRKRSYSAGNASQLEOLSRARRSGGELYIDVEBEME TVEGSTGRIKGERGVTANGVASVESVLOEKRGLYDDEREME TVEGSTGRIKGERGVTANGVASVESVLOEKRGUTDENGVSH MLKGELQAAGSKKVUKATMAQPYSKVVEAVVGTRDGMVGSH MLKGELQAAGSKKVUKATMAQPYSKVVEAVVGTRDGMVGSH MDLVDTCVGTSVETNSVGISCPPECKNKVVGFELPHNIMIVKER VEMHBRCAGRSVEMCDKSVSVESVCETGSNTEESVINDLTLLKT NLNLKEVRS IGGGGCSVDVTSVSFKCCARGGWTEAVSQVEAAV MAVPRTADQDTSTDLEOVHQPTNTETATLIESCTNTCLSTLDKQ TSTGTVETRTVAVGBGRVENDINSSTKRSIGGGTLLSGHSGFDR PSAVKTRESGVGIN INDNIVIVGLKMRTIACCPPPQLTVGLTASR RSVEVGDDPVESSLENPQPQAPLGMMTSLDHYIGRICKLADGQQ TLLLENYSELLBARGGERGUND INSTITUSISCSTLIAGSHSGFDR RSVEVGDDPVESSLENPQPQAPLGMMTSLDHYIGRICKLADGQQ TLLLENYSELLBARGGERGUNGDNINGOLLGTASR	ļ	2472	693	2986	IPPKTKLELOKH\ LTTLT\ NODODOTT
RLDMLKNRAKRSLTESLESILSRGKARACIQHSISYDJDASLS STLSNTSKEPSVCEKEALPISSESSKLLGSSEDLSDASSESHLPE BPAPLSPOOAPRRRANTLSFPIECCEPPOPARGSPCVSQRKIM RYHSVSTETPHERKIPFEKANHLGDSGGTPVKTRHSWRQOIFL RVATPOKACDSSRYEDVSELGELPPRSPLEFVCDCPPGPPPE EKRRTSREIRELWCKALIGLILLERMEKENOKLOASENDLLINKR LKLDYBEITPCLKEVTTVWEKMLSTPGRSKIKFDMEKMHSAVGQ GVP\RHINGERIWKFLAEDGLILLHRMEKENFOKLOASENDLLINKR LKLDYBEITPCLKEVTTVWEKMLSTPGRSKIKFDMEKMHSAVGQ GVP\RHINGERIWKFLAEDGLINKHGPPSKQOPKDVPYKELLKOLT SOOHALLIDLGRTFPTHPYFSAQLGAGGLSLYNILKAYSLLDGS VGYCQGLSFVAGILLHMSEEBAFKMLKFLMFDMGLRKOYRPDM IILCIOMYOLSRLHDVHRIEBEIGFSLYAAPWFLTMF ASGPPLGFVARVFPMIFLQGTEVIFKVALSLLGSHKPLILQHEN LETTVDFIKSTLPNLGLVOKKTINQVFEMDIJAKQLQAYEVEYH VLQEELIDSSPLSDNQRMDKLEKTNSLSKKONDLLEDLQVANG RIQSLEATIEKLISSESKLKQAMLTLELERSALLQTVEELRRS AKPSDREPECTQPEPTGD **SQLFFFWGGKAGDILSGDQDKEOKDPFYFETPYGYQLDLDFLK* YVDDIQKGMTIKKLINQKRKSVPVPCPEPRTTSGQGGIWTSTES* LSSSMSDDNKQCPNFLIARSQVTSTEISKPPPPLETSLPFLTIP ENRQLPPPSPGLEKHNLHVYKTLMETRRLEGBRATMOMTPGBF RRPRLASFGGMGTTSSLDSFVGSGNINPARHOLONGYGGMDYG SYAPAAPTTSSMGSSIKHSPLSSGISTPYTNVSPMHLQHIRBQM AIALKRLKELBEQVRTIPLVKISVLOEKRGLUSOLKNORAA SQINVCGVRKRSYSAGNASQLEOLSRARRSGGELYIDVEBEME TVEGSTGRIKGERGVTANDVKISVLOEKRGLUSOLKNORAA SQINVCGVRKRSYSAGNASQLEOLSRARRSGGELYIDVEBEME TVEGSTGRIKGERGVTANGVASVESVLOEKRGLYDDEREME TVEGSTGRIKGERGVTANGVASVESVLOEKRGUTDENGVSH MLKGELQAAGSKKVUKATMAQPYSKVVEAVVGTRDGMVGSH MLKGELQAAGSKKVUKATMAQPYSKVVEAVVGTRDGMVGSH MDLVDTCVGTSVETNSVGISCPPECKNKVVGFELPHNIMIVKER VEMHBRCAGRSVEMCDKSVSVESVCETGSNTEESVINDLTLLKT NLNLKEVRS IGGGGCSVDVTSVSFKCCARGGWTEAVSQVEAAV MAVPRTADQDTSTDLEOVHQPTNTETATLIESCTNTCLSTLDKQ TSTGTVETRTVAVGBGRVENDINSSTKRSIGGGTLLSGHSGFDR PSAVKTRESGVGIN INDNIVIVGLKMRTIACCPPPQLTVGLTASR RSVEVGDDPVESSLENPQPQAPLGMMTSLDHYIGRICKLADGQQ TLLLENYSELLBARGGERGUND INSTITUSISCSTLIAGSHSGFDR RSVEVGDDPVESSLENPQPQAPLGMMTSLDHYIGRICKLADGQQ TLLLENYSELLBARGGERGUNGDNINGOLLGTASR	- 1		1	ļ	TICKL BOLDERY OF THE WOLLD THE EVOKER PRINE OR ENEL
STLSMTSKEPSVCEKEALPISSSTKLIGSSDLSSDSSHLPE EPAPLSPOOAFRRRANTLSHFPIECOEPPOPARGSPCVSQRKLM RYHSVSTETPHERKIPFESKANHLGOSGGTPVKTRHSWRQOIFL RVATPOKACDSSRYEDYSELGELPPRSPLEVCEOFPGPPPE EKRATSELRELWQKALLQOILLIMMERENQKLOASENDLLMKR LKLDYEBITPCLKEVTTVWEKMLSTPGRSKIKFDMERMHSAVGQ GVP\RHHRGETWKFLAEOFHLKHOFPSKQOPKDVPYKELLKOLT SQOMAILIDLGRTFPTHPYFSAGLAGGLSIYNILKAYSLLDOE VGYCQUSFVAGILLIMMSEEBAFKMLKFLMEDWGLRKOYAPDM IILQIOMYOLSRLHDVHRDLVINHLEBHEIGPSLYAAPWFLTMF ASGPFLGFVARVFDMIFLOFUTYFKVALSLLGSHKPLHLIQHEN LETIVDPIKSTLPNLGLVQMEKTINQVFEMDIAKOLQAYEVEYH VLQEELIDSSPLSDNORMDKLEKTNSSLRKONLDLEDLQVANG RIQSLEATIEKLLSSESKLAQAMLTELERSALLQTVEELRRS AKPSDREPECTQPEPTGD KSQLFCFWGGKAGDILSGQODKECKDFYFVETFYGYQLDLDFLK YVDDIQKGNTIKRLNIQKRKKPSVPCPEPPRTTSGQGGIWTSTES LSSSNSDDNKQCNNFILARSQVTSTPISKPPPLETSLPPLTTIP ENROLPPSSFOLFKHLHVYKTLMETRRILGERATMOMTFGEF RRPRLASFGGMGTTSSLPSFVGSGNNNPAKHQLONGYQGNGDVG SYAPAAPTTSSMGSSIRTBPLSSGISTPVTNNSPMHLQHIRBOM ATALKRLKELEEQVRTIPULOVKISVLOEEKRQLVSGLKNORAA SQINVCGVRKSYSAGNASOLEOLSRARRSGGELYIDYEEEME TVEGSTORIKEFROLVTAMQALEGKRIDDSCEASSELRENGEC RSVAVGAEENMNDIVVTHAGSRSCKDAAVGTLVENENCUSVTE ANLGWMEADKEIELOQOTIESLKERIYLLEVQLRETTHDREMT KLKGELQAAGSKKVDKATMAQPLUFSKVVEAVLTURQWSH MDLUDTCVGTSVETNSVGISCQPECKNKVVGFELEMNWIVKER VEMHDRCAGRSVEMCDKSVSVEYSVVETGSNTEESVNDLTLLKT NLNLKEVRSIGGGCSVDVTVCSPKECASRGVNTEAVSQVEAAV MAVPRTADQDTSTDLEOVHQPTNTETATLIESCTNTCLSTLDKQ TSTGTVETRTVAVGEGRGVKDINSSTKRSIGGTLLSGHSGFDR PSAVXTKESGVGUNINDNIVLOLKMRTIAGCEPPQLTVGLTASR RSVEVGODPVESSLENPQPQAPLGMMTLDCHTRICKLLADOQ TLLAENSELAEAFGEPELSGRINGSLINGOLUSTISSTENDELTAR	- 1]		TAGE DROLLE ADRONDHIHLIGEMKOTSOMANENICEEL DROLLED
BPALSPOQAFRRANTICSHFPIECOEP PODRAGESPGYSORKLM RYHSUSTETPHERKIPESKANHLIGDSGGTPVKTRRHSWRQDIFL RVATPOKACDSSRYEDYSELGELPPRSPLEPVCEOGPFGPPDE EKKRTSRELRELWQKALLQQILLLRWEKENOKLQASENDLLNKR LKLDYEEITPCLKEVTTVWEKMLSTFGRSKIKFDMEKMHSAVGQ GVPVRHINGEIWKFLAGEPHLKHQFPSKQQPKDVPYKELLKOLT SQQHAILIDLGRTFFTHPYFSAOLGAGQLSLYNILKAYSLLDOZ VGYCQGLSFVAGILLLHMSEEBAFKMLKFLMFDMGLRKOVRPDM IILQIOMYQLSRLLHDVJHRDLNHLBEHEIGPSLYAAPWFLMF ASGPPLGFVARVFDMIFLQGTEVIFKVALSLLGSHKPLLIQHEN LEFIVDFIKSTLPNLGLUVQMEKTINGVFEMDINKOLQAYEVEYH VLQEELIDSSPLSNNGMDKLEKTMSSLRKONLDLLEGLQVANG RIQSLEATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRRR AKPSDREPBECTOPEPTGD KSQLFCFWGGKAGDILSGDQDKEOKDPYFVETPYGYQLDLDFLK YVDDIQKGNTIKRLNIQKRRRPSVPCPPBPRTTSGQQGIWTSTES LSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLFFLTIP ENRQLPPPSPQLPKHNLHVTKTLMETRRLEGERATMOMTFGEP RAPRLASFGGMGTTSSLPSFVGSONHNPAKHQLQNGYQGNGDYG SVAPAAPTTSSMGSS RHSPLSSGISTPVTNVSPMHLQHIRRQM AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNORAA SQINVCGVRKRSYSAGNASOLEQLSRARRSGGELYIDTEEEME TVEGSTQR KEFROLL/TADMOALBOKIQDSCEASSELRENGEC RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVERNCGVSVTE AMLGVMTEADKEIELQOQTIESLKEKTYRLEVOLRETTHDREMT KLKGELQAAGSRKKUVRAAIMAQPLVFESKVVBAVVGTRDDMVGSH MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWIVKER VEMBDCAGGRSVEMCDKSVSVEVVENVGTNETESVUDLITLIKT NLINLKEVRSIGCGDCSVDVIVCSPKECASRGVNTEAVSQVERAAV MAVPRTADODTSTDLEOVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETTRVAVGGGRCVDINSSKTKTRSIGVGTLLSGHSGFDR PSAVXTKESGVGQININDNYLVGLKMRTIACGSPDCLTVGLTASR RSVGVGDDPVGSSLENPQPQAPLIGMMTGLDHYTERIQKLLAEQO TLLLAENSELBLAEAFGEPHSOMSSLNSOLL STLASTRENDELSC	I		1		(ALDRIDAN ANASTITESTES I I SECURA SCI OPUCTOURING SON S
RYHSVSTEPHERKIPESKANHLGDSGTPVKTRHSWRQOIFL RVATPQKACDSSSRYEDYSELGELPPRSPLEPVCEDGPFGPPPE EKKRTSRELRELWQKAILQQILLERMEKENGALQASENDLINKR LKLDYEEITPCLKEVTTVWEKMLSTEGRSKIKFDMEKMHSAVGQ GVP\RHHRGETWKFLAEQFHLKHQFPSKQDYBDVPYKELLKOLT SQQHAILIDLGRTFPTPYFSAQLGAGQLSLYNILKAYSLDQE VGYCQGLSPVAGILLLHMSEEBAFKMLKFLMFDMGLRKQVRPDM IILQIQMYQLSRLHDYHRLUPHLEHEIGPSLYAAPWFLTMF ASGPFLGFVARVFMIFTQGTEVIFFVALSLLGSHKPLILQHEN LETTVDFIKSTLPNLGLVQMEKTINQVFEMDLAKQLQAYEVETH VLQEELIDSSPLSDNQRMDKLEKTNSSLKKQNLDLLEQLQVANG RIQSLEATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRRS AKESDREPECTQPPPTGD \$4074 KSQLFCFWGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLK YVDDIQKGNTIKRLNIQKRRKPSVPCPFFRTTSQQGINTSTES LSSSNSDDNKQCNFFLLARSQVTSTFFISKPPPPLETSLPFLTIP ENNQLPPPSFQLFKRHLHVTKTLMETRRLEGERARMQMTPGEP RRPRLASFGGMGTTSSLDSFVGSGNHNPAKHQLQNGYGGNGDYG SVAPAAPTTSSMGSSIRHSPLSSGISTFVTNVSPHHLGHIRBQM AIALKRLKELEBQVRTIPVLQVKISVLQEEKRQLVSQLKNORAA SQINVCGVRKRSYSAGNASGLEOLSRARRSGGELYIDYEEEME TVEQSTOR IKEFRQL\TAMQALEQKIQDSSCEASSELRENGEC RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMNCGVSVTE AMLGVMTEADKEIELQQQTIESLKKIYTRLEVGLRETHDREMT KLKGELQAASRKKVURAAMQPLVFEKVVEAVVQTRDQMVGSH MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMWWIVKER VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTESVUDLTLLKT NLNKEVRSIGGGDCSVDTVCSPKECASRGNTEENVDLTLLKT NLNKEVRSIGGGGCSVDTVCSPKECASRGNTEENVGDLYKGRA MAVPRTADQDTSTDLEOVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETTVAVGRGGRVKDINSSTKRSIGVGTLLSGHSGFDR PSAVXTKESGVQQININDNYLVGLKMRTIACGSPDCLTVGLTASR RSVGVGDDPVGSSLENPQPQAPLIGMMTGLDHYTERIQKLLAEQO TLLAENSELLAEAGGEPHSMOMSLNSOLL STLASTRENDELSC	- 1		į į		STLSNTSKEPSVCEKEALPISESSPYLLCSSPDLCSPD
RVATPQKACDSSSPLENELDYSELGELDYBRSPLEPUCEDGPGPPPE EKKRTSRELRELWQKAILQQILLLRMEKENQKLQASENDLINKR LKLDYEEITPCLKEVTTVEKMGTTPGRSKIKFDMERMHSAVGQ GVP\RHHRGEIMKFLAEQFHLKHGFPSRSKIKFDMERMHSAVGQ GVP\RHHRGEIMKFLAEQFHLKHGFPSRSKIKFDMERMHSAVGQ GVP\RHHRGEIMKFLAEQFHLKHGFPSRKQVREDVPKELLKOLT SQOHAILIDLGRTFPTHPYFSAQLGAGQLSLYNILKAYSLLDGE VGYCQGLSPVAGILLHDYHRDLYNHLBEHEIGESLYAAPWFLTMF ASGPPLGFVARVFDMIFLQGTEVIFKVALISLGSHKPLILQHEN LETTVDPIKSTI.PNIZLQMEKTINQVFEMDIAKQIQAYEVEYH VLQEELLDSSPLSDNQRMDKLEKTNSSLRKCMLDLLEQLQVANG RIQSLEATIERLLSSESKLKQAMLTLELERSALLQTVEELRRRS AKPSDREPECTOPEPTGD SQLFCFWGGKAGDILSGDQDKEQKDFYFVETPYGYQLDLDFLK YVDDLQKGNTIKKLNIQKKRKRSVPCPEPRTTSGQGIMTSTES LSSSNSDDNKQCPWFLIARSQVTSTISKPPPLETSLPFLTIP ENRQLPPPSPQLPKHNLHVTKTLMETRRLEQERATMCMTPGEF RRPRLASFGGMGTTSSLDSFVGSNENPAKRQLONGYQGNGDYG SXAPAAPTTSSMGSSIRHSPLSSGISTPYTNVSPMHLOHIRBOM ATALKRIKELEEGQVRTIPVLQVKISVLQEEKRQLVSQLKNORAA SQINVCGVRKRSYSAGNASQLEQLSSCERSSELRENGEC RSVAVGAEEMMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMT KLKQELQAAGSRKVDKATMAQPLVFSKVVEAVVOTRDQMUSSH MDLVDTCVGTSVETNSVGISCOPECKNKVVGPELPMNWIVKER VEMHBRCAGRSVEMCDKSVSVEVSVCETGSNTTESVMDLTLLKT NLNLKEVRSIGCGDCSVDVTVCSFKECASRGWMTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTGTVETTTVAUGRGRKVDINSSTKTRSIGVGTLLSGHGFDR PSAVXTKESGVGQININDNIVGLKKMTIACGPPQLTVGLTASR RSVGVGDDFVGSSLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ TLLAENYSELABAFQEPHSOMGSLMSOLISTISSTRUMMS	- 1		1		EPAPLSPOOAEPPRANTE CHIEFE
RVATPQKACDSSSPLENELDYSELGELDYBRSPLEPUCEDGPGPPPE EKKRTSRELRELWQKAILQQILLLRMEKENQKLQASENDLINKR LKLDYEEITPCLKEVTTVEKMGTTPGRSKIKFDMERMHSAVGQ GVP\RHHRGEIMKFLAEQFHLKHGPFSKQVRKDYKELLKQLT SQOHAILIDLGRTFPTHPYFSAQLGAGQLSLYNILKAYSLLDQE VGYCQGLSPVAGILLHMYHEBEHEIGESLYAAPWFLTMF ASQPPLGFVARVFDMIFLQGTEVIFKVALSLIGSHKPLILQHEN LETTVDPIKSTLPNLQUMEKTINQVFEMDIAKQLQAYEVEYH VLQEELLDSSPLSDNQRMDKLEKTNSSLRKCMLDLLEQLQVANG RIQSLEATIERLLSSESKLKQAMLTLELERSALLQTVEELRRRS AKPSDREPECTOPEPTGD SQLFCFWGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLK YVDDLQKGNTIKKLNIQKKRKRSVPCPEPRTTSGQGIMTSTES LSSSNSDDNKQCPMFLIARSQVTSTISKPPPLETSLPFLTIP ENRQLPPPSPQLPKHNLHVTKTLMETRRLEQERATMCMTPGEF RRPRLASFGGMGTTSSLDSFVGSNENPAKRQLONGYQGNGDYG SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLOHIRBOM AIALKRLKELEGQVRTIPVLQVKISVLQEEKRQLVSQLKNORAA SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEME TVEGSTQRIKEFRGL\TADMGALEGKQDSSCEASSELRENGEC RSVAVGAEEMMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMT KLKQELQAAGSRKVDKATMAQPLVFSKVVEAVVOTRDQMVGSH MDLVDTCVGTSVETNSVGISCOPECKNKVVGPELPMNWIVKER VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTTESVMDLTLLKT NLNLKEVRSIGGGDSVDVTVCSFKECASRGWMTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTGTVETTTVAUGRGRKVDINSSTKTRSIGVGTLLSGHGFDR PSAVXTKESGVGQININDNIVGLKKMTIACGPQOTVGLTASR RSVGVGDDFVGSSLENDPQPQAPLGMMTGLDHYIERIQKLLAEQQ TLLAENYSELABAFGEPHSOMGSLMSOLISTISSINGHLAEQ	- 1		1		PYLICUSTRANCE OF PLECOEPPOPARGSPGVSQRKLM
EKKRTSELRELWGKAILQOILLIRMEKENQKLQASENDLINKR LKLDYEEITPCLKEVTTVWEKMLSTPGRSKIKFDMEKMHSAVGQ GVP\RHRGEIWKFLAECPHIKHGFPSKQPKDVPYKELLKOLT SQOHAILIDLGRIFFPHPYFSAQLGAGQLSLVNILKAYSLLDQE VGYCQGLSFVAGILLIHMSEEEAFKMLKFLMFDMGLKGYRPDM IILQIQMYQLSRLLHDYHRDLYHHLEBEEIGPSLYAAPWFLTMF ASGPPLGFVARVFDMFFLQGTEVIFKVALSLIGSHKPLILQHEN LETIVDFIKSTLPNLGLVQMEKTINQVFEMDIAKQLQAVEVEYH VLQEELIDSSPLSDNQRMDKLEKTNSSLRKGNLDLLEQLQVANG RIQSLEATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRS AKPSDREPECTQPEPTGD S416 27 4074 KSQLFCFWGGKAGDILSGDODKEOKDPYFVETPYGYQLDLDFLK YVDDIQKGNTIKRLNIQKRRKPSVPCPEPRTTSGQQGIWTSTES LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTIP ENRQLPPPSPQLPKHNLHVTKIMETRRLEGERATMOMTPGFF RRPRLASFGGMGTTSSLPSFVGSGNINPAKHQLQNGYQGNGDYG SXAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIRRQM AIALKRLKELEEQVRTIPVLOVKISVLQEEKRQLVSOLKNORAA SQINVCGVRKRSYSAGNSGLEQLSRARRSGGELYIDYEEEME TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEC RSVAVGAEENMNDIVVYHRGSRSCKDAVGTLVEMRNGGVSVTE AMLGVMTEADKEISLQOQTISSLKEKIYRLEVQLRETTHDREMT KLKGELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTEDQWGSH MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMWWIVKER VEMHBRCAGRSVEMCDSSVEVESVECTGSNTESSVNDLTLLKT NLNLKEVRSIGCGDCSVDVTVCSPKECASRGWNTEAVSQVEAAV MAVPRTADQDTSTDLECVHOPTNTETATLIESCTNTCLSTLDKQ TSTQTVETTTVAVGRGKVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPPQPQAPLGMMTGLDHYIERIOKLLAEQQ TLLAENVSELABAFGEPHSOMGSLNSOLISTISSTRENMENE	- 1		1		TATAS VOLET PREKKIJE ESKANHI GDGGGTDWTDDUGWDGGTD
LKLDYBEITPCLERVITUMEKNISTEGRSKIRFDMEKMHSAVEQ GVPQRHHRGEIWFLAEGFHLKHQFPSKQQPKDVPYKELLKOLT SQQHAILIDLGRTFPFHYFSAQLGAGQLSLYNILKAYSLLDQE VGYCQGLSFVAGILLLHMSEEBERKMLKFLMFDMGLKRQYRPDM IILQIQMYQLSRLLHDWHRDLVNHLEEHEIGPSLYAAPWFLIMF ASGPPLGFVARVFDMIFLQGTEVIFKVALSLLGSHKKPLILQHEN LETIVDFIKSTLPNLGLVQMEKTINQVFEMDIAKQLQAVEVEYH VLQEELLDSSPLSDNQRMDKLEKTMSSLRKONLDLLEQLQVANG RIGSLEATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRS AKPSDREPECTOPEPTGD 5416 27 4074 KSQLFCFWGGRAGDILSGDDKEOKDPYFVETPYGYQLDLDFLK YVDDIOKGNTIKRLNIGKRKKPSVPCPEPFRTTSGQQGIWTSTES LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPLETSLPFLTIP ENRQLPPPSPQLPKHNLHVYKTLMETRRRLEQERATMQMTPGEF RRPLASFGGMGTSSLSPSFVGSGNHNPAKHQLQNGYQGNGDYG SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIRBQM AIALKRLKELEEQVRTIPVLQVKISVLQBEKRQLVSQLKNORAA SQINVCGVKRKSYSANSOLEQLSRARRSGELYIDYEEEME TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEC RSVAVGAEEMMNDIVVYHRGSRSCKDAAVGTLVEMRNGGVSVTE AMLGVMTEANKEILQQQTIESLKEKIYRLEVQLRETTHDREMT KLKQELQAAGSRKKVDKATMAQPLVFSKVVGFELPMNWHIVKER VEMHSRCAGRSVEMOKSUSVEVSVCETGSNTEESVNDLTILLKT NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFINTETATLIESCTNTCLSTLDKQ TSTQTVETRTVAVGEGRVKDINSSTKRSIGVGTLLSGHSGFDR PSAVXTKESGVGQININDNYLVGLKWRTIACGSPPQLITVGLTAGR RSVGCDDPVGESLENDQPQAPLGMMTGLDHYIERIQKLLAEQQ TLLAENYSELAEAFGEPHSOMSLUNGLISSLESDNEHMARD	- [i . i		1 ************************************
GVP\RHRRGEIWKPLAEOFHLKHQFPSKQQPKDVPYKELLKOLT SQOHAILIDLGRTFPTHPYFSAQLGAGQLSLYNILKAYSLLDQE VGYCQGLSFVAGILLHMSEEBAFKMLKFLMFDMGLRKQYRPDM IILQIQMYQLSRILDHMSEEBAFKMLKFLMFDMGLRKQYRPDM IILQIQMYQLSRILDHRJERDHYNLBEHEIGPSLYAAPWFLTMF ASQPPLGFVARVFDMIFLQGTEVIFKVALSLLGSHKPLILQHEN LETIVDFIKSTLFNLGLVQMKTINQVFEMDIAKQLQAVEVEYH VLQEELIDSSPLSDNQRMDKLEKTNSSLRKONLDLLEQLQVANG RIQSLEATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRRS AKPSDREPECTQFEPTGD KSQLFCFWGKKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLK YVDDIQKGNTIKRLNIQKRRKPSVPCPFPRTTSGQQGIWTSTES LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPDFETSLPFLTIP ENRQLPPSPSQLPKSYSSGNHPARHQLQNGYYGRNDYG SYAPAAPTTSSMGSSIRHBFLSSGISTPYTNVSPMHLQHIRBQM ATALKRLKELEEQVFIIVLQVKISVLQEEKRQLVSOLKNQRAA SQINVCGVRKRSYSSGNASQLEGLSRARRSGGELY1DYEEEBME TVEQSTQRIKEFROL\TAMQALEQKIQDSSCEASSELRENGEC RSVAVAAEEMMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE AMLGVMTEADKEIELQQOTIESLKEKTYRLEVQLRETHDREMT KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSH MDLVDTCVGTSVETNSVGISCQPECKNKVVGFELPMNWTIVKER VEMHDRCAGRSVENCOKSVSVESVSVETGSNTEESVNDLTLLKT NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV MAVPRTADQDTSTDLEOVHQFINTETATLIESCTNTCLSTLDKQ TSTQTVETRTVAVGEGRVKDINSTTRTSIGVGTLLSGHSGFDE PSAVXTKESGVQDININDNYLVGLKMRTIACGPPQLITVGLTASR RSVGVGDDPVGSSLENDEQPQARIGMMTGLDHYIERIQKLLAEQQ TLLAENYSELAEAFGEPHSOMGSLUNGLISCSNDEWNCR	- 1				EKKRTSRELRELWOKATLOOTLIT BMEKENOKT OF CHESTFOFFE
SQHAILIDIGERTPTHYFSAQLGAGQLSLYNILKQLT SQHAILIDIGERTPTHYFSAQLGAGQLSLYNILKQLT VGYCQGLSFVAGILLHMSEEEAFKMLKFLMFDMGLRKQYRPDM IILQIQMYQLSRLHHDYHRDLYMHLBEHBIGBSLYAAPWFLTMF ASQPPLGFVARYPDMIFLQGTEVIFKVALSLLGSHKPLILQHEN LETIVDFIKSTLPNLGLVQMEKTINQVFEMDIAKQLQAYEVEYH VLQEELIDSSPLSDNQRMDKLEKTNSSLRKQNLDLLEQLQVANG RIQSLEATIEKLLSSESKLKQAMLTLEDERSALLQTVEELRRRS AKPSDREPECTQPEPTGD SQLPCFWGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLK YVDDIQKGNTIKRLNIQKRRKPSVPCPEPRTTSGQQGIWTSTES LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTIP ENRQLPPPSPQLPKHNLHVTKTLMETRRRLEGERATMQMTPGEF RRPRLASFGGMCTTSSLPSFVGSGNINPAKHQLQNGYQGNGDYG SVAPAAPTTSSNGSSIRHSPLSSGISTPVTNVSPMHLQHIREQM AIALKRLKELEEQVRTIPVLQVKISVLQEERRQLVSQLKNQRAA SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEME TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEC RSVAVGAEENNNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE AMLGVMTEADXEIELQQQTIESLKEKIYRLEVQLRETTHDREMT KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSH MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWHIVKER VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTESSVNDLILKKT NLINLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTGTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPPQOAPLGMMTGLDHYIERIQKLLAEQQ TTLAENYSELAEABFGEPHSOMGSLNSOLLTSLESSINDNA	-1		í		LKLDYEETTDCI KENTERINGKA ON TO THE AND KINDLINKR
SQHAILIDIGERTPTHYFSAQLGAGQLSLYNILKQLT SQHAILIDIGERTPTHYFSAQLGAGQLSLYNILKQLT VGYCQGLSFVAGILLHMSEEEAFKMLKFLMFDMGLRKQYRPDM IILQIQMYQLSRLHHDYHRDLYMHLBEHBIGBSLYAAPWFLTMF ASQPPLGFVARYPDMIFLQGTEVIFKVALSLLGSHKPLILQHEN LETIVDFIKSTLPNLGLVQMEKTINQVFEMDIAKQLQAYEVEYH VLQEELIDSSPLSDNQRMDKLEKTNSSLRKQNLDLLEQLQVANG RIQSLEATIEKLLSSESKLKQAMLTLEDERSALLQTVEELRRRS AKPSDREPECTQPEPTGD SQLPCFWGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLK YVDDIQKGNTIKRLNIQKRRKPSVPCPEPRTTSGQQGIWTSTES LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTIP ENRQLPPPSPQLPKHNLHVTKTLMETRRRLEGERATMQMTPGEF RRPRLASFGGMCTTSSLPSFVGSGNINPAKHQLQNGYQGNGDYG SVAPAAPTTSSNGSSIRHSPLSSGISTPVTNVSPMHLQHIREQM AIALKRLKELEEQVRTIPVLQVKISVLQEERRQLVSQLKNQRAA SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEME TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEC RSVAVGAEENNNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE AMLGVMTEADXEIELQQQTIESLKEKIYRLEVQLRETTHDREMT KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSH MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWHIVKER VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTESSVNDLILKKT NLINLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTGTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPPQOAPLGMMTGLDHYIERIQKLLAEQQ TTLAENYSELAEABFGEPHSOMGSLNSOLLTSLESSINDNA	- [CVID DIVINGENT TOWERMEST PGRSKIKFDMEKMHSAVGQ
VGYCQGLSFVAGILLHMSEEAFKMLKFLMFDMGLRKQYRPDM IILQIQMYQLSRLHDYHRDLYNHLEEHEIGESLYAAPWFLTMF ASQFPLGFVARVFFMMIFLQGTEVIFKVALSLLGSHKPLILQHEN LETIVDFIKSTLPMIGLVQMEKTINQVFEMDIAKQLQAYEVEYH VLQEELIDSSPLSDNQRMDKLEKTMSSLRKQNLDLLEQLQVANG RIQSLEATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRRS AKPSDRFPETGPPTGD KSQLFCFWGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLK YVDDIQKGNTIKRLNIQKRRKPSVPCPEPRTTSQQQIWTSTES LSSNSDDDNKQCPNFLIARSQVTSTPISKPPPLETSLPFLTIP ENRQLPPPSPQLFKHNLHVTKTLMETRRRLEQERATMQMTPGEF RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYG SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIREQM AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAA SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEME TVEQSTORIKEFROL/TADMQALEGKIQDSSCEASSELRENGEC RSVAVGAEENMDIVVYHRGSRSCKDAAVGTLVEMRNCGSVTE AMLGVMTEADKEIELQQOTIESLKEKIYRLEVQLRETTHDREMT KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSH MDLVDTCVGTVETTNSVGISCQPECKNKVVGFELPMNWWIVKER VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT NLNLKEVRSIGCGCSVDVTVCSPKECASRGVNTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQPTINTETATLIESCTNTCLSTLDKQ TSTQTVETRTVAVGEGGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPPQQAPLGMMTGLDHYIERIQKLLAEQQ	ļ				1 OAL WUUKGETMKLTVEOLHIKHOLDGKOODKDAAAAA 1
IILQIQMYQLSRLLHDYHRDLYNHLEHEIGPSLYAAPWFLTMF ASQPPLGFVARVFDMIFLQGTEVIFKVALSLIGSHKPLILQHEN LETIVDFIKSTLPPLIGLVQMEKTINQVFEMDIAKQLQAYEVEYH VLQEELIDSSPLSDNQRMDKLEKTNSSLRKQNLDLLEQLQVANG RIQSLEATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRS AKPSDREPECTQPEPTGD KSQLFCFWGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLK YVDDIQKGNTIKKLNIQKRRKPSVPPCPEPRTTSQQGIWTSTES LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTIP ENRQLPPPSPQLPKHNLHVTKTLMETRRRLEQERATMQMTPGEF RPPRLASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYG SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIREQM AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNORAA SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEME TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEC RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMT KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVQTRDQMVGSH MDLVDTCVGTSVETNSVGISCQPECKNKVVGPEDPMWWIVKER VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLITLLKT NLNLKEVRSIGCGDCSVDVTVCSPKECASRGWTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETRTVAVGRGRVKDINSSTKTRSIGVGTLLSCHSGFDR PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPQQAPLGMMTGLDHYIERIQKLLAEQQ TLLAENYSBLAEAFGEPHSCMSSLMSQLISTLSSTREIMKORD	1		i i		1 OKKIMI DIDUGKTE ETHPYFSAOT GAGOT GT VNTT VAVOY - DOD
ASOPPLGFVARVFDMIFLQGTEVIFKVALSLLGSHKPLILQHEN LETIVDFIKSTLPNLGLVQMEKTINQVFEMDIAKQLQAYEVEYH VLQEELIDSSPLSDNQRMDKLEKTNSSLRKQNLDLLEQLQVANG RIQSLEATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRS AKPSDREPECTOPEPTGD KSQLFCFWGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLK YVDDIQKGNTIKRLNIQKRRKPSVPCPEPRTTSGQQGIWTSTES LSSSNSDDNKQCPNFLIARSQVTSTFISKPPPPLETSLPFLTIP ENRQLPPSPPQLPKHNLHVTKTLMETRRLEQERATMQMTFGEF RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYG SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIREQM AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSOLKNQRAA SQINVCGVKRSYSAGNASQLEQLSRARRSGGELYIDYEEEMME TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEC RSVAVGAEENMNDIVYYHRGSRSCKDAAVGTLVEMRNCGVSVTE AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMT KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSH MDLVDTCVGTSVETNSVGISCQPECKNKVVQFELPMNWIVKSR VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVXTKESGGGQININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPPQPQALIGMNTGLIDHYIERIQKLLAEQQ TLLLAENYSELLAEAFGEPHSOMGSLMSOLITHUSETNSVMLORD	- 1		i		VGYCQGLSFVAGILLIHMSEEEAEKMI.KELMEDMGLDVOND
LETTUPTIKSTLPNIELQGTEVTFKVALSLLGSHKPLILQHEN VLQEELIDSSPLSDNQRMDKLEKTMSSLRKQNLQAYEVEYH VLQEELIDSSPLSDNQRMDKLEKTMSSLRKQNLDLLEOLQVANG RIQSLEATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRS AKPSDREPECTOPEPTGD KSQLFCFWGGKAGDILSGDQDKEOKDPYFVETPYGYQLDLDFLK YVDDIQKGNTIKRLNIQKRRKPSVPCPEPRTTSGQQGINTSTES LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPLETSLPFLTIP ENRQLPPPSPQLPKHNLHVVKTLMETRRRLEQERATMOMTPGEP RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYG SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIREQM AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAA SQINVCGYKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEME TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEC RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE AMLGVMTEADKEIELQQQTIESLKEKIVRLEVQLRETTHDREMT KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRQDMVGSH MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWWIVKBR VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETRTVAVGBGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ TLLAENYSELAEAFGEPHSOMGSLNGOLISTLSINGNACH	1		l f		III.OIOMYOLSPILUDVIDDI VALLE TANDRE LATE DAG DRKQYRPDM
LETTUPTIKSTLPNIELQGTEVTFKVALSLLGSHKPLILQHEN VLQEELIDSSPLSDNQRMDKLEKTMSSLRKQNLQAYEVEYH VLQEELIDSSPLSDNQRMDKLEKTMSSLRKQNLDLLEOLQVANG RIQSLEATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRS AKPSDREPECTOPEPTGD KSQLFCFWGGKAGDILSGDQDKEOKDPYFVETPYGYQLDLDFLK YVDDIQKGNTIKRLNIQKRRKPSVPCPEPRTTSGQQGINTSTES LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPLETSLPFLTIP ENRQLPPPSPQLPKHNLHVVKTLMETRRRLEQERATMOMTPGEP RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYG SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIREQM AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAA SQINVCGYKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEME TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEC RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE AMLGVMTEADKEIELQQQTIESLKEKIVRLEVQLRETTHDREMT KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRQDMVGSH MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWWIVKBR VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETRTVAVGBGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ TLLAENYSELAEAFGEPHSOMGSLNGOLISTLSINGNACH	1				ACCEPT CENTER OF THE PROPERTY O
VLQEELIDSSPLSDNQRMDKLEKTNSSLRKONLDLLEQLQVANG RIQSLEATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRRS AKPSDREPECTQPEPTGD KSQLFCFWGGKAGDILSGDQDKEQKDPYFVETFYGYQLDLDFLK YVDDIQKGTITKRLNIQKRRKPSVPCPEPRTTSQQGIWTSTES LSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTIP ENRQLPPPSPQLPKHNLHVTKTLMETRRLEQERATMOMTPGEF RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYG SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIREQM AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAA SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEME TVEQSTQRIKEFROL\TADMQALEQKIQDSSCEASSELRENGEC RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMT KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSH MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELEMNWIVKER VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT NLINLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETRTVAVGBGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ TLLAENYSELAEAFGEPHSOMGSLMSQLISTLSSINGTMARD	1				1 ADDIFFUGE VARVEDMIELOGTEVTERVALGELICGIVAL TE ATTACK
RIQSLEATIEKLLSESKLKQAMLTLELERSALLQTVEELRRRS AKPSDREPECTQPEPTGD KSQLFCFWGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLK YVDDIQKGNTIKRLNIQKRRKPSVPCPEPRTTSGQQGIWTSTES LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTIP ENRQLPPSPQLPKHNLHVTKTLMETRRLLEQERATMOMTPGEF RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYG SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPHHLQHIREQM AIALKRIKELBEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAA SQINVCGVRKKSYSAGNASQLEQLSRARRSGGELYIDYEEEME TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEC RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMT KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSH MDLVDTCVGTTSVETNSVGISCQPECKNKVVGPELPMNWWIVKER VEMHDRCAGRSVEMCDKSVSVEVSVCTGSNTEESVNDLTILKT NLNLKEVRSIGCGDCSVDVTVCSPKECASRGWNTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKILAEQQ TLLAENYSELAEAFGEPHSOMSSLNSOLISTLSSTRENDENOR			ſ		DELL OF INSTREME GLVOMEKTINOVERMOTATOLOGYPHINE
ARPSDREPECTOPEPTGD ARPSDREPECTOPEPTGD KSQLFCFWGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLK YVDDIQKGNTIKRLNIQKRRKPSVPCPEPRTTSGQQGIWTSTES LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTIP ENRQLPPPSPQLPKHNLHVTKTLMETRRRLEQERATMQMTPGEF RRPLASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYG SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIREQM AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNORAA SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEME TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEC RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMT KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSH MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWWIVKER VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPQVQAPLGMMTGLDHYIERIQKLIAEQQ	1				VLQEELIDSSPLSDNORMDKI.EXTMCCI.DXOXX.DX.TO.
SALES COPEPTED XSQLPCFWGGKAGDILSGDODKEQKDPYFVETPYGYQLDLDFLK YYDDIQKGNTIKRLNIQKRKKPSVPCPEPRTTSQQGIWTSTES LSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTIP ENRQLPPPSPQLPKHNLHVTKTLMETRRRLEQERATMQMTPGEF RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYG SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIREQM AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAA SQINVCGVRKSYSAGNASQLEQLSRARRSGGELYIDYEEEME TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEC RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMT KLKQELQAAGSRKKVQKATMAQPLVFSKVVEAVVQTRDQMVGSH MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWWIVKER VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVXTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ TLLAENYSELAEAFGEPHSGMGSLNSQLISTLESTNSVMRAAR	1				RIOSIEATIEVI I COROVE VOLUME TO THE REAL PROPERTY OF THE PROPE
SALES COPEPTED XSQLPCFWGGKAGDILSGDODKEQKDPYFVETPYGYQLDLDFLK YYDDIQKGNTIKRLNIQKRKKPSVPCPEPRTTSQQGIWTSTES LSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTIP ENRQLPPPSPQLPKHNLHVTKTLMETRRRLEQERATMQMTPGEF RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYG SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIREQM AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAA SQINVCGVRKSYSAGNASQLEQLSRARRSGGELYIDYEEEME TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEC RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMT KLKQELQAAGSRKKVQKATMAQPLVFSKVVEAVVQTRDQMVGSH MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWWIVKER VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVXTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ TLLAENYSELAEAFGEPHSGMGSLNSQLISTLESTNSVMRAAR	1	1	ł		AKOCODODO
ASQLPCFWGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLK YVDDIQKGMTIKRLNIQKRRKPSVPCPEPRTTSGQQGIWTSTES LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTIP ENRQLPPPSPQLPKHNLHVTKTLMETRRLEQERATMQMTPGEF RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYG SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIREQM AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAA SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEME TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEC RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMT KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSH MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWIVKER VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETTTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVXTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ TLLAENYSELAEAFGEPHSOMGSLNSOLISTLSSTNEWKORER	Г	5416	27	4024	AMISEREFECTOPEPTGD
LSSNSDDNKQCPNFLIARSQVTSTPISKPPPLETSLPLTIP ENRQLPPPSPQLPKHNLHVTKTLMETRRLEQERATMQMTPGEP RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHQLQMGYQGNGDYG SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIREQM AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAA SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEME TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEC RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMT KLKQELQAAGSRKVDKATMAQPLVFSKVVEAVVQTRDQMVGSH MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWHIVKER VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETTTVAVVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVXTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ TTLLAENYSELAEAFGEPHSOMGSLNSOLISTLSSTNEWKORD	1	- 1		4074	KSQLFCFWGGKAGDILSGDQDKEOKDPYFVETPYGYOLDI DELV
ENROLPPPS POL PKHNIARS QVTSTPI SKPPPPLETS LPFLTIP ENROLPPPS POL PKHNLHVTKTLMETRR LLEGERATMOMTPGEF RRPRLAS FGGMGTTS SLPS FVGSGNHNPAKHQLQNGY QGNGD YG SYAPAAPTTSSMGSS I KHSPLS SGISTPVTNVS PMHLQHIREGM AIALKRLKELEEQVRTI PVLQVKI SVLQEEKRQLV SQLKNORAA SQINVCGVRKRSYSAGNAS QLEQLSRARRS GGELY IDYEEEME TVEQSTQR I KEFROL YTADMQALEQKI QDSSCEASSELRENGEC RSVAVGAEENMNDI VVYHRGSRSCKDAAVGTLVEMRNCGVSVTE AMLGVMTEADKEIELQQOTIESLKEKIYRLEV QURETTHDREMT KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSH MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWI VKER VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEES VNDLTLLKT NLNLKEVRS IGCGDCS VDVTVCSPKECAS RGVNTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETT VAVGEGRVKDINSSTKTRS IGVGTLLSGHSGFDR PSAVXTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTAS R RSVGVGDDPVGSSLENPQPQAPLGMMTGLDHY IER IQKLLAEQQ TLLAENYSELAEAFGEPHSOMGSLNSOLISTIS STRIMKORDER	ı	J	1	•	1 1 1 D T Q N G N I I A K D N I O K K K K K K K K C C C C C C C C C C C
RRPARASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYG SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIREQM AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAA SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEME TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEC RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMT KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRQMVGSH MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWMIVKER VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETRTVAVGEGGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVXTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ TLLAENYSELAEAFGEPHSOMGSLNSQLISTLSSTNEWKORD	1	1	i i	1	LSSSNSDDNKOCDNELTARCOMMONDERS
RRPARASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYG SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIREQM AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAA SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEME TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEC RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMT KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRQMVGSH MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWMIVKER VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETRTVAVGEGGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVXTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ TLLAENYSELAEAFGEPHSOMGSLNSQLISTLSSTNEWKORD		ł	1		ENDOLDED CONTROL DIAKSQVISTPISKPPPPLETSLPFLTIP
SYAPAAPTTSSMGSSIRHSPLSGISTPVTNVSPMHLQHIREQM AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAA SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEME TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEC RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMT KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSH MDLVDTCVGTSVETNSVGISCQPECKNKVVDFELPMNWWIVKER VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ TLLAENYSELAEAFGEPHSOMGSLNSOLISTLSSTNEWKORD	1	i	I		LEARQUEEPSPQUEKHNLHVTKTIMETDDDI.EOEDARMOMADOOD
AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAA SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEME TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEC RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMT KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSH MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWWIVKER VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVKTKESGVGQININDNYLVGLKNRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ TLLAENYSELAEAFGEPHSOMGSLNSOLISTLSSTNEWKORD	1	[i	- 1	AMERICASE GGMGTTSSLPSEVGSGNUNDA PUOT OMOVOONORS
SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEME TVEQSTQRIKEFRQL\TADMQALEQLSQDSSCEASSELRENGEC RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMT KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSH MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWWIVKER VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETTVAVVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVXTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIGKLAEQQ TLLAENYSELAEAFGEPHSOMGSLNSOLISTLSSINSUMWORD	1	- 1	ļ		SYAPAAPTTSSMGSSIRHSDI.SCTCHDYMYYCD
TVEQSTQRIKEFRQL\TADMQALEQLSRARRSGELYIDYEEEEME TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEC RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE AMLGVMTEADKEIELQQOTIESLKEKIYRLEVQLRETTHDREMT KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSH MDLVDTCVGTSVETNSVGISCQPECKNKVVGFBLPMNWWIVKER VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETTVAVVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVXTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ TLLAENYSELAEAFGEPHSOMGSLNSOLISTLSSINSVAVOR	1	1	i	í	ATALKEL FROM TRIBELESSELSTPVTNVSPMHLQHIREQM
TVEQSTQRIKEFRQL\TADMQALEQLSRARRSGELYIDYEEEEME TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEC RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE AMLGVMTEADKEIELQQOTIESLKEKIYRLEVQLRETTHDREMT KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSH MDLVDTCVGTSVETNSVGISCQPECKNKVVGFBLPMNWWIVKER VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETTVAVVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVXTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ TLLAENYSELAEAFGEPHSOMGSLNSOLISTLSSINSVAVOR	1		})	ATABICATIVE DELEGARTIPATION NICHTARIA
RSVAVGAEEMMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE AMLGVMTEADKEIELQQOTIESLKEKIYRLEVQLRETTHDREMT KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSH MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWWIVKER VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVMDLTLLKT NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETTVAVAGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVXTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ TLLAENYSELAEAFGEPHSOMGSLNSOLISTLSSTNEWKORD	ı				DQINVCGVRARSISAGNASOLEOLSRAPPSCGPLVIDVERPRING
AMUSVATEABENNINDI VVYHRGSRSCKDAAVGTLVEMRNCGVSVTE AMLGVMTEADKEIELQQOTIESLKEKIYRLEVQLRETTHDREMT KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSH MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWWIVKER VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVXTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGSSLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ TLLAENYSELAEAFGEPHSOMGSLNSOLISTLSSINSVAVOR	1	į		Į.	TYPESTER LABRED LIADMONT. FOR TODGCCCARCON A PROSON A
KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDGMVGSH MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWMIVKER VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ TLLAENYSELAEAFGEPHSOMGSLNSQLISTLESTNENWCAGR	1	1	í	1	RSVAVGAEENMNDIVIVUDGEDECTION
KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDGMVGSH MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWMIVKER VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ TLLAENYSELAEAFGEPHSOMGSLNSQLISTLESTNENWCAGR	1	i	i	ſ	AMI CUMTEA DYDTHE CONTROL CONT
MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWHIVKER VEMHORCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEASVQVEAAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVKTKESGVGQININDNYLVGLKNRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ TLLAENYSELAEAFGEPHSOMGSLNSOLISTLSSINSVEVER	ı	ł	Į.	}	THOUSE TELEVICION IN THE PROPERTY OF THE PROPE
VEMHDRCAGRSVEMSUSVEVSVCETGSNTEESVNDLTLLKT NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ TLLAENYSELAEAFGEPHSOMGSLNSOLISTLSSINSVMVOROR	ŀ	i	1	į.	ADAQEDQAAGSKKKVDKA'IMAODI.VEQVAXEXIAXOODDAAGE
NLNLKEVRS IGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ TLLAENYSELAEAFGEPHSOMGSLNSOLISTLSSINSVMVOROR	Į	- E	i	1	MDLVDTCVGTSVETNSVGTSCOPECVATURE TO THE TOTAL TOTA
NLNLKEVRS IGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ TLLAENYSELAEAFGEPHSOMGSLNSOLISTLSSINSVMVOROR		j	I	ı	VEMHORCAGRSVEMODYGVOVOVOVOVOVOVOVOVOVOVOVOVOVOVOVOVOVOVO
MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVXTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ TLLAENYSELAEAFGEPHSOMGSLNSQLISTLSSINSVMVQ	1	- 1	f	ľ	VARIABLE AGREE VEHICLES VSVEVSVETCONTERCIAIN TO THE TARE
TSTQTVETTALEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVXTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ TLLAENYSELAEAFGEPHSOMGSLNSQLISTLSSINSVMVQ		- 1	1	j	NAME AND TREE CONTRACTOR OF CONTRACTOR OF THE PARTY OF TH
PSAVXTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ TLLAENYSELAEAFGEPHSOMGSLNSQLISTLSSINSVAVOR		- 1		l	TWAVERIADQUISTULEOVHOFTNTETATI.TECOMITECT COLDINA
RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ TLLAENYSELAEAFGEPHSOMGSLNSQLISTILSENEGHVGS	1	ı	1	1	TSTOTVETRTVAUGRCBUVDINGCT
RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ TLLAENYSELAEAFGEPHSOMGSLNSQLISTILSENEGHVGS		j	l	Į.	DEAUXTUREGUEGATATA
TLLAENYSELAEAFGEPHSOMGSLMSOLISTLSSINGSMYGROR		1	í	1	FORVALABOUNG INTONYLVCI, KMPTTACCDDOL TOOL TOOL TO
1 DEFINITION OF THE PROPERTY O		1	j		NO 1G 1GDDF 1GESUENPOPOAPI, CMMTCI, DUVIED TOVI 1 2 200
EELRNPDFQKTSLGKITGSYLGYTCKCGGLQSGSPLSSQTSQPB		ļ		ſ	TLLAENYSELAEAFGEPHSOMGGI MOOT TOWN CONTROL TOWN
THE WASTERVILLE SAFEALT CONTROL OF THE PROPERTY OF THE PROPERT				1	EELRNPDFOKTSLGVIMGO:
	-				ZANDERAL I GSYLGYTCKCGGLQSGSPLSSQTSQPE

Deginning not clocation corresponding to first amino acid amino ac	SEO	Predicted	Predicted end	
Noticeotide Cocation Corresponding to first College Coll	_	I.	1	Amino acid segment containing signal peptide
Cortesponding Coffree Cortesponding Coffree Co	NO:			Glutamic Acid F-Phenylalaning C-Clusica
LeLeucine, M=Methiconine, N=Asparagine, Definite Colimanine, N=Arginine, Arginine, Colimanine, N=Arginine, S=Serine, T-Threonine, V=Valine, Columanine, N=Arginine, S=Serine, T-Threonine, V=Valine, Columanine, N=Aughangine, P-P-Deline, Q=Glutamine, N=Aughangine, P-P-Deline, Q=Glutamine, N=Aughangine, P-P-Deline, Q=Glutamine, N=Aughangine, P-P-Deline, Q=Glutamine, N=Aughangine, P-P-Deline, Q=Glutamine, N=Aughangine, P-P-Deline, Q=Glutamine, N=Aughangine, P-P-Deline, Q=Glutamine, N=Aughangine, P-P-Deline, Q=Glutamine, N=Aughangine, P-P-Deline, Q=Glutamine, N=Aughangine, P-P-Deline, Q=Glutamine, N=Aughangine, P-P-Deline, Q=Glutamine, N=Aughangine, P-P-Deline, Q=Glutamine, N=Aughangine, P-P-Deline, Q=Glutamine, N=Aughangine, P-P-Deline, Q=Glutamine, N=Aughangine, P-P-Deline, P-P-Deline, Q=Glutamine, N=Aughangine, P-P-Deline, Q=Glutamine, N=Aughangine, P-P-Deline, Q=Glutamine, N=Aughangine, P-P-Deline, Q=Glutamine, N=Aughangine, P-P-Deline, Q=Glutamine, N=Aughangine, P-P-Deline, Q=Glutamine, N=Aughangine, P-P-Deline, Q=Glutamine, N=Aughangine, P-P-Deline, Q=Glutamine, N=Aughangine, P-P-Deline, Q=Glutamine, N=Aughangine, P-P-Deline, Q=Glutamine, N=Aughangine, P-P-Deline, Q=Glutamine, N=Aughangine, P-P-Deline, Q=Glutamine, N=Aughangine, P-P-Deline, Q=Glutamine, N=Aughangine, P-P-Deline, Q=Glutamine, N=Aughangine, Q=Glutamine, N=Aughangine, Q=Glutamine, N=Aughangine, Q=Glutamine, N=Aughangine, Q=Glutamine, N=Aughangine, Q=Glutamine, Q=Glutamine, N=Aughangine, Q=Glutamine, Q			1 :	H=Histidine T=Tsoleucine K-Lucine
To fitte amino acid residue of seino acid control of residue of seino acid sequence		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
### amino acid sequence sequen			amino acid	P=Proline, Q=Glutamine, R=Arginine.
### Tryptophan, Y=Tyrosine, X=Unknown, *=Stop amino acid sequence Codon, /=possible nucleotide deletion,			residue of	S=Serine, T=Threonine, V=Valine,
sequence seq	1	1	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Sequence Appossible mucleotide insertion]		sequence	Codon, /=possible nucleotide deletion.
STILKS IMKKKOGNNOSNASAKNIQEVGI INGGYETTSSIDDESS SSSSSSDDEDDE IT SYLEREEEEEBERTRAMACHIANTISGI KSARVEDBMQVQECPEKVEIREKYELSEKNISACHIANTISGI KSARVEDBMQVQECPEKVEIREKYELSEKNISACHIANTISGI SPDULRYVIILLADGORDTHALHTSVSISSFETIVALLIADDATOKTY HQKKAGYTPIMIALALAVEREKUMETVELFIGGGOLVMAKASQAG GTALMIAVSIGRI IMPUKGILLACGADVN 1QDBEGSTALMCASEHY HQKKAGYTPIMIALALAVEREKUMETVELFIGGGOLVMAKASQAG GTALMIAVSIGRI IMPUKGILLACGADVN 1QDBEGSTALMCASEHY HQKKAGYTPIMIALALAVEREKUMETVELFIGGGOLVMAKASQAG GTALMIAVSIGRI IMPUKGILLACGADVN 1QDBEGSTALMCASEHY HQKKAGYTPIMIALALAVEREKUMETVELFIGGGOLVMAKASQAG GTALMIAVSIGRI IMPUKGILLACGADVN 1QDBEGSTALMCASEHY HVEYTALGAG SCOTTERS THE STATE OF THE STATE		sequence	<u> </u>	\=possible nucleotide insertion)
ESSSSEDDECOVIETPLEBEREEEEDBTGMASGHHANNTEGL KSARVEDEMOVGECEPEKVE IRERVELSEEMCHLEKNTING PRALITSKOMRFCLINTLOHEWFRVSSOKSA PANWODY LAAFFAT SPDULRYVINLADGMANTALVSVSHAMFE VILLIDADVCNVU HOMAGAYPPIMLADAAVEAEKOMET VELLICADVCNUM HOMAGAYPPIMLADGAAVEAEKOMET VELLICADVON LODGAAVEA GTALMAAVSHARTDWKCALLAGADVN LODGATUMACASHAGAC GTALMAAVSHARTDWKCALLAGADVN LODGATUMACASHAGAC HVEIVELLLAQPGCKSHLEDNOGSTALS IALEAGHKOLAVLLYA HVEIVELLLAQPGCKSHLEDNOGSTALS IALEAGHKOLAVLLYA HVEIVELLLAQPGCKSHLEDNOGSTALS IALEAGHKOLAVLLYA HVEIVELLLAQPGCKSHLEDNOGSTALS IALEAGHKOLAVLLYA HVEIVELLLAQPGCKSHLEDNOGSTALS IALEAGHKOLAVLLYA HVEIVELLLAQPGCKSHLEDNOGSTALS IALEAGHKOLAVLLYA HVEIVELLLAGAGCKSTALS IALEAGHKOLAVLLYA HVEIVELLLAGAGCKSTALS IALEAGHKOLAVLLYA HVEIVELLLAGAGCKSTALS IALEAGHKOLAVLLYA HVEIVELLLAGAGCKSTALS IALEAGHKOLAVLLYA HVEIVELLAGAGCKSTALS ISLEVENSKALS IALEAGHKOLAVLLYA HVEIVELLAGAGCKSTALS ISLEVENSKALS IALEAGHKOLAVLAGAGKA ALAKELLEEDOWTTI PVIQVELS ISLEVENSKALS IALEAGHKOLAVCAGKAA ALAKELLEEDOWTTI PVIQVELS IN STANTSINGHAGHKOLAVA HVENDSTOKLIS HERAGAGCHAGAGCHAGAGCHAGAGCHAGAGAGAA ALAKELLEEDOWTTI PVIQVELS IN STANTSINGHAGAGCKAAA ALAKELLEEDOWTTI PVIQVELS IN STANTSINGHAGAGAAA ALAKELLEEDOWTTI PVIQVELS IN STANTSINGHAGAGAAA ALAKELLEEDOWTTI PVIQVELS IN STANTSINGHAGAAA ALAKELLEEDOWTTI PVIQVELS IN STANTSINGHAGAAA ALAKELLEEDOWTTI PVIQVELS IN STANTSINGHAGAAA ALAKELLEELE OOTH TESSKAL YALEAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	I			QEVGTSEGKPISSLDAFPTQEGTLSPVNLTDDQIAAGLYACTNN
RSARVEDEMQVQECEPEKVSIRERYELSEMHASCHLIKITIINI PRALITSKUMR ERUSSOKSA PAMWODYIAAFEAT SPOULRYVINLADGMONTALHYSVSHSMFEIVKLLIDADVCNVD HONKAGYTP IMAALAAVERKOMRIVEELFOGWAKAGAGA QTALMLANJHORIDANTALHYSVSHSMFEIVKLLIDADVCNVD HONKAGYTP IMAALAAVERKOMRIVEELFOGWAKAGAGA QTALMLANJHORIDANVACLLACGADVNIQDDEGSTALMCASEHG HVEIVKLLIAAQGCONHLIAASOUNGODEGSTALMCASEHG HVEIVKLLIAAQGCONFILIAASOUNGSVASITATISKE PETPTGYOLDLUFLK YVDDIOKONTI KRINIOKRKESPUETERTTSGQGI HTSTES LSSSNEDINKGCONFILIAASOUNTSTPISKEP PETETSLEPTITI ENKOLPPSPOLDKINLHUTKTLMSTERRLEGERATMONTTOEP RREPLASPGGMONTTSTLES VERSCUSSCHAPAKAGOVSOLNOVAA AIALKELEELEEDEVRTITIVLOVISIVLOERKEKVSOLKINORAA SQIINVCGVURKESVSAKANSOLEGISRARRSGGELYIDVEEEME TVEOSTORIKEPTGOVITAVOHADELOKYSISVEEME TVEOSTORIKEPTGOVITAVOHADELOKSUSUSUSTA AMUSVATARABAGAGASEKVUDKATWAQPLUFSKVVEAVOVTROMMOSH MUDUTCUGTSVETNINGISLEKKIYIRLEUQURETTIDIRAM KIKOGLQAAGSKKUDKATWAQPLUFSKVVEAVOVTROMMOSH MUDUTCUGTSVETNINGISLEKKIYIRLEUQURETTIDIRAM KIKOGLQAAGSKKUDKATWAQPLUFSKVVEAVOVTROMMOSH MUDUTCUGTSVETNINGISLEKKIYIRLEUQURETTIDIRAM KIKOGLQAAGSKKUDKATWAQPLUFSKVVEAVOVTROMMOSH MUDUTCUGTSVETNINGISLEKKIYIRLEUQURETTIDIRAM KIKOGLOAGSVEMCDKSVEVSVETSVETSKUSTESVIVILLIKT KIKOGLOAGSVEMCDKSVEVSVETSKVETSESVADILLIKT KIKOGLOAGSVEMCDKSVEVSVETSKVETSESVADILLIKT KIKOGLOAGSVEMCDKSVEVSVETSKVETSESVADILLIKT KIKOGLOAGSVEMCDKSVEVSVETSKVETSESVADILLIKT KIKOGLOAGSVEMCDKSVEVSVETSKVETSESVADILLIKT KIKOGLOAGSVEMCDKSVEVSVETSKVETSESVADILLIKT KIKOGLOAGSVENDOLOKSVETSKVETSKVETSKVETSKVETSVETSKVETSKVETS	1		1	ESTLKSIMKKKDGNKDSNGAKKNLQFVGINGGYETTSSDDSSSD
PRALTSKOMR FCLINTLOGEWFRVSSORS A PROMODY LARPER A SPDULRYVI INLADGORNATALYSSHENET INLALIDADVCONVO HONKAGYTP IMIAALAAVEAEKOME IVEELIFICGGUNARASQAG GTALMIANSHERI DWIKGLIACADAVI QODGATIMACASHEM WELVILLILAQGCKOKHLEDNGSTALS IALEAGHKULAVILLYA HVETVALLILAQGCKOKHLEDNGSTALS IALEAGHKULAVILLYA HVETVALLILAQGCKOKHLEDNGSTALS IALEAGHKULAVILLYA HVETVALLILAGAGTORI REMITERS OF THE STORY TO THE STORY OF THE STO	1		· ·	ESSSSESDDECDVIEYPLEBEEEEEDBDTRGMAEGHHAVNIEGL
SPOVLKYVINLADGMONTALHYSVSHSNPEIVKLLIDADVCNVD HOWAGNTYPI HAJALAAVEROKMIVEELEJGEVONKAGSGAC GTALMAAVSHGRIDMIVKGLLACGADVNIODGGSTALMGASEHG HVEIVKLLIA/GCCKONHEINGSVONGSTALSIALAGEHGHAVILLYA HVISTAKAGSPGTBRIGRETSPOPTHRGSFD 27 4074 KSOLFCFHGGGGAGDLISSGDQDFYEFFFYGYOLDLOFIK YVDDIOKGNTI KRLNIOKRKESPVCTEPRTTSGGGINTSTES LSSSNSDNKGCNFLIARSGVONTSTPISKEPPLETSLEPTIID ENROLPPSPOLDKIRNLUTKTLMSTERRLEGERATMONTTGEF RERELASFGGMGGTTSSLES FUSGSGNHBPAKHGUNSQLKNORAA AIALKELEELEEQVATIFYLVOKISVLGERKROVSQLKNORAA SQINVCGVRKRSYSAGNASGLEGISRARRSGGELYIDYSEEME TVEGSTORIKERFGQI\TITAVGALEGKVONSQLKNORAA SQINVCGVRKRSYSAGNASGLEGISRARRSGGELYIDYSEEME TVEGSTORIKERFGQI\TITAVGALEGKVONSQLKNORAA SQINVCGVRKRSYSAGNASGLEGISRARRSGGELYIDYSEEME TVEGSTORIKERFGQI\TITAVGALEGKVONSQLKNORAA SQINVCGVRKRSYSAGNASGLEGISRARRSGGELYIDYSEEME TVEGSTORIKERFGQI\TITAVGALEGKVONSQLKNORAA SQINVCGVRKRSYSAGNASGLEGISRARRSGGELYIDYSEEME TVEGSTORIKERFGQI\TITAVGALEGKVONSQLKNORAA SQINVCGVRKRSYSAGNASGLEGISRARRSGGELYIDYSEEME TVEGSTORIKERFGQI\TITAVGALEGKVONSQLKNORAA SQINVCGVRKRSYSAGNASGLEGISRARRSGGELYIDYSEEME TVEGSTORIKERFGQI\TITAVGALEGKVONSQLKNORAA KIKAGELQAAGSRKKUDARTRAGPLYFSKVVERVOYTCHOMMIVKER RELIKERGELGAAGSRKKUDARTRAGPLYFSKVVERVOYTCHOMMIVKER VEHBRCAGRSVENDOLGVRGTVTSTATLICETTIOLERFT TVEGSTORIKERFTORICHTORYTCHOMMITTAVALLICHER RELIKERTSTATUTTAVALLICHERFTORICHTORYTCHOMMITTAVALLICHERGFTOR PSANKTKESGORGCONSTORICHTORYTCHOMMITTAVALLICHERGFTOR PSANKTKESGORGCHOMMITTAVALLICHERFFUNSALLICHERGFTOR RESULVENDPORTSLIGKTTOSVLCYTCKCOGLOGGEPLASGAGAE GOVUTSBEKUS ELBAPPTOECHSPONLINGUL TARGAGATA SPOURYT INLABONGATALHYSVSHANGELINGULAGULARANGAGA GOVUTSBEKUS ELBAPPTOECHSPONLINGUL TARGAGATAL SPOURYT INLABONGATALHYSVSHANGELINGULAGULARANGAGA GOVUTSBEKUS ELBAPTOECHSPONLINGUL TARGAGATAL SPOURYT INLABONGATALHYSVSHANGELINGULARANGAGAE PSANLTSKOMSFCLATHGAGAENGAGAALVOYOLARAAGAGAE GOVUTSBEKUS ELBAPTOECHSPONLOFT SCESSESDBECHTORYTGANTANGODDEGGTALMCAGEG PSANLTSKOMSFCLATHGAGAENGAGAENGAGAENVARAPEN CHARACTARAGAGAGAENGAG	ŀ			KSARVEDEMQVQECEPEKVEIRERYELSEKMLSACNLLKNTIND
HQNKAGYTPIMI-ALJAAVEAEKUMRIVELEFGCGUNRAKASQAG GTALMIANSHRIDWKCHLIACASAVVI QUDEGETALMCASEHG HVEIVULLIAQPGCKSHLEDNGSTALS IALERGHKOIAVILLYA HVEIVULLIAQPGCKSHLEDNGSTALS IALERGHKOIAVILLYA HVEIVULLIAQPGCKSHLEDNGSTALS IALERGHKOIAVILLYA HVEIVULLIAQPGCKSHLEDNGSTALS IALERGHKOIAVILLYA HVEIVULLIAQPGCKSHLEDNGSTALS IALERGHKOIAVILLYA HVEIVULLIAGSQUTSIPJISKPPPTGYGULDEFEK SUNDIOKGNITI KENIOKRIKSVEVECEPRITYSCOGIHTSTES LSSSNSDDNKQCNFLIARSQUTSIPJISKPPPTGYGULDEFEK ENROLPPSPGLEKHILHVYKIMSTRRELDGETMONTPCEF RRPILASSGGGHTTSSLDSFVGSGHHBPAHGLONGYGONDYG SYAPAPTSKASSISHRSILSGISTPTVNYSPMHIGHIREOM AIALKRILEELEEQVRTI PVLQVKISVLGEKRGUVSGLKORRA SQINVCGVKRSYSAGNASQLGJEARRRSGGLYJDYEBEEME TVROSTORIKEFRGQATLAMQALEGKIDGSSCERSSELRENGEC RSVAVGABERMINDIVVYHRGSSCCDAAVCHYDDRWGSSH MLKOZIQAASRKVUKATHAGALUSKASCCDAAVCHYDDRWGSSH MLKOZIQAASRKVUKATHAGALUSKASCCDAAVCHYDDRWGSH MLKOZIQAASRKVUKATHAGALUSKASCCDAAVCHYDDRWGSH MLKOZIQAASRKVUKATHAGALUSKASCCDAAVCHYDDRWGSH MLKOZIQAASRKVUKATHAGALUSKASCCDAAVCHYDDRWGSH MLKOZIQAASRKVUKATHAGALUSKASCCDAAVCHYDDRWGSH MLKOZIGATSTOLLEVHGFTNTTTATLIESCTNICLISTLDKG TSYQTVETRTVAVGEGRVKOINSSTKTRSIGVGTLLSGHSGFDR PSAVKTESSOVGCININDNILGIARRTIACGTILLSGHSGFDR PSAVKTKESSOVGCININDNILGIARRTIACGTILLSGHSGFDR PSAVKTKESSOVGCININDNILGIARRTIACGATUTVALDAGA RSVGVGUDPVGESLENDPQDALIGMMTGLHYHIRITOKLLEQQ TLLLARNYSELARAFGCHHSKGMSLINSGLISTLISINSMKSASTT EELRRPPDCKTSIGKITGSYLGYTCKGGLGSGSPLSSOTSOPE ORVGTSEGRIS SSLDAPPTGCGTLSPVILITOHIRITOKLLEQQ TLLLARNYSELARAFGCHHSKGMSLINSGLISTLISINSMKSASTT EELRRPPDCKTSIGKITGSYLGYTCKGGLGSGSPLSSOTSOPE ORVGTSEGRIS SSLDAPPTGCTLSPVILITOHIRITOKALIYACTNI ESTILKSIMKKRONNOBINGAKRILQFVGINGGYETTSSDDSSSSD ESSSSSDEDECTLTSPVILITOHIRAGALYACTNI ESTILKSIMKKRONNOBINGAKRILQFVGINGGYETTSSDDSSSSS ESSSSDEDECTLTSPVILITOHIRAGALYACTNI ESTILKSIMKASCONINGAKAGAGAGAACKACHALVYATIND PKALTISKOMRFCLATICHDERFYRSSOXASI AWANGAATTHO PKALTISKOMRFCLATICHDERFYRSSOXASI AWANGAATTHO PKALTISKOMRFCLATICHDERFYRSSOXASI AWANGAATTHO PKALTISKOMRFCLATAGACHAUCHAACAACKACKACHAVRACAACKACHAVRACAACKACHAVRACAACKACHAVRACAACKACHAVRACAACKACHAVRACAACKACHAVRACAACKACHACHACHACHACHACHACHACHACHAC	1			PKALTSKOMRFCLNTLQHEWFRVSSQKSAIPAMVGDYIAAFEAI
GTALMLAVSHGRIDWYKGLLACGADVIQDEGSTALMCASEHG HVEIVALLAQPGCNGHLEDBORSTALSIALFAGHKDIAVILIYA HVEIVALLAQPGCNGHLEDBORSTALSIALFAGHKDIAVILIYA HVEIVALAQPGCNGHLEDBORSTALSIALFAGHKDIAVILIYA HVEIVALAQPGCNGHLEDBORSTALSIALFAGHKDIAVILIYA HVEIVALAQPGCNGHLEDBORSTALSIALFAGHKDIAVILIYA HVEIVALAQPGCNGHLEDBORSTALSIALFAGHKDIAVILIYA YVDDIOKGNTIKRINIOKRRYBSVPCFERTTSSCOGTHTSTES LSSNSDDNKQCNFLIARSQVTSTPISKPPPLETSLPFLTIP ENRCLPPSPQLPHHLHVTKILMETRRALEQGRATMONTEGEF RRPALSFEGGGGTTSSLPFYGSGNINPAKHGLQNGYGCNGDYG SYAPAAPTTSSMGSSIRHSPLSSGISTPVTRVSPMHLGHIREQM ALALRALKELEGQVRTIPYLQVKISULGGRANSGUSQLKONGRAA SQINVCGVRKRSYSAGNAGOLEQLSRARRSGGGLYIDEEEME TVEGSTORIKEFRGL\TANQALEGKINGDSCCRASSERERGIGE RSVAVGARENNNDIVVYHRGSRSCKDAAVGTIJPMENGGSVTTK ANLGVWTERDKEFELQLOTTESLKEETIYAUCURSTTHDEMT KLKQGLQAAGSRKKUDKATMAQPLVPSKVVEAVUQTPDOMYGSH MULVDTCVGTVETSVTNSVGISCOPECKNEVULDRETTHDEMT KLKQGLQAAGSRKKUDKATMAQPLVPSKVVEAVUQTPODMYGSH MULVDTCVGTTVETSVTNSVGISCOPECKNEVULDRETHORDEMT KLKQGLQAAGSRKKUDKATMAQPLVPSKVVEAVUQTPODMYGSH MAVPRTADODTSTDLEQVHQPTNTETATLISCTTTCLSTLDKO TSTQTVETTTVAVGEGRVCHUTSSTKTSSTCTLLSCHSCTTLACG PSAVTKESGYGGININDNTLVGIRRTIAGGPPDIJTALLALBOO TULARNYSELARAFGEPHSQMGSLNSQLISTLSSINSVMKSAGT EELRINDPOKTYSINSTKTSSTCTLSGTLASCHSCTTLACGROP PSAVTKESGYGGININDNTLVGIRRTIAGGPPDIJTALFALABOO RUTTSGKTSGKTTSAUGHTCHTSTTALISSTNSVMKSAGT EELRINDPOKTYSINSTKTSSTVATCAGGPLSSONGSTTSSDSSSS ESSSSSDDCCUTIETPILEREEEEDDETRGMAGHHAVITIGL KSARVEDBMQVQSCEPEEVISLAGTCKAGGSPLSSONGTTSSDSSSSS ESSSSSDDCCUTIETPILEREEEEDDETRGMAGHHAVITIGL KSARVEDBMQVQSCEPEEVISLAGACKHLQFVCHTSSTDSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	}			SPDVERIVINLADGNGNTALHYSVSHSNFEIVKLLI,DADVCNVD
#WEIVKLLIAQPGCNOHLEDNOSTALSIALEAGHRDIAVILLYA #WEINAKAGSPETTRICARKTSPOPTHEGST 5417 27 4074 ***SOLFCFWGGTAGGILSGDONEGKDFYFVETPGYGDLDIDEK #WEIVAKAGSPETTRICARKTSPOPTHEGST LSSSNSDDNKQCNPILARSQVTSTISKPPPLETSCOGIMTSTES LSSSNSDDNKQCNPILARSQVTSTISKPPPLETSCOGIMTSTES LSSSNSDDNKQCNPILARSQVTSTISKPPPLETSCOGIMTSTES LSSSNSDDNKQCNPILARSQVTSTISKPPPLETSCOGIMTSTES LSSSNSDDNKQCNPILARSQVTSTISKPPPLETSCOGIMTSTES LSSSNSDDNKQCNPILARSQVTSTISKPPPLETSCOGIMTSTES LSSSNSDDNKQCNPILARSQVTSTISKPPPLETSCOGIMTSTES LSSSNSDDNKQCNPTLARSQVTSTISKPPPLETSCOGIMTSTES RRFRLASFGGMGTTSSLPSFVGSGNINDAKUGLONGVGAA SQINVCGVKRSYSAGANAGUEQUSTRRENGELYDFUTIP AILARKEKELEEQUPTIPVLOYKISVLQEEKRQLNGVAAA SQINVCGVKRSYSAGANAGUEQUSTRRENGELYDFUTGEEMB TYEOSTORIKEFRQL\TAMQAELYSKVVEAVVGTLOPEMTGAT ANLGVWTEADASSRKKVDKATMAQELYSKVVEAVVGTLOPEMTGAT ***RUNDAYTCAGTSVETMSVGSTGOPECKNKVVEAVVGTROPMGSH** MDLVDTCVGTSVETMSVGSTGOPECKNKVVEAVVGTROPMGSH** MDLVDTCVGTSVETMSVGSTGOPECKNKVVEAVVGTROPMGSH** MDLVDTCVGTSVETMSVGSTGOPECKNKVARVEAVERDWAAA** MAPRETAQDOTSTDLEQVYGTTMTCTLESVGRTEAVSQVEAV MAPRETAQDOTSTDLEQVYGTTMTCTALIESCTNTCLSTLDKG TSTQTVETRTVAGGGETVGLINSTKTISTGOTLLSGSFOR PRAVKTRESGVGGININDNTLVGLKWRTIAGGPPGTTAGLAEQO** RSTGVGVDDPVGSELENEYQDAAJGGMSLASQUSTGLISTLSSINSWKASAT EELRAPDPGVTSIGKTITGSVAGTCAGCIGAGSPLSSOTTGOPE QRVGTSEGKPISSGLAAFGEPBSQWGSLNSQLISTLSSINSWKASAT EELRAPDPGVTSIGKTITGSVAGTCAGCIGAGSPLSSOTTGOPE QRVGTSEGKPISSGLAAFGEPBSQWGSLNSQLISTLSSINSWKASAT EELRAPDPGVTSIGKTITGSVITGAGGTETTSSDDSSSS ESSSESSDBCDVTSPPLEEEBEEDEDTROMAEGHHAVNI EGL KSARVEDBMQVQSCEPEFLYSINGSVAGAKALGVVEILAGAGVATON PKALTSKDMRFCLNTLGIEMFRVSSGKSAIPANVGDYIAAFEA SPPULRYVIALAGGGNTALHYSVSHSNFTLSACALLKUTIND PKALTSKDMRFCLNTLGIEMFRVSSGKSAIPANVGDYIAAFEA SPPULRYVIALAGGGNTALHYSVSHSNFTLSACALCALKUTING PKALTSKDMRFCLNTLGIEMFRVSSGKSAIPANVGDYIAAFEA SPPULRYVIALAGGGNTALHYSVSHSNFTLSACALCALKUTING PKALTSKDMRFCLNTLGIEMFRVSGKSAIPANVGDYIAAFEA SPPULRYVIALAGGGNTALSGOPTHATSPGTTHAGSP LDGGGVEKLOPPOPUKEMBIGSGDAABAGAACHUR PRED LDGGGVEKLOPPOPUKEMBIGSGGAABACAACHUR PRED LDGGVEKLOPPOPUKEMBIGSGGAABACAACHUR PRED LDGGVEKLOPPOPUKEMBIGSGGAABACAACHUR PRED PKGVVALLSSSTROMAGRO	1		!	OTAL MI AVOUGD TOWN KG I A GOAD TO THE CONTROL OF T
5417 27 4074 KSQLFCFMGKAGDILGROPMERGEFD VETPGGOLDLOFLK YODLOKONTIKRLNIOKRRYBSYDCFBERTISGGOLTWISTEES LSSNSDINGKCOPNELLASQUTSTIELS SSNSDINGKCOPNELLASQUTSTIELS ENGLASFGGGUTSSLES REPRLASFGGGGTTSSLES REPRLASFGGGGTTSSLES REPRLASFGGGTTSSLES REPRLASFGGGTTSSLES REPRLASFGGGTTSSLES REPRLASFGGGTTSSLES REPRLASFGGGTTSSLES REPRLASFGGGTTSSLES REPRLASFGGGTTSSLES REPRLASFGGGTTSSLES REPRLASFGGGTTSSLESPTOSGNINDRAGGGTOKOTOG SVAPAAPTTSSMGGSIRHBJLSSGISTPUTNESPMILGHIRGM ALAKRILKELBEQUPTIPULGUSGISTPUTNESPMILGHIRGM ALAKRILKELBEQUPTIPULGUSGISTPUTNESPMILGHIRGM SQUNVCGVYRKSYSAONASGLEGISTRAKTGGGLYIDVEBEEME TVROSTGRIREFRQLUTSAMGGSKCUDAKAMGGLEVENKINGRAA SQUNVCGVYRKSYSAONASGLEGISTRAKTGGGLYUTDEEBEME REVAVAGBEMNOIVVYIRGSRSKCHAAVGTLVENKINGGVSVTR AMLGVVRTRADVETSLEQUTTESLKERIYELEVGLRETHDREMT REVAVAGBEMNOIVVYIRGSRSKCHAAVGTLVENKINGUSVTR AMLGVVRTRADVETSULGGVDECKNKVVQPELDMANGIVKR MDLVDTCVGTSVETNSVGISGQDECKNKVVQPELDMANGIVKR VEHBRCAGRSVEMCASSVSVEVSVEVGTSSTEESVIDLITLIKT NIALKEVASIGGCDCSVDVTVGSPKSCASRGVNTEAVSQVEAV MAVPRTADOJTSTLLEGVOJTTNITGTATISTOTICLSTLDKG TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVOTLLSKGNESSOVEAV MAVPRTADOJTSTLLEGVOJTNITGTATISTOTICLSTLDKG TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVOTLLSKGNESSOVEAV MAVPRTADOJTSTLLEGVOJTNITGTATISTOTICLSTLDKG TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVOTLLSKGNESSOTSOPE PSAVKKRSSGGOININDNIVLOLKNRTISSINSVMKSAST EELRIPDPOGNTSILGKITGSVLGTTCKCGGLOSGSPLSSOTSOPE OEVGTSEGKITSLAAFTGEBTSLGGGSLINGGLAAGLIAAVTRATIN ESTLKSINKKKDGINKDSNGAKKALGPVGINGGTETSSDDSSSD ESSSSSDDECVITEPULEEREEEDEDLOTAGGTATAGTAN ESTLKSINKKKDGINKDSNGAKKALGPVGINGGTETSSDDSSSD ESSSSSEDDECVITEPULEEREEEDEDLOTAGGTHAFFIN SKPLUKTULLAGDGCVGFRUFFULSTRETVALLEGAGGVANKAGAGG QTALMLAVSKGGITDMVGCLHEFFUNSSKSGAIPANGGHTAAFFIN ESTLKSINKKRDGENKFLORGHTMSGGGAAGALUNGKAGAGA QTALMLAVSKGGITDMVGCLHEFFUNSKAGAGGTAMAGGGAAGAULUNGKAGAGA QTALMLAVSKGGITDMVGCHAFFUNSKAGAGAGAULUNGKAGAGAGAURUNGKAGAGA QTALMLAVSKGGITDMVGCHAFFUNSKAGAGAGAULUNGKAGAGAGAURUNGKAGAGA GREDERVINGKAGAGGGTATLAGGGAGAULUNGKAGAGAGAURUNGKAGAGA CORGENERVENGERPSDAGGGGAGAGAULUNGKROBAGSPFR GGREVAURHERSBORGFROMGGGGAAGAULUNGKROBAGSPFR GREGAVDPREUBFRSVGGGAGAGA				HVEIVKIJI AODGONGHI EDNDOGONI CIAL EAGUNDIAIR AND
### SOLFCFWGGGAGGILSGDONEGKDFYFVETFGYGDLDEFLE ### SYDDIOKGNIT KRINIOKRENSYPCETFT SOGGIMTSTES LSSSNSDNKQCNPLIARSGVTSTISKPPPPLETSPHTITSG ### SYDDIOKGNIT KRINIOKRENSYPCTE PETTSGOGGIMTSTES LSSSNSDNKQCNPLIARSGVTSTISKPPPPLETSLPFITIT ### ENROLPPPS POLEVHILHVITTUMETRER PETTSGOGGIMTSTES LSSSNSDNKQCNPLIARSGVTSTISKPPPPLETSLPFITIT ### ENROLPPPS POLEVHILHVITTUMETRER PETTSGOGGIMTSTES ### SYDAPAPTISSMGSIT REPRUSSGIT STEVER SHELL PROVIDED ### STAPAPTISSMGSIT REPRUSSGIT STEVER SHELL PROVIDED ### STAPAPTISSMGSIT STAPARSH STANGAL SEGURI TYPE SEEME ### STAPAPTISSMGSIT STAPARSH STANGAL SOINVICGWKRSYSANGALDELQUERREN SHELL PROVIDED ### STAPAPTISSMGSIT STAPARSH STANGAL SEGURI TYPE SEEME ### STAPAPTIS STANGAL SEGURI STANGAL SEGURI TYPE SEEME ### STAPAPTIS STANGAL SEGURI TYPE SEGUR TYPE SEGURI TYPE SEGURI TYPE SEGUR TYPE SEGUR TYPE SEGUR TYPE SEGUR TYPE SEGUR TYPE SEGUR TYPE SEGUR TYPE SEGUR TYPE SEGUR TYPE	1		ł	HVNFAKAOSPGTPRI GRKTSPGPTHPGGED
YVDIOKGNTIKENIOKRRIBSVECEPERTISGOGGIWTSTES LSSNSBODNKCCPMFLIARSGOVTSTIPLEPITITE ENRCLPPSPOLIPHINLHVIKTIARSGOVTSTIPLEPITITE ENRCLPPSPOLIPHINLHVIKTIARSGOVTSTIPLEORATMOMTEGEP RRPILASFGOMSTISSLEPSVGSGEMPHOLORGYGOMODY SYAPAPTTSSMISSIHSPLSSGISTPVINVSPHHLOHTREOM AIALKERLEBOURTIPULOVICISVLOERKOLUSOLORGAA SQINVCGURKRSYSAGNASCLEOLERKOLUSOLORGAA SQINVCGURKRSYSAGNASCLEOLERKOLUSOLORGAA SQINVCGURKRSYSAGNASCLEOLERKOLUSOLORGAA SQINVCGURKRSYSAGNASCLEOLERKOLUSOLORGAA SQINVCGURKRSYSAGNASCLEOLERKOLUSOLORGAA SQINVCGURKRSYSAGNASCLEOLERKOLUSOLORGAA SQINVCGURKRSYSAGNASCLEOLERKOLUSOLORGAA SQINVCGURKRSYSAGNASCLEOLERKOLUSOLORGAA SQINVCGURKRSYSAGNASCLEOLERKOLUSOLORGAA SQINVCGURKRSYSAGNASCLEOLERKOLUSOLORGAA SQINVCGURKRSYSAGNASCLEOLERKOLUSOLORGAA SQINVCGURKRSYSAGNASCLEOLERGELINDEWSURL RENGLOWSTAGNASCHEOLERGE TVEGOTORT LADMONITUTUR STATE SUCCESSION TO THE CONTROL OF THE CONTROL O	5417	27	4074	KSOLFCFWGGKAGDILSGDODKEOKDDYFYFTBYGYOLDLDFLY
LSSSSSDDNKQCPNFLIARSQVTSTP1SKPPPPLETSLPFLTIP ENRQLPPSPOLPHRILMTYKTMETRELEOERATMOMTEGE RRPRLASFGGMGTTSSLPSFVSGGHHPAKHQLQKYQGMGDYQ SYAPAAPTTSSMGSS IRBSPLSSGTVTNVSPHHLGHTREOM AIALKRLKELEEQURTT PVLQWKISVLQEEKRGLYSQLMQRAA SQINVGGVKRSYSAGANSOLEQLERRRRSGGELYIDYEEEEME TVEQSTQRIKEFRQL\TAJMQALEQKTQDSCEASSELRENGEC RSVAVGAEENINDTVVYHRGSRSCCDAAVGTLVERRNCGVSVTK AMLGVWTIRADKEI ELQQGYTIESLKKKIYRLEVQLEKTTHDREATT KLKQELQAAGSRKVDKATMAQPLVFSKVVGAVVGTRDQWUSH MDLVDTCVGTSVETNSVGISCQPECKNAVVGPELPMNMH YIKER VEHHRCAGRSVURGTSCAPECKNAVVGPELPMNMH YIKER VEHHRCAGRSVURGTSCAPECKNAVVGPELPMNMH YIKER VEHHRCAGRSVURGTSCAPECKNAVVGPELPMNMH YIKER VEHHRCAGRSVURGTSCAPECKNAVVGPELPMNMH YIKER VEHHRCAGRSVURGTSCAPECKNAVVGPELPMNMH YIKER VEHRRCAGRSVURGTSCHTCASSVUTLENSVORTELSVIDLTLLKT MIALKEVKSIGCGGGSVODTVICS PRECEASROWTEAVSQVEAAV MAVPRTADQDTSTDLEQVAQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETTTAVACEGREVKUNISSTKATSGVSTLLSGSFOR PSAVKTKESGVGGININDNYLUGUKRRILACGPQITTGLTASR RSVGVCDDDVCGSLERPQPQAPLGMMTGLOHYIERIGKLÄGEQFOR PSAVKTKESGVGGININDNYLUGUKRRILACGPQITTGLTASR RSVGVCDDDVCGSLERPQPQAPLGMMTGLOHYIERIGKLÄGEGP PSAVKTKESGVGGININDNYLUGUKRRILACGPQITTGLTASR RSVGVCDDDVCGSLERPQCTSLASVENSTANSVMKSAST EELRNPDPGVKTSLKATTGSYLGYTCKGJGGSFPLSSOTSQPE QBVGTSECKP; SSLDAPPTQEGTLSPVALTDDQIAAGLIYACTNN ESTLKSIMKKRDNKDSNASKNUQFVGINGGFTSSDDSSGS BSSSESDDECDVTETYFLEEEEEEDDTTGMARGHHAVNIEGL KSARVEDBMQVGSCEPEKVSIRERYFLSSEMSAACHLKKTIND PKALITSKMRFCLNTLGHEWFRVSSGSAPAMVGDVIAAFREAI SPDVLRYVINLABONGNTALHYSVSHSNETEIVKLLLDADVCNVD HONKAGYTPINLAALAAVBARGNDRIVGHEWFRVGSGTALMCASSGAG QTALMLAVSHGRIDMWGCSCEPELGCGGVVAKASQAG QTALMLAVSHGRIDMWGCSCAPPTHRGSFD SPERAGGBMETGAAECTYDDALLGILGWGNVQDFLRULFGFTYR KDFTRLLRHPSDRMFPPGBAAGLULQVFKYPDHMARQDDEKR RQLEKEKTRREEEEBAKTYSAAAARKEPVPVPVVGETRIVTK EDGGCGVKVLVNLSKVGEVWNNALLGGEPT IDIDKINKERSMATVDE EDGAVLDRLIFPDTHCHLOGRVGDAFGGTAMCASSERG GREYPAMFHISBAUG DGGCVEKVLYGPPOPSTAGARGERGRKIKVNMKHPBPADA KDPASLPGC/LGF JORGANGRAGEVFR JEPI LERIGOGGOGGCCARGFTGRENKIKVNMKHPBPADA KDPASLPGC/LGF JORGANGRURERDREVTWANGKLFRHINTESILMSL BCGCNENTCWGKKLRRAEVLDERVKWYKLGEGERPLGWWVLGG VKKLQVLCPHSRDPKVVADGEGCFLVRDVFR	1			YVDDIOKGNTIKRLNIOKRRKPSVPCPEPRTTSGOOGIWTSTES
ENROLPPSPOLPHHILMTYRTHLEOERATMOMTEGEE RRPILASFGGMSTTSSLDFSVGSGHNEPAKHOLONGYGONGDYG SYAPAAPTTSMGSSIHSPLSSGISTVYNVSPHILOHIREOM AIALKRIKELEGOVRITPVLOVKISTVOLPERKOLVSOLKONGRAA SOINVCGVKKRSYSAGMASOLBOLISRARRSGGELTDVTNUSVERKOLVSOLKONGRAA SOINVCGVKKRSYSAGMASOLBOLISRARRSGGELTDVTREEMME TVEGSTGRIKEFROLV-JA-MQALBOKYOLDSSCRASFBLERGIER RSVAVCABERIMMDIVVYHRGSRSCKDARVGTUVEMRINGCVSVTK AMIGWYTERADKEIELQOGTIESLKEKTYRLEVOLRETHIREMT KLKOELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRQWYGSH MDLVDTCVGTSVETNAVGISCQPECKNKVVGPELEMMWRIVKER VEMBERGARSVEMOLKSVSVEVSVCSTGSNTEESVYDALTLIKT KLKOELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRQWYGSH MDLVDTCVGTSVETNAVGISCQPECKNKVVGPELEMMWRIVKER VEMBERGARSVEMOLKSVSVEVSVCSTGSNTEESVYDALTLIKT KLKOELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRQWGSH MDLVDTCVGTSVETNAVGISCQPECKNKVVGPELEMMWRIVKER VEMBERGARGSVEMOLKSSTKVDKATMAQPLVFSKVVEAVVQTRQWGSH MDLVDTCVGTSVETNAVGISCQCKSVSVEVSVCSTGSNTEESVYDALTLIKT KLKOELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTELEMMWRIVKER VEMBERGARSVEMOLKSSTSVESVEVSVCSTGSNTEESVYDALAK MAPRATAQDOTSTDLERGVRGFTATLIESCTTTCLSTLDKO TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVTLLSANSTVAN RSVGVSDDPVGESLENPQPQADLGMMTGLDHYIERIOKLLAGGG TLLAENYSEGALGARGTPROGGALGSTALITSGSTLGKTGSVLGVTTKCGGLOSGSPLSSCTSOPE PSAVKTKESGVGOININDRIVLOGLAMGTALLTSGKLATSON ESTLKSIHKKKEGORKDSNOAKKNLQFVGINGGYETTSDDSSSD ESSSESSDDEGDVIETY LEEPEREEDEINDGALACTNIN ESTLKSIHKKKEGORKDSNOAKKNLQFVGINGGYETTSDDSSSD ESSSESSDDEGDVIETY LEEPEREEDEINGAACHLIKATIND PKALISKAMRRCLINTLGHENPTVSOSLAPAMVGOVAACTNIN ESTLKSIHKKKEGORKDSNOAKKNLQFVGINGGGETTSDDSSSD ESSSESDDEGDVIETY LEEPEREEDEINGAACHLIKATIND PKALISKAMRRCLINTLGHENPTVSOSLAPAMVGOVAACTNIN ESTLKSIHKKEGARTATURGHENPTSVAGATAACHACKSCAA CYTALLAUSHGRIDMVGCEPEKVEIREYELSEKNILSANA CYTALLAUSHGRIDMVGCEPEKVEIREYELSGRMCLACKSCAA CYTALLAUSHGRIDMVGCACAACHVPOVAACASAACA CYTALLAUSHGRIDMVGCACAACHVPOVAACAACAACAACHVPA HVERAAQASGPGTRAGGENERYTMACHTACKKLTHARGAACAACAACHVPAACAACAACHVPAACAACHVPAACAACAACHVPAACAACAACHVPAACAACAACHVPAACAACHVPAACAACAACHVPAACAACAACHVPAACAACAACHVPAACAACAACHVPAACAACAACHVPAACAACAACHVPAACAACAACHVPAACAACAACHVPAACAACAACHVPAACAACHACHTACAACAACAACHVPAACAACAACHVPAACAACAACHV	[LSSSNSDDNKQCPNFLIARSOVTSTPISKPPPPLETSLPFLTTP
RRPRLASFGGMTTSSLPSFVGSGNINDRAKHQLONGYGGNGDYG SYAPAAPTTSSMGSSIRHSPLSSG1STPVTNYSMHLQHTREGM AIALKRILKELEDURTIFVLOVKISVLQEEKRQLVSOLJKNGRAA SOINVCOVKRSFYSKANASQLEDISRRSGGEKIYDYEEEMS TVEOSTORIKEFRQL\TA\manaledniopsscasselrenge RSAVAGAERNMOIVVTHRGSRSCKDAAVGTLUPERRNGGVSTYE ANLGVMTEADKEIELQQGTIESLKERIYHLEVQLKETTHDREMT KLKQELQAAGSRKKUDKATHAQELVFSKVVUSGTLORWGSH MDLVDTCVGTSVETNSVUSICQDECKIKVVGPELDRWMWIVKER VEHEDRCAGRSVEMCDKSVSVEVSUCETGSNTEESVHDLITLIKT NIALKEVRSIGGGDCSVDVTVCSPKEASRGVNTEAVSQVEAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCINTCLSTLDKO TSTQTVTGTTVAVAGESVKVDINSTKSIGVGTLLSGHSGFDR PSAVKTKESGVGOININDNILVGLKMRTIACGPPDITUGLTASK RSVGVGDDPVGSSLENDPQDQAPLGMGLHSQLYSLSGNSGHSGNISTLSSINSVMKSAST EELRNPDPCKTSLGKTTGSVLGATCCGGLOSGSPLSSOTSQDE QBVGTSEGKPISSLDAPPTQEGTLSVNLTDDQIAAGLVACTNN ESTLKSIMKKKDGMAGKNGSNAKUNGDLSTTLSSINSVMKSAST EELRNPDPCKTSLGKTTGSVLGATCKCGGLOSGSPLSSOTSQDE QBVGTSEGKPISSLDAPPTQEGTLSVNLTDDQIAAGLVACTNN ESTLKSIMKKKDGMAGNAGNAGAUSTTSSDDSSSD ESSSSSDDECDVIEYPLEEEEEEDEDTRGMAGGHTANNIEGL KGARVEDDMQVGCCEPKVSIRRFYFLSSKANLACHLKNTIND PRALITSKMMRCLANTLGHERMVSGSSAIPAMVGDYIAAPSAI SPEVLRYVINLADGNGNTALHTSVSISRFFYLSIKALACHLKNTIND HANKAGYTPINLAALAVAREKUMTSLALALACACHN HONKAGYTPINLAALAVAREKUMTSLALALACACHNVIGHT HUSIVKLLLAQPGGNGHTGMAGGHTANCASEBIG HVEIVKLLLAQPGGNGHEDNDGSTSLALACASEBIG HVEIVKLLLAQPGGNGHEDNDGSTSLALACASEBIG HVEIVKLLLAQPGGNGHEDNDGSTSLALACASEBIG HVEIVKLLLAQPGGNGHEDNDGSTSLALACASEBIG HVEIVKLLLAQPGGNGHEDNDGSTSLALACASEBIG GRUEBEKTRREEBEARTVSAAAARERPUPVPVQEIEIDSTTEL DGGQEVEKVQPPGPVKEMMAGGGRAAARGAAGVACALVVVK GGGVSVALSSSIRVAMGERPTGAAAALVLLOUFKTPDHMARQDDERR RCLEEKKTREEBEARTVSAAAARERPUPVPVQEIEIDSTTEL DGGQEVEKVQPPGPVKEMMAGGGRAAARGAAGVACALVVVK GGGVSVALSSSIRVAMLEGGEPTDLIGNTRESSLASL EPGGVLUNILSKVGEVMWALILEGEPTDLIDKTNERSSMATVDE EDQAVLDALTTPDTHQKLQGKPOSHKUMKHKRERSMATVDE EDQAVLDALTTPDTHGAUGACGERSKHKVNNKHDERADA KDPASLPGC/LOG/DCVPRAPSSTROUNGSGRGRARAKNNKKHDERADA KDPASLPGC/LOG/DCVPRAPSSTROUNGLIKURINTSLESLASL EPGGVUNDSKVGETRYBESBORGDDDTDLICTGVSCGHTINPR VALRRMRCCARTESGTSTSGNSTYTIGGATRICTGVNROSKT VALRRMRCCARTESGTSTSGNSTYTIGGATRICTGVNROSKT VALRRMRCCARTESGTSTSG	1	ł		ENROLPPPSPOLPKHNLHVTKTLMETRRRLEOERATMOMTPGEF
SYAPAAPTTSSMGSSIRHSPLSSGISTPYTNYSMHLQHIREGM AIALKRIKELEOVATT PULQVILSULGERKQLUSQLKNORAA SQINVCGVRKRSYSAGNASQLEQLSRARRSGEGLYIDYEBEEME TVEGSTORI KEPRGU TA-MOALDELOBSCERASSEIRENGEC RSVAVGAEENMODIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTR ANLGYMTBADKEIELQQGYLTESIKERIYBLEVQLRETTHDREMT KIKQELQAAGSRKKVDKATMAQPLYPSKVVEAVQTROMOSH MDLVDTCVGTSVETNSVGISCPECKNKVVGAPQTROMOSH MDLVDTCVGTSVETNSVGISCPECKNKVVGAPQTROMOSH MDLVDTCVGTSVETNSVGISCPECKNKVVGAPQTROMOSH MDLVDTCVGTSVETNSVGISCPECKNKVVGAPQTROMOSH MDLVDTCVGTSVETNSVGISCPECKNKVVGAPQTROMOWHIVER VPHPBRCAGRSVEMCDKSVSVEVSVCGTGSNTESSVGDLTLLKT NIAHLKEVRSIGGGDCSVDVTVGSPKECASRGWTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTHTATLISECTNTCLSTLDKO TSTQTVETRTVAVGEGRVKDINSTKTRSIGVGTLLSGHSGFDR PSAVKKRESGVQCININDNIVLOKHTIALGSPOITVGLTASH RSVGVCDDPVGESLENDPQPAPLGMMTGLDHYIRRIGKLLAEQQ TLLAENTSELABARFGEBRSQMGSLNSQLISTLSSINSVKKSAST EELRNPDPQKTSLGKTTGSVLGVTCXCGGLOSGSPLSSCTSQPE QRVGTSECKPISSLDAPPTQEGTLSFVULTDQIAAGLYACTNN ESTLKSINKKKDGNKOSNGKKNLGVVGINGGYETTSDDSSSD ESSSSSSDDECDVIEVPLEEEEEEDEDEDTGMAGHHAVNIEGL KSARVEDBMQVQCECEPKVSIRRFYLSSKNLSACNLIKNTTIMD PKALTSKDMRPCLNTLQHEMFRVSSGSAIPAMGDYIAAFBAI SPOURTYVINLABORGTATAHYSSGSSAIPAMGDYIAAFBAI SPOURTYVINLABORGTATAHYSSGSSAIPAMGDYIAAFBAI SPOURTYVINLABORGTATAHYSSGSSAIPAMGDYIAAFBAI SPOURTYVINLABORGTATAHYSSGSSAIPEVGAUAAASSGG CYALMAUSHGGIDMVGCLLACCADVIODDEGSTALMGASSEIG HVEIVKLLLAQPGCNGHLEDNDGSTALSIALBAGHKDIAVLLYA HNYFAXAQSPGTPRLGKTSPGFTHRGSFD GRAUBSGMMETGAAEUTOAALLGILDHWGNVODPERVLFGFLYR KIDFYRLLRHSDRMGFPCAAQALVLQVFKTFDHMARQDDEKR RGLEEKHREEEEBARTVGAAAABFEPVPVPVQETEIDSTTEL DGHQEVERVQPPGPVKRMAILGSCEAAPCAVAGAAEVPR\PEDFI LEPIGOFONPDSVAGAVRENYTHSGOYTDLERVTUPVERHVK GKQVSVALSSSSTRVAMLEENGERVLMSGKLTHKINTESLMSL EPGKCYLVNLSKVGEYWMAILEGEEPTDLOIRKRRSWATTVDE ECQAVLDRLITPDTHQKLQGKPQSHBLKVHMEKKRMAABAEC GREEKEKREEEBARTGGAAGAEVPR\PEDFI LEPIGLTLARQQAVGEGERPLGVWNNAKHPERADA KDPASLPCQ/LGP/DCVPRAPSSSYCDDCMKLAANITYEIL PQRIQOMGOSPCTAEBHGKKLLERTRSQQSARTRLQEMERFPH ELEAILTARQQAVEDEBUSCCCCPLVRNNAKNNHEPERADA KDPASLPC/LGP/DCVPRAPSSSYCDDCMKLAANITYEIL PQRIQOMGOSPCTAEBHGKKLLERTRSQCSARTRLOEMERFPH ELEAILTARAQQAVEDBUCGCCPLVRO	J		İ	RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHOLONGYOGNGDYG
SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEMEM TVESSYGRIKEFRGYLTAMAALDEVIDSSCEASSEIRENGEC RSVAVGAEENMIDIVVYHRGSSCKDAAVGTLYEMRINGGVSVTE AMIGWYNTEADKEILEJQQTIESIKETYLEWQLRETTHDREMT KLKOELOAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDOMVGSH MDLVDTCVGTSVETNSVG1SCQPECKNKVVGPELPMWWIJVKER VEMEDRCAGRSVEMCDKSVSVEVSVCGTGSNTEESVANDLTLLKT NIANLKEVRSIGGDCSVDVTVCSPKBCASRGWTEAVSQVEAAV MAVPRATADQDTSTDLEQVHOFTBTTATLIESCTNTCLSTLDKK TSTQTVETRTVAVGEGRVKDINSSTKTRSIGGGTLLSGHSGFDR PSAVRKKESGVGOININDNILVGHTTACOPPOI TVGGITLASG RSVGVCDDPVGESLENPQPQAPLGMMTGLDHYIRRIGKLLAEQQ TLLEARVSELARAFGEPHSQMGSLISTLSSINSVMKSAST EELRNDPGKTSLGKHTGSVLGVTCKGGLQSGSPLSSGTSQPE QEVGTSEGKPISSLDAPPTQBGTLSPVHLTDDIAAGLYACTNN ESTLKSINKKEGNKOSNGAKNIGVFVGINGGYETTSDDSSSD ESSSSSSDDECDVIEVFLEEEEEEDEDTGMAGHHAVNIEGL KSARVEDDMQVGCEFERVSIRERFYLSEKMLSACULKNTIND PKALTSKDMRFCLNTLGHEMFRVSSQKSAI FAMGGDY IAAFBRI SPULRYVINLABORGTAHHAVGSCKSAI FAMGGDY IAAFBRI SPULRYVINLABORGTAHHAVGLACADVIODDGGSTALUKNTIND PKALTSKDMRFCLNTLGHEMFRVSSQKSAI FAMGGDY IAAFBRI SPULRYVINLABORGTAHHAVGLACADVIODDGGSTALUKNTIND PKALTSKDMRFCLNTLGHEMFRVSSQKSAI FAMGGDY IAAFBRI SPULRYVINLABORGTAHAVGCLACADVIODDGGSTALMCASBCG QTALMLAVSHGRI DMVKGLLACADVIODDGGSTALMCASBCG HVBIVKLLLAQPGCNGHLEDNDGSTALSIALEAGHKOIAVLLYA HVNFAKAQSPGTPRLGRKTSPGFTHRGSFD HVBIVKLLLAQPGCNGHLEDNDGSTALSIALEAGHKOIAVLLYA HVNFAKAQSPGTPRLGRKTSPGFTHRGSFD GRADHAVGSKERKFEEEBARTVSAAAABARDVPDVPUGETISTTEL DGHQEVERVQPPGFVKEMRAIGSGEAEDCAVAGABEVPR\BPD-I LPRIGGFORNPDS VRAGAVRENYTHSODYTDLERVRUPEKHVVK GKQVSVALSSSSTRVAMLEENGERVLMSGKLTHKINTESSLHSL EPKCLVLUNLSKUGEVRWNAILEGEEPTDLDIKNKERSMATVDE EQAVLDRLTPDYHQKLQGKPGSHRKWNNKHERSMATVDE EGAVLDRLTPDYHQKLQGKPGSHRKWNNKHERSMATVDE EGAVLDRLTPDYHQKLQGKPGSHRKWNNKHERSMATVDE EGAVLDRLTPDYHQKLQGKPGSHRKWNNKHERSMATVDE EGAVLDRLTPDYHQKLGGKPGSHRKWNNKHPERADA KDPASLPGC/LIG/DCVGPLENGBVCTGCDGMKLAANNIYEIL PQRIQQMGSPCIABEHGKKLLERTREQQSARTRLQEMERPH BELBILIBARQQAVEDESSNEGGSCDDGMKLAANNIYEIL PQRIQQMGGSPCIABEHGKKLLERTREQCGCPLVVNNGSKT VCKLQVLCDEHSRDPKVSDEDCGGCCPLVVNNGSKT VCKLQVLCDEHSRDPKVSDEUCGCCPLVVRLOERTGNVTNLERF	ļ	1		SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLOHIREOM
TVEGSTORI KEPRQL \tammaqalegkiqdsscrasselerngec RSVAVGAERIMNDIVVYHRGSKDAAVGTLVBWRNCGGSVTYE AMLGVATEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMT KLKQELQAAGSRKKVQKATMAQPLVFSKVVEAVVQTIEDMYGH MDLVDTCVGTSVETMSVGISCQPECKNKVVQPELPMWHIVVER VEHEDRCAGRSVEMCDKSUSVEVSVCETGSNTEESVADLTLLKT NLANLKEVRSIGGCDCSVDTVTVSFYERGSRTEESVADLTLLKT NLANLKEVRSIGGCDSVDTVTVSFYERGSRTEESVADLTLLKT NLANLKEVRSIGGCDSVDTVTVSFYERGARGAVTTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVTETRTVAVAGEGRVADINATLAGSPPQITVGLTASK RSVGVGDPEVGESLENPQQPAGHTTLAGGPPQITVGLTASK RSVGVGDPEVGESLENPQQPAGHTTLAGGPPQITVGLTASK RSVGVGDPEVGESLENPQQPAGHTTLAGGPPQITVGLTASK RSVGVGDPEVGESLENPQPQAGHTTLAGGPPQITVGLTASK RSVGVGDPEVGESLENPQPAGHTSVHATDQIAAGLYACTIN ESTLKSIMKKLGHNKDSNGAKNLQFVGINGGTETISSIDSSD GESSSSSDDEGDVITSPLEEEEEDEDTRGMAGGHAVNIEGL ESTLKSIMKKLGHNKDSNGAKNLQFVGINGGTETISSDSSD SESSSSDDEGDVITSPYLEEEEEEDEDTRGMAGGHAVNIEGL KSARVEDEMQVQSCEPEKVEIRERYELSERNLSACKLLKNTIND PKALITSKMMFCHINIGHEMPKSQKSAIPAMGYIAAFEAI SPDVLRYITILADGRGNTALHYSVSHSNFEIVKLLLDADVCNVD HQNKAGYTPINLAALAAVEREKDMRIVEELFGGGDVNAKASQAG QTALMLAVSHGRIDMVKCLLACGADVNIQDEGSTALMCASEHG HVBIVKLLLAQPGCNGHLEDNDGSTALSIALBAGHKDIAVLLYA HVMFAKAGSFGTPFILGRNTSSPGTPHRGSFD HVBIVKLLLAQPGCNGHLEDNDGSTALSIALBAGHKDIAVLLYA HVMFAKAGSFGTPFILGRNTSSPGTPHRGSFD SVPRAGGMBTGAABELYDDALLGILGHVGNOPELEVLFGFILYR RQELEEKIRRKEEEEAKTVSAAAAEKEPVDVVQEIEIDSTTEL DCGQEVEKVEVPPGFVKKBHAGSQCRAEPGAVAGAAEVPR\EPPI LRRIGEGFQKNPFDSYNGAVERNYTWSGDYTDLEVRYPVFKHVVK GKQVSVALSSSIRVAMLEENGERVLMGGKLTHKINTESSLWSL EPPKCVLVNLSKVCEYPWNAILEGEPIDIDKINKERSMATVDE EEGAVLDRLITPTYHQKLQGKPQSHELKVHEMLKKGWDAEGSPFR GRFDPAMFNISPGAVOPSKYCSDCOMKLAANRIVETIL PQRIQOWQOSPCIABEHGKLLERIREGOGSARTLLQEMERPH VALRHMERCYAKYBSQTTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPEHSRDPLVQWKLDEFGSRONTATMTN RAGLLALMLHQTTQHDPLTTDLRSSADR 5420 117 1733 NEBGGACPFKGGASGRILLSERDFGSVAGGEERPLGWWVLIGG	1	1		AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAA
RSVAVGAERIMMDIVVYHRGSRSCKDAAVGTLVEMMINCGGVUTE AMGUVTTEADKEIELQQQTIELELQQOTIELEKTHIPEMT KLKQELQAAGSRKKUDKATMAQPLVPSKVVEAVVQTRDQMVGSH MDLVDTCVGTSVETMSVGISCQPECKNKVVQPELPMNWMIVKER VEMBRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT NLMLKEVRSIGCDCSVDVTVCSPKECASRGVNTEAVSQVEAAV MAVPRADQDTSTDLEQVNQFTNTEATILIESCTNTCLSILDKO TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVKYKESGVGGININDNYLKMRTIACGPDOITVGLTASH RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLASCQ TLLAENYSELARAFGEPHSQMSSLNSQLISTLSSINSVMKSAST EELRNPDPCKTSLGKITGSYLGYTCKCGGLQGSGPLSSOTSQPE QRVGTSEGRFISSLDAPPTQEGTLSPVNLTDDQIAAGLVACTNN ESTLKSIMKKROGNKDSNGAKNLOFVGVINGGYETTSSDDSSD ESSSSSDDDCDVIEYPLEEBEEBEDDDTRGMAGHHAVNIEGL KSARVEDEMQVQSCEPEKVEIRERYFLSEKMLSACNLLLKNTIND PKALTISKMMRFCLNTLGHEMPRVSQXSAIPANVGGYIAAFFRI SPDVLRYVINLADGNGNTALHYSVSHSNFFIVKLLLDADVCNVD HQNKAGYTPIMLAALAAVAERKUTVEELFGGGUNAKASQAG QTALMLAVSHGRIDMVKGLLACGADVNIODDEGSTALMCASEHG HVBIVKLLLAQAGCNGHLEDNGCKNLOFMORGVOPFLRVLFGFLYR KNDFYRAGGMETGAAELYDOALLGIGLOWGVOPFLRVLFGFLYR KNDFYRLLRHENBENGFPFGAAALVLQVEKTFDHMARQDDEKR RQELEEKIRRKEEEEAKTVSAAAAEKEPVPVPVQEIELDSTTEL DGHGEVEKVQPPGPVKEMAHGSALAVDVPLVPDFLRVLKG GKQVSVALSSSIRVAMLEENGERVLMSGCHHKINTESSLWSL EBGKCVLNNLSKVGEYWNAILEGEEPIDDKINKRSMATVDE EEQAVLDRLITPDYHQKLQGKPGSHELKVHEMLKKGMDAEGSPFR GGRFPDAMFINISPGAVGF GGRFPDAMFINISPGAVGF SESACEAFGRKSEEEGRRSDTSGFGRSRKHKVUNKHPERADA KOPASLPQC/LGP/DCVRPAQPSSKVCSDDCCMKLAANRIVEIL PQGIQOMQOSPCIAEEHGKKLLERIRECOSARTRLQEMERRFH VKLIKANGECXAKYESQTSFGSMYPTRIEGATRLOFMERRFH VKLIKANGECKYAKYESQTSFGSMYPTRIEGATRLOFMERRFH VKLIKANGECKYAKYESGTSFGSMYPTRIEGATRLOFDVPGNET PQRIQOMLOGSPCIAEEHGKKLLERIRECOSARTRLQEMERRFH VKRIMBECXAKYESGTSFGSMYPTRIEGATRLPCDVYNPQSKT VKRIGOVLCPPHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKKRRAEVDLERVRWWKLBELEFGERNVRTAMTN RAGLLALMLHIGTTQHPLTTDLRSSABG 117 NEGGAGGFFKKGBEGRREGNERVSWYLGGEERPLGWWWLIGG	1			SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEME
AMIGWATERDAKETELQQQTTESLKEKTYRLEVQLRETTHDREMT KLKQELQAAGSKKKUVKATMAQUPSKVVBAVVQTRDQWUGSH MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNMIVKER VEMHDRCAGRSVEMCDKSVSVEVSVCETGSTETSETSUDITLLKT NLANLKSVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTNTSTATLIESCTNTCLSTLDKQ TSTQTVGTERTVAVAGERVKQINSTKTRSIGVGTLLSGHSGFDR PSAVKKESGVGOININDNYLVGLKMRTIACGPPQITVGLTASR RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYTERTQKLLASCQQ TELLAENYSELARAFGEPHSQWGSTNSQLISTLSSINSVWKSAST EELRNDPPQKTSIGKITGSYLGYTCKCGGLQSGSPLSSISTSQVEXSAST EELRNDPPQKTSIGKITGSYLGYTCKCGGLQSGSPLSSGTSQPE QBVGTSEGKPISSLDAPPTQESTPVALITDQLAAGLVACTNN ESTLKSIMKKRGONKDSNGAKKNLQFVGINGGYETTSSDDSSD ESSSSEDDECDVIEYPLEEBEBEBEDTBRAAGGHAVNIEGL KSARVEDEMQVQGCEPERVETRERYELSBKMLSACHLKNTIND PKALTSKDMRFCLNTLGHENFRVSSQXSAIPAWGDYIAAFBAI SPDVLRYVINLAADGKNTALHYSVSHSNFEIVKLLLDADVCNVD HONKAGYTPIMLAALAAVBAEKDMRIVSSHSASIPAWGDYIAAFBAI SPDVLRYVINLAADGKNTALHYSVSHSNFEIVKLLLDADVCNVD HONKAGYTPIMLAALAAVBAEKDMRIVSSHAGHENGASEHG WHEIVKLLLAQPGCNGHLEDDAGDSTALSIALEAGHKDIAVLLYA HWAFAKAGSPGTPRLGRKTSPGPTHRGSFD SVPRRAGGOMETGAABELYDOALGIUNGVKVGDFLRVLFGFLYR KTDFYRLLRHPSDRNGFPPGAAQALVLQVFKTPDHMARQDDEKR RQLEEKIRRKEEBEAKTVSAAAAEKEPVPVVQEIEIDSTTEL DGGQVEKVQPPGPVKEMAHGSGAEAPGAVAGAAEVPR\EPPI LPRIQGQFQKNPDSYNGSVALSSSSIRVAMLEENGERVLMGGKLTKKINTESSLUSL EGGKCVLIVILSKVGGYWMNATLEGEEPIDIDKINKERSMATVDE EGQAVLDRLTPDYHQKLQGKPQSHEKVMGKHEMKKMDAEGSPFR GQRFDPAMFNISPGAVQF SSESACEAFGRRKSEEGERRSDTGGFGRSKHKVDWKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAARRIVEIL PQRIQOMQQSPCIABEHGKKLLERIRECOSARTRLQEMERRFH VALRHMERCYAKYESOTSFGSMYPTRIEGATRLFCDVYNPQSKT VCKRLQVLCPPHSREGEGRSDTVLDFVGYSCGHFINPR VALRHMERCYAKYESOTSFGSMYPTRIEGATRLFCDVYNPQSKT VCKRLQVLCPPHSRDPKYPADEVGCPLVRVVFLITGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRVWKLDELEFGERNVRTAMTNIN RAGLLALMLHIGTIQHDPLTTDLESSADR SPADO				TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEC
KLKOSŁOAGSRKKUDKATMAQPLUFSKVEADVOTRDOMVGSH MDLUDTICVETSVETNSVGI SICQPECKIKVVOPELPINNWI LYKER VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT NLNLKEVRSIGCODCSVUDTVCSPELPINNWI LYKER VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT NLNLKEVRSIGCODCSVUDTVCSPELBANGOVEANV MAVPRTADQDTSTDLEQVHOFTNTETATLIESCTRICLSTLDKQ TSTQTVETRTVANGEGRVKDINSTIKTSIGVGTLLSGRSGFDR PSAVKTKESSVGGININDNIVGIKHRITIACGPDI,TVGLITASR RSVGVGIDPVGESLEMPQPQAPLGMMTGLDHYIERIQKLLAGQ TLLAENYSELLARAFGEPHSQMSGLNSOLISTLSSINSVMKSAST EELRNDPGKTSIGKITGSYLGYTCKCGGLQSSSPLSSGTSGPE QRVGTSEGKPISSLDAFPTQEGTLSSVUNLTDDQIAAGLYACTINN ESTLKSIMKKRONKDNSNGAKKNLQPVGINGGTETTSSDDSSD ESSSSSEDDECDVIEYPLEEEEEEDEDTRGMAEGHHAVNIEGL KSARVEDEMQVORCEPEKVEIRFYLLSKRINGACKLLKNTIND PKALTSKOMRFCLNTI,OHEMFRVSSQXSAIPAMVGDYIAAFEAI SPDVLRYVINLADGNONTALHYSVSGXSAIPAMVGDYIAAFEAI SPDVLRYVINLADGNONTALHYSVSGXSAIPAMVGDYIAAFEAI SPDVLRYVINLADGRONTALHYSVSGXSAIPAMVGDYIAAFEAI SPDVLRYVINLADGRONTALHYSVSGXSAIPAMVGDYIAAFEAI SPDVLRYVINLADGRONTALHYSVSGXSAIPAMVGDYIAAFEAI SPDVLRYVINLADGRONTALHYSVSGXBAIPAMVGDYIAAFEAI SPDVLRYVINLADGRONTALHYSVSGXBAIPAMVGDYIAAFEAI SPDVLRYVINLADGRONTALHYSVSGXBAIPAMVGDYIAAFEAI SPDVLRYVINLADGRONTALHYSVSGXBAIPAMVGDYBCSTALKASEHG HVBIVLLLIAQPGCNGHLEBNSTALSTEERJFKDGNAMCSPGRE GRADLAGAELYPOALLGILQPVGNVQDFLRVLFGFLYR KTDFYRLRHRPSDRWGFPFGAAQALVLQVFKTFDHMARQDDEKR RQLEEKIRRKEEEEAKTVSAAAAEREPVPVVQEIEIDSTTEL DCHQEVEKVQPPGPVKEMMAGSQEAEPGAVAGAAEVDR,PEPJI LPRIGSGFGKNPDSVNGAVRENYTNSQDYTDLEVRVPVPKHVVK GKQVSVALSSSSIRVAMLEENGERVLMEGKLTHKINTESSLWSL EPGKCVLVNLSKVGEYMMAILEGEEPJDIJKINKERSMATVDE EBGAVLDALTPDYHQKLQGKPGSHBLKVHEMLKKGWDAEGSPFR GGRFPDAMFNISPGAVQF GGRFSSSTSTOAMLEGERSPFLGFRABEG SESACEAFGRRKSEEEGRRSDTSGFGRRSHKVNMKHPERADA KDPASLPQC/LOP/DCVRPAQPSSKYCSDDCGMKLANRTYEIL PQRIQOWQOSPCIAEEHGKKLLERIRREQQSARTHLCGMERRFH ELEAILBARQQAVREDEESNEGDSDDTDLGITCVSCCHPINPR VALRAMERCYAKYESGTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRQVLCPEHSRDPKVPADEVCCGCPLVRDVFELTTGDFCRLPK RQCNRHYCWERLRRAEVDLERKRWWKLDELFEGERNDKTAMTN RAGLALMLHGTIGVDEPLTDLRSSADR				RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE
MDLVDTCVGTSVETNSUGISCOPECKIKVVGPELPRINWHIVERE VEMHDRCAGRSVEMCDKSVSVEVSVCETGSITESSVDDLTLLKT NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVITEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVTLLSGSFOR PSAVKTKESGVGQININDNYLVGLKWRITACCGPOI-TVGLTASR RSVGVGDDPVGSELERPQPQDALGMMTGLDHYIERTQKLLAEQQ TLLAENYSELARAFGEPHSQMSLNSQLISTLSSINSVMKSAST EELRNDFQKTSIGKTTGSYLGYTCKGGLQSGSPLSSGTSQPE QBVGTSEGRP ISSLDAPPTQEGTLSFVNLTDDQIAAGLYACTNN ESTLKSIMKKRONKDSNGKKNLQFVGINGGYETTSSDDSSD GSSSSDDBECDVIEPVLEEEBEEDDTRGMAEGHHAVNIEGL KSARVEDEMQVQECEPEKVEIRERYELSEKMLSACULLKNTIND PRALITSKDMRFCLNTLQHEWFRVSSGXSAIPAMVGDYIAAFBAI SPDVLRYVINLADGRONTALHYSVESHSPEIVKLLLDADVCNVD HQNKAGYFTIMLAALAAVEAEKDMRIVEELFGCGDVNAKASQAG OTALMAUSHIGEIDMVGGLLAGADVNIODDEGSTALMCASEHG HVEIVKLLLAQPGCNGHLEDNDGSTALSIALBAGHKDIAVLLYA HVWFAKAGSPGTTRLGRKTSPGFTHRGSFD SVERRAGGDMETGAAELYDQALGILGHVONVQDFLRVLFGFIJYR KTDFTRLLHRPSDRNGFPFGAAQALVLQVFKFFDHMARQDDEKR RCLEKKIRKKEEEAKTVSAAAEKEPUVVPVEIEIDSTTGL DGHQEVEKVQPPGPVKEMAHGSQBAEAPGAVAGAAEVPR\EPPI LPRIQSQFCKNPDSVNGAVRENYTNSQDYTDLEVKVPVPKHVVK GKQVSVALSSSSIRVAMLEBROFVLMSGKLTHKINTESSLWSL EPGKCVLVNLSKVGEFWMNA LLEGEEPIDIJKINKERSMATVDE EEQAVLDRLTPDYHQKLQGKPQSHELKVHEMLKKGWDAEGSPFR GGRFDPAMFNISPGAVQF SSEACEAFGRKSEEGGRSTDTSGFGRSRKFINKMWKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PQRIQONGSPCIABEHGKKLLERTRREQGSARTHLGEMERFFH ELEAILLBAKQQAVREDEESNEGDSDDTDLOIFCVSCCHPINPR VALRRIMERCYAKYESOTSFGSNYPTRIGATRLFCDYVNPQSKT VCKRQVLCPERSOPKVPADEVCCCPLVRDVPELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVWYKLDELFEGERNVRTAMTN RAGLLALMLHGTTIOGDEPTTLRLSSADR	1	Į.		WI CORI ON A CERVITARIA THE SERVICE OF THE SERVICE
VEMEDRCAGRSVEMCUSSVEVGETGSTEESUNDLITLIKT NIAINLKEWRSIGCGGCSUDVIVUSSPKCASRGWITEAVSQVEAAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVKTKESGVGQININDLYGLKMRTIACGPPGI TVGLTASR RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLASQQ TLLAENYSELAEAFGEPHSQWGSLNSQLISTLSSINSVMKSAST EELRNDPPKKTSLGKITGSYLGYTCKCGGLOSGSBLSSGTSQPE QRVGTSEGKPISSLDAPPTQEGTISPVALTDQLAAGLYACTNN ESTLKSIMKKKDONKDBNGAKKNLQFVGINGGYETTSSDGSSD ESSSSSDDECDVIEYPLEEEEEEDDTRGMAEGHHAVNIEGL KSARVEDEMQVQCCEPEKVSITRRYSLGSKHLSACNLLKNTIND PKALTSKDMRFCLNTLQHEWRRVSSQXSAIPAMVGDVIAAFEAI SPDVLRYVINLADGNGNTALHYSVSHSNFEIVKLLDADVCNVD HONKAGYTPINLAALAAVEAEKOMRIVEELFGCGDVNAKASQAG QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG HVBIVKLLLAQPGCNGHLENDNGSTALSIALEAGHKDIAVLIYA HVMFAKAGSFGTTRLGRKTSFGPTHRGSFD SVPRAGGDMETGAAELYDQALLGILQHVGNVQDFLRVLFGFLYR KTDFYRLLRHPSDRMGFFFGAAQALUQVKFTPHMARQDDEKR RQELEEKIRKEEEEAKTVSAAAAEKEPVDVPVQEIEIDSTTEL DCHQEVEKVQPPGPVKEMAHGSQEAEAFGAVAGAAEVPR\RPPI LPRIQSFGKOKNPDSYNGAVENTWSQDYTDLEVRVPVPKHVVK GKQVSVALSSSIRVAMLEENGERVLMEGKLITKINTESSLWSL EFGKCVLVNLSKVGEVWNNAILEGGEFIDIDKINKERSMATVDE EEGAVLDRLTBYPTYQKLQGFLGWNDTEESPFLGFRAAEEC GGRFDPAMFNISFGAVQF GGRFDPAMFNISFGAVQF STSEACEAFGRRKSEEEGRRSDTSGFGRSKHKKWNKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PQRIQQWQQSPCIAEEHGKKLERIRREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSGHFINPR VALRHMERCYARYESGTSFGSMYPTHIGGATRLFCDVYNPQSKT YCKRQVLCPHSRDPKVPADEVCGCPLVROVPELTGDFCRLPK PCRCULVHLERSPREVPRADEVCGCPLVROVPELTGDFCRLPK RCCCHLVCHSLRRAEVDLERVRWYKLDELFEQERNVRTAMTN RAGLALMLHQTIQDPLTTDLRSSADR	j			MDLUDTCUCTCUCTCUCTCLCCODECUMENTARIA
NINIKEVRSIGGEDESVDVTUCS PRECASRGYNTEANSQUEAAV MAVPRIADODISTDLEGGYVAGTINTEATLIESCTNTCLSTLDKQ TSTQTVETRTVAVGEGRVKDINSSTKTRS IGVGTLISCHSGFDR PSAVKTKESGVGGININDNILVGLKMRTIACGPPQITUGLTASR RSVGVCDDPVGESLENPQDQAPLGMMTGLDHYIERIGKLARQQ TLLAENYSELAEAGEPHSQMGSLNSQLISTLSSINSVMKSAST EELENPPGOKTSLGKITGSLYGTKCGGLQSGSPLSSQTSQPE QEVGTSEGKPISLDAPPTQEGTLSPVNLITDQTAAGLYACTNN ESTLKSIMKKKDGNKDSNGAKKNLQFVGINGGYETTGSDDSSSD DESSSSEDDEDVIEYPLEEBEEDEDDLTGMAGGHHAVNIEGL KSARVEDEMQVQECEPEKVEIRERYELSEKMLSACNLLKNTIND PKALTSKOMFCLNTLQHEMFRVSSQKSAIPAMVGDYIAAFEAI SPDVLRYVINLADGNGNTALHYSVSHSNFEIVKLLLDADVCNVD HQNKAGYTPIMLAALAAVEAEKOMRIVELEGCGDVNAKASQAG QTALMLAVSHGRIDMWGLACGADVNIODDEGSTALMCASEHG HVBIVKLLLAQFGCNGHLEDNDGSTALSIALEAGHKDIAVLLYA HWFAKAQSFGTPRLGRKTSPGPTHRGSFD SVFRAGGDMETGAAELYDQALLGILQRVGNVQDFLRVLFGFLYR KTDFYRLLRHPSDRMGFPPGAAQALVLQVFKTFDHMARQDDEKR RQLEEKIRRKEEEEAKTAAAAEKEPUPVPVQEIELDSTTEL DCHQEVEKVQPPGVKEMAHGSQEAEAPGAVAGAAEVPR\EPPI LPRIQEGFGKNDDSYNGAVRANTWRGDYTDLEVRVPVPKHVVK GKQVSVALSSSIRVAMLEENGERVLMEGKITHKINTESSLWSL EPGKCVLVNILSKVGEVWANILEGGEPIDIDKINKERSMATVDE EEGKCVLVNILSKVGEVWANILEGGEPIDIDKINKERSMATVDE EEGKCVLVNILSKVGEVWANILEGGEPIDIDKINKERSMATVDE EEGKCVLVNILSKVGEVWANILEGGEPIDIDKINKERSMATVDE EEGKCPLVANILSKVGEVRANDENGFFGSFFLGFRAAEEG SESEACEAFGRRKSEEEGRSDTSGFGRSKKHKVNWKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PQRIQQQQSPCIAEBHGKKLERIRRQQSARTRQEMERRFH ELEAIILRAKQQAVREDEESNEGDSDDTDLJCYCSGHINPR VALRHMERCYARYESGTSFGSMYFRIEGATRLFCDVYNPQSKT YCKRGOVLCPHSRDPKVPADEVCGCPLVRAVPVELECDFCLPK RQCNRHYCWEKLRRAEVDLERVRWYKLDELFEQERNVRTAMTN RAGLALALHLHQTIQHDPLTTDLRSSADR				VEMHDRCAGRSVEMCDKSVSVEVSVSVSVSVSVSVSVSVSVSVSVSVSVSVSVSVS
MAVPETADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETBTVAVQGEGRVLDINSTKTRSIGVGTILISGHSGFDR PSAVKTKESGVGQININDNYLVGLKMRTIAGGPQJ.TVGLTASR RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKILAEQQ TILLAENYSELLAEAFGEPHSQGSLNSQLISTLSSINSVMKSAST EELRNPPFQKTSLGKITGSYLGYTCKCGGLQSGSPLSSQTSQPE QEVGTSEGKPISSLDAPPTQEGTLSPVNLTDDQIAAGLYACTNN ESTLKSIMKKKCMKOSNGAKKNLQFVGINGGYETTSSDGSSD ESSSESDDECDVIEYPLEEEEEEEDDTGMAEGHHAVNIEGL KSARVEDEMQVQECEPPEVETREMEYELSEKMLSACNLLKNTIND PKALTSKDMRFCLNTLQHEWFRVSSQXSAIPAMVGDYIAAFEAI SPDVLRYVINLADGNGNTALHYSVSSGXSAIPAMVGDYIAAFEAI SPDVLRYVINLADGNGNTALHYSVSSGNSAIPAMVGDYIAAFEAI SPDVLRYVINLADGNGNTALHYSVSHSNFEIVKLLDADVCNVD HONKAGYTPIMLAALAAVEABKOMRIVEELFGCGGVNAKASQAG QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG HVBIVKLLLAQPGCNGHLEDNDGSTALSIALBGHKDIAVLLYA HVNFAKQSPGTTRLCRKKTSPGFTHRGSFD 5418 24 1133 SVPRAGGDMETGAAELYDQALLGILOHGGNOODFLRVLFGFLYR KTDFYRLLKHPSDRMGFP PGAAQALVLQVFKTFDHMARQDDEKR RQELEEKIRRKEEEEAKTVSAAAAEKEPVEVPVQEIEIDSTTEL DCHQEVEKVQPPGPVKEMAHGSQEAEAGAAVGAAEVRN\RPPI LPRIQEQFGKNPDSYNGAVRENTWSQDYTDLERVEVPYRHIVK GKQVSVALSSSIRVAMLEENGERVLMSGKLTHKINTESSLWSL EPGKCVLVNLSKVGEWWNAILBEGEFIDIDKINKERSMATVDE ESQAVLDRLTFPYHQKLQGAPGSHELKVHEMLKKGMDAEGSFFR GGRFDPAMFNISFGAVQF 5419 1395 259 GTHPLDPDLVSRTSVQGPLMTMACPGMSDTEESPFLGFRAAEEG SESSACEAFGRRKSEEEGRRSDTSGFGRSKHKVNWHPPERADA KDPASLPQC/LGF/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PORIQOMQOSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH ELEAILRAKQQAVREDEESNEGDSDDTDLQIRCVSGHPINPR VALRHMERCYARYESGTSGSMYBTIEGATRLFCDVYNPQSKT YCKRLQVLCPBHSNDPKVPADEVCGCPLVROVPLETGDFCRLPK PCCNRHYCWEKLRRAEVDLERVRWYKLDELFEQERNVRTAMTN RAGLALMLHGTIQHPLTTDLRSSADR	1 .			NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSOVEAAV
TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVKTKESGVGOININDNYLVGLKMRTIACGPPQI-TVGLTASR RSVGVGDDPVGESLENPQPQAPLIGMMTGLDHYIERICKLLAEQQ TLLAENYSELAEAFGEPHSQMGSLISGLISTLSSINSVMKSAST EELERNPPPGVTSLGKITGSYLGYTCK.GGGLGSGSPLSGOTSQPE QEVGTSEGKPISSLDAFPTQEGTLSPVNLTDDQIAAGLYACTNN ESTLKSIMKKKGMKDSNGAKKNLQFVGINGGYETTSSDDSSSD ESSSSESDDECDVILEPYLEEEEEEDEDEDETTGMAEGHHAVNIEGL KSARVEDEMQVQGCEPEKVEIRERYELSEKMLSACNLLKNTIND PKALTSKDMRFFCLNTLQHEWFRVSGXSAIPANVGDVIAAFEAI SPDVLRYVINLADGNGNTALHYSVSHSNFEIVKLLLDADVCNVD HONKAGYTFIMLAALAAVEAEKDMRIVELLFGCGDVMAKASQAG QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG HVBIVKLLLAQPGCNGHLEDNDGSTALSIAALEAGHKDIAVLLYA HVMFAKAQSFGTPRLGRKTSPGPTHRGSFD \$VPRAGGDMETGAAELYDOALIGILQHVGNVQDFLRVLFGFLYR KTDFYRLLRHPSDRMGFFPGAAQALVLQVFKTFDHMARQDDEKR RQELEEKIRRKEEEEAKTVSAAAAEKEPUPVQEIEIDSTTEL DCHQEVEKVQPPGPVKEMAHGSQPAAGAAEVPR\EPPI LPRIQEGFQKNPDSYNGAVRENYTWSQDYTDLEVRVPVKHVVK GKQVSVALSSSIRVAMLEENGERVLMGKLTHKINTESSLWSL EPPKCVLVNLSKVGSYWANALLEGEEPIDIDKINKERSMATVDE EEQAVLDRLTFDYHQKLQGKPQSHELKVHEMKKKGMDAGGSPFR GQRFDPAMFNISPGAVQF \$CHPLDPDLYSTSVGQFLMTMACPGMSDTEESPFLGPRAAEEG SESEACEAFGRRKSEEEGRRSDTSGFGRSKKHVNWKHPERADA KOPASLPQC/LGF/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PCRRIQWOGPCTAEEHGKKLLERIRREQQSARTRLCPEMERRFH ELEAILLRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHFINPR VALRHMERCYAKYESQTSFGSMYPTRIEGATTALFCDVYNPQSKT YCKRLOVLCOPHSSRDPKYPADEVCGCPLYNDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRWYKLDELFFQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR	}			MAVPRIADODISTDLEOVHOFINITETATLIESCINICLSTLOKO
PSAVKTKESGYGOININDNYLVSLKMRTIAGGPPOLTVGLITASR RSVGVGDDPVGSLENPQDADLGMMTGLDHYIERIQKLLAEQQ TLLAENYSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSAST EELRNPDFQKTSLGKITGSYLGYTCKGGGLQSGSPLSSQTSQPE QBVGTSEGKPISSLDAFPTQEGTLSSVULTDDQLAAGLYACTNN ESTLKSIMKKKGDKDSNGAKKNLQFVGINGGYETTSSDDSSD ESSSESDDECDVIEYPLEEEEEEDEDTRGMAEGHHAVNIEGL KSARVEDEMQVQECEPERVEIRERYSLSKMLSACHLLKNTIND PKALTSKDMKFCLNTLQHEWFRVSSQXSAIPAMGDVIAAFEAI SPDVLRXVINLADGNGNTALHYSVSHSNFEIVKLLLDADVCNVD HONKAGYTPIMLAALAAAVEAEKDMRIVELLLGADVNIQDDEGSTALMCASEHG HVBIVKLLLAQFGCNGHEDDNGSTALSIALEAGHKODIAVLLYA HVMFAKAQSPGTPRLGRKTSPGPTHRGSFD 5418 24 1133 SVPRAGGDMETGAAELYDOALGILGLGHVGNVODFLRVLFGFLYR KTDFYBLLRHPSDRWGFPPGAAGALVLQVFKTPHMARQDDEKR RQELEEKIRRKEEEBAKTVSAAAAEKEPVPVVQEIEIDSTTEL DCHGCVEKVQPPGPVKEMAHGSGREAEAGAVAGASEVPRPPPI LPRIQEGFQKNPDSYNGAVRSNYTMSGDYTDLEVVPVPKHVVK GKQVSVALSSSIRVAMLEENGERVLMGGKLTHKINTESSLWSL EPGKCVLVNLSKVGEYWMAILLEGEFPIDIDKINKERSMATVDE EEGAVLDRLTFDYHQKLGGKPQSHBLKVHEMKKKMDABESPFR GGRFDPAMFNISPGAVQF 5419 1395 259 GTHPLDDDLJSTSVQGPLMTMACPGMSDTEESPFLGPRAAEEG SESEACEAFGRRKSEEEGRRSDTSGFGRSRKHKVNKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PQRIQOMQOSPCIAEBERDKKLLBERIRERQOSARTRLQEMERFPH ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHFINPR VALRHMERCYAKYESQTSFGSMYPTRIEGATTRLFCDVYNPGSKT YCKRLGVLCQFHSKDPLYADEVCCGPLVROVFELIGGDFCRLPK RQCNRHYCWEKLRRAEVUDLERVRVWYKLDELFPQERNVTRAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR		•		TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR
RSVGVGDDPVGESLENPQDQAPLGMMTGLDHYIERIQKLLAEQQ TLLAENNYSELABAFGEPHSQMGSLNSQLISTLSSINSVMKSAST EELRNPDPQKTSLGKITGSYLGYTCKCGGLQSGSPLSSQTSQPE QBVGTSEGKPISSLDAPPTQEGTLSPVNLITDDQIAAGLYACTNN ESTYLKSIMKKKDGNNOGAKKNLQFVGINGGYETTSSDDSSD ESSSSEDDECDVIEYPLEEEEEEDEDTRGMAEGHHAVNIEGL KSARVEDEMQVQECEPEKVSIRERYFLSEKMLSACKLLKNTIND PKALTSKDMRFCLNTIQHEWFRVSGXSAIPAMGDYIAAFEAI SPDVLRYVINLADGNGNTALHYSVSHSNFEIVKLLLDADVCNVD HONKAGYTPIMLAALAAVEREKDMRIVEELFGCGDVNAKASQAG QTALMLAVSHGRIDMVKGLLACGADVNIODDESTALMCASEHG HVBIVKLLLAQPGCNGHLEDNDGSTALSIALEAGHKDIAVLLYA HNNFAKAQSPGTPRLGRKTSPGTHRGSFD SVFRAGGDMBTGAABLYDOALLGILQHVGNVQDFLRVLFGFLYR KTDFYRLLRHPSDRMGFPPGAAQALVLQVFKTFDHMARQDDEKR RQELEKIRRKEEEEAKTVSAAAAEKEPVDVPVQEIEIDSTTEL DCHQEVEKVQPPGPVKEMAHGSQBEAFQAVWAGABEVPR\PPPI LPRIQSOFQKN PDS XNGAVRENYTWSQDYTDLEVRVPVPKHVVK GKQVSVALSSSIRVAMLEENGERVLMEGKLTHKINTESSLWSL EEGKCVLIVILSKVGEFYWMAILEGGEFIDIDKINKFRSMATVDE EEGAVLDRLTFDYHQKLQGKPQSHELKVHEMLKKGWDAEGSPFR GQRFDPAMFNISPGAVQF SSEACEAFGRRKSEEEGRRSDTSGFGRSRHKVNWKHPERADA KDPASLPQC/LGP/DCVVBAPGSSKYCSDDCGMKLAANRIYEIL PQRIQQWQQSPCIABEHGKKLEERIRREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHPINPR VALRHMERCYAKYESQTSFGSMYPTRIEGGATRLCCDVYNPQSKT YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEQERNVTTAMTN RAGGLALMHLIQTIQHDPLITDLRSSADR	1			PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQLTVGLTASR
EEILRNPDFQKTSLGKITGSYLGYTCKCGGLQSGSPLSSQTSQPE QBVGTSEGKPISSLDAPPTQEGTLSPVNLTDQIAAGLYACTNN ESTLKSIMKKKDGNKDSNGAKKNLQFVGINGGYETTSSDDSSSD ESSSSESDDECDVIEYPLEEEEEEDDTRGMAEGHHAVMIEGL KSARVEDEMQVQCEPEKVEIRERYELSEKMLSACNLLKNTIND PRALTSKDMRFCLNTLQHEWFRVSSQXSAIPAMVGDYIAAFEAI SPDVLRTVINLADGNGNTALHYSVSHSHFEIVKLLLDADVCNVD HQNKAGTPINLAALAAVEAEKDMRIVEELFGCGDVNAKASQAG QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG HVBIVKLLLAQPGCNGHLEDNDGSTALSIALEAGHKDIAVLLYA HVMFAKAQSPGTPRIGRKTSPGPTHRGSFD 5418 24 1133 SVFRAGGDMETGAAELYDQALLGILCHVGRVQDFLRVLFGFLYR KTDFYRLLRHPSDRMGFPPGAQALVLQVFKTFDHMARQDDEKR RQLELEEKIRRKEEEEAKTVSAAAAEKEPVPVPVQEIEIDSTTEL DGHQEVEKVQPPGPVKEMAHGSQEAEAPGAVAGAAEVPR\EPPI LPRIQEGFQKNPDSYMGAVRENYTMSQDYTDLEVRVPVPKHVVK GKQVSVALSSSSIRVAMLEENGERVLMEGKLTHKINTESSLWSL BFGKCVLVNLSKVGEFWWNAILEGEEPIDIDKINKERSMATVDE EEQAVLDRLTFDYHQKLQGKPQSHBLKVHEMLKKGWDAEGSPFR GGRFDPAMFNISPGAVQF 5419 1395 259 GTHPLDPDLVSTTSVQGPLMTMACPGMSDTEESPFLGPRAAEEG SESEACEAFGRKSEEEGRRSDTSGFGRSRKHKVNWKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYELL PQRIQQWQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHPINPR VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVNNPQSKT YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRWYKLDELFFQGRNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR	1			RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEOO
QRVGTSEGKPISSLDAFFTQEGTLSPVNLTDDQLAAGLYACTNN ESTLKSIMKKKDGNKDSNGAKKNLQFVGINGGYETTSSDDSSDD ESSSSEDDECDVIEYPLEEEEEEDEDTRGMAEGHHAVNIEGL KSARVEDEMQVQBCEPEKVEIRERYELSEKMLSACNLLKNTIND PKALTSKDMRFCLNTLQHEWFRVSSQKSAIPAMVGDYIALFEAI SPDVLRVVINLADGNGNTALHYSVSHSNFEIVKLLLDADVCNVD HQNKAGYTPIMLAALAAVEAEKDMRIVEELFGCGDVNAKASQAG QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG HWBIVKLLLAQPGCNCHLEDNDGSTALSIALBAGHKDIAVLLYA HVMFAKAQSPGTPRLGRKTSPGPTHRGSFD 5418 24 1133 SVPRAGGDMBTGAAELYDQALULQVFKTFDHMARQDDEKR RQELEEKIRRKEEEEAKTVSAAAAEKEPVPVPVQBIEIDSTTEL DCHQEVEKVQPPGPVKEMAHGSQEAEAPGAVAGAAEVPR\EPPI LPRIQEGFQKNPDSYNGAVRENYTWSQDYTDLEVRVPVPKHVVK GKQVSVALSSSIRVAMLEENGERVLMEGKLTHKINTESSLWSL EPGKCVLVNLSKVGEYWWNAILEEGEPIDIDKINKERSMATVDE EEQAVLDRLTFDYHQKLQGKPQSHELKVHEMLKKGWDAEGSPFR GQRFDPAMFNISPGAVQF 5419 1395 259 GTHPLDDDLVSRTSVQGPLMTMACPGMSDTEESPFLGPRAAEEG SESEACEAFGRKSEEEGRRSDTSGFGRSRKHKVNWKHPERADA KOPASIPQC/LGP/DCVRPAQPSSKYCSDDGMKLAANRIYEIL PQRIQQWQQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRPH ELEAIILRAKQQAVREDESBNEGDSDDTDLQIFCVSCCHPINPR VALRIMMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPPHSRDPKVPADEVCGCPPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR	1			TLLAENYSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSAST
ESTLKSIMKKKDONKDSNGAKKNLQFVGINGGYETTSSDDSSSD ESSSESDDECDVIEYPLEEEEEEDDTRGMAEGHHAVNIEGL KSARVEDEMQVQSCEPEKVEIRERYELSEKMLSACNLLKNTIND PKALTSKDMRFCLNTLQHEWFRVSSQKSAIPAMVGDYIAAFEAI SPDVLRYVINLADGNGANTALHYSVSHSNFEIVKLLLDADVCNVD HQNKAGYTPIMLAALAAVEAEKUMRIVEELFGCGDVNAKASQAG QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG HVBIVKLLLAQPGCNGHLEDNDGSTALSIALEAGHKDIAVLLYA HVNFAKAQSPGTPRLGRKTSPGPTHRGSFD SVPRAGGDMETGAAELYDQALLGILQHVGNVQDFLRVLFGFLYR KTDFYRLLRHPSDRMGFPPGAAQALVLQVFKTPDHMARQDDEKR RQELEEKIRRKEEEEAKTVSAAAAEKEPVPVPVQEIEIDSTTEL DCHQEVEKVQPPGVKEMAHGSQBAEAPGAVAGAAEVPR\EPPI LPRIQEGFQKNPDSYNGAVRENYTWSQDYTDLEVRVPVPKHVVK GKQVSVALSSSIRVAMLEENGERVLMSGKLTHKINTESSLWSL EPGKCVLVNLSKVGEYWWNAILEGEPIDIDKINKERSMATVDE EEQAVLDRLTFDYHQKLQGKPQSHELKVHEMLKKGWDAEGSPFR GQRFDPAMFNISPGAVQF 5419 1395 259 GTHPLDPDLVSRTSVQGPLMTMACPGMSDTEESPFLGFRAAEEG SESEACEAFGRRKSEEEGRRSDTSGFGRSRKHKVNWKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PQRIQQWQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHPINPR VALRHMERCYAKYESQTSFGSMYPTRIGATRIFCDYNPQSKT YCKRLQVLCPPHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR	1			EELRNPDFQKTSLGKITGSYLGYTCKCGGLQSGSPLSSQTSQPE
ESSSESDECDVIEYPLEEEEEEEDDTRGMAEGHHAVNIEGL KSARVEDEMQVQECEPEKVEIRRYELSEKMISACNILKNTIND PKALITSKDMRFCLNTIQHEWFRVSSQKSAIPAWGDYIAAPEAI SPDVLRYVINLADGNGNTALHYSVSHSNFEIVKLLLDADVCNVD HQNKAGYTPIMLAALAAVEAEKDMRIVEELFGCGDVRAKASQAG QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG HVEIVKLLLAQPGCNGHLEDNDGSTALSIALEAGHKDIAVLLYA HUNFAKAQSPGTTRLGRKTSPGPTHRGSFD SVPRAGGDMETGAAELYDQALLGILQHVGNVQDFLRVLFGFLYR KTDFYRLLRHPSDRMGFPPGAAQALVLQVFKTFDHMARQDDEKR RQELEEKIRRKEEEBAKTVSAAABEKEPVPVVQVEIEIDSTTEL DGHQEVEKVQPPGPVKEMAHGSQEAEAPGAVAGAAEVPR\EPPI LPRIQEGFQKNPDSYNGAVKENYTMSQDYTDLEVRVPVPKHVVK GKQVSVALSSSSIRVAMLEENGERVLMEGKLTHKINTESSLWSL EFGKCVLVNLSKVGEYWMNAILEGEEPIDIDKINKERSMATVDE EEQAVLDRLTFDYHQKLQGKPQSHELKVHEMLKKGWDAEGSPFR GQRFDPAMFNISPGAVQF 5419 1395 259 GTHPLDPDLVSRTSVQGPLMTMACPGMSDTEESPFLGPRAAEEG SESEACEAFGRRKSEEEGRRSDTSGFGRSRKHKVNWKHPERADA KDPASLPQC/LOF/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PQRIQOWQQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDESNEGDSDDTDLQIFCVSCGHPINPR VALKHMERCYSKYSQTFSGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRWYKLDELFEQERNVRTAMTN RAGLLAIMLHQTIQHDPLTTDLRSSADR	1			QRVGTSEGKPISSLDAFPTQEGTLSPVNLTDDQIAAGLYACTNN
KSARVEDEMQVQECEPEKVETRERYELSEKMLSACNILKNTIND PKALTSKDMRFCLNTLQHEWFRVSSGXSAIPAWGDYIAFFEAI SPPDVLRYVINLADGNGNTALHYSVSHSHDFEIVKLLLDADVCNVD HQNKAGYTPIMLAALAAVEAEKDMRIVEELFGCGDVNAKASQAG QTALMLAVSHGRIDMVKGLLACGADVNIODDEGSTALMCASEHG HVEIVKLLLAQPGCNGHLEDNDGSTALSIALEAGHKDIAVLLYA HVNFAKAQSPGTPRLGRKTSPGPTHRGSFD SVPRAGGDMETGAAELYDQALLGILQHVGNVQDFLRVLFGFLYR KTDFYRLLRHPSDRWGFPCAAQALVLQVFKTPDHMARQDDEKR RQLEEKIRRKEEEEAKTVSAAAAEKEPVDVPVQEIEIDSTTEL DGHQEVEKVQPPGPVKEMAHGSQEAEAPGAVAGAAEVPR\EPPI LPRIQEGFQKNPDSYNGAVKENYTWSQDYTDLEVRVPVPKHVVK GKQVSVALSSSIRVAMLEENGERVLMEGKLTHKINTESSLWSL EPGKCVLVNLSKVGEYWWNAILEGEEPIDIDKINKERSMATVDE EEQAVLDRLTFDYHQKLQGKPQSHELKVHEMLKKGWDAEGSPFR GGRFDPAMFNISFGAVQF S419 1395 259 GTHPLDPDLVSRTSVQGPLMTMACPGMSDTEESPFLGPRAAEEG SESEACEAFGRRKSEEEGRRSDTSGFGRSRKHKVNNKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL FQRIQQWQQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHPINPR VALRHMERCYSARYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR	1			ESTEKSIMKKKDGNKDSNGAKKNLQFVGINGGYETTSSDDSSSD
PKALTSKDMRFCLNTLQHEWFRVSSQKSAIPAMVGDYIAAPEAI SPDVLRYVINLADGNGNTALHYSVSHSNFEIVKLLLDADVCNVD HQNKAGYTPIMLAALAAVEAEKDMRIVEELFGCGDVNAKASQAG QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG HVBIVKLLLAQPGCNCHLEDNDCSTALSIALEAGHKDIAVLLYA HVNFAKAQSPGTPRLGRKTSPGPTHRGSFD SVPRAGGDMBTGAAELYDQALLGILQHVGNVQDFLRVLFGFLYR KTDFYRLLRHPSDRMGFPPGAAQALVLQVFKTFDHMARQDDEKR RQELEEKIRRKEEEEAKTVSAAAAEKEPVPVPVQEIEIDSTTEL DCHQEVEKVQPPGPVKEMAHGSQEAEAPCAVAGAAEVPR\EPPI LPRIQEQFQKNPDSYNGAVRENYTWSQDYTDLEVRVPVPKHVVK GKQVSVALSSSIRVAMLEENCERVLMEGKLIHKINTESSLWSL EPGKCVLVNLSKVGEYWWNAILEGEEPIDIDKINKERSMATVDE EEQAVLDRLTFDYHQKLQGKPQSHELKVHEMLKKGWDAEGSPFR GQRFDPAMFNISPGAVQF SESEACEAFGRRKSEEEGRRSDTSGFGRSRKHKVNWKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PQRIQQWQSPCIABEHGKKLLERIRREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHPINPR VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLERAEVDLERVRWYKLDELFEQERNVRTAMTN RGGLALMLHQTIQHDPLTTDLRSSADR			•	ESSSSESDDECDVIEYPLEEEEEEEDEDTRGMAEGHHAVNIEGL
SPDVLRYVINLADGRÖNTALHYSVSHSNFEIVKLLLDADVCNVD HQNKAGYTPIMLAALAAVEAEKDMRITVEELFGCGDVNAKASQAG QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG HVEIVKLLLAQPGCNGHLEDNDGSTALSIALEAGHKDIAVLLYA HVNFAKAQSPGTPRLGRKTSPGPTHRGSFD SVPRAGGDMETGAAELYDQALLGILQHVGNVQDFLRVLFGFLYR KTDFYRLLRHPSDRMGFPPGAAQALVLQVFKTFDHMARQDDEKR RQELEEKIRRKEEEEAKTVSAAAAEKEPVPVPVQEIEIDSTTEL DGHQEVEKVQPPGPVKEMAHGSQEAEAPGAVAGAAEVPR\EPPI LPRIQEQFQKNPDSYNGAVRENYTMSQDYTDLEVRVPVPKHVVK GKQVSVALSSSIRVAMLEENGERVLMEGKLTHKINTESSLWSL EPGKCVLVNLSKVGEYWWNAILEGEEPIDIDKINKERSMATVDE EEQAVLDRLTFDYHQKLQGKPQSHELKVHEMLKKGWDAEGSPFR GQRFDPAMFNISPGAVQF SESEACEAFGRRKSEEEGRRSDTSGFGRSRKHKVNWKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PQRIQQWQQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHPINPR VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRWYKLDELFEQERNVRTAMTN RAGLALMLULQTIQHDPLTTDLRSSADR 5420 117 1733 NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG			•	RAARVEDEMQVQECEPEKVEIRERYELSEKMLSACNLLKNTIND
HONKAGYTPIMLALAAVEAEKDMRIVEELFGCGDVNAKASQAG QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG HVEIVKLLIAQPGCNGHLEDNDGSTALSIALEAGHKDIAVLLYA HVNFAKAQSFGTPRIGRKTSPGPTHRGSFD 5418 24 1133 SVPRAGGDMETGAAELYDQALLGILQHVGNVQDFLRVLFGFLYR KTDFYRLLRHPSDRMGFPPGAAQALVLQVFKTFDHMARQDDEKR RQELEEKIRRKEEEEAKTVSAAAAEKEPVDPVQEIEIDSTTEL DGHQEVEKVQPPGPVKEMAHGSQEAEAPGAVAGAAEVPR\EPPI LPRIQEQFQKNPDSYNGAVRENYTWSQDYTDLEVRVPVPKHVVK GKQVSVALSSSIRVAMLEENGERVLMEGKLTHKINTESSLWSL EPGKCVLVNILSKVGEYWWNAILEGEEPIDIDKINKERSMATVDE EEQAVLDRLTFDYHQKLQGKPQSHELKVHEMLKKGWDAEGSPFR GQRFDPAMFNISPGAVQF 5419 1395 259 GTHPLDPDLVSRTSVQGPLMTMACPGMSDTEESPFLGPRAAEEG SESEACEAFGRRKSEEEGRRSDTSGFGRSRKHKVNWKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PQRIQQWQQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCCHPINPR VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEQERNVRTAMTN RAGGLALMLHQTIQHDPLTTDLRSSADR 5420 117 1733 NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWWWVLGG		<u> </u>		SPDVI.RYVINIADGNCNTALHYCUCUCHERTUUTTT DANYON
QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG HVBIVKLLLAQPGCNGHLEDNDGSTALSIALEAGHKDIAVLLYA HVNFAKAQSPGTPRLGRKTSPGPTHRGSFD SVPRAGGMBTGAAELYDQALLGILQHVGNVQDFLRVLFGFLYR KTDFYRLLRHPSDRMGFPPGAAQALVLQVFKTFDHMARQDDEKR RQELEEKIRRKEEEEAKTVSAAAAEKEPVPVPVQEIEIDSTTEL DCHQEVEKVQPPGPVKEMAHGSQEAEAPGAVAGAAEVPR\EPPI LPRIQEQFQKNPDSYNGAVRENYTWSQDYTDLEVRVPVPKHVVK GKQVSVALSSSIRVAMLEENGERVLMEGKLTHKINTESSLWSL EPGKCVLVNLSKVGEYWWNATLEGEEPIDIDKINKERSMATVDE EEQAVLDRLTFDYHQKLQGKPQSHELKVHEMLKKGWDAEGSPFR GQRFDPAMFNISPGAVQF 5419 1395 259 GTHPLDPDLVSRTSVQGPLMTMACPGMSDTEESPFLGPRAAEEG SESEACEAFGRKSEEEBGRRSDTSGFGRSRKHKVNWKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL FQRIQQWQQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHPINPR VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR 5420 117 1733 NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG]	j	•	HONKAGYTPIMLAALAAVEAEKDMPTVEFI.FCCCDMANY3COAC
HVEIVKLILAQPGCNGHLEDNDGSTALSIALEAGHKDIAVLIYA HVNFAKAQSPGTPRLGRKTSPGPTHRGSFD SVPRAGGDMETGAAELYDQALLGILQHVGNVQDFLRVLFGFLYR KTDFYRLRHESDRMGFPPGAAQALVLQVFKTFDHMARQDDEKR RQELEEKIRRKEEEEAKTVSAAAAEKEPVPVPVQEIEIDSTTEL DGHQEVEKVQPPGPVKEMAHGSQEAEAPGAVAGAAEVPR\EPPI LPRIQEQFQKNPDS YNGAVRENYTWSQDYTDLEVVVPVPKHVVK GKQVSVALSSSIRVAMLEENGERVLMEGKLTHKINTESSLWSL EPGKCVLVNILSKVGEYWWNAILEGEEPIDIDKINKERSMATVDE EEQAVLDRLTFDYHQKLQGKPQSHELKVHEMLKKGWDAEGSPFR GQRFDPAMFNISPGAVQF S419 1395 259 GTHPLDPDLVSRTSVQGPLMTMACPGMSDTEESPFLGFRAAEEG SESEACEAFGRKSEEEGRRSDTSGFGRSRKHKVWWKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PQRIQQWQQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHPINPR VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR 5420 117 1733 NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWWWVLGG	1			QTALMLAVSHGRIDMVKGLLACGADVNTODDEGGTALMCAGEUG
HVNFAKAQSPGTPRLGRKTSPGPTHRGSFD 5418 24 1133 SVPRAGGDMETGAAELYDOALLGILQHVGNVQDFLRVLFGFLYR KTDFYRLLRHPSDRMGFPPGAAQALVLQVFKTFDHMARQDDEKR RQELEEKIRRKEEEEAKTVSAAAAEKEPVPVPVQEIEIDSTTEL DCHQEVEKVQPPGPVKEMAHGSQEAEAPGAVAGAAEVPR\EPPI LPRIQEQFQKNPDSYNGAVRENYTWSQDYTDLEVRVPVPKHVVK GKQVSVALSSSIRVAMLEENGERVLMEGKLTHKINTESSLWSL EPGKCVLVNLSKVGEYWWNAILEGEEPIDIDKINKERSMATVDE EEQAVLDRLTFDYHQKLQGKPQSHELKVHEMLKKGWDAEGSPFR GQRFDPAMFNISPGAVQF 5419 1395 259 GTHPLDPDLVSRTSVQGPLMTMACPGMSDTEESPFLGPRAAEEG SESEACEAFGRRKSEEEGRRSDTSGFGRSRKHKVNWKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PQRIQQWQQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHPINPR VALRHMERCTAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPPHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRYCWEKLRRAEVDLERVWYKLDELFEQERNVRTAMTN RAGLLALMHQTIQHDPLTTDLRSSADR 5420 117 1733 NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG		ľ		HVEIVKLLLAQPGCNGHLEDNDGSTALSIALEAGHKDIAVII.VA
SVPRAGGDMETGAAELYDQALLGILQHVGNVQDFLRVLFGFLYR KTDFYRLLRHPSDRMGFPPGAAQALVLQVFKTPDHMARQDDEKR RQELEEKIRRKEEEEAKTVSAAAAEKEPVPVPVQEIEIDSTTEL DGHQEVEKVQPPGPVKEMAHGSQEAEAPGAVAGAAEVPR\EPPI LPRIQEQFQKNPDSYNGAVRENYTWSQDYTDLEVRVPVPKHVVK GKQVSVALSSSIRVAMLEENGERVLMEGKLTHKINTESSLWSL EPGKCVLVNLSKVGEYWWNAILEGEEPIDIDKINKERSMATVDE EEQAVLDRLTFDYHQKLQGKPQSHELKVHEMLKKGWDAEGSPFR GQRFDPAMFNISPGAVQF 5419 1395 259 GTHPLDPDLVSRTSVQGPLMTMACPGMSDTEESPFLGPRAAEEG SESEACEAFGRRKSEEEGRRSDTSGFGRSKKHKVNWKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PQRIQQWQQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHPINPR VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPFHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR 5420 117 1733 NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG		· .		HVNFAKAQSPGTPRLGRKTSPGPTHRGSFD
KTDFYRLLRHPSDRMGFPPGAAQALVLQVFKTFDHMARQDDEKR RQELEEKIRRKEEEEAKTVSAAAAEKEPVPVPVQEIEIDSTTEL DGHQEVEKVQPPGPVKEMAHGSQEAEAPGAVAGAAEVPR\EPPI LPRIQEQFQKNPDSYNGAVRENYTWSQDYTDLEVRVPVPKHVVK GKQVSVALSSSSIRVAMLEENGERVLMEGKLTHKINTESSLWSL EPGKCVLVNLSKVGEYWWNAILEGEEPIDIDKINKERSMATVDE EEQAVLDRLTFDYHQKLQGKPQSHELKVHEMLKKGWDAEGSPFR GQRFDPAMFNISPGAVQF 5419 1395 259 GTHPLDPDLVSRTSVQGPLMTMACPGMSDTEESPFLGPRAAEEG SESEACEAFGRRKSEEEGRRSDTSGFGRSKKHKVNWKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PQRIQQWQQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHPINPR VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPFHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR 5420 117 1733 NEAGGACPFKGGASGRLYLSFRLPRVSVAGCEERPLGWVWVLGG	5418	24	1133	SVPRAGGDMRTGAAELYDQALLGILQHVGNVQDFLRVLFGFLYR
RQELEEKIRRKEEEEAKTVSAAAAEKEPVPVPVQEIEIDSTTEL DGHQEVEKVQPPGPVKEMAHGSQEAEAPGAVAGAAEVPR\EPPI LPRIQEQFQKNPDSYNGAVRENYTMSQDYTDLEVRVPVPKHVVK GKQVSVALSSSIRVAMLEENGERVLMEGKLTHKINTESSLWSL EPGKCVLVNLSKVGEYWWNAILEGEEPIDIDKINKERSMATVDE EEQAVLDRLTFDYHQKLQGKPQSHELKVHEMLKKGWDAEGSPFR GQRFDPAMFNISPGAVQF 5419 1395 259 GTHPLDPDLVSRTSVQGPLMTMACPGMSDTEESPFLGPRAAEEG SESEACEAFGRRKSEEEGRRSDTSGFGRSRKHKVNWKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PQRIQQWQQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHPINPR VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR 5420 117 1733 NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG	[KTDFYRLLRHPSDRMGFPPGAAQALVLQVFKTFDHMARODDEKR
DGHQEVEKVQPPGPVKEMAHGSQEAEAPGAVAGAAEVPR\EPPI LPRIQEGFQKNPDSYNGAVRENYTWSQDYTDLEVRVPVPKHVVK GKQVSVALSSSIRVAMLEENGERVLMEGKLTHKINTESSLWSL EPGKCVLVNLSKVGEYWWNAILEGEEPIDIDKINKERSMATVDE EEQAVLDRLTFDYHQKLQGKPQSHELKVHEMLKKGWDAEGSPFR GQRFDPAMFNISPGAVQF 5419 1395 259 GTHPLDPDLVSRTSVQGPLMTMACPGMSDTEESPFLGPRAAEEG SESEACEAFGRRKSEEEGRRSDTSGFGRSRKHKVNWKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PQRIQOWQQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHPINPR VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR 5420 117 1733 NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG	1 1		!	RQELEEKIRRKEEEEAKTVSAAAAEKEPVPVPVQEIEIDSTTEL
LPRIQEQFQKNPDSYNGAVRENYTWSQDYTDLEVRVPVPKHVVK GKQVSVALSSSIRVAMLEENGERVLMEGKLTHKINTESSLWSL EPGKCVLVNLSKVGEYWWNAILEGEEPIDIDKINKERSMATVDE EEQAVLDRLTPDYHQKLQGKPQSHELKVHEMLKKGWDAEGSPFR GQRFDPAMFNISPGAVQF 5419 1395 259 GTHPLDPDLVSRTSVQGPLMTMACPGMSDTEESPFLGPRAAEEG SESEACEAFGRRKSEEEGRRSDTSGFGRSKHKVNWKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PQRIQQWQQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHPINPR VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR 5420 117 1733 NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG	, ,	ļ	ı	DGHQEVEKVQPPGPVKEMAHGSQEAEAPGAVAGAAEVPR\EPPI
EPGKCVLVNLSKVGEYWWNAILEGEEPIDIDKINKERSMATVDE EEQAVLDRLTFDYHQKLQGKPQSHELKVHEMLKKGWDAEGSPFR GQRFDPAMFNISPGAVQF S419 1395 259 GTHPLDPDLVSRTSVQGPLMTMACPGMSDTEESPFLGPRAAEEG SESEACEAFGRRKSEEEGRRSDTSGFGRSRKHKVNWKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PQRIQQWQQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHPINPR VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR 5420 117 1733 NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG	Į (}		LPRIQEQFQKNPDSYNGAVRENYTWSQDYTDLEVRVPVPKHVVK
EEQAVLDRLTFDYHQKLQGKPQSHELKVHEMLKKGWDAEGSPFR GQRFDPAMFNISPGAVQF 5419 1395 259 GTHPLDPDLVSRTSVQGPLMTMACPGMSDTEESPFLGPRAAEEG SESEACEAFGRRKSEEEGRRSDTSGFGRSRKHKVNWKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PQRIQQWQQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHPINPR VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPFHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR 5420 117 1733 NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG	į į			GKQVSVALSSSSIRVAMLEENGERVLMEGKLTHKINTESSLWSL
GQRFDPAMFNISPGAVQF 1395 259 GTHPLDPDLVSRTSVQGPLMTMACPGMSDTEESPFLGPRAAEEG SESEACEAFGRRKSEEEGRRSDTSGFGRSRKHKVNWKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PQRIQQWQQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHPINPR VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHOPLTTDLRSSADR 5420 117 1733 NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG	 	ł		EPGKCVLVNLSKVGEYWWNAILEGEEPIDIDKINKERSMATVDE
5419 1395 259 GTHPLDPDLVSRTSVQGPLMTMACPGMSDTEESPFLGPRAAEEG SESEACEAFGRRKSEEEGRRSDTSGFGRSRKHKVNWKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PQRIQQWQQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHPINPR VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR 5420 117 1733 NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG	j }	j		CORPORANTE A CORPORATE A CORPORATE A CORPORATE A CORPORAT
SESEACEAFGRRKSEEEGRRSDTSGFGRSRKHKVNWKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PQRIQQWQQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHPINPR VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR 5420 117 1733 NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG	5419	1395	250	
KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PQRIQQWQQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHPINPR VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR 5420 117 1733 NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG		1333	עכ.	GIRLDYDLVSKTSVQGPLMTMACPGMSDTEESPFLGPRAAEEG
PQRIQQWQQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHPINPR VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR 5420 117 1733 NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG		ļ		KDDASI.BOC/I CD/DCMDAODCCVVCCDDCCVVV
ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHPINPR VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR 5420 117 1733 NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG		1		PORTOOWOOSPOTAERHOUVILERTBRECOGARDA CONTEST
VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR 5420 117 1733 NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG	[[İ		ELEAIILRAKOOAVREDERSNEGDEDDTDI OTEGUS COURTES
YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR 5420 117 1733 NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG	ļ 1	}		VALRHMERCYAKYESOTSEGSMYDTETEGATELEGDIVADOGYM
RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR 117 1733 NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG	j j	1		YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCDI.DV
RAGLLALMLHQTIQHDPLTTDLRSSADR 5420 117 1733 NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG		•	ſ	RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEOERNVRTAMTM
117 1733 NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG				RAGLLALMLHQTIQHDPLTTDLRSSADR
GGFLPARPPRAQRHLGFSHAEQSMEAPDYEVLSVREQLFHERIR	5420	117	1733	NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG
	L			GGFLPARPPRAQRHLGFSHAEQSMEAPDYEVLSVREQLFHERIR

SEC	Predicted		
ID	Predicted	Predicted end	
NO:		nucleotide	
110.	1	location	
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan Y=Typogine Waline,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	1	Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			FCIISTIFE NUCLEOTIDE insertion)
1	[1	ECIISTLIFATLYILCHIFLTRFKKPAEFTT\GMMKMPPSTRL/
- 1	})	TOURIST THATALGAVILLIPEST TSNEW, LCI DDARWY AND THE
- }		1	DITTODANDVE DESNUSLI EL MUPAVERTROPORARIA CONTENENT
ı		1	1 12 1 V VILLIADI I DEVEGNOWVASA TVDKNIVA NIDEGI VIDEVIDIO III
- 1	1	}	1 TO TO CLOT LIGATION CONTROL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE T
	i	i	T VET COAT BEAALI KKI CNPTSCWI DI DMFI I UPOVI AT OPONI-
			LEKKKKASAWUKNLGYPLAMICI.T.VI.TCI CIII TIIA TIIT
	ĺ	1	EARLY FROM DO I SUGUEST SKI CERCANTOUR TENT AGE COMME
Ì	1	1	T TOO F OF TOO BEEN THE TANK OF TANK OF THE PROPERTY OF THE PR
- 1	j	1	TRFDLLGDFGRFNWLGNFYIVFLYNAAFAGLTTLCLVKTFTAAV
5421		L	RAELIRAFGERE
3421	117	1733	NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG
1	1	1	GGFLPARPPRAQRHLGFSHAEQSMEAPDYEVLSVREQLFHERIR
1	ſ		ECIISTLLFATLYILCHIFLTRFKKPAEFTT\GMMKMPPSTRL/
			LLELCTFTLATALGAVILLI DEGLIGORETT GMMKMPPSTRL/
- 1	4		LIELCTFTLAIALGAVLLLPFSIISNEVLLSLPRNYYIQWLNGS
1	,		LIHGLWNLVFLFSNLSLIFLMPFAYFFTESEGFAGSRKGVLGRV
- 1	1		YETVVMLMLLTLLVLGMVWVASAIVDKNKANRESLYDFWEYYLP
{	1 1		YLYSCISFLGVLLLLVCTPLGLARMFSVTGKLLVKPRLLEDLEE
1	1 1		QLYCSAFEEAALTRRICNPTSCWLPLDMELLHRQVLALQTQRVL
	1		LEKRRKASAWQRNLGYPLAMLCLLVLTGLSVLIVAIHILELLID
- 1	1		1 DIE IN KONGGISEGOVSESKEGSFRAVIOTATI TOULADOGENION
1	1		1 100 P DE ROCKERWHOTAMTOI TONCVCI.I.VI.CCAT OVERDER CO.
	1 1		TRFDLLGDFGRFNWLGNFYIVFLYNAAFAGLTTLCLVKTFTAAV RAELIRAFGERE
5422	3	1263	
j	1 1	2003	SCGESLPTWLAGASRPGIGRKGGAWGGRGGSSPAQVLLSPGPVF
- 1	1 1		I AND CHANGED AND CHANGE OF THE COLOR OF THE
	1 !		1 THE TYPE OR THE PROPERTY OF
- 1	1		*** VDEREDDWARVMVEKSRMGVV/DDGTOVEOT TVRVVV VD==
- [! !	ı	I TO TO BRING TORMS FOLD GGMT TTCFMT OF UDTM DATE THE AREA
i	1		I TO THE TAX TO THE TA
1	1 1		DINGS PLUGRWYPPAAVAANCUNIT DIMIDOORT TICOT TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL T
1	i		DIDIGIONORMALGITOVVISDITMEN DOMENT DIVERSOR
	1		**************************************
5423	3186		DE LONG TOUR TOUR PROPERTY OF THE PROPERTY OF
}] 3200	905	GVSMALGEEKAEAEASEDTKAOSYGDGSCDEDELDY DGENGE
]	í	TERMENEGGELSPVWGAEGIPAPTCWTCTDDCCDGDAUADA
	1 1	1	**************************************
	1		201 X1 DODERT LICSGHDAD PRODDET, ADT DOAT DE GOODES
ı	1	Ì	TO THE PROPERTY OF THE PROPERT
1	1 (ľ	ODER CONTROL OF THE COURSE OF
1	1		CAGADI VACIMACVLPDSLPPSPDPHQDI MIDNIERED * * ****
-	1 1		YPLRPGPQLPKHLDSRVPADPVLQDSGVDLDSFSVSPASTLKSP
}]	i i	TNVSPNCPPAEATALPFSGPREPSLKQWPSRVPQKQGGMGLASW
	1 (}	SQLASTPRAPGSRDARWERREPALRGAKDRLTIGKHLDMGSPQL
Ì		i	RTRDRGWPSPRPEREKRTSQSARRPTCTESRWKSEEEVESDDEY
1	[]		LALPARLTQVSSLVSYLGSISTLVTLPTGDIKGQSPLEVSDSDG
i	ĺ	(PASFPSSSQSQLPPGAALQGSGDPEGQNPCFLRSFVRAHDSAG
l i	ĺ	1	EGSLGSSOALGYSSCLI PERDON DATE TO THE SEVRAHDSAG
1 1],	EGSLGSSQALGVSSGLLKTRPSLPARLDRWPFSDPDVEGQLPRK
1	1	1.	GGEOGKESLVQC\VKTFC\CQLEELICWLYNV\ADVTDHGTPAR
j 1	ļ	 	SNLTSLK\SSLQLYRQFKKDIDEHQSLTESVLQKGEILLQCLLE
		<i>!</i> ;	NTPVLEDVLGRIAKQSGELESHADRLYDSILASLDMLAGCTLIP DKKPMAAMEHPCEGV
5424	3186		PROFIDAMENTOLEGY
1 1	ļ	1 '	GVSMALGEEKAEAEASEDTKAQSYGRGSCRERELDIPGPMSGEQ
1 1	i	1 .	TRUESEGGII OF VWGAEGI PAPTCWTCTDDCCDCDATTCDCC I
, 1	ſ	•	WINDE VALKSBEAUSGLEPATMGSGDIJI SGESOUPVIVI COOR
}		, -	20 1 O TO DERILLICS GROAD PEDDDGT AND DOAT DE COORTEGE
) (ſ	1 ^	OCHO QUINO VIO PUSA A O PRESCRITO REPORTATION DE LA COMPONIDA
	1	1	SHARVSSSLEPVVPOEPSSVVGLGDDDOWGDODVDGGGDDAGG
1 1	1	, ,	Add D P VAC I WALVE PDS L PDS DDDUS DI MINDATUR VEDIT I DAME
	1	1 -	THE GEOLOGICAL DESKY PADPVI ODSGVDI DEREVIEDS CON 1100
<u> </u>		1	'NVSPNCPPAEATALPFSGPREPSLKQWPSRVPQKQGGMGLASW
			ALIGOGRAPH MANAGEMENT AND AND AND AND AND AND AND AND AND AND

Deginning	SEO	Predicted	Drodinted and	
No: nucleotide location corresponding to first corresponding to first amino acid residue of amino acid residue of amino acid sequence sequ	_	I .	Predicted end	Amino acid segment containing signal peptide
Cocation Corresponding Cofirst Statement Cofirst Cofirst Statement Cofirst Statement Cofirst Statement Cofirst Statement Cofirst Statement Cofirst Statement Cofirst Cof				(A=Alanine, C≈Cysteine, D=Aspartic Acid, E=
corresponding to first amino acid serious of serious of sirst amino acid residue of amino acid sequence serious of amino acid sequence seq	1	•		Glutamic Acid, F=Phenylalanine, G=Glycine,
amino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid sequence **Tryptophan, Y=Tyrcosine, X=Unknown, *=Stop Codon, /=possible mucleotide deletion, Codon, /=possible mucleotide deletion, Codon, /=possible mucleotide insertion **Tryptophan, Y=Tyrcosine, X=Unknown, *=Stop PAPPESSSSSQSQUPSGCLMTRESUPSGCAMERGEREVESDOBY REPERSORS PAPPESSSSQSQUPSGCAMERGEREVESDOBY RESPECTATION TO THE MINOR TH	1			H=Histidine, I=Isoleucine, K=Lysine,
amino acid residue of amino acid sequence should be acid sequence should be acid seq	1			L=Leucine, M=Methionine, N=Asparagine,
residue of amino acid sequence	1	l .		P=Proline, Q=Glutamine, R=Arginine.
### ### ### ### ### ### ### ### ### ##	1		I.	S=Serine, T=Threonine, V=Valine,
sequence Codon, /-possible nucleotide insertion SQLASTERAPOSEDARMEREPALEGARDRITICHALDMOSPOL REDRECHPEN SQLASTERAPOSEDARMEREPALEGARDRITICHALDMOSPOL ALAPARITOVSSILVSYLGSISTITYTETEDIKOGSPLEVSDDDSY LALAPARITOVSSILVSYLGSISTITYTETEDIKOGSPLEVSDDDSY RASPYSSSSGQULPYSSCHLKTRESLEPARLDRWFFSDPDVEGGLER SQLASTERAPOSSCHLKTRESLEPARLDRWFFSDPDVEGGLER SQLASTERAPOSSCHLKTRESLEPARLDRWFFSDPDVEGGLER SQLASTERAPOSSCHLGVANGER COLLEINGNIVALDHOTHOTRAR SQLASTERAPOSSCHLGVANGER COLLEINGNIVALDHOTHOTRAR SQLASTERAPOSSCHLGVANGER COLLEINGNIVALDHOTHOTRAR SQLASTERAPOSSCHLGVANGER COLLEIGNIVALDHOTHOTRAR SQLASTERAPOSSCHLGVANGER COLLEIGNIVALDHOTHOTRAR SQLASTERAPOSSCHLGVANGER COLLEIGNIVALDHOTHOTRAR SQLASTERAPOSSCHLGVANGER COLLEIGNIVALDHOTHOTRAR ALASATAGAPH, LAGGICUMANI SYMAPHITE DEPLYPOT KYELGRALYLGWASASLISIGGLCLCSACCOSDEDRARASRRY VALAVSVAMPATATADDEGDSS SEKVERNARLEVALGERPENTY KYELGRALYLGWASASLISIGGLCLCSACCOSDEDRARASRRY VALAVSVAMPATADDEGDSS SEKVERNARLEVALGERSCHLVLIPYSLA ACKOLSVUSPULPGLALVLLGWRRVEDEKESIGRARAQLLDDERGLERAP KYELGRALYLGWASASLISIGGLCLCSACCOSDEDRARASRRY VALAVSVAMPATADDEGDSS SEKVERNARLEVALGUNGSPOLL KYELGRALYLGWASASLISIGGLCLCSACCOSDEDRARASRRY VALAVSVAMPATADDEGDSS SEKVERNARLEVALGUNGSPOLL KYELGRALYLGWASASLISIGGSOPAPPEPPEPPEPPEPPEPPEPP ARAMARDPOSSGGOPAGGAAGRALANUTISSGERICHULVIPYSLA ACKOLSVUSPULPGLALVLURREVALDERSPEPPEPPEPPEPPEPP ARAMARDPOSSGGOPAGGAAGRALANUTISSGERICHULVIPYSLA GAVGLSVUSPULPGLALVLURREVALDERSPEPPEPPEPPEPPEPPEPPEPPEPPEPPEPPEPPEPPEP	- i		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Ston
Sequence Appossible nucleotide insertion	j	amino acid	sequence	Codon, /=possible nucleotide deletion
SOLASTEAPGESEARMEREPALGRAKOPLITICHLUMSOFIL RTERROR/SPEPEREKTSCSARMERITCTESSINKSEEWESDDORY LALPARLITUVSSLUSYLSSISTITUTLETGID INGGSELEVEDDORY LALPARLITUVSSLUSYLSSISTITUTLETGID INGGSELEVEDDORY LALPARLITUVSSLUSYLSSISTITUTLETGID INGGSELEVEDDORY BASPPSSSOSQU-PROPALAGGSOSPD-KOONPOTERSYVEANDSAG EGSLGSSQALGVSSCLLKTEPSLPARLDEWPFDDDVEGGLERK GEGGKESLUCV, VKTETC\COLLEGLICHLUMYLYN-UPTHOTPAR SNLTSLK\SSLQLYROPKKOIDENGSLTSSVLKKGETLLQCLLE PTPVLEDVLGRI KANGSGELESIBARDLYDS LLASLAGGGTLIP DEKAMMAMERICCSU STEDENSTÄNGNERPTUAPTINSMAVETFOFFMATVGLIMLGVTLP NSYMRVSTYNGNVITTATI LEIGHLGLIGLAGLGCTLINGGELESKE ARLAATAGAH\LIGGICGNAVI\SWYAPNITR\DPSDPLYROP RENGRALINGARSLISTIGGICLICSACCOSSDEDPAASARRY 1QARYSVAPVATSQCGGSSFGKYGNALRUVALCRGPRCLPT XYELGARLYGUSASLISTIGGICLICSACCOSSDEDPAASARRY 1QARYSVAPVATSQCGGSSFGKYGNALRUVALCRGPRCLPT XYELGARLYGUSASLISTIGGICLICSACCOSSDEDPAASARRY 1QARYSVAPVATSQCGGSSFGKYGNALRUVALCRGPRCLPT XYELGARLYGUSASLISTIGGICLICSACCOSSDEDPAASARRY 1QARYSVAPVATSQCGGSSFGKYGNALRUVALCRGPRCLPT XYELGARLYGUSASLISTIGGICLICSACCOSSDEDPAASARRY 1QARYSVAPVATSQCGGGGGAGGAACALAVLISTGURLUVILITYCHSGOLDERPAASARRY 1QARYSVAPVATSQCGGGGGGAGGAACALAVLISTGURLUVILITYCHSGOLDERQA XTSSCGLGRADP PROCTIFICTSTVELGSEVAQVAPPLQVINGUSAC XXELTICALTUVANGRAD DAVIS STEPPLOLIDINGOMPICAGGAGGAACALAVLISTGURLUVILITYCH XXELTICALTUVANGRAD DAVIS STEPPLOLIDINGOMPICAGGAGGAACALAVLISTGURLUVILITYCH XXELTICALTUVANGRAD DAVIS STEPPLOLIDINGOMPICAGGAGGAACACALAVLISTGURLUVILITYCH XXELTICALTUVANGRAD DAVIS STEPPLOLIDINGOMPICAGGAGGAACACALAVLISTGURLUVILITYCH XXELTICALTUVANGRAD DAVIS STEPPLOLIDINGOMPICAGGAGGAACACALAVLISTGURLUVILITYCH XXELTICALTUVANGRAD DAVIS STEPPLOLIDINGOMPICAGGAGGAGAACACALAVLISTGURLUVILITYCH XXELTICALTUVANGRAD DAVIS STEPPLOLIDINGOMPICAGGAGGAGAACACALAVLISTGURLUVILITYCH XXELTICALTUVANGRAD DAVIS STEPPLOLIDINGOMPICAGGAGAACACACACACACACACACACACACACACACAC	j	sequence	1	\=possible nucleotide insertion)
RTRIBEGHS PREPERATESGARRITCTESSINKSEERVESDIDEY IALDRALITOVS SUNFIGISITUTLETION INCOSELEVISIBLE PASPESSSS GOOLPEGAALGSGDPEGGPFCFRESTVEANIBES ESSIGSSGAGUS VSCALVERS LOVER PARALGRIFFDEWEGGBER GESIGSSGAGUS VSCALVERS LOVER PARALGRIFFDEWEGGBER SINISK SSIGLY WARP KAIDBEST LOVER LICELLE BYPPUEDUER LAKGSGELSEIRDRIPS ILASLOMLAGCTLIP DER HAMPAMERIP CONTROL THAT I FEITHER SCATDLEVYNCKEFSML AND STOVEN WANT THAT I FEITHER SCATDLEVYNCKEFSML AND STOVEN WANT THAT I FEITHER SCATDLEVYNCKEFSML AND STOVEN WANT THAT I FEITHER SCATDLEVYNCKEFSML AND STOVEN WANT THAT I FEITHER SCATDLEVYNCKEFSML AND STOVEN WAS THE THAT I THAT I OFFICIAL GRAPHITA DESDELTEST YOAD VOUND THAT I THAT I OFFICIAL GRAPHITA DESDELTEST YOAD VOUND WAT THAT I CHARLES AND THE SCATDLEVYNCKEFSML AND SCATCH WAS AND THAT I THAT I OFFICIAL GRAPHITA DESDELTEST YOAD VOUND WAS AND THAT I THAT I OFFICIAL GRAPHITA DESDELTEST YOAD VOUND WAS AND THAT I THAT I OFFICIAL GRAPHITA DESDELTEST YOAD VOUND WAS AND THAT I THAT I OFFICIAL GRAPHITA DESDELTEST YOAD VOUND WAS AND THAT I THAT I OFFICIAL GRAPHITA DESDELTEST YOAD VOUND WAS AND THAT I THAT I OFFICIAL GRAPHITA DESDELTEST YOAD VOUND WAS AND THAT I THAT I OFFICIAL GRAPHITA DESDELTEST YOAD VOUND WAS AND THAT I THAT I OFFICIAL OF			<u> </u>	SOLASTPRAPESEDARWERREDAT. PCAKER TICKUL DMCOPOL
LALPARITOYSSLUSYLGSISTLYTUPTGDIKGGSPLEWSDBDG PASSPSSSAGQUPEGAALQGGGDPGGGNESPVRAMDSAG EGSIGSSQALGVSSGLIKTRESLPARLDRWFFSDDDVEGGLERK GGEGKESLUCVKTFC\CQLEELLCLLYNDTHGTPAR SNLTSLK\SIGUYRGFKDDDHGGLESVUQKGETLLQCLE NTPVLEBVLGRIRANGGELSHADRLYSTLANGAGCTLISV SNLTSLK\SIGUYRGFKDDDHGGLESVUQKGETLLQCLE NTPVLEBVLGRIRANGGELSHADRLYSTLANGAGCTLISV EKKMMAMERICGGV S125 1086 115 GFCFFFFLGRIGHGPRVLHFTYSMAVETFGFFNATVGLINLGVYLP NSYMFVSTVHGNVTTNTIFENLWFSCATDSLGVYNGKEFFSML ALSGYIQACRALNTATLLIGFGLLLGTAKCTGCLESR KRUGATAGAFR\LIPGIGGMVAI\SWAPMITR\DFSDPLYGF KYELGRAYLVGMSSALISILGGCLCSACCGDDFASARRF TOAPVSWFVATDDEGDSFGKYGRNALKVAALCGPRCLPTA REGERGING FFYSKLIGGRFUPVVAFFFRFRINGGLELSR REGERGING FFYSKLIGGRFUPVVAFFRFRINGGLEDSFOR PANALNEDFGGGODGGGGAGGAGGAGAFTFFRINGGELSR REGERGING FFYSKLIGGRFUPVVAFFRFRINGGLEDSFOR GANGLSGGDAGGAAGGAGAFTFRINGGELSR REGERGING FFYSKLIGGRFUPVVAFFRFRINGGLEDSFOR GANGLSGGAFFFFRINGFSAGGGGGGGGGGAGGAGGAGAFTRINGGELDER LLAFTVARAVEGGODGGGGAGGAGGAGAFTRINGGLEDFOR REGERGING FFYSKLIGGRFUPVAFFRFRINGLEDFORG REGERGEN FFYSKLIGGRFUPVAFFRFRINGLEDFORG REGERGEN FFYSKLIGGRFUPVAFFRFRINGLEDFORG REGERGEN FFYSKLIGGRFUPVAFFRFRINGLEDFORG REGERGEN FFYSKLIGGRFUPVAFFRFRINGLEDFORG REGERGEN FFYSKLIGGRFUPVAFFRFRINGLEDFORG REGERGEN FFYSKLIGGRFUPVAFFRFRINGLEDFORG REGERGEN FFYSKLIGGRFUPVAFFRFRINGLEDFORG REGERGEN FFYSKLIGGRFUPVAFFRFRINGLEDFORG REGERGEN FFYSKLIGGRFUPKAFFRFFTLOTHNYGHTHLDLIFGGELSISG THIMDSLAFLLYDPRILLYVELDPLOVALFRFRINGLEDFORGHLUPKAFF REGERGEN FFYSKLIGGRFUPKAFFRFFTLOTHNYGHTHLDLIFGGSSLIGE REGERGEN FFYSKLIGGRFUPKAFFRFTLOTHNYGHTHLDLIFGGSSLIGE REGERGEN FFYSKLIGGRFUPKAFFRFTLOTHNYGHTHLDLIFGGSSLIGE REGERGEN FFYSKLIGGGGGVHLARLEWISLISGABELGEVQUWM VSSRPDPSSALILVYNLDRAQDLLANGAFFRFTLODEGGGELVOW VSSRPDPSSALILVYNLDRAQDLLANGAFFRFTLODEGGGENVAFFTLOTHNYGHTHLDLIFGGRFUPKAFFRFTLODEGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA	1	J.	j	PTPDPCWPCPPPPPPPPCCCARPOTTCPPCPPUCTPCT
PASPPSSSSQQLPFGAALQGSGDPEQGNPCFLRSPVRAIDSAG BESIGSSGALGVSGILLITRSPLPAALIDRP EDVESGUPER GGEGGESILVQC/VKTPC\CQLEELICALINV\ADVIDHETPAR SILTSIK\SSLGVPROPKSGILLIGCLIE NTPVLEDVLGRIAKQGSELSEHADRLYDSILASLDMLAGGTLIP DEKEMMAMEHPICEDV 115 GFCFSFSLGHQPFRVLHFTMSMAVETFGFFMATVGLIMLIGVTLP SYRWSTVHONVITNTI TERNIFSCATESLGYNCKEFPSML ALSGY1QACRALMITAILLIGFLGLLLIGTAGLRCTNIGGLELSRK AKLAATAGAPT\LPG1GGMAY \LWAYSPTFATTGGELSRK AKLAATAGAPT\LPG1GGMAY \LWAYSPTFATTGGELSRK XAKLAATAGAPT\LPG1GGMAY \LWAYSPTFATTGGELSRK XYELGSALYLGWSASLISILGGLCLCSACCCGSDEDPAASARR YQAPVSWPWAYTSDGEGGSSFGYGYRNALRANGEPRGLFTA PKREGFGROFPFYSNLRGPRCPVPVAPPRRPRVHJSHGPGOAK NOSMEVALISEGSGUPTSGEGFSFSFMOPSABSBPTDQP PAAHAKPDPGSGOOPAGGAAGRALAVLTSFGRRLLIVITPVLA GAVGLSVGFVLFGLALYLGWRRYNDEKENSLRARQLDDEGOL TAXTLMSHRELEAWSSPDVEAREMLINKYLQWOPPLOQYMEK LLARTVAPAVRSGNPHLOTFTFRVELGERDRI IGVVHOOR REQITLIBLNI SYGONOTOWEKSPERGEMINTUTTCTSCTUDELIN DELARCULSSKOKYVKGLI BGKSDPYANDRLOTTTCTSCTUDELIN ROWGETYSNVHLVPRILLIVALPUPDLOVANDRLOTTTCTSCTUDELIN ROWGETYSNVHLVPRILLIVALPUPDLOVANDRLOTTTCTSCTUDELIN ROWGETYSNVHLVPRILLIVALPUPDLOVANDRLOTTTCTSCTUDELIN ROWGETYSNVHLVPRILLIVALPUPDLOVANDRLOTTTCTSCTUDELIN ROWGETYSNVHLVPRILLIVALPUPDLOVANDRLOTTTCTSCTUDELIN ROWGETYSNVHLVPRILLIVALPUPDLOVANDRLOGSSGONSKLIVM RUSSRLITGALTUTLARILLTARBELFARPPLOPOSOGNINDOV RODSRLITGALTUTLARILLTARBELFARPPLOPOSOGNINDOV RODSRLITGALTUTLARILLTARBELFARPPLOPOSOGNINDOV RODSRLITGALTUTLARBELFARPREPLOPOSOGNINDOV RODSRLITGALTUTLARGENING ROGSOVILARGE RUSSRLITGALTUTLARGENING ROGSOVILARGE RUSSRLITGALTUTLARGENING ROGSONSKLIVM RUSHRLITGALTUTLARGENING ROGSONSKLIVM RUSHRLITGARGENING ROGSONSKLIVM RUSHRLITGARGENING ROGSONSKLIVM RUSHRLITGARGENING ROGSONSKLIVM RUSHRLITGARGENING ROGSONSKLIVM RUSHRLITGARGENING ROGSONSKLIVM RUSHRLITGARGENING RUSSRGSGERSPERIG REKUS VHOCKSLEGONG ROGSOPPANDERSSSSSGSSEPEIG GGPHITTSSAPPVANDELTOPT GENUTLENING REFERING ROGSONSKLIVM RUSHRESPEIG GGPHITTSSAPPVANDELTOPT GENUTLENING REGILLOLING RUSSRGFRORSPENDOV RUSHRLITGALTUTLARGENING ROGSONDAPR REGILLOLING RUSSRGFRORSPENDOV RUSHREDPROGSONSKRIPM RUSSRGPPSRATILVANDROD RUSHRESPEIGUNG RUS	i	1		TAL DADI TOUCCI HOW GOTOTI WITH THE THE THE
EGSIGSSQALGVSSGILKTRESIPARLDRWFFSDPDUEGGLERK GGGGGKESLVCC\NTFC\CQLEBLICALVADTHGHTPAR SNLTSLK\SLQLYRGPKXDIDEHGSLTESVLQKGETLLQCLLE MTPVLEDVLGRIAKQGGELSEHADRLYSTLLGLLAGCTLIP DEKDWAMMERPCECV 115 GGCFSPSIGHAQGGGGVSHADRLYSTHATVOLINLGVTLP NSYMRVSTVHGNVITTNTIFENLMFSCATDSLGVTNCWRFSPML ALSGYLQACRALWTAILLGFCLLLGLTGLGLLGTTIGGELSRK ARLAATAGAPH\LIPGICGMWAT\SWAPFHITR\DFSDPLYRGT KYELGPALVLGWASALISILGGCLCSACCGDEDAAGARRY VQAPVSWFVATSDQEGGSFGKYGRNARVAALGGPRCLETA PKKRGPGRGPPYSNLGRGPREPVVAPPRFRVALVALGGPRCLETA PKKRGPGRGPPYSNLGRGPREPVVAPPRFRVALVALGGPRCLETA PKKRGPGRGPPYSNLGRGPREPVVAPPRFRAGAGLDDEEQL ARTILWSHRELPAWSPPDVSACRERGFSFSFNDQPSAPSAPBTDGP PAAHARPDPGSGGOPAGAGRALAVLTSFGRRLUVLIPYVLA GGVCLSVGFVLFGLALYLGMRKPUDEKKSHLGIGVNGWGC LLAETVAPAVGSNPLGTTFTRVELSEBFLGUVGFRAGAGLDUCCCA CAUCLSVGFVLFGLALYLGMRKPUDEKKSHLGIGVNGWGC KEQILLDLNISYYGDVQIDVEVKKYFCKAGVKGMQLIGVLRVIL EPLIGLEFVGAVSGFFIRAFTDLINVTGMIJTGLSSLSS TMIMDSIAAFLVLPNRLLVFLVDLIQDVAQLSSPLPRGIIRHL LAARGLSKKDKYVGLIGGKGGVALKEBJSLJCSVLQWMWG VSSRPDPBSAALLVVLPNRLLVFLVDLIQDVAQLSSPLPRGIIRHL LAARGLSKKDKYVGLIGGKGVALKEBJSLJCSVLQWMWG VSSRPDPBSAALLVVLPNRLLVFLWDLIQDVAQLSSPLPRGIIRHL LAARGLSKDKYVGLIGGKGGVALKEBJSLJCSVGVGSVDAPPG WOLSIQDVTGSKAVYSTGCVGARBWFJDFAVDLAGTGSVLDGENGLVGKV VSSRPDPSSAALLVVLDRAQDLAWTSELYPPQLKKGNKEDPI WOLSIGDVTGSKAVYSTGCVGABPSDPTAVLRLGTGSVLDGVBSUDGSGSVDAPPG PCHTTPDSQGGGGTHVLRHULBGADLIAKDRFLGGLVKKKSDPY VKLKLAGSSFSRSVVGELDIBFSREDVLGVMSLGFUNGSSVDAPPG PCHTTPDSQGGGGTHVLRHVLBQADLIAKDRFLGGLVKKKSDPY VKLKLAGSSFSRSVVGELDBFRGFSPSPFDFDGGSSVDAPPG PCHTTPDSQGGGGGVALGSLIPJSELLVJLTWLTL SGGGGGVALLBAQLGILVGGGGGGVALGSLIPJSELLVJLTWLTA SGGGGGVALLBAQLGILVGGGGGGVALGSLIPJSELLVJLTWLLA CANGLSVGFVUYGGGGGTGVALGSLEPJSELLVJLTWLLA GGGGSTGVERLDSPRGSTMERSFSSSSLSEPFLS GGGFFHITSSAPPVQFBCATHRAGSFSSSSSSSFFISH LGKVOLDLAFTOLSGGARWFVDLDENGGGSFAPSDPTDQP PAAHAKPDPGSGGGGPAGAGAGALAVLTSGGRRLDVTLDWYLGG CAGGSVGVFLQGGGGTGVALGRAFYDAGVKLTDVSGFLDVGVK LGKVGLDAFTOLALLVLGWRAYDBERSFSFSFSFBERBEL LGKVOLDLAFTOLALLVLGWRAYDBERSFSFSFSFSFBERBEL LGKVOLDLAFTOLALLVLGWRAYDBERSFLAGVLDGWGK LLAETVPAPAVGGGGGGGVALGERUSCHSKLGVCRWMG VSSRPDPPSAALLVARRUFFLGGLVKGKS	ľ	1	ł	DAGE PROCESSION TO THE PROPERTY OF THE PROPERT
GGEGGESLVQC\VKTPC\CQLEBILCINVA\ADVIDHOTBAR SNITSIK\SS\DLYRGPKXDIDEHQSILESVIQKGELILQCILE NTPVLEDVLGBIAKQSGELSSHADRLYDSILASLDMLAGGTLIP DKKNMAMEHPCEQV 115 GFCFSFBLGHQFPRVLHFTYMMAVETFGFFMATVGLIMLGVTLP SYRWSTVHONVITNTI TENLWFSCATDSLGYNCKBFPSML ALSGY1QACRALMITAILLGFLGLLLGTAGLKCTHIGGLELSRK ARLAARAGAPT\LIPGIGGMAY\SWASAFILSGYNCKBFPSML ALSGY1QACRALMITAILLGFLGLLLGTAGLCCTSGEDBPAASARRP VQAPVSWPWAYTSDQEGGSSFKYGYRNALRAVGEPGSCHT KYELGFALYLGWSASLISILGGLCLCSACCCGSDEDPAASARRP VQAPVSWPWAYTSDQEGGSSFKYGYRNALRAVGEPGSCHT KYELGFALYLGWSASLISILGGLCLCSACCCGSDEDPAASARRP VQAPVSWPWAYTSDQEGGSSFKYGYRNALRAVGEPGSCHT KYELGFALYLGWSASLISILGGLCLCSACCCGSDEDPAASARRP VQAPVSWPWAYTSDQEGGSSFKYGYRNALRAVGEPGSCHT KYELGFALYLGWSASLISILGGLCLCSACCCGSDEDPAASARRP VQAPVSWPWAYTSDQEGGSSFKYGYRNALRAVGHPGGAK KYELGFALYLGWSASLISILGGLCLCSACCCGSDEDPAASARRP VQAPVSWPWAYTSDQGGGGAPGGAGAGALAVLTISFGRKLLJVLIPVYLA GAVGLSVGFVLFGLALYLGWRRYNDEKRSILRARQLDDEGOL TAKTLMSHRELFAWSSFDVEGERSALLAVILTSPCRILLUTLIPVYLA GAVGLSVGFVLFGLALYLGWRRYNDEKRSILRARQLDDEGOL TAKTLMSHRELFAWSSFDVEKARWANGABALAVLTSPCRILLIPVYLA LAAFGLSSKOKYVKGLIEGKSDFYALVARLGTCTTCCSSVIDELIN LAAFGLSSKOKYVKGLIEGKSDFYALVARLGTCTTCCSSVIDELIN LAAFGLSSKOKYVKGLIEGKSDFYALVARLGTCTTCCSSVIDELIN LAAFGLSSKOKYVKGLIEGKSDFYALVARLGTCTTCCSSVIDELIN LAAFGLSSKOKYVKGLIEGKSDFYALVARLGTCTTCCSSVIDELIN LAAFGLSSKOKYVKGLIEGKSDFYALVARLGTCTTCCSSVIDELIN LAAFGLSSKOKYVKGLIEGKSDFYALVARLGTCTTCCSSVIDELIN VKLAKGSRFPDFPAPLGGGGQVILARLBWISLSJSDAELGEGUVQNW UGSRRJATGALTCALTUPLARLLTARBERFRFPLQDPSGSMIDLIVOK UGSRRJATGALTCALTUPLARLLTARBERFRFPLQDPSGSMIDLIVOK UDSRRJATTGALTTTULSGFLDDFMITLEDVPSGRILLIGL ERLTFPRFTARABERVLYDDLINGFRANDENSERSLILGT UKKLAGRSFRSTERVVREDLINGFRANDENSERSSLILGERILIGL ERLTFPRFTARABERVLYDDLINGFRANDLIST WEBABD LPEKKSTHILSPFATLTTULSGFLDFMITLEDVPSGRILLIGL ERLTFPRFTARABERVLQUMSLGSLELDISELLUNGFRANDLINGG GGFPHITSSAFPENEPLEDLBOAGRAKLDVYKDGAGSGFORSEPLIN KKTTLSPFFINEFFFENEPLEDLBOAGRAKLDVYKDGAGSFTSFREREL LGRVQLULABTULGGGGGGGAAGAGALAVITSGGRADDLIDGLSCLILD LAARGLSKNOKYVGLIEGKSGROPPAAVLGITDFUCKSTUPELDI PAHAMSTABABLUNDRAGGSFORMATHIOPAGGSSTORPRIVA KLUMBILLAGRGSGFORMATHIOPAGSSTO	ŀ	J	}	PASTPSSSQSQLPPGAALQGSGDPEGQNPCFLRSFVRAHDSAG
SNLTSLK\SSLQLYRQPKKDIDBHGSLIESVLQKGREILLQCLIE NTPVLEDVLGRIAKQGGELISEKADRLYSTILDALGACTLIP DRKPMAMERIPCEDV SYRRYSTHONVITTITITERILAFSCATDSLGVYRCMERPSML ALSGYIQACRALMITAILLGFLGLLIGHGALGKTRIGGLESRK ARLAATAGAPH\LIPGICGLUGHGALGKTRIGGLESRK ARLAATAGAPH\LIPGICGLUGHGALGKTRIGGLESRK ARLAATAGAPH\LIPGICGLUGHGALGKTRIGGLESRK ARLAATAGAPH\LIPGICGMAT\SWAPHITR\DFSDPIPGT KYELGAPLYLGMSSALISILGGLCSCACCOEDPAASARRP VQAPVSWPVATSDQEGDSSGRYGRNALEVAALCGPRCLPTA PKKRGPGRGPPYSNLRGRPREPVPAPPRFRUHSHGGPSOAK NCSWEVAYLPSEAGSLIF 5426 42 3435 ATSSGSLGRAPPRGGTWERSPGEGFSSFRDDFSAPSTDGP PAAHARPDPGSGGOPAGAGRALAVLTSFGRRLUVLIPYVLA GRVCLSUGFVLFGLALYLGMRVRDEKRSILGIGKVSHCOGA KEQILLDLNISYYGDVGIDVEKKYFCKAGVKGMQLIGVLRVIL EPLIGLIPYVAGVAGNFFIRRFTRUSINGSTUGKVHPOGA KEQILLDLNISYYGDVGIDVEVKKYFCKAGVKGMQLIGVLRVIL EPLIGLIPFVAGANGFIRRFTDLINWTGMILGFGLSISSIS TMIMDSIAAFLVLPNRLLVPLDDLQDVAQLRSPLPRGIIRHL LAARGISSKOKYVGLIGGKSDYAVLNLGTGSVVIDELID POMGETYSWMHEVPGOGISVEVFDKDDPXDDFLGRWKLDVGKV VSSRPDPPSAALLVVLDRAQDLPMVTSELYPPQLKKGMKEDN WOSSRAPLFGGGGGGVHLREWISLISDGFDYSVDLEDVGRVDGKDV KDDSRALTGALTLELARLLTAPELILDOMFQLSSGGRSVDAPPR PCHTTPDSOGGTEHVLRIHVLBAQDLJAKDRFLGGUKKGKSDPY VKLKLAGSSFSRGVVREDLINFRENDFYGESVDLEDER DKDLDKDDFIGRCKVRLTTVLNSGFLDSWILTEDVPSGRILML ERUTPPFAABLEBVLQVNSLSLEILPSELLVAQDLCLDRWFTL SGGGGGVVLBAQGGTGVULDSLEAPSELLVAQLCLDRWFTL SGGGGGVVLBAQGGTGVULDSLEAPSELLVAQLCLDRWFTL SKGGGGVVLBAQGGTGVULDSLEAPSELLVAQLCLDRWFTL SKGGGGVVLBAQGGTGVULDSLEAPSELLVAQLCLDRWFTL SKGGGGVVLBAQGGTGVULDSLEAPSELLVAQLCLDRWFTL SKGGGGVVLBAQGGTGVULDSLEAPSELLVAQLCLDRWFTL SKGGGGVVLBAQGGTGVULDSLEAPSELLVAQLCLDRWFTL SKGGGSVGVLBAQGGTGVULDSLEAPSELLVALVAGCLDRWFTL SKGGGSVGVLBAQGGTGVULDSLEAPSELLVALVALVAGCULDRWFTL SKGGLILDLINSVYHGCGSARWYDLDMNCKGSS TATTJWSHRELPANVSFDVEKARGKRDVAGMGAHDUEDGEG CARTSVFFLUGALLVLCKRAVGDERESTARGRLDDEGG TARTLYMSHRELPANVSFDVEKARGKRDVAGMGAHDUEDGEG TARTLYMSHRELPANVSFDVEKARGKRDDVAGKGMOHGVLRVLL EPLICOLPFYGGGGGGVULDRAFTLUNGGRVENDER VSSRPDPSAALLVARNELPERDFALDLERGELGVCKNENDER VSSRPDPSAALLVARNELPERGGGGGOVALRESLEGVLDWMG VSSRPDPSAALLVARNELPERGGGGGOVALRESLEGVLDWMG VSSRPDPSAALLVARNELPERGGGGGOVALRESLEGVLDWMG VS]	1	EGSLGSSQALGVSSGLLKTRPSLPARLDRWPFSDPDVEGQLPRK
S425 1086 115 GFCFSFSLGHQPFRULPFTMSMAVETFGFFMATVGLINLGVTLP SYMNSTYHORYTHORYTHTIST IFENLHSSCALULIGUTLE SYMNSTYHORYTHORYTHTIST IFENLHSSCALULIGUTLGUTLS AKLAATAGAPH\LIPSICGUMAI\SWALALGRERGLIGGELSRK AKLAATAGAPH\LIPSICGUMAI\SWALALGRERGLIGGELSRK AKLAATAGAPH\LIPSICGUMAI\SWALALGRERGLIPTA VQAPVSMPVATSDQEGGDSSFGKYGRNAALGRERGLIPTA PKKRGPGRGPFPYSNLRGRPRVVPAPPRPRPRVLHSHGPSQAK NCSMEVALINJSFSAGSLIF 5426 42 3435 ATSSGSLGRADPPRGTMERSPGGEFSPSPMOGSASSPFTDGP PAHAKNPDESGGGDAPGAGAGALALAULAUWAPPLGQYMEK LIABTVAPAVRGSNPHLOTFTTTRULGERDLUDTEQL TAKTLMSRELPAMVSTPDVEKAEMINLOUWAPPLGQYMEK LIABTVAPAVRGSNPHLOTFTTTRULGERDLULDEGLINKT GAVULSVGFVLFGLALYLGWRRVEDKERSLEGRDLUNLTPVLA GAVULSVGFVLFGLALYLGWRRVEDKERSLEGRDLUNLTPVLA GAVULSVGFVLFGLALYLGWRRVEDKERSLEGRDLUNLTPVLA GAVULSVGFVLFGLALYLGWRRVEDKERSLEGRDLUNLTPVLA GAVULSVGFVLFGLALYLGWRRVEDKERSLEGRDLUNLTPVLA GAVULSVGFVLFGLALYLGWRRVEDKERSLEGRDLUNGWNE KEQILLIDIN SYVDOWLD UDVEKKEYPCKGWOLHGULRVIL EPLIGDLPFVGAVSMFFIRFTLDINNTGMTNLDI PGLSSLSD TMIMDSLAAPLVLPNLLLVPLVDLDLOVDSEPLERGILINLT EPLIGDLPFVGAVSMFFIRFTLDINNTGMTNLDI PGLSSLSD TMIMDSLAAPLVLPNLLLVPLVDLDLOVDSEPLERGRILINL EPLIGDLPFVGAVSMFFIRFTLDINNTGMTDLURSPLERGRILINL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTOTFCSSVIDELIN VOSSRPDPPSAALILVVULDBLADOLDHAMTSENPERGLESVALDONN VSSRPDPPSAALILVVULDBLADOLDHAMTSENPERGLESVALDONN VSSRPDPSAALILVVULDBLADOLDHAMTSENPERGLESVALDONN VSSRPDPSAALILVVULDBLADOLDHAMSSENPORGSSVIDEN WOLLSIGDVTOESKAVYSTNCPVMBERFFFFLQDPGSSGLIDNV VKLLLAGRSFFSHVVEEDLANFRINSEYPEVITTSVFQOGLERVFL RUMMFILLYDSSELECFFTVPGCPGANDVDSISNPQRGSSVALDA KLUMRILVLDSSELECFFTVPGCPGANDVDSISNPQRGSSVALDA KLUMRILVLDSSELECFFTVPGCPGANDVDSISNPQRGSSVALDA RUMMFILLYBDSSELECFFTVPGCPGANDVDSISNPQRGSSVALDA RUMMFILLYBPPTAABLEVLOVNSLICTONSAALAALISTMERABD LPLKETKHT, SYATLTVUGGSHCTVLTINSSFTDERFRIGHTNAAPAGAP PROTTETSPFTAABLEVLOVNSLICTONSAALAALISTMERABD LPLKETKHT, SYATLTVUGGSHCTVLTSSFTDERFRIGHTNAAPAGAP RUMMFILLYBPTABLEUQUNGSOVARVDLMINNKDKOSS ATSSGSLGRADDFPGGTMERSFEGGESTSPENDFDFSAPSDPTDDF PAAHAKAPPPSAALVAURSPROGESTSPENDFGSAPSDPTDDF PAAHAKAPPSAASSPPLAGGGGGABGAAVILTSFRRITLUTIVTVIL PROTTETSPFTAARAGAPAGAPA	1	l		GGEQGKESLVQC\VKTFC\CQLEELICWLYNV\ADVTDHGTPAR
S425 1086 115 GFCFSFSLGHQPFRULPFTMSMAVETFGFFMATVGLINLGVTLP SYMNSTYHORYTHORYTHTIST IFENLHSSCALULIGUTLE SYMNSTYHORYTHORYTHTIST IFENLHSSCALULIGUTLGUTLS AKLAATAGAPH\LIPSICGUMAI\SWALALGRERGLIGGELSRK AKLAATAGAPH\LIPSICGUMAI\SWALALGRERGLIGGELSRK AKLAATAGAPH\LIPSICGUMAI\SWALALGRERGLIPTA VQAPVSMPVATSDQEGGDSSFGKYGRNAALGRERGLIPTA PKKRGPGRGPFPYSNLRGRPRVVPAPPRPRPRVLHSHGPSQAK NCSMEVALINJSFSAGSLIF 5426 42 3435 ATSSGSLGRADPPRGTMERSPGGEFSPSPMOGSASSPFTDGP PAHAKNPDESGGGDAPGAGAGALALAULAUWAPPLGQYMEK LIABTVAPAVRGSNPHLOTFTTTRULGERDLUDTEQL TAKTLMSRELPAMVSTPDVEKAEMINLOUWAPPLGQYMEK LIABTVAPAVRGSNPHLOTFTTTRULGERDLULDEGLINKT GAVULSVGFVLFGLALYLGWRRVEDKERSLEGRDLUNLTPVLA GAVULSVGFVLFGLALYLGWRRVEDKERSLEGRDLUNLTPVLA GAVULSVGFVLFGLALYLGWRRVEDKERSLEGRDLUNLTPVLA GAVULSVGFVLFGLALYLGWRRVEDKERSLEGRDLUNLTPVLA GAVULSVGFVLFGLALYLGWRRVEDKERSLEGRDLUNLTPVLA GAVULSVGFVLFGLALYLGWRRVEDKERSLEGRDLUNGWNE KEQILLIDIN SYVDOWLD UDVEKKEYPCKGWOLHGULRVIL EPLIGDLPFVGAVSMFFIRFTLDINNTGMTNLDI PGLSSLSD TMIMDSLAAPLVLPNLLLVPLVDLDLOVDSEPLERGILINLT EPLIGDLPFVGAVSMFFIRFTLDINNTGMTNLDI PGLSSLSD TMIMDSLAAPLVLPNLLLVPLVDLDLOVDSEPLERGRILINL EPLIGDLPFVGAVSMFFIRFTLDINNTGMTDLURSPLERGRILINL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTOTFCSSVIDELIN VOSSRPDPPSAALILVVULDBLADOLDHAMTSENPERGLESVALDONN VSSRPDPPSAALILVVULDBLADOLDHAMTSENPERGLESVALDONN VSSRPDPSAALILVVULDBLADOLDHAMTSENPERGLESVALDONN VSSRPDPSAALILVVULDBLADOLDHAMSSENPORGSSVIDEN WOLLSIGDVTOESKAVYSTNCPVMBERFFFFLQDPGSSGLIDNV VKLLLAGRSFFSHVVEEDLANFRINSEYPEVITTSVFQOGLERVFL RUMMFILLYDSSELECFFTVPGCPGANDVDSISNPQRGSSVALDA KLUMRILVLDSSELECFFTVPGCPGANDVDSISNPQRGSSVALDA KLUMRILVLDSSELECFFTVPGCPGANDVDSISNPQRGSSVALDA RUMMFILLYBDSSELECFFTVPGCPGANDVDSISNPQRGSSVALDA RUMMFILLYBPPTAABLEVLOVNSLICTONSAALAALISTMERABD LPLKETKHT, SYATLTVUGGSHCTVLTINSSFTDERFRIGHTNAAPAGAP PROTTETSPFTAABLEVLOVNSLICTONSAALAALISTMERABD LPLKETKHT, SYATLTVUGGSHCTVLTSSFTDERFRIGHTNAAPAGAP RUMMFILLYBPTABLEUQUNGSOVARVDLMINNKDKOSS ATSSGSLGRADDFPGGTMERSFEGGESTSPENDFDFSAPSDPTDDF PAAHAKAPPPSAALVAURSPROGESTSPENDFGSAPSDPTDDF PAAHAKAPPSAASSPPLAGGGGGABGAAVILTSFRRITLUTIVTVIL PROTTETSPFTAARAGAPAGAPA	j	Ì	1	SNLTSLK\SSLQLYRQFKKDIDEHQSLTESVLQKGEILLQCLLE
DEKEMBAMBHICEGU OFCSPSIGHOFPRUNFTMSMAVETFGFFMATVGLINLGUTLE NSYMVSTHORVITINTIFENLMFSCATDSLGYTNCWFFPSML ALSGYIQACRALMITAILLGFIGLLGLAGETANTIGGLESRK AKLAATAGAPH LILPGICGMVAI VSWYAFNITR\DFSDELVRGT KYELGPALLVLGWSASLISI LIGGLGLCSCOSCEDPARASRRP VOAPVSMPVATSDOEDSSFGKYGRMALRVAALCROPSCLPTA PKRKGPGROFP PYSNLINGBRPRV DVAPPRPRPRULHSGPBOAK NCSWEVAYLPSEAGSLIF PKRKGPGROFP PYSNLINGBPRV DVAPPRPRPRULHSGPBOAK NCSWEVAYLPSEAGSLIF ATSGSLGERDPPGGGTMERESEGESPEE PROOFSAFSDPTOOP PAALAKEDPGSGOOPACPGAGEALAVLITSFGRRLIVLI PVILA GRAVELSVERVLFUGLALYLGHRRVAUDEKENSKRARGLUDDEED LAATVAPAWRSDRFLOTFTFTRVELGSKDER I IGVKVHPGOR KEGILLDINI SYVDDVQ IDVEVKKYP CKAWGOLHGVLEVIL LAATVAPAWRSDRFLOTFTFTRVELGSKDER I IGVKVHPGOR KEGILLDINI SYVDDVQ IDVEVKKYP CKAWGOLHGVLEVIL LAATVAPAWRSDRFLOTFTFTRVELGSKDER I IGVKVHPGOR KEGILLDINI SYVDDVQ IDVEVKHYP CKAWGOLHGVLEVIL LAATVAPAWRSDRFLOTFTFTRVELGSKDER I IGVKVHPGOR KEGILLDINI SYVDDVQ IDVEVKHYP CKAWGOLHGVLEVIL LAATVAPAWRSDRFLOTFTFTRVELGSKDER I IGVKVHPGOR KEGILLDINI SYVDDVQ IDVEVKHYP CKAWGOLHGVLEVIL PPLIGDLEP VOAVSMFT IRRPTLID INNTGMINLOUPGLSSIST TMIMDS I AAFLVLAPRILITA DEL ILDOWGLESSGENGEL IVA VSSRPDPSSAALILVAVILDRADDI ANTSTEDER POKGETT EVMHVEV POGG LEVEVY DENDEDFIGMKLDVGKV LOAS VLDOWFPLOGGGGVHARLEMISLISDAELGEVLOWNOM VSSRPDPSSAALILVAVILDRADDI ANDROLESSGENGEL IVA KLUMARILLADSSEI CPPTVPGCCPAMDVDSSNPCHESSGLENGEL IVA KLUMARILLADSSEI CPPTVPGCCPAMDVDSSNPCHESSGLENGER IVA KLUMARILLADSSEI CPPTVPGCCPAMDVDSSNPCHESSGLENGER IVA KLUMARILLADSSEI CPPTVPGCCPAMDVDSSNPCHESSGLENGER DERLITSPRPTAARLEW LAVAGOLHIN STENSEN IVABEAC LERITYPPTAARLEW LAVAGOLHIN STENSEN IVABEAC LERITYPPTAARLEW LAVAGOLHIN STENSEN IVABEAC LERITYPPTAARLEW LAVAGOLHIN STENSEN IVABEAC LERITYPPTAARLEW LAVAGOLHIN STENSEN LERITA STENSELLUL I PUTLA GROWGHT STENSEN IVABCOLD STENSEN IVABCOLD STENSEN IVABCOLD STENSEN ERKUS I VHGCGSGROPAGEN LAVATSGSSLEBER BEDFDOO KRETTLA SPENERE BELDEAGRARLDOVALLIMY SS ERKUS I VHGCGSGROPAGEN LAVATSGSSLEBER BEDFDOO KRETTLA SPENERE BELDEAGRARLDOVALLIMY SS ERKUS LAVAGOLD STENSEN STENSEN LEDING LOVAGOLD RAVAGOLD RAVAGOLD RAVAGOLD RAVAGOLD RAVAGOLD RAVAGOLD			İ	NTPVLEDVLGRIAKQSGELESHADRLYDSILASLDMLAGCTLTP
SYAROS THERWITTEN TERMINISCATORS INTO SUPPORT ALSOYIOACRAIMITAILLIGHIGILLIGIAGING CHESSER ARCHATAGAPI (I.PGI COMMAI) SWARATITR (DESDLIVEGT KYELGRALYLGWSASLISILGGLICSACCGSDEDASARRE YOAP VSWAVISDQREDSSFCKYGRMARWALCROPACLDTA EKRAGEGROF PY SWARGEREPUVAPPREPERVLHHGPSOAK KOSMEVANIPSEAGSLIF ATSSGSLGRADP PRGGTMERSPGEGPSPSPRUMPEDPASASRRED ATSSGSLGRADP PRGGTMERSPGEGPSPSPRUMPEDPASASRRED ATSSGSLGRADP PRGGTMERSPGEGPSPSPRUMPEDPASASRED ATSSGSLGRADP PRGGTMERSPGEGPSPSPRUMPEDPASASRED ATSSGSLGRADP PRGGTMERSPGEGPSPSPRUMPEDPASASPDTDOP TARTLYMSREPLAMWS PPD VEKABULNISTGGRELIVLI PVYLA GAVGLSVGPVLFGLALYLGWRRVARDEKERSLRARGULDDEEQL TARTLYMSREPLAMWS PPD VEKABULNISTGGRELIVLI PVYLA GAVGLSVGPVLFGLALYLGWRRVARDEKERSLRARGULDDEEQL TARTLYMSREPLAMWS PPD VEKABULNISTGGRELIVLI PVYLA GAVGLSVGPVLFGLALYLGWRRVARDEKERSLRARGULDDEEQL LLARTVAPAVRGSSPBLOTFFTENDELGSKUPLI I GRVKHPOGR KEQILLDLIN SYVLOVOLU DEVKKYFCKAWGOLHGVURVI EPLIGDLPPVGAVSMFFIREPTLD INNTOMINLD I FGELSISD TMIMDSIARPLVLPNELLUPLUPLDDOLOVAGWPLIGWUNGWS VSSRDPSSALILVVVLDRADDOLBMYTSERPFGLOFGGSGINGEV WOLSTQDVTGESRAVYSTOLOVWEREPFFFFLODPGGGLUVGNWG VSSRDPPSSALILVVVLDRADDOLBMYTSENPORGSSGDNAPPR PCHTTPDSGGGGGGGVHLRLEWISLLSDABELGGUVGKKSDPY VKLKLAGRSFRSHVVEEDLINFRWEVFFEVITTS VFGGELEVEVF DKDLOKDDFLGGCKCVLLTVUNSGFLDEWILGEDVSGGELLVL ERILFRPPTAABLEBULOVNSLICTONGSABLALALLISITMERADD LPLKKTETKLSPATATITUGSGSHCWALTISHSSSLGEREPILS GGPPHITSSADEVLONGSGENTAVILSTGSSLGEREPILS GGPPHITSSADEVLONGSGENTAVILSTGSSLLIVANDSCLLDRAPTIL SGGGGVLLARGUSTLSPATATUGSGSHCWATISHSSSLGEREPILS GGPPHITSSADEVLONGSGETGVLGSSHCTAVILSTGSSLLGREPILS ERILFYSINGERGSGDPAGGGGGAAVILTSFGRALLUTIVAYSC GGPPHITSSADEVLONGSHCHAINSTGSSSLGSREPILS GGPPHITSSADEVLONGSHCHAINSTGSSSLGSREPILS GGPPHITSSADEVLONGSHCHAINSTGSSLGSSSLGSREPILS GGPPHITSSADEVLONGSHCHAINSTGSSLGSSLGSREPILS GGPPHITSSADEVLONGSHCHAINSTGSSLGSSLGSREPILS GGPPHITSSADEVLONGSGTTENDERGTKRETSG KKRTLSPFREREBELDLDGARRALDVILSTGRALLUTIVAY ATSSGSLGRADPFRGGGTTERSFCGGFSFSPDDDGFSAPSDPTDQF PAAHAKPPDFGGGGQPAGGAGGALAVILTSFGRILLUTIVAY ATSSGSLGRADPFRGGGTTERSFCGGFSFSPDDDGFSAPSDPTDQF		<u> </u>	ł	
NSYWRSTHORNUTINTIFERLINFSCATDSIGVYNCWEFFSMI. ALSGYIOACRAIMTHAILEGFIGLLIGEFIGINGTONICELISEK ARLAATAGAPH\ILPGICGUMAI\SWARNITR\DFSDLYPGT KYELGPAL\UGANSALISILEGFIGLICACCOSEDDRASARR VQAPUSWMPVATSDCEODSSFCKYGRNALRVAALCROPECLPTA PKREGEGGFPYSNINGERBFREVPVAPPRRPRVLHSHGPSCAK NCSWEVAYLPSEAGSLIF PARAIKEDPGSGGOPAGPGAAGGALAVLTSFGREIDTDGP PARAIKEVARL STORRILAVLIFVYLA GAVGLSVGFVUFGLAVLUKHRVRURKERBARGOLLDDEEQL TAKTUMSKREILPAWUSFPDUERKERLANULVAQVWPFLOGUMEK LLAFTVAPAVGSSPBLOTPTTTPVELEGRARGOLLDDEEQL TAKTUMSKREILPAWUSFPDUERKERLANULVAQVWPFLOGUMEK LLAFTVAPAVGSSPBLOTPTTTPVELEGRARGOLLDDEEQL TAKTUMSKREILPAWUSFPDUERKERLANULVAQVWPFLOGUMEK KEQILLDINISVYDUVOLDVEVKKYPCKAGVKMOLHGVLEVIL EPLIGOLPFVQAVSMFPIRRTVLDINITGHTNILDIFGLSSIST TMINDSLAAFLVLPANTGSSPBLOTPTTTPVELEGRARGOLLDDEEQL LAASTVAPAVGSSPBLOTPTTTPVELEGRARGOLLDDEEQL VKQLILDINISVYDUVOLDVEVKKYPCKAGVKMOLHGVLEVIL EPLIGOLPFVQAVSMFPIRRTVLDINITGHTNILDIFGLSSIST TMINDSLAAFLVLPANTSVARTORTSPLOTPTGLSSISTELPFCLKKCMKEPN WOLSIQOVTQBSKANYSTNCPVWEBAFFFFLQDPGGSGLOVQ KODSRALIVAGATURATULPAQDLIANGFLORFUNGKKEPN WOLSIQOVTQBSKANYSTNCPVWEBAFFFFLQDPGGSLDVOV KODSRALITGALTLPLARLITAFELLIADPHOGESSVDAPPR PCHTTPDSGPGTETHURITAVBAQDLIANGFLISDFUNGKKSDPY VKKALAGRSFRSHVVWEBLDFRUNGVFFSSGPNSRLWM KLOMRILLVARGGFTGFTTHVARTUNGSFLDEWIT DKOOLONDELEGEFF DKOOLONDELGEFF DKOOLONDELE	5425	1086	115	GFCPSPSLGHOPPRVLHPTMSMAVETFGFFMATVGLLMLGVTLD
ALSGYIOACRALMITAILLGELGILGIAGIACTNIGGLELSRK ARLAATAGAPH\LIGE ICGWAAI\SWAPHTR\DESDEDPAASARRD VQAPVSWPVATSOGEDS SFKYKGRAIRWAALCGEPCLPTA PKKRGPGGFPFYSNLGGRERYPVAAPDERDEPPARCHISHGPSQAK NCSBEVAYLPSEAGSLIF 5426 42 3435 ATSSGSLGRADPPRGCTMEXSFGEGFSPE PRIDGESAFSDPTTQF PANAKRAPDCSGGOPAGPGAAGGALAVLITSFGRELIVLIFYVLA GAVGLSVGFVLFGLALYLGWRRVRUBEKRSLRAAGLLIDDEGOL TAKTLYMSHEELPAWVSFPDVEKAEWLIKKTVAQVMFLGQUMFL LLAETVARAVRGSMPHLOTTFTRVELGEKPLRITGVEVHFGQR KEQILLDINISYVGVQIDVEVKKYFCKGGVKMQLHGVLRVIL EPHLIGGLFVGAVSMFFIRFTDLINNTGWTNLDIPGLSSLSD TMIMDSIAAFLVLPNRLUFSLVPDLQDDVAQLRSPJPGGIIRIHL LAARGLSSKOKYVKGLIGEKSDPYAJVELGTOTFCSRVJDELIN POMGETYEMWHEVPGGGIEVEVFFKDDDKDDFLGRMKLDDVGK VSSRDPPSAAILVVALDRAQDLPMVTSELYPPQLKKGNKEPNP WOLSTQDVTOESKAVYSTNCPVWEAFPFLQDPSGGEDLVQV KUDSRALTLGALTLPLARLITAFELILDQWFGLSSGENGELVW KLUMRITULDSSEICFFTYPGCCGAMVEDENPRGGAVSCADPP PCHTTPDSGFGTERVLRITVLERQDLIAKDRFLGGLVKGKSDPY VKIKLAGSFSSHVVRGLVDNSLOTORSERPLQDPSGGENEVEW PKIKLAGSFSSHVVRGULVSSLOTORSERPLQDPSGGENEVEW PKIKLAGSFSSHVVRGULVSSLOTORSERPLQDPSGGENEVEW PKIKLAGSFSSHVVRGULVSSLOTORSERPLQDPSGGENEVEW PKIKLAGSFSSHVVRGULVSSLOTORSERPLQDPSGGENEVEW PCHTTPDSGFGTERVLRITVLNSGFLDEWLTLEDDYSGRIHLELL ERTIPPPTAABLEEVLQVSSLOTORSERPLATALISTMERABD LPLKKSTKILSPYATLTVGDSSHKKKTISGTSAPVMDESASFLI RKPHTSSLELQVRGGGTGVLGSLSIPLSELLAVAGCLDRWFTL SGGGOPHITSSAPEV\RQCHTTVUSSLEDGLARAALLSIVMERABD LPLKKSTKILSPYATLTVGDSSHKKKTISGTSAPVMDESASFLI RKPHTSSLELQVRGGGTGVLGSLSIPLSELLAVAGCLDRWFTL SGGGOPHITSSAPEV\RQCHTHVUSPLEAPAGPLGQCKLDLWFTL SGGGOPHITSSAPEV\RQCHTHVUSPLEAPAGPLGQCKLDLWFTL GAVGLSVGFVLFGIALYLGWRRVDEKERSLRARAGLDDEGOL TAKTLYMSHERLPAWVSPFDVEKAEMTUNQVWPFLGGYMEX LLAETVAPAVRGSNPHLOTFTFTRVELGEKPLRITIPLVVLA GAVGLSVGFVLFGIALYLGWRRVDEKERSLRARAGLLDDEGOL TAKTLYMSHERLPAWVSPFDVEKAEMTUNQVWPFLGGRMKLDVGWEX LLAETVAPAVRGSNPHLOTFTFTRVELGEKPLRITIPL LAARGLSKKKYVVGLIECKSDPYALVRLGTOTFCSRVIDELNI PQWGSTYEVWHEVPGQGETVFVPDKDCPARKDLDVGKYMFG VSSRPDPFSAAILVYLDSSSICTPTVPGCCPARMYSLENDFREFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF				NSYWRYSTVHGNVITTNTIFENIWESCATDSIGVYNCUPEDCAL
ARLAATAGAPH\LIGGICGMVAI\SWYAPNITEDBEDLYPGT XYBLGPALVIGMSASLISLIGGICLGCACCGSDEDPAASARR YQAPVSWPVATSDQEGDSSFGKYGRNALRVAALCGCPRCLPTA PKKEPGRGPPPYSHLEGRERPVVAPPRPPRVLHSHOPSQAK NCSWEVAYLPSEAGGLIP 3435 ATSSOSLIGRADPPRGCTHEXSPGGFSPSPMDQFSAFSDPTDQP PAAHAKPDPGSGGPAPGAAGEALAVLTSFGRRLLVULTSYVLSH GAVGLSVGFVLFGLALVLGMRRVRDEKKENSLRAARQLLDDEEQL TAKTLIWASRELPAMVSPPDVEKAEWLIKKVAQVWPFLGQYMEK LLAETVAPAVRGSWPHLOTTFTFRVELGERFLEN LGVKVHPGQR KEQILLDLNISTVGDVQLDVEVKKYFGAVGKWGULHGVGLWEVIL EPLIGDLPFVGAVGMFFIRRPTLDINNTGMTNLLDIFGLSSLSD TMIMBISLAAFVLVPNRTLUVFUVPDLOQLGSSPLBGFIRIHL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTOTFCSRVIDEELN POMGETTEVTWHEVPGGCGQVHLKLWISLLSDAEKLEQUVQNNWG VSSRPDPPSAALLVAVLDRAQDLDWTLSPPDGKESCHEN WVQLSIQDVTOGSKAVVSTNCCVWBEAFRFFLQDPSGCBLDVQ KDDSRALLTGALTIPLARLLTABELILDQMFQLSSSGFNBRUM KLWRILLLDSSTCFPTVPGCCPGAWDVDGENPGRGSSVDAPPR PCHTTPDSOFTENUR.RIVLEAQDLIAKDFTLGGLWGKSDPY VKIKLAGRSFRSHVVREDLERFMRWEVEVIVTSVPGGLEEVEVF DKDLDKDDFLGRCKVKLTTVLNSGFLDEWLTLEDVPSGRCHLHLL ERRITPRPTAABLEEVLQVRSCTGVLASSLGTVLSAAAALLSITWREAD LPLKKGTKHLSPYATLTVGDSSHKTKCTSGTSAPWWDESASFLI RKPHTSSLEDLYNGGCTGVLGSLSDLSPAGLGGVKURNFTL SSGQGVLLRAQLGILVSGHSGVVRHSHSYSHSSSLSEEPELG GGPHITTSAPPV\RGRTVLSGHSGVVRSHSHSYSHSSSLSEEPELG GGPHITTSAPPV\RGRTVLSGHSGVVRSHSTGNARTSO KKRTLSPFFNRFWERLDDEAQRKLAVLLOWDPLGGWFTL SSGQGVLLRAQLGILVSGHSGVVRNSHSTMRRFSD ERRLVSIVHGCRSLRONGRDPPDPYVSLLLLEDRINGGTKRRTSO KKRTLSPFFNRFWERLDDEAQRKLAVLTSGRRLJAVLTSVTAYSE ERRLVSIVHGCGSLRONGRDPPDPYVSLLLLEDRINGGTKRRTSO KKRTLSPFFNRFWERLDDEAQRKLAVLTSGRRLJAVLTSVTAYSE ERRLVSIVHGCGSLRONGRDPPDPYVSLLLLEDRINGGTKRRTSO KKRTLSPFFNRFWERPBLDDEAQRKLAVLTSGRRLJAVLTSVTA GAWGLSVGFVLFGLALYLGWRRVDEKERSLEARAGLLDDEQL TARTLYMSHRELPAMVSPPDVEKAEMTLVQAWPPLGGYMEX LLGEVADABAGELAVLTSGRRLDVRVL EPLIGGLBFVGAVSWFFTRFFTLDINMTMMTHLLDIGGLKGKNENPL PAAHAKPPDGGGGGGTEVEVENDEAGRGNAVGMLHGWLVL EPLIGGLBFVGAVSWFFTRFFTLDINMTMMTHLLDIGGLKGKNENPL POMGETTSVAMMEVPGGGGGGTEVEVENDEDFLGANKLNOURVL LGASULDDWPPLGGGGGGTEVEVENDEDFLGANKLNOURVL LGASULDDWPPLGGGGGGTEVEVENDEDFLGANKLNOURVL LGASULDDWPPLGGGGGGGTEVEVENDEDFLGANKLNOURVL LGASULDDWPPLGGGGGGGTEVEVENDEDFLGANKLNOURVL KLWMEI	1		1	ALSGYTOACRALMITATILICET CLILICIA CLICARIA PORTECT PARAMETERS
KYELGPALYLGWSASLISILGGLCLGSACCGSDEPDARSARRP VQAPVSWPVATSDGEDSSFKYGMIRVALCGRPCLPTA PKKRGPGGFPYSNLRGRPRYVYAPPRPRPRVLHSHGPSQAK NCSWEVAYLPSEAGSLIF 5426 42 3435 ATSSGSLGRADPPRGTMESSPGEGFSVEPRDGPSAFSDPTDQP PAHAKRPBCPGGGDAGAGEALVISTGRRLHVI PYVLA GAVCLSVGFVLFGLALYLGWRRVNDEKERSLPARGQLLDDEQL TAKTLYMSKRED,PANVSFPDVEKERSLPARGQLLDDEQL TAKTLYMSKRED,PANVSFPDVEKERSLPARAGQLLDDEQL TAKTLYMSKRED,PANVSFPDVEKERSLPARAGQLLDDEQL TAKTLYMSKRED,PANVSFPDVEKERSLPARAGQLLDDEQL TAKTLYMSKRED,PANVSFPDVEKERSLPARAGQLLDDEQL TAKTLYMSKRED,PANVSFPDVEKERSLPARAGQLLHOLEQUM LLAETVAPAVRGSNPHLQTFTFTRVELGKVBRI IGVKVHFGGR KEQILLDLNISYVODQGIDVVEKYFYCKAGVKROUHGVLKVIL EPLIGDLFFVGAVSMFFIRFTLDINYMSMINLDIPGLGSLSS TMIMDSIAAFLVLPRILLVPLUPDLQDDVAQLRSPDFRGG IIR IHL LARGGLSSKOKYVKGLI GEKSDPYALVSLGTOTFCSRVIDBELIN PQMGETYEVMYHEVPGGEIEVEVFPKDDDKDDFLGRMKLDDVGKV LOASVLDDWFPLQGGGQQVHLREBNISLLSDAREKLGQU/QNNW VSSRPDPPSAAILVVYLDRAQDLMVTSELYPPQLKKGNKEPNP MVQLSIQDVTOESKAVYSINCEVWBEAFFLQDPSOGEDLVQV KDDSRALTLGALTLJDLARLLTAPELILDQWFQLSSGFNBRLYM KLUMRILLVLDSSEICTFTVPGCCGAMUSEPPLQDFNSGGSVDAPR PCHTTPDSOFGTBRVLRIHVLBAQDLIAKDRFLGGLVKGKDPY VKLKLAGSFFSHVVRGUNSSLTOTVABGDLENGVBFVDAPFR PCHTTPDSOFGTBRVLRIHVLBAQDLIAKDRFLGGLVKGKDPY VKLKLAGSFFSHVVRGUNSSLTOTVABGDLENGVBFTLHELL ERTPPRPTAABLEEVLQVSSLTOTVABGLAALLSIVMBRAD LPLKKGTKHLSPYATLTVGDSSHKKTSTSGTSAPVMDESASPLI RKPHTSSLEDLQVRGCGTGVLGSLEDLSELVADQLCLDRWFTL SSGGGQVLLRAOLGILUSQHSGVBAKKKTSGTSAPVMDESASPLI RKPHTSSLEDLQVRGCGTGVLGSLEDLSELVADQLCLDRWFTL SSGGGGVLLRAOLGILUSQHSGVBAKKKTSGTSAPVMDESASPLI RKPHTSSLEDLQVRGCGTGVLGSLEDLSELVADQLCLDRWFTL SSGGGGVLLRAOLGILUSQHSGVBAKKKTSGTSAPPDETDQP PAHAKPPPPGGGQQPAGAGAGALALVAQVADPLGQVMLT LGKVOLDLABTDLSGGVARWYDLAUNDKMSSS MSGEREL 5427 42 3435 ATSSGSLGRADPPRGTMERSPGGSPSPSDMOPSAPSDPTDQD TAMMSLAARLLVLNPRLLVPLVDLQDLQALSPLPRGTIRHL LAARGLSKKKYVVKGLIEGKSDPYALVRLGTGTFCSRVILDELN PQMGTYEVMHEWPGGEIEVEVFDKDDFNDCDFLGRKLLDVGKV LQASVLDDMFPLQGGGQVHRLEWLSLLSDAREKLGVLQRNMG VSSRDPPSAAILVYLDSSSLICTPTVGCPCGAMVGMOLGHGVLRVLL EPLIGDDFVGASKAYVSINCPVWEERFLQDPGOSGUNDAPR PCHTTPDSQRGTFHVLRTHVLEAQDLIAKDRPLGGLVKKKSDPY VKLKLAGSSFSHVVRECHLDRWRMEWPTVSV				AKLAAMACADUL TA DOLOGUMATA GUMA MATARA ARANGA ARANGA MATARA ARANGA MATARA ARANGA MATARA ARANGA MATARA ARANGA MATARA ARANGA MATARA ARANGA MATARA ARANGA MATARA ARANGA MATARA ARANGA MATARA ARANGA MATARA ARANGA MATARA ARANGA MATARA ARANGA MATARA ARANGA MATARA ARANGA MATARA ARANGA MATAR
YQAPVSWBVATSDQGGDSSTGKYGRNALKYAALCKGPRCLPTA PKKBGPGGFFFYSBLIGRPRPVPVADPRPRPRVLHSIGPSQAX NCSWEVAYLPSBAGSLIF ATSGSJGRADPFBGGTFERSPGEGPSSSMDQFSAGSDPTDQF PARHAKPDPGSGGDAGCBAAGCBALAVLTSFGRELLVLIPVYLA GAVGLSWGFVLFGLALVIJGMRRVMEKRSIKARAQLLDDEEQL TAKTLYMSHRELPAMVSPPDVEKAEMINKIVAQVWPFLGQYMEK LLAETVAPANGSNPHLQTFTFTRVELGSFURIIGVKVHFGQR KEQILLDLANISVUGDVQIDVEVKKYFCKAQVKMQLHGVLRVIL EPLIGDLFFVGAVGMFFIRRFTLDINNTGMTHLLDIFGLSSLSIS TMIMDSIAAFLUPRRLLVPLLVPDLDQVAQLKSPLPRGIRIHL LAARGLSSKDKYVKGLIBGKSDPYALVRLGTTGFCSRVIDBEIN POMGETFEVMVHEUPGGEIEVEVPDKDPDKDFLGRMKLDVGKV LQASVLDDWFPLQGGGGGVHIRLEWIJSLSDAEKLEQVLQWNNG VSSRPDPSAAILVVALDRAQDLHSELLDOMPGLSSGFRSLLVM KLUMRILVILDSSEICFPTVPGCPGAMDVDGSBUPQRGSSVDAPR PCHTTPDSOFGTEHVLRHVLEAQDLIAKORFLGGLIVKGKSDPY VKLKLAGRSFRSHVVREDLBFRRNEVFEVIVTSVPGGELEVEVF DKDLDKDDFLGRCKVRLTTVINGSFLBFLALTLEDVFGGSSFRSLLVM KLUMRILVILDSSEICFPTVPGCPGAMDVDGSBUPQRGSSVDAPR PCHTTPDSOFGTEHVLRTHVLEAQDLIAKORFLGGLIVKGKSDPY VKLKLAGRSFRSHVVREDLBFRRNEVFEVIVTSVPGGELEVEVF DKDLDKDDFLGRCKVRLTTVINGSFLBKTLTIGOTASPWNDESASFLI RKPHTESLELQVRGGGTGVLGSLSLBLLVADQLCLDBWFTL SSGGGVLLRAQLGILVSGHSGVEARSHSYSHSSSSLSEEPPLIS GGFPHTTSSAPVN, VQRLTHVDSBLABLLJSTLMADALCLDBWFTL SSGGGVLLRAQLGILVSGHSGVEARSHSYSHSSSSLSEEPPLIS GGFPHTTSSAPVN, VQRLTHVDSBLADALLSTLMADALCLDBWFTL SSGGGVLLRAQLGILVSGHSGVEARSHSYSHSSSSLSEEPPLIS GRENVSIVHGCRSLRQGGRDPPDPYVSLLLLPDKNGTKRRTSQ KRTLSPFENRFRBELPLDBEAGRAPDGLGGVRKTTSG KRSTLSPFENRFRBELPLDBEAGRAPDGLGAPASDEAPDTDGP PAAHAKPDPGSGGQPAGPGAAGEALAVLTSGGRELLVLITHVYLA GAVGLSVGFVLFGLALVLGWRRYDEKERSLRARGLLDDEEQL TAKTLYMSHRELPAWSFPDVEKGRSGVMADHGVLRVIL EPLIGDLFFVGAAVMFFIRRFTLDINMTGMTNLDIFGLSSLSD THMDSIAAFLULPRUVPGCHEVGAVGMVGMURVLRVLL EPLIGDLFFVGAAVMFFIRRFTLDINMTGMTNLDIPGGSSLSD THMSSIAAFLUGAVSFPDVERGAGGGGVANLDVGKULVCKUL CASVUDDWFPLQGGGGGVVHRLEWLSLLSDAEKLEQVLQWMG VSSRDPPSAAILVVILDRAQDVINVTSGLYPPOLKGKREPNP MVOLSIGDVTGESKAVYSTGCPWBERFRFFLDDFOSSSGPNSRLYM KLVMRILVDSSSICTFFTVDGCGGABVDDFSSSGPDABLYM KLVMRILVLDSSSICTFTVDGCGGEVVSVTDGSSSGPNSRLYM KLVMRILVLDSSSICTFTVTDGCGGLEVEVFV	1			VYPLODALVI CHOREL TOTAL COLOR CONTROL TO THE COLOR COL
PKKRGPGRGFPYSNLRGRPRPVPVAPPRRPRVLHSHGPSOAK NCSMEWAYLPSBAGSLIF ATSGSLGRADPRGGTMERSPGEPSSPENDQFSAPSDPTQF PAHAKREPDGSGGQDAPGAAGAELAVLTSFGRRLLVLIPVYLA GAVGLSVGFVLPGLALYLGWRRVRDEKERSLRARQLLDDEEQL TAKTLYMSHRELDARWSFPDVEKAEWLINKIVAQVWPFLGQYMEK LLAETVAPAVRSNPHLQTFTFTKELGERDIRI (JOKVHPGQR KEQILLDLANISYGDVQI QUBEVKKYFCKAGVKGMQLHGVLRVIL EPLIGDLPFVGAVSMFFIRRFTLDITKGMTLLDIPGLSSLSD TMINDSIAAFLVLPNRLLVPLVPDLQDVAQLSPLPRGIIRIH LAARGLSSKDKYVKGLIEGKSDPYALVRLGTOTFCFSVIDEELN POMGETYEMVHEVSGQSIEVEVFDKDDDKDDFLGRMKLDVGKV LOASVLDDWFPLGGGGQVHLRILBLSJSDAKKLOQULQNNWG VSSRPDDPSAALLVVYLDRAQDLDMYTSELYPPQLKKGNLEPNP MVQLSIQDVTQESKAVYSTNCPVWEEBFFLQDPQSGBLDVQV KUMRILLYLDSSEICFFTVPGCPGAMPUDSENPQRGSSVDAPPR PCHTTPDSGFGTEHVLRIHVLEAQDLLDMYTSELYPPQLKKGNLEPNP WKLKLAGRSFRSHVVREDLBFRNRDFFEVIVTSVFGGELEVEVF DKDLDKDDFLGGGKVRLTIVLNSFELTLAGRRILGVKGKSDPY VKLKLAGRSFRSHVVREDLBFRNRDFFEVIVTSVFGGELEVEVF DKDLDKDDFLGGGKVRLTITVLNSFELTLAGRRILGVKGKSDPY VKLKLAGRSFRSHVVREDLBFRNRDFFEVIVTSVFGGELEVEVF DKDLDKDDFLGGGKVRLTTVLNSFELTLAGRRILGVKGKSDPY VKLKLAGRSFRSHVVREDLBFRNRDFFEVIVTSVFGGELEVEVF DKDLDKDDFLGGGKVRLTTVLNSFELTLAGRRILGVKGKSDPY VKLKLAGRSFRSHVVREDLBFRRNSFSSSSLSEEPFELS GGPPHITSSAPEVLQNBSLIGTTKISQTSAPVMBSASPLI RKPHTESLELQVGGETGVLGSLSLELSELLADQLCLDRWFTL SGGGQVLLRAQGGTGVLGSLSLEDLSELLADQLCLDRWFTL SGGGQVLLRAQGGTGVLGSLSLEDLSELLADQLCLDRWFTL SGGGQVLLRAQGGTGVLGSLSLEDLSELLADQLCLDRWFTL SGGGGVLLRAQGGGTGVLGSLSCHARDSTSSSSSSFREREEL LGKVQLDLAETDLSQGVARWJDLMONKDKGSS TATSGSSLGRADPFRGGTMERSFGEGFSPSPMDGPSASSBPTDOP PAAHAKPPDGSGGQPAGFGAAGLAAVITSFGRRLLULLIPVLA GAGLSSKDKYVGLLAGWRVDBKERSLRAARQLDDEEQL TAKTJWSHRELDAWSFPDJEKAEWLINLIVAQWPFLGGYMEK LAARGLSSKDKYVGLLAGWRVDBKERSLRAARQLDDEEQL CLASVLDDWFPLQGGGQQVHLRLEWLSLLSDARKLEQVLOWMIG VSSRPDPSAAILVYALDRAADLPWTSLYPPQLKKMKLDVGK LAARGLSSKDKYVGLIEGKSDPYALVRIGTTCSRVIDEEN PQMSTTYDWHREYPGGGETEVEVFROPDCDFLGGKNLDVGK VSSRPDPSAAILVYALDRAADLPWSGSSGPNSBLYM KLVMR ILVDSSEICFFTTYPGCFGAMVDDESSGPNSBCRA				NO DISCIPLINATION AS LIST LIGGLE CLCSACCEGS DEDPAASARRP
S426 42 3435 ATSSGIGRADPROGTMERSPGEPSPSEMDOPSAPSDPTDOP PARAKREDPOSGGOPAGEAAGEALAVLTSFGRELLVLIPVYLA GAVGLSVGVLPGLALYIGMERVRDEKRSIRAAROLLDBEGU TAKTLYMSHRELPAWVSPPDVEKAEWLINKIVAQVMPFLGGYMEK LLAETVAPANGSNPHLOTFTFTRVELGERPIRIIGWKHPGOR KEQILLDLNISYVGDVQIDVEVKKYKAGVKGMQLHGVLRVIL EPLIGDLPFVGAVSMFFIRRFTLDINNTGMTMLDDIPGLSSLSD TMIMDSIAAFLVLIPMRLLVPLVPDUOPAQLSSPJPRGIIRIHL LAARGLSSKDKYVKGLIEGKSDPYALVRLOTDFCSRVIDBELM POMGETYEMVMEUR POGGEIEVUFDOTDFCSRVIDBELM VSSRPDPPSAALLVVYLDRAQDLPMYTSELYPPQLKKGNKEPMP WOLDSIQDVTOPSKAVVSTNCPVWEERFFFLQDDSGELDVQV KDDSRALTLGALTLPLARLLTAPELILDQMFQLSSGGPNSRLM KLVMRILVLDSSEICFPTVPGCGSGEVUNDSDENPQRGSSVDAPPR PCHTTPDSGFGFHVLRIHVLEAQDLIAKDRFLGGLWGKSDPY VKKLKAGRSFRSHVVREDLMFRIMEVFEVUTVSVPGGELEVEVP DKOLDKODFLGRCKVRLTTVLNSGFLDEWLITLEDVPSGRLHLRL ERITPPRFTABLEEVLQVNGSLSLDLSELLVADGLCLDRWFFIL SSGGGVLARAGLGILVSGRSGGVARSHSYSHSSSSEEPPELS GGPHTTSSAPEV\RQRLTHVDSPLEARBLAAALLSIYMBRAED LPLRKGTKHLSPYATLITVGDSSHKTKTISGTSAVWBGSASFLI- RKPHTESLELQVRGEGTGVLGSLSLDLSELLVADGLCLDRWFFIL SSGGGVLARAGLGILVSGRSGGVARSHSYSHSSSSISEPPELS GGPHTTSSAPEV\RQRLTHVDSPLEAPAGPLGGVKLTLWYTSE ERKLVSIVIGGCSLRONGROPPPDYLLLLDPDINGTKRRTSG KKRTLSPERNERFFENELPLDEAGRRLDDVKNSNSSFMSREREL LGEVOLDLAFTDLSGGVARWYDLMOMKDKGSS 5427 42 3435 ATSSGLGRAPPPRGGTMERSPGGFSFSPENDGPSAPSDPTDQP PAAHAKPPDGSGGQPAOFGAAGEALAVLTSFGRRLLDVLIVVILA GAGGLSVGFVLFGLALVLGRRKVDFERSERJRAARGLDDEEQL TAKTLYMSHRELPAWVSFPDVEKAEKININGTVHEGKERLDDEEQL TAKTLYMSHRELPAWVSFPDVEKAEKININGTVHEGKERLDDEEL LAETVAPAVRGSSHPHLOTFTFTRVELGEKREIRAARGLDDEEQL TAKTLYMSHRELPAWVSFPDVEKAEKININGTVHYDFGCSSSD TMIMDSIAAFLULDRINGTVENGERSPRANGTVHYDFGCSSSD TMIMDSIAAFLULDRINGTVENGERSPRANGTVHYDFGCSSSD TMIMDSIAAFLULDRINGTVENGERSPRANGTVHYDFGCSSSD PQMGETTYSWMHSFYGGGLEVSFVPDFDCDFLGRKKLDVGVV LQASVLDDWFFLQGGGGQVHKLEMISLLSDARKLEGVLQNMWG VSSRPDPFSAAILVVTLDRAQDLPRSLEVPDOTTGSSRVLDVGKKENDPP MVOLSIQDVTOESKAVYSTNCPVWEEAFRFFLQDPQSGELDVOV KDDSRALTLGALTLPLARFLLTAPELILDQWFGLSSSGPNSRLYM KLVMRILVLDSSSICFFTFVPGCGRAMDVDSSSPORGSSVDAPPR PCHTTPDSQFGTERVLRIHVLBAQDLIAKDRFLOGLVKKKSDPY VVKLKLAGRSFRSHVVSELDLMPRINGSVLUTSUVTSGGEGUEVEVF	1	j		IQAPVSVMPVATSDQEGDSSFGKYGRNALRVAALCRGPRCLPTA
ATSSOSLGRAD PREGTMERSEGESSES MODESASED PTOOP PAHAKREPDESSEGODAS CHARGERLAVLTSFORRILDITYVIA GAVGLSVGPVLPGLALYLGWRRVRDEKERSLRARQLLDDEEQL TAKTLMWSRELDAWVS PDVEKAEWLINKIVAQVWPFLGQYMEK LLAETVAPAVRSSNPLOTFTFTRVELGERPIRI (JEWKHPGQR KEQILLDLANISYGDVQIDEVKKYFCKAGVKGMQLHGVLRVIL EPLIGDLPFVGAVSWFIRFTENTIOTHGMTHLLDIPGLSSLSD TMINDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRHL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTOTFCSRVIDEELN POMGETYEVMVHEVSGOSIEVEVVPDKDPDKDDFLGRMKLDVGKV LOASVLDDWFPLGGGGQVHLRILBALSJSDAKKLSQVLQWNWG VSSRPDDFSAAALVVYLDRADDLPMVTSELYPPQLKKGNNEPNP MVQLSIQDVTQESKAVYSTNCPWHEEAFRFFLQDPQSGELDVQV KDDSRALTLGALTLPLARLTAVELLDGWFGLSSSGPNSRLWM KLVMRILVLDSSEICFPTVPGCCGAMPLVDSENPQRGSSVDAPPR PCHTTPDSGFGTEHVLRIHVLEAQDLLAKORSDPY VKLKLAGRSFRSHVVREDLMFRWNEVFEVIVTSVFGGELEVEVF DKDLKDDFLGGGKVRLTIVNLSTELSTLATVENGSSKLVAKGKSDPY VKLKLAGRSFRSHVVREDLMFRWNEVFEVIVTSVFGGELEVEVF DKDLKDDFLGGGKVRLTTVINGSEBLENILTEUNYPSGRHLHLL ERLTPRPTAABLEEVLQVNSLIGTOTKSAELAAALLSIYMREAED LPLKKGTKHLSPVATLTVGDSSFKTSISTSSTSSHSEFFELS GGGPHITSSAPEVLQVNSLIGTOTKSAELAAALLSIYMREAED LPLKKGTKHLSPVATLTVGDSSFKTSISTSHSSSSLSEEPFELS GGGPHITSSAPEVLQRGSLTOTUSSLSLEISLALVADQLCLDRWFTL SSGGGVLRAQLGSLVGGROPPDPYVSLLLLPDDINGTKKRTSQ KRTLSPEFNERFEBLELDBEAQRGBLGVVLTMYYSE ERRLVSIVHGCRSLRQGGROPPDPYVSLLLLPDINGTKKRTSQ KRTLSPEFNERFEBLELDBEAQRGBLGVVSVNSSSFRGREEL LGKVQLDLAETDLSQGVARWYDLMONKDKGSS STRGFEEL LGKVQLDLAETDLSQGVARWYDLMONKDKGSS KRTLSPEFNERFEBLEPLDEAQRGELAVLTSGTGRLLULTIPVLA GAGGLSVGFVLFGLALVLGWRRYDEKERSLRAARQLDDEEQL TAATLYMSHRELPAWVSFPDVEKAEWLNKIVAQVWPFLGGYNEK LLAETVAPAVRGSNPHLOTFFTRVELGERKELRAPGGVRGMQHLAVLI EPLIGDLFFVGANSWFFIRRPTLDINWGMYNLDLIDGLSSLSD TMMDSIAAFLLURLLVLDVQDQLAGSELPGGIRHL LAARGLSSKDKYVKGLIEGKSDPYALVRIGTOTFCSRVIDEELN PQWSTTYEVMHEVPGGGEEVEVSFYDCROPKORDLDDEEQL LAARGLSSKDKYVKGLIEGKSDPYALVRIGTOTFCSRVIDEELN PQWSTTYEVMHEVPGGGEEVEVSFYDCROPKORDLDSSSGPNSELYM KLVMR ILVDSSLICTFTVDGCGBAWDVDSENDGRGSSVDAPPR PCHTTPDSQFGTENVLRIHVLEAQDLIAKDRFLOGLVKKKSDPY VKLKLAGAGSFRSHVVYGLDLNPRVINGEVSUSTVOTSSVDAPSPROGSSVDAPPR PCHTTPDSQFGTENVLRIHVLBAQDLIAKDRFLOGLVKKKSDPY VKLKLAGRSFRSHVVEDLDNPRUMESVITUSTSVOGGLEUVGV				PKKRGPGRGPFPYSNLRGRPRPVPVAPPRPRPRVLHSHGPSQAK
PARIAR PDROSGOPAGEGAGEALAVITS CRRILULI PYYLA GAVGLSUGFVLFGLALY LGWRRVIDEKEKSURARA GLIDDEEQL TAKTLYMSHRELD PAWNS PPDUS KAEWLINKI VAQWEFLGQYMEK LLAETVAPAVRGSNPHLOFTFTRVELGEK PLRI I GVKVHPGQR KEQILLDLINIS YUGDVQIDVEVKKYEK GKGVKGMQLIGVLEVIL EPLIGDLPFVGAVGMFPI RRPTLDINNTGMTMLDIPGLSSLSI TMIMDSIAPLLVJRNRLLVPLUPDLODVAQLRSPLPRGIIR IHL LAARGLSSKOKYVKGLIEGKDPYALVELGTQTFCSRVIDEELIN PQMGETYEWWHEVPGQEIEVEVFFKDPDKDDFLGRNKLDVGKV UGAS VLDDWFPLGGGGGQVHLREWISLLSDAEKLEQVLQMNWG VSSRPDPPSAAILVYLDDRAQDLPWTSELYPPGLKKGNKEPNP MVQLS IQDVTQESKAVYSTNCPWEERFFFLQDPGSGELDVQV KDDSRALTIGALTLPLARILTAPELILDOWFOLSSGEPNSILWM KLWMRILVILDSSEICFPTVPGCAMDVDDSENPGRGSVDAPPR PCHTTPDSOFGTEHVLRI HEVLEAQDLIAKDRPLGGLVKCKSDPY VKLKLAGRSFRSHVVREDLNPRWNEYEVIVTSVPGGELEVEVF DKDLDKODFLGRKKVRLTTVLNSGFLDEWILLEDVPSGEHLRL ERLTPRFTAABLEEVLQVNSLIOTQKSSELAAALLSIYMERAED LPLKKKTKHLSFYATLTVODSSHTKKTISQTSAPVDWESSFIL RKPHTESLELQVRGEGTGVLGSLSLPLSELLVADQLCLDRWFTL SGOGGOVLLRAQLGILVSQHGSVHSHISYSHSSSLSEEPPLG GGPHTTSSAPEV\RGRITHVDSPLEAPAGPLGQVKLTJWYSE ERLLVSIVIGGSLELQRORGPPVSULLLPDKNRGTKRRTSQ KKRTLSPEPNERFEWELPLDEAQRRKLDVSUNSSIFMSRREEL GROGVLLFAGLELVGAWGAWDLDANKKOSS 5427 42 3435 ATSSGSLGRADPPRGGTMERSFEGESFSEMDGPSAPSDPTDQP PAAHAKPDPGSGQDPAGGAAGEALAVLTSGGRRLLVLIPVVLA GAVGLSVGFVLFGLALVIJOMRVDEKERSLRARQLLDDEEQL TAKTLYMSHRELPAAVSFPDVEKABULNKTVAQVWPFLGOYMEX KEGILLDLNI SYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVYL EPLIGDLFVCAVSMSFILLYBURGEKPLIR ILVKVHPGOR KEGILLDLNI SYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVYL EPLIGDLFVCAVSMSFILRRFTLDINNTGMTNLDIPGLSSLSD TMMDSIAAFLVLPRRILVPLVPDLQDVAQLASPJERGIIRIHL LAARGLSSKDKYVKGLIEGKSDPYAJVKLTQTFCSRVIDEELN PQMGETYEWMHEVPGGEIEVEVPTDDDPDCDPLKKGMKEPNP MVOLSIQDPTQGSGGVHLREBELSLLSDAKKEQULQNING VSRRPPPSAAILVYLDRADDFTGSSVDAPPR PCHTTPDSQFTSWMINDFUNDEVPURGSSVDAPPR PCHTTPDSQFTSWMINDFUNDEVPURGSSSVDAPPR PCHTTPDSQFTERVLAR LIVLLEAQDLIAKDRGSSVDAPPR PCHTTPDSQFGTERVLAR LIVLLEAQDLIAKDRGSSVDAPPR PCHTTPDSQFGTERVLAR LIVLLEAQDLIAKDRGSSVDAPPR PCHTTPDSQFGTERVLAR LIVLLEAQDLIAKDRGSSVDAPPR PCHTTPDSQFGTERVLREDVURDEVPURVEVPURDGGLIVKKSDPY VKLKLAGRSFRSHVAN EDLIAPRINGEVFULVTEVPUGGLIVKKSDPY VKLKLAGRSFRSHVAN E	5426			
GAVGLSVGFVLFGLALYLGWRRVDBEKESLRARAQLIDDEEQL TAKTLWASHRELDEWVSFPDVSKASEULKIVAQVWPFLGQYMEK LLAETVAPAWGSONPILGYFTFRVELGEKPLRIIGVKVHEGGR KEQILLDLNISYVGDVQIDVEVKKYFCKGVKGWCLHGVLRVIL EPLIGDLFVGAVSMFFIREPTLDINWTGMYNLDIGLSSLSD TMINDSIAAFLVLPNRLLVFLVPDLDDVAQLRSPLFRGIIRIHL LAARGLSSKDKYVKGLIEGKSDPALVVKIGTGTSENDIBELIN FQWGETYEVMVHEVPGQEIEVEVFPKDPDKDDFIGRMKLDVGKV LQASVLDDWFPLGGGGQGVHLRLEWISLISDAEKLEQVLQWNWG VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP MVQLSIQDVTQESKAVYSTNCPVWEEAFFFLQDPSGELDVQV KDDSRALTIGAAITLPLARLITAFELILDQWFGLSSGGPNSRLVM KLVWRILYLDSSEICFPTVPGCPGAWDVDSENPGRGSSVDAPPR PCHTTPDSOFGTBHVLRHVLBAFELISGLWKGKSDPY VKLKLAGSSFRSHVVREDLNPRWNBVFSVITSVPGGELEVEVF DKDLDKDDFIGRCKVRLTTVLNSGFLDEWITLEDVPSGEHLVGL ERLTPRPTABLEEVLQVNSLIQTGKSSEALAAALLSIYMERAED LPLEKGTKHLSFYATLTVDDSSHKTKTISGTSAPVWDESASFII RKPHTESLEQVGREGTGVLGSLIJSELLVANDLCLCDRWFTL SSGGGGVLLRAGLGILVSGHSGVEAHSHSYSHSSSSLSEEPBLS GGPPHTTSSAPEV,RRDITHVDSLEAPAGFLGVKKITLWYSE GGPHTTSSAPEV,RRDITHVDSLEAPAGFLGVKKITLWYSE GGPHTTSSAPEV,RRDITHVDSLAPAGFLGVKLTLWYSE GREKLVSIVHGCRSLRQNGRDPPDPYVSLLLIPDKNRGTKRRTSQ KRRTLSPEFNREFFWEIFLDEAQRRKLDVSVKSNSFFMREREEL LGKVOLDLAETDLSGGVARWVDLAUVTSGGRRLLVLTPGVLA GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRARQLLDDEEQL TAKTLYMSHRELPAWVSFPDVEKABLAVLTSGGRRLLVLTPQVLA GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRARQLDDEEQL TAKTLYMSHRELPAWVSFPDVEKABURNTLYQVWFFLGQYMEX LLAETVAPAVRGSNPHLQTFTFTEVLGERFLRIIFUKHVHPGQR KEGILLDLNISYCGDVGIDVEVKKYFCKAVKGMOLHGVLRVIL EPLIGDLPFVGANSWFFIRRFTLDINWTGMTNLIDTGLSSLSD TMIMDSIAAFLVLPNRLLVPLVPDLODVAQLRSPLPRGIIRIHL LAARGLSSKDKYVKGLIEGKGDPYALVRLGTGTFCSVVIDERIN PCWGETYSVMVHEVPGGEIEVEVPDKDDFLOGMKLDVGKV LGASVLDDWFFLQGGGGQVHLRLEWLSLLSDAEKLEQVLQWNWG VSRPPPSAAILVYNDRAGLDWYTSELYPPOLKKKKKEPNP MVOLSIODVTGESKAVYSTNCPVWEEAFRFFLQDPGOSCDLDVGV KDDSRALTLGALTLAPELILDLDWFGLSSSSODAPPR PCHTTPDSGFCTBRVILAIHVLEAQDLIAKDRFLGCLVKKSDPY VKLKLAGRSFFSHVYREDLBPRNNEVFEVVIVSTVGGLEVEVF	3426	} 42	3435	ATSSQSLGRADPPRGGTMERSPGEGPSPSPMDQPSAPSDPTDQP
GAVGLSVGFVLFGLALYLGWRRVDBEKESLRARAQLIDDEEQL TAKTLYMSHRELDEAWUSPFDVSKASELIKIVAQVWPPLGQYMEK LLAETVAPAWGSONPILGYFTFRVELGEKPLRIIGVKVHPGGR KEQILLDLNISYVGDVQIDVEVKKYFCKGVKGWCLHGVLRVIL EPLIGDLPFVGAVSMFFIREPTLDINWTGMYNLDIGLSSLSD TMINDSIAAFLVLPNRLLVFLVPDLDDVAQLRSPLPRGIIRIHL LAARGLSSKDKYVKGLIEGKSDPALVVKIGTGTSENDEELIN POMGETYEVMVHEVPGOEIEVEVFPKDPDKDDFIGRMKLDVGKV LQASVLDDMPPLGGGGQVHLRLEWISLISDAEKLEQVLQMNWG VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP MVQLSIQDVTQESKAVYSTNCPVWEEAFFPLQDPOSGLDVQV KDDSRALTIGAAITLPLARLITAFELILDQWFGLSSGGPNSRLVM KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPGRGSSVDAPPR PCHTTPDSOFGTBHVLRHVLBAPELIDEQLWKGKSDPY VKLKLAGSSFRSHVVREDLNPRWNBVFSVTYSVPGGELEVEVF DKDLDKDDFLGRCKVRLTTVLNSGFLDEWITLEDVPSGEHLKE ERLTPRPTABLEEVLQVNSLIQTGKSSABLAAALLSIYMERAED LPLEKGTKHLSPYATLTVODSSHKTKTISGTSAPVWDESASFII RKPHTESLEQVGREGTGVLGSLIJSELLVANDLCLCRWFTL SSGQGVLLRAGLGILVSGHSGVERHSHSYSHSSSSLSEPPELS GGPPHTTSSAPPEV,RRITHVDSLEAPAGPLGOVKLTLWYYSE GGPHTTSSAPPEV,RRITHVDSLEAPAGPLGOVKLTLWYYSE GGPHTTSSAPPEV,RRITHVDSLEAPAGPLGOVKLTLWYYSE GREKLVSIVHGCRSLRQNGRDPPDPYVSLLLIPPKNRGTKRRTSQ KRRTLSPEPNRFFWEIPLDEAQRRKLDVSVKSNSFFMREREEL LGKVOLDLAETDLSGGVARWYDLMNKUKGSS ATSSGSLGRADPPRGGTMERSFGESFSFSPMDQPSAPSDPTDOP PAAHARPPDGSGGPAGGGAAGEALAUTJSFGGRELLVLIPPVILA GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLLDDEEQL TAKTLYMSHRELPAWVSFPDVEKAEMLNVTAQVWFFLGGYMEK LLAETVAPAVRGSNPHLQTFTFTEVLEGERPLRIIGVKVHPGQR KEGILLDLNISYCGDVGIDVEVKKYPCKAGVKGMOLHGVLRVIL EPLIGDLPFVGANSWFFIRRFTLDINTGMTMLIDTPGLSSLSD TMIMDSIAAFLVLPNRLLVPLVPDLODVAQLRSPLPRGIIRIHL LAARGLSSKDKYVKGLIEGKGDPYALVRLGTGTFCSVIDEELIN PQWGGTYSVMVHEVPGGGERSVFVDKDDFLOGRMKLDVGKV LQASVLDDWFPLQGGGGQVHLRLEWLSLLSDAEKLEQVLQWNWG VSRPPPSAAILVAVDRADDWYSELPPPGLKKKKKEPNP MVOLSIODVTGESKAVYSTNCPVWEEAFRFFLQDPGOSCDLDVGV KDDSRALTLGALTLAPLILTAPELILDLDWFGLSSSGDDSRLYM KLVMRILYLDSSEICFFTVDGCGAMDVDSENPQRGSSVDAPPR PCHTTPDSQFGTHEVLRILTAPELILDLQWFQLSSSGDDAFLYW KLLWRILYLDSSEICFFTVDGCGAMDVDSENPGRSSVDAPPR PCHTTPDSQFGTERVLARILTAPELLILDLQWFULVSGULVEVY VKLKLAGRSFRSHVYRCDLMPRNNEVFEVIVTSVGVGGLEVEVF	J			PAAHAKPDPGSGGQPAGPGAAGEALAVLTSFGRRLLVLIPVYLA
TAKTLYMSHRELPAMUS FPDVE KAEWLINKTUAQUWPPLGQYMEK LLAETVAPAVIRGSSHHLOTT EVELGEK PLR I I GUKVEHPGOR KEQILLDLNI SYVGDVQIDUEVKKYFCKAGVKGMQLHGVLRVIL EPLLIGDLFFVGAVSMFF FIRFTI DI INWTGMTNILLDIFGLSSLSS TMIMDS IAAFLVLPNRLLVSLVPDLQDVAQLRSP LPRGI IR IHL LAARGLSSKDKYKVKGLEGKSDEVALDVALGTOTFCSRV IDEELIN POMGETYEVMVHEVPGGEI EVEVPTRDEPDLNDDFIGRMKLHOVGKV LQAS VLDDWFPLGGGGGQVHLRLEWLSLLSDAEKLEGVLQMNNG VSRPDPPSAAILUVVLDRADLDFWYSELTYPPQLKKGMKEPMP MVQLS I QDUTGESKAVYSTRCPWBEBFRFFLQDPQSORLDVQV KDDSRALTLGALTLPLARLTAPEL ILDQWFQLSSSGFNSRLYM KLVMR ILYLDSSEICFPTVPGCFGAMDVDSENPQRGSSVDAPPR PCHTTPDSOFGTBHVLRIHVLEAQDLIAKDRFIGGLVKCKSDPY VKLKLAGRSFRSRVLVEDLDNFRWNBEVFEVIVTSVPGGGELEVEVFF DKDLDKNDFFLGRCKVSLTTVLNSGFLDEWLTLSDVSSGFHLRL ERLTPRFTABALEEVLQVNSLIGTOKSABLAALLSI YMERABD LPLRKGFKHLSPVATLTVGDSSHKTTCI SCTSAPVMDESAS PLI RKPHTESLELQVAGEGTGVLGSLSLPLSE ELLVADQLCLDRWFTL SGCQGVLLRAQIGILVSGHSGWEAHSHSYSHSSSSLSEPPLS GGPHITTSSAPEV\RQRLTHVDSPLBEALVADQLCLDRWFTL SGCQGVLLRAQIGILVSGHSGWEAHSHSYSHSSSSLSEPPLS GGPHITTSSAPEV\RQRLTHVDSPLBEALVADQLCLDRWFTL SGCQGVLLRAQIGILVSGHSGWEAHSHSYSHSSSSLSEPPLS GRENVSIVHGGSLSLRONGRDPPDPPYVSLLLLPRKMGTKRRTSQ KKRTLSPENBERFEWELPLDEAQRRLDVSVKSNSSFMSREREL LGKVOLDLAETDLSGCVARW VDLMDINKDKSSS 5427 42 3435 ATSSGSLGRADPPRGGTMERSPGEGFSFSPMDQPSAPSDPTDQP PAAHAKPDPDSGGQPAGPAAGEALAVITSFGRRLLVLIPVYLLA GANGLSVGFVLFGLALYTLGMRVDREKESLFARARQLLDDEEQL TAKTLYMSRRELPAWWSPDVBKABLINKIVAQVWPFLGQYMEK LLAETVAPAVGSNSPHLOTFTRVELGKERLRI IGVKHPGOR KEGILLDLNISVGSDVOIDVEVKKYFCKAGVKGMOLHGVLRVIL EPLIGDLFPVGANSPHFLRFTVEVLGKERLRI IGVKHPGOR KEGILLDLNISVGSDVIDVEVKKYFCKAGVKGMOLHGVLRVIL EPLIGDLFPVGANSPHFLRFTVEVLGKERLRI IGVKHPGOR KEGILLDLNISVGSDVIDVEVKKYFCKAGVKGMOLHGVLRVIL EPLIGDLPPVGANSPHFLRFTVEVLGKERLRI HULDLDFULSSLD TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGTIRIHL LAARGLSSKOKVVKGLIEGKSDPYALVRLGTTFTFCRVIDEELIN POMGETTEWWENEVENGPDENDFLGRMKLDVGKV LQSSVLDDWFPLQGGGGVHLRLEWLSLLSDAEKLEGVLQWNMG VSSRPPPSAAILTVVPLDRADLPATSSLTPPOLKKKMKENDP MVGLSIQDVTQESKAVYSTNCPVWBEBAFFFLQDPOSGELDVQV KDDSRALTLGALTLDARLLTAPELILDOWPGLSSSGFNSRLYM KLWMSILVLDSSEICFPTVPGCFGAMDVDSRPGRGSSVDAPPR PCHTTPDSGCFGT		1		GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAAROLLDDEEOL
LLAETVAPAVRGSNPHLOTFTFTRVELGEKPLRI IGWKVHPCQR KEQILDLNISYVGDVQIDVKYPYCKQRVGMCHGURVIL EPLIGDLFFVGAVSMFFIRRFTLD INWTGMTNLLDIPGLSSLSD TMIMDSIAAFLVLPNRLLVPLVPLDQDVAGLRSPLPRGIIRIHL LAARGLSSKKYVKGLIEGKSDPYALVRLGTOFTCSRV 1DEELN PQMGETYEVWVHEVPGGEIEVEVPUKDRDPKDDFLGRMKLDVGKV LQAS VLDDWFPLGGGGGQVAHRLEWIJSLLSDAEKLEGVLQMMG VSSRPDPPSAAILVVYLDRAQDLDMVTSELYPPQLKKGNKEPNP MVQLSIQDVTQGSKAVYSTNCYWEEAFRFFLQDPQSQELDVQV KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSGFNSRLYM KLVMRILYLDSSBICFFTVPGCCGAMPUDSENPQRGSSVDAPPR PCHTTPDSOFGTHVURI RHVLPAQDLIAKDRFLGGLVKKSDPY VKLKLAGRSFRSHVVKEDLNPRNNEVFEVIVTSVPGGELEVEVF DKDLDKDDFLGGCKVKLTTVLBGFDDEWLTLEDVPSGRLHLRL ERLTPRPTAABLEEVLQVNSLIGTOFKSABELAALLSIYMERAED LPLRKGTKHLSPYATLTVGDSSHKTKISGTSAPVMDESASFLI RKPHTESLELQVRGEGTGVLGSLSLELSELLVAQCLCLDRWFIL SSGGGQVLLRAQGGILVSGHSGVEAKSHSYSHSSSLSEEPELS GGPPHTTSSAPEV\RQRLTVDSLEAPASFLGQVKLTLMYYSE ERKLVSIVIGCRSLRONGRDPPDPYVSLLLLPDKNRGTKRRTSQ KKRTLSPEFFNERFEWELPLDEAQRRKLDVSVKSNSSFMSREREL LGKVOLDLAETDLSGCVARWYDLMDNKDKGSS 5427 42 3435 ATSSGSLGRADPPRGGTMERSPGEGFSFSPMDQFSAPSDPTDQP PAAHARPPDESGGQPAFGGAGALAVLTSFGRRILLVITPVLA GAVGLSVGFVLFGLALYLGWRRVDEKERSLRARQLLDDEEQL TAXTLYMSHELPAWVSFPDVEKAEWLNIVAQVWFFLGQVMEK LLAETVAPAVRGNNPHLOTFTFTRVELGEKERLIGVKVHPGQR KEGILLDLNISVYGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL EPLIGDLFPVGAVSMFFIRRFULDINTMTGMTHLDLIPGLSSLSD TMIMDSIAAFLULPRRLLVPLUPDLQDVAQLRSPLPRGIIRTHL LAARGLSSKDKYVKGLIEGKSDPYALVRGTGTFCSRVIDEELN PQWGETYEVMVHEVPGQEIEVEVFFKDPDKKGKREPNP MVGLSIQDVFGSKAVYGGLIEGKSDPANDLSSRPGRGSVDAPPR PQWGETYEVMVHEVPGQEIEVEVFFKDPDKDFLGRMKLDVGKV LQASVLDDWFPLQGGGGQVHLRLEMLSLLSDAEKLEQVLQWNMG VSSRPPPSAAILVVYLDRAQDPATSSLVPPOLKKGNKEPNP MVGLSIQDVTGSKAVYSTNCPVMEEAFRFFLQDPOSGELDVQV KDDSRALTLGALTLPLARLTAPELILDDFPLGSSSGPNSRLYM KLVMRILYLDSSEICFPTVPGCPGGAMDVDSSPPGRGSSVDAPPR PCHTTPDSGPGTEHVLRTHVLEAQDLIAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVYNEELNFRWFESVITVSPGGELEVEVF]		TAKTLYMSHRELPAWVSFPDVEKAEWLNKIVAOVWPFLGOVMEK
KEQILLDINISYVGDVQIDVEVKKYPCKAGVKGMQLHGVLRVIL EPLIGDLPFVGAVSMFFIRRPTLDINNTGMTRLDIFGLSSLSD TMINDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL LAARGLSSKNKYVKGLIGKSDEYALVRLGTQTFCSRVIDEELM PQMGETYEVMYHEVPGQEIEVEVPDKDPDKDDPLGRMKLDVGKV LQASVLDDWFPLQGGGQGVMLRLEWLSLLSDAEKLEQVLQWNMG VSSRPDPPSAAILVVVLDRAQLDPWTSELYPPQLKKGNKEPNP MVQLSIQDVTQESKAVYSTNCPVWEBAFRFPLQDPQSGLDVQV KDDSRALTLGALTLPLARLLTAPELLIDQMFQLSSGFNSRLYM KLVMRILYLDSSICPTYPGGCGAMDVDSENPQRGSSVDAPPR PCHTTPDSOFGTHVLRIHVLEAQDLLAKDRFLGGLVKCKSDPY VKLKLAGRSFRSHVVEBCDLMFNEWFEVEVTYTSVPGQELEVVCY DKDLDKADFLGRCKVRLTTVLNSGFLDEWLTLEDVPSGRLHLRL ERLTPRPTABLEEULQVNSLIQTQKSAELAAALLSIYMERAED LPLKKGTKHLSYTATITVGDSSKKTKTISCTSAPVWBESASILI RKPHTESLELQVRGEGTGVLGSLSLPLISELLVADQLCLDRWFTL SGGGQVLLRAGOLGILVSGGVEARIGHSYSHSSSSLSEEPELS GGPPHITSSAPEV\RQRLTHVDSPLEAPAGPLGQVKLTLWYSSE ERKLVSIVHGCRSLRQNGRDPPDYVSLLLLPDKNRGTKRRTSQ KKRTLSPERNERFEWELPLDEAQRRKLDVSVKSNSSFMSREREL LGKVOLDLAETDLSGGVARWYDLMDNKDKGSS KKRTLSPERNERFEWELPLDEAQRRKLDVSVKSNSSFMSREREL LGKVOLDLAETDLSGGVARWYDLMDNKDKGSS ATSSGLGRADPBGGGGAGGAAGALAVLTSFGRRLLVLIPVYLA GAVGLSVGFVLFGLALYLGWRRVFDSKERSLRARQLLDDEEQL TAKTLYMSKRELPAWWSFPDVKAEKINNIVAQVWPFLGQVMEX LLAETVAPAVRGSNPHLOTFTFTRVELGEKPLRIIGVKVHPGQR KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL EFFLIGDLFFVGAVSMFFIRRFTLDINMTGMTMLDIPGLSSLSD TMMDSIAAFLVLPNRLLVPLVPDLQDDVAQLRSPLPRGIIRIHL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTYFTCSRVIDBELN PQMGETYEWWINEVPGQEIEVEVFDKDPKMKEPNP MVGLSIQDVTQESKAVYSTNCPVWEBEAFRFFLQDPGSGELDVQV VSSRPDPPSAAILVVYLDRAGQDLPMVTSELYPFOLKKGNKEPNP MVGLSIQDVTQESKAVYSTNCPVWEBEAFRFFLQDPGSGELDVQV KDDSRALTLGALTLPLALLTAPELILDOWFGLSSGPNSRLYM KLVMRILYLDSSEICFPTVPGCPGAWDVDESPPGRGSSVDAPPR PCHTTPDSQFGTEHVLRITVLEAQDLJAKDRFLGGLVKGKSDPY VKLKLAGRSFFRSHVVYREDLINFRWFEVEVITSVEYGGELEVEVF		1		LLAETVAPAVRGSNPHLOTFTFTRVELGEKPLRI IGVKVHPGOP
EPLIGDEPTVGAVSMFFIRRPILD INNTGMTMILDIPGLSSLSD TMIMDSTARAFULPNRILUPSLYDDLODVAQURSPLPRGIIRIHL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTGTFCSRVIDEELIN PQMGETYEVMYHEVPGGEIEVEVPKDPDKDDFLGRMKLDVGKV LQASVLDDWSPLQGGGGGVHLRLEMISLISDAEKLEGVLQWMMG VSSRPDPSAAILVVYLDRAQDLPMVTSELYPPQLKKGMKEPNP MVQLSIQDVTQESKAVYSTNCPVWEBAFRFFLQDPGSGELDVQV KDDSRALTLGALTIPLARLLTAPELILDQWFQLSSGSPNSRLYM KLVMRILYLDSSEICFPTVPGCFGGAMDVDSENPQRGSSVDAPPR PCHTTPPSGFGTEHVLRIHVLEAQDLIAKDRFLGGUVKGKSDPY VKLKLAGRSFFSHVVREDLNPRWNEVFEVIVTSVPGQELEVEVF DKDLDKDDFLGRCKVRLTTVLINSGFLDEMLTIEDVPSGRLHLRL ERRIPPRFTABALEEVLQUNGLSLSPLSELLVADQLCLDRWFFL SCGGQVLLRAQLGILVSQHSGVEAHSHSYSHSSSLSEEPELS GGFPHTTSSAPEV\RQRLTTVJSLFJAPAGPLGGVKLTLWYSE ERRLVSIVHGCRSLRQNGRPPDPPVSLLLLPDRNGRTKRTSQ KKRTLSPENBERFWELPLDEAQRRKLDVSVKSNSFMSREREL LGKVOLDLAETDLSQGVARWYDLWNDKKGSS KKRTLSPENBERFWELPLDEAQRRKLDVSVKSNSFMSREREL LGKVOLDLAETDLSQGVARWYDLWNDKKGSS ATSSGSLGRADPPRGGTMRFSPGEEPSPSDMDQPSAPSDPTDQP PAAHARPDPGSGGQPAGPGAAGEALAVLTSGRRLLVLIPVYLA GAVGLSVGFVLFGLALVLGWRVRDEKERSLRAARQLLDDEEQL TAKTLYMSHRELPAWSFPDVEKAEWLNKLVAQVWPFLGGYMEK LLAETVAPAVRGSNPHLQTTFTRVELGEKFLRIIGVKVHFGQR KEGILLDLMISYYGDVG1DVEVKKYFCKAGVKGMOHAVRURVIL EPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD TMIMDSIAAFLVLYBNRLLVPLVPELDQDVAQLRSPLFRGIIRIHL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTGTGTCSRVIDEELN PQMGETYEWMYHBVPGGEIBVEVPGKDPDKDDFLGRMKLDVGKV LQASVLDDWFPLQGGQGQVHLRELGKSDPYALVRLGTGTTCSRVIDEBLN PQMGETYEWMYHBVPGGEIBVEVPGKDPDKDDFLGRMKLDVGKV LQASVLDDWFPLQGGQGQVHLRLEWLSLLLSDAEKLEQVLQWNWG VSSRPDPPSAAILVYLLDRAQDLPMYTSELYPPGLKKGNKEPNP MVOLSIQDVTQESKAVYSTNCPWWEAFFRFFLQDPGSGELDVOV KDDSRALTLGALTIPLARRLLTAPELLLDMPGLSSCSPORSLYM KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQFGTEHVURIHVHLEAQDLJAKDRFLGGUKGRSDPY VKLKLAGRSFFRSHVVREDLLDNRNNEVPEVIVTSVPGGELBVEVF VKLKLAGRSFRSHENVYREDLURBFLRFFLCDDPGGELBVEVP VKLKLAGRSFRSHENVERDLDNRNNEVPEVIVTSVPGGELBVEUF VKLKLAGRSFRSHENVERDLDNRNNEVPEVIVTSVPGGELBVEUF VKLKLAGRSFRSHENVERDLDNRNNEVPEVIVTSVPGGELBVEUF VKLKLAGRSFRSHENVERDLDNRNNEVPEVIVTSVPGGELBEVEUF VKLKLAGRSFRSHENVERDLDNRNNEVPEVIVTSVPGGELBEVEUF	1	1		KEQILLDLNISYVGDVOIDVEVKKYFCKAGVKGMOLHGVI.PVTT
TMINDSTARFLUPLNPUDLOWAQLESPLENGIRIHL LAARGLSSKDYWKGLIEGKSDPYALVRIGTOTFCSRVIDEELN POWGETYEVMVHEVPGQEIEVEVFDKDPDKDPFLGRMKLDVGKV LQAS VLDDWFPLGGGGGGVHLRLEWISLLSDAEKLEQULQWNWG VSSRPDPPSAAILVYLDGDDLPMYTSELYPPOLKKGKENPN MVQLSIQDVTQESKAVYSTNCPVWEBFFFFLQDPGSQELDUQV KDDSRALTLGALTLPLARDLIDAPGLISSGSPNSRLYM KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSOFGTEMVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLYDRWBVFFEVIVTSVPGGELEVEVF DKDLDKODFLGRCKVRLTTVLNSGFLDEWLTLEDVPSGRLHLRL ERLTPRFTAABLEEVLQNTSVASELDLOTGKSAELAAALLSIYMERAED LPLRKGTKHLSPYATLTVGDSSHKTKTISQTSAPVWDESASFLI RKPHTESLELQVRGEGTGVLGSLSPLSELLVADQLCLDRWFTL SSGGGVLLARQLGILVSQHSGVEAHGHSYSHSSSLSEEPPELS GGPPHTTSSAPEV\RQRLTHVDSPLEAPAGPLGQVKLTLWYYSE ERKLVSIVHGCRSLRQNGRDPPDPYVSLLLLPDRINGTKRRISQ KKRTLSPEPNERFEWELPLDEAQRRKLDVSVKSNSFYRGREL LGRVOLDLAETDLSQGVARWYDLMDNKDKGSS ATSSGSLGRADPPGGGTMESPEGEGPSPEPDPGPSAPSDPTDQP PAAHAKPDPGSGQPAGPGAAGEALAVLTSFGRRLLVLIPVYLA GAVGLSVGFVLFGLALYLGWRRVBEKERSLRAARQLLDDEEQL TAKTLYMSHRELPAWUSFPDVEKAEMLNKLVAQVWPFLGQVMEX LLAETVAPAVRGSNPHLOTFTFTRVELGEKPLRIIGVKVHFGQR KEGLILDLNISYVGDVOLOVEKKYFCKAGVKGMQLHGVLRVIL EPLIGDLPFVGAVSMFFIRRPTLDINNTGMTNLDIPGLSSLSD TMMDSIAAFLVLPNRLLUFLVPLDLOVAQLRSPLPRGIIRIHL LAARGLSSKDAVYVKGLIEGSDPYALVRLGTOTTCSRVIDBELN POWGETYEWMYHEVPGGEIEVEVPDDPDKODPLGRMKLDVGKV VSSRPDPFSAAILVYVLDRLDVBLLFOTTCTSRVIDBELN POWGSTYEWMYHEVPGGGEIEVEVPDRODRODPLGRMKLDVGKV VSSRPDPFSAAILVYVLDRAQDLPMYTSELYPPOLKKRNKEPNP MVGLSIQDVTGESKAVYSTNCPWWEAFFFFLODPGSGELDVOV VKDDSRALTLGALTIPLARRLLTAPELLDLORPGJSSVDAPPR MCLSIQDVTGESKAVYSTNCPWWEAFFFFLODPGSGELDVOV VKDDSRALTLGALTIPLARRLLTAPELLDLORPGJSSVDAPPR PCHTTPDSGFGTEHVLRIHVLEAQDLLAKDRFLGGLVKGRSDDPY VKLKLAGRSFFRSHVVREDLENPRNNEVFEVVTUSTSVGGGLEBVEVP VKLKLAGRSFFRSHVVREDLENPRNNEVFEVVTUSTSVGGGLEBVEVP VKLKLAGRSFFRSHVVREDLENPRNNEVFEVVTUSTSVGGGLEBVEVP VKLKLAGRSFFRSHVVREDLENPRNNEVFEVVTUSTSVGGGLEBVEVP VKLKLAGRSFFRSHVVREDLENPRNNEVFEVVTUSTSVGGGLEBVEVP	1	1		EPLIGDI.PFVGAVSMFFIRRPTI.DINIJTGMTNI.LDIDGI.GGI.GD
LAREGLSSKDKYVKGLIEGKSDPYALVRLGTOTFCSRVLDEELN POWGETTEVMHEVPGQETEVEVPDKDDKDDFLGRMKLDVGKV LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWWG VSSRPDPPSAAILVVYLDRAQDLPWTSELTYPPQLKKGNKEPNP MVQLSIQDVTQESKAVYSTNCPWEEBAFRFFLQDPGSQGLDVQV KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSGPNSRLYM KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQFGTEHVLRITVLBGGDULTAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLNPRWNEVFEVITVSVPGGELEVEVF DKDLDKNDFLGRCKVRITVLNSGFLDEWUTLEBUPSGRLHERL ERLTPRPTAABLEEVLQVNSLIQTQKSAELAAALLSIYMERAED LPLRKGTKHLSPYATLTVADSGFLDEWUTLEDVPSGRLHERL SGGGQVLLRAQLGILVSGHSGVEAHSHSVSHSSSSLSEEPELS GGPHITSSAPEV\RQRLTHVDDSPLEAPAGFLCQVKLTLWYYSE ERRLVSIVHGCRSLRQNGRDPPDPYVSLLLLPPKNRGTKRRTSQ KKRTLSPEFMERFEWELPLDEAQRRKLDVSVKSNSSFMSREREL LGKVGLDLAETDLSGVARWYDLMDMKGGSS SKYTTLSPEFMERFEWELPLDEAQRRKLDVSVKSNSSFMSREREL LGKVGLDLAETDLSGVARWYDLMDMKGGS ATSSQSLGRADPPRGGTMERSPGEGPSPSPMDQPSAPSDPTDQP PAAHAKPDPGSGGQPAGPGAAGEALAVLTSFGRRLLVLIPVYLA GAVGLSVGFVLFGLALVIGWRRVDBKERSLRAARQLLDDEEQL TAATLYMSHRELPAWVSFPDVEKAEWLNKIVAQVWPFLGQYMEK LLAETVAPAVRGSNPHLOTFTFTRVELGEKPLRIIGVKVUPFGQR KEGILLDLNISYVGDVGIDVEVKKYFCKAGVKGMQLHGVLRVIL EPPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD MIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIRIHL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTGTFCSRVIDEELN PQWGETYEVWHREVPGGEIEVEVFDKDPDRDDFLGRMKLDVGKV LOASVLDDWFPLQGGQGVHLRLEWLSLISDAEKLEQVLQWNMG VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKGRKEPNP MVGLSIQDVTQESKAVVSTNCPVWEEAFFFFLQDPGSGELDVQV KDDSRALTLGAATLPLARLTAPELLIDOWFGLSSGPNSRLYM KLVMRILYLDSSEICPPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQFGTTEHVLRIHVLEADQLIAKDRFLGGLVKCKSDPY VKLKLAGRSFRSHVVREDLMPRWNEVFEVIVVSVGGGLEVEVF	j	ļ j		TMIMDSIAARI.VI. DNDI I.VDI VDDI ODVAOI BEDI DDESTED
POWGETYEVMYHEVPGQEIEVEVPDKNDPKDDFLGRMKLDVGKV LQAS VLDDWPPLQGGGGQVUHRLEWLSLLSDAEKLEQVLQWNWG VSSRPDPPSAAILVYYLDRAQDLPMYTSELYPPQLKKGNKEPNP MVQLSIQDVTQESKAVYSTNCPWEEAFRFFLQDPQSQBLDVQV KDDSRALTGALTLPLARLLTAPELILDQWPQLSSSGPNSRLYM KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVYREDLNPRWNEWFEVVITSVPGGELEWEVF DKDLDKODFLGRCKVRLTTVLNSGFLDEWLTLEDVPSGRLHLRL ERLTPRPTAABLEEVLQVNSLITQTKSBELAAALLSIYMERAED LPLKKGTKHLSPYATLTVGDSSHKTKTSISGTSAPVWDESASFLI RKPHTESLELQVRGEGTGVLGSLSLPLSELLVADQLCLDRWFTL SGGQVLLRAQLGILVSQURGVEAHSHSYSHSSSLSEBFELS GGPHITSSAPEV\RQRLTHVDSPLEAPAGPLGQVKLTLWYYSE ERKLVSIVHGCRSLRQNGRDPPDPYVSLLLLPDKNRGTKRRTSQ KKRTLSPEFNERFEWELPLDEAQRRKLDVSVKNSSFMSREREL LGKVOLDLAETDLSQGVARWYDLMDNKDKGSS ATSSQSLGRADPPRGGTMERSPEGEPSPSMDQPSAPSDPTDQP PAAHAKPDPGSGQDPAGPGAAGEALAVLTSFGRRLLVLIPVYLA GAVGLSVGFVLFGLALVIGWRRVRDEKERSLRAARQLLDDEEQL TAKTLYMSHRELPAWSFPDVEKABRINKIVAQVWPPLGGYMEK LLAETVAPAWRGSNPHLTFFTRVELGEKPLRIIGVKVHPGQR KEQILDLNISYVGDVQIDVEVKKYFCKAGVKMQLHGVLRVIL EPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLDIFGLSSLSD THIMDSIAAPLVLPRILDILVPDLQDVAQLRSPLPRGITRIHL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN POWGETYEWMHEVPGGEIEVEVFDKDPDKDDFLGRMKLDVGKV USSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP MVOLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPGOGGLDVOV KDDSRALTLGAATLTLARPELILDDWFLGSSGPENSLYM KLUMRILYLDSSEICPFTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQFGTEHVLRIHVLEADDLIAKDRFLGGLVKCKSDPY VKLKLAGRSFRSHVVREDLIPPRWNEVFEVIVTSVPGQELEVEVF	1	j i		LAAPGLCCVDVVVVCLIEGVCDDVALIDY GEGERSPERGIIRIHL
LQAS VLDDWFPLQGGGQVHLRLEWI.SLLSDAEKLEQULQWMWG VSSRPDPPSAAILVVYLDRAQDI.PWTSELYPPQLKKGNKEPNP MVQLSIQDVTQESKAVYSTNCFVWEEAFRFFLQDPQSGELDVQV KDDSRALTLGALTI.PLARILITAFELILDQWFQLSSGENSRLYM KLVMRILYDDSSEICFFVTGCGGAWDVDSENPQRGSSVDAPPR PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY VKLKLAGRSFFSHVVREDLNPRMINEVFEVITSVFGGELEVEVF DKDLDKDDFLGFCKVKLTTVLNSGFLDEWITLEBUPSGRLHIRL ERLTPRFTAABLEEVLQVNSLIGTQKSAELAAALLSIYMERAED LPLKKGTKHLSPYATLITVGDSSHKTKTISQTSAPVWDESASFLI RKPHTESLELQVRGEGTGVLGSLSLELSELLVADQLCLDRWFTL SSGQGQVLLRAQLGILVSQHSGVGAHSHSYSHSSSSLSEEPELS GGPHITSSAPEVV,RGUTHVDSPLEAPAGFLGQVKLTLWYYSE ERKLVSIVHGCRSLRQNGRDPPDPVVSLLLLPPKNRGTKRRTSQ KKRTLSPEFNERFEWELPLDEAQRRKLDVSVKSNSSFMSREREL LGKVOLDLABTDLSGQVARWYDLMDNKGKSS ATSSGSLGRADPPRGGTMERSPGEGPSPSPMDQPSAPSDPTDQP PAAHAKPDPGSSGQPAGPGAAGEALAVLTSFGRRLLVLIPVYLA GAVGLSVGFVLFGLALVLJWRRVRDEKERSLRARQLLDDEEQL TAKTLYMSHRELPAWVSPDVEKAERLINKIVAQVWPFLGQYMEX LLAETVAPAVRGSNPHLQTFTFTRVELGEKPLRIIGVKVHPGQR KEQILLDLNISYVGDVQIDVSVKKYFCKAGVKGMQHGVLRV°IL EFFLIGDLPFVGAVSMPFTRRPTDLINWTGMTNLDLIPGLSSLSD TMIMDSIAAPLVLPRRLLVPLVPDDLQDVAQLRSPLPRGIIRIHL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTGTFCSRVIDEELN POWGETYEVMVHRVPGGGIEVEVFDKDPDNKDDFLGRMKLDVGKV LOASVLDDWPPLQGGGGGIVHCRLEMLSLSDAEKLEQVLQWMWG VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPIPP MVGLSIQDVTQESKAVYSTNCPVWEAFRFFLQDPQSGELDVOV KDDSRALTLGAATLPLARALTAPELILDDWFQLSSGPNSRLYM KLVMRILYLDSSEICPPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQFGTTBHVLRIHNLEADDLIAKDRFLGGLVKCKSDPY VKLKLAGRSFRSHVVREDLMPRWNEVFEVIVTSVGQGLEVEVF	1 1	1		DOMGETVERMULEGICATION
VSSRPDPSAALTUVILDRAQDLPMVTSELYPPQLKKGNKEPNP MVQLS IQDVTQESKAVYSTNCPVWEAFRFPLQDPQSQELDVQV KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSGPNSRLYM KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLNPRWNEVFEVIVTSVPGGELEVEVF DKDLDKDDFLGRCKVRLITTVLNSGFLDEMITLEDVPSGRLHLRL ERRITPRPFPABLEEVLQVNSLIQTQKSAELAAALLSIYMERAED LPLRKGTKHLSPYATLTVGDSSHKTKTISQTSAPVWDESASFLI RKPHTESLELQVRGESTGVLGSLSLPLSELLVADQLCLDRWFTL SSGGGQVLLRAQLGILVSGNESVEAHSHSYSHSSSLSSEPELS GGPPHITSSAPEV\RQRLTHVDSPLEAPAGPLGQVKLTLWYYSE ERKLVSIVHGCRSLRQNGRDPPDPYVSLLLLPDKNRGTKRRTSQ KKRTLSSFFNERFBELPLDEAQRKLDVSVKSNSFMSRERERL LGKVOLDLAFTDLSGGVARWYDLMDNKDKGSS ATSSQSLGRADPPRGGTMERSPGGEDFSPMOPSAPSDPTDQP PAHAKPPGSGGGPAFGGAAGEALAVUTSFGRRLLVLIPVYLA GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLLDDEEQL TAKTLYMSHRELPAWVSFPDVEKAEWLNKLVAQVWFFLGGYMEX GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLLDDEEQL TAKTLYMSHRELPAWVSFPDVEKAEWLNKLVAQVWFFLGGYMEX LLAETVAPAVRGSNFPHLOTFTFTRVELGSKPLRI IGVKVHPGGR KSGILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL EPLIGDLPFVGAVSMFFIRPTLDINNTGMTNLLDIPGLSSLSD TMIMDSIAAFLVLDRNFLLVPLVPDLODVAQLRSPLPRGITRIHL LAARGLSSKDKVVKGLIECKSDPYALVRLGTQTFCSRVIDEELN PQWGETYEVMVHEVPGQEIEVEVFDKDPDKDDFLGRMKLDVGKV LGASVLDDWFPLQGGQGQVHLRLEBWLSLLSDAEKLEGVLQMNMG VSSRPDPPSAAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP MVQLSIQDVTQESKAVYSTNGCVWEEAFFFFLQDPQSGLDVQV KDDSRAITLGALTLPLARLLTAPELLILDQWFQLSSSGPMSRLYM KLVMRILYLDSSEICFPTVPGCPGAWDVDSSNPQRGSSVDAPPR PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKKSDPY VKLKLAGRSFRSHVVREGLNPRWNEVFEVITSVPGQELEVEVF]	i i		POWGETTEVMVHEVPGQETEVEVFDKDPDKDDFLGRMKLDVGKV
MVQLSIQDVTQESKAVYSTNCPVWEEAFRFPLQDPQSQELDVQV KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGFNSRLYM KLWWRILYLDSSEICPTVPGCCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQFGTEHVURIHVLEAQDLIAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLNPRWNEVFEVIVTSVPGQELEVEVF DKDLDKDDFLGRCKVRLTTVLNSGFLDENLTLEDVPSGRLHLRL ERLTPRPTABLEEVLQVNSLIQTQKSAELAAALLSIYMERAED LPLRKGTKKLSPYATLTVDDSSHKTKTISQTSAPVWDESASFLI RKPHTESLELQVRGEGTGVLGSLSLPLESLLVADQLCLDRWFTL SSGGGQVLLRAQLGILVSOHSGVEAHSHSYSHSSSLSEEPELS GGPPHITSSAPEV\RQRITHVDSPLEAPAGPLGQVKLTLWYSE ERRLVSIVHGCRSLRQNGRDPPDPYVSLLLLPPKNRGTKRRTSQ KKRTLSPEFNERFEWELPLDEAQRRKLDVSVKSNSSFMSREREL LGKVOLDLAETDLSQGVARWYDLMDNKKGSS ATSSQSLGRADPPRGGTMERSPGEDSPSPMDQPSAPSDPTDQP PAAHAKPDPGSGGQPAGGAAGEALAVLTSFGRRLLVLIPVYLA GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLLDDEEQL TAKTLYMSHRELPAWFSPDVEKABULMKIVAQVWPFLGQYMEK LLAETVAPAVRGSNPHLQTFTFTRVELGEKPLRIGVKVHPGGR KSQILLDLNISYVGDVQIDVVKKYFCKAGVKGMQLHGVLRVIL EFPLIGDLPFVGAVSMFFIRRPTLDINMTGMTNLDIPGLSSLSD TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL LAARGLSSKDKYVKGLIECKSDPYALVRLGTQTFGCSVIDEELN PQWGETYEVWHEUPGQEISVEVFDKDDPKDDFLGRMKLDVGKV LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWNWG VSSRPDPPSAAILVYYLDRAQDLPMVTSELYPPQLKKGNKEPNP MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV KDDSRALTLGALTLPLARLLTAPELLLDQWFQLSSSGPNSRLYM KLVMRILYLDSSEICFPTVPGCGGAWDVDSSNPQRGSSVDAPPR PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKKSDPY VKLKLAGRSFRSHVVYREDLNPRNWEVFEVITSVPGGELEVEVF		[LOAS VLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWNWG
KDDSRALTIGAETLPLARLLTAPELILDQWFQLSSGPNSRLYM KLVMRILVLDSSBICFPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQFGTEHVURIHVLERQDLTAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLNPRWNEVFEVIVTSVPGGELEVEVF DKDLDKDDFLGRCKVRLTTVLNSGFLDEWLTLEDVPSGRLHLRL ERLTPRPTABELEEVLQVNSLIQTQKSAELAAALLSIYMERAED LPLKKGTKHLSPYATLTVGDSSHKTKTISQTSAPWDESASFLI RKPHTESLELQVGEGTGVLGSLSLPLSELLVADQLCLDRWFTL SSCQGQVLLRAQLGILVSQHSGVEAHSHSYSHSSSSLSEPFLS GGFPHITSSAPEV\RQRLITHVDSPLEAPAGFLGQVKLTLWYYSE ERKLVSIYHGCRSLRQNGRDPPPDYVSLLLLPDKNRGTKRRTSQ KKRTLSPEFNERFEWELPLDEAQRRKLDVSVKSNSSFMSREREL LGKVQLDLAETDLSQGVARWYDLMDNKDKGSS ATSSQLGRADPPRGGTMERSPGEGPSPSPMDQPSAPSDPTDQP PAAHAKPDPGSGGQPAGPGAAGALAAVLTSFGRRLLVLIPVYLA GAVGLSVGFVLFGLALYLGWRVVDEKERSLRAARQLLDDEFQL TAKTLYMSHRELPAWVSFPDVEKAEWLNKIVAQVWPFLGQYMEK LLAETVAPAVRGSNPHLQTTFTRVELGERPLRIIGVKVHPGQR KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL EPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD TMIMDSIAAFLVLPRRLLVPLVPDLQDVAQLRSPLPRGTIRIHL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN PQWGETYEVMVHEVPQGQGQVHLRLEWLSLLSDAEKLEQVLQWMNG VSSRPDPPSAAILVVYLDRAQDLPMYTSELYPPQLKKGNKEPNP MVOLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPGSGELDVQV KDDSRAITLGALTILPLARLLTAPELILDDWFGLSSSGPNSRLYM KLVMRILYLDSSEICPPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQPGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY	1 :	!		VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP
KDDSRALTIGAETLPLARLLTAPELILDQWFQLSSGPNSRLYM KLVMRILVLDSSBICFPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQFGTEHVURIHVLERQDLTAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLNPRWNEVFEVIVTSVPGGELEVEVF DKDLDKDDFLGRCKVRLTTVLNSGFLDEWLTLEDVPSGRLHLRL ERLTPRPTABELEEVLQVNSLIQTQKSAELAAALLSIYMERAED LPLKKGTKHLSPYATLTVGDSSHKTKTISQTSAPWDESASFLI RKPHTESLELQVGEGTGVLGSLSLPLSELLVADQLCLDRWFTL SSCQGQVLLRAQLGILVSQHSGVEAHSHSYSHSSSSLSEPFLS GGFPHITSSAPEV\RQRLITHVDSPLEAPAGFLGQVKLTLWYYSE ERKLVSIYHGCRSLRQNGRDPPPDYVSLLLLPDKNRGTKRRTSQ KKRTLSPEFNERFEWELPLDEAQRRKLDVSVKSNSSFMSREREL LGKVQLDLAETDLSQGVARWYDLMDNKDKGSS ATSSQLGRADPPRGGTMERSPGEGPSPSPMDQPSAPSDPTDQP PAAHAKPDPGSGGQPAGPGAAGALAAVLTSFGRRLLVLIPVYLA GAVGLSVGFVLFGLALYLGWRVVDEKERSLRAARQLLDDEFQL TAKTLYMSHRELPAWVSFPDVEKAEWLNKIVAQVWPFLGQYMEK LLAETVAPAVRGSNPHLQTTFTRVELGERPLRIIGVKVHPGQR KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL EPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD TMIMDSIAAFLVLPRRLLVPLVPDLQDVAQLRSPLPRGTIRIHL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN PQWGETYEVMVHEVPQGQGQVHLRLEWLSLLSDAEKLEQVLQWMNG VSSRPDPPSAAILVVYLDRAQDLPMYTSELYPPQLKKGNKEPNP MVOLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPGSGELDVQV KDDSRAITLGALTILPLARLLTAPELILDDWFGLSSSGPNSRLYM KLVMRILYLDSSEICPPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQPGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY		l i		MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV
KLWRILYLDSSEICFPTVPGCPGAMDVDSENPQRGSSVDAPPR PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLINPRWMEVFEVIVTSVPGQELEVEVF DKDLDKDDFLGRCKVRLTTVLNSGFLDEWLTLEDVPSGRLHLRL ERLTPRPTABBLEEVLQVNSLIQTQKSAELAAALLSIYMERAED LPLKKGTKHLSPYATLTVGDSSHKTKTISGTSAPVWBESASFLI RKPHTESLELQVRGEGTGVLGSLSLPLSELLVADQLCLDRWFTL SSGQGVLLRAQUGILVSQHSGVEHHSHSYSHDSSSLSEEPELS GGPPHITSSAPEV\RQRLTHVDSPLEAPASPLGQVKLTLWYYSE ERKLVSIVHGCRSLRQNGRDPPDPYVSLLLLPDKNRGTKRRTSQ KKRTLSPEFNERFEWELPLDEAQRRKLDVSVKSNSSFMSREREL LGKVOLDLAETDLSQVARWYDLMDNKKGSS ATSSQSLGRADPPRGGTMERSPGEGPSPSPMDQPSAPSDPTDQP PAAHAKPDPGSGQQPAGPGAAGEALAVLTSFGRRLLVLIPVYLA GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLLDDEEQL TAKTLYMSHRELPAWVSFPDVEKAEWLINKIVAQVWPFLGQYMEK LLAETVAPAVRGSNPHLQTFTFTRVELGEKPLRIIGVKVHPGQR KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL EFLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD TMIMDSIAAFLVJPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEBLN PQWGETTEVMVHEVPGQEIEVEVFDKDPPKDDFLGRMKLDVGKV VSRPDPPSAAILVVILDRAQDLPMVTSELYPPQLKKGNKEPNP MYOLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV KDDSRALTLGALTLPLARLLTAPELLIDQWFQLSSSGPNSRLYM KLVMRILYLDSSEICPFTVPGCGPGAWDVDSENPGRSSVDAPPR PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRPLGGLVKKSBPP	1	ĺ	•	KDDSRALTLGALTLPLARLLTAPELILDOWFOLSSSGPNSRLVM
PCHTTPDSGFGTEHVLRIHVLEAQDLIAKDRPLGGLIVKGKSDPY VKLKLAGRSFRSHVVREDLNFRWNEVFEVIVTSVPGQELEVEVF DKDLDKDDFLGGCKVRLTTVLNSGFLDENTTLBDVPSGRLHLRL ERLTPRPTABBLEEVLQVNSLIQTQKSAELAAALLSIYMERAED LPLRKGTKHLSPYATLTVGDSSHKTKTISGTSAPVWDESASFLI RKPHTESLELQVRGEGTGYLGSLSLPLSELLVADQLCLDRWFTL SSGQGQVLLRAQLGILVSQHSGVEAHSHSYSHSSSSLSEEPELS GGFPHITSSAPEV\RQRETHVDSPLEAPAGPLGQVKLTLWYYSE ERKLVSIVHGCRSLRQNGRDPPDPYVSLLLLPDKNRGTKRRTSQ KKRTLSPEFNERFEWELPLDEAQRRKLDVSVKSNSSFMSREREL LGKVOLDLAETDLSQGVARWYDLMDNKDKGSS 5427 42 3435 ATSGSGLGRADPPRGGTMERSPGEGPSPSPMDQPSAPSDPTDQP PAAHAKPDPGSGQPAGPGAAGEALAVLTSFGRRLLVLIPVYLA GAVGLSVGFVLFGLALVLGWRRVRDEKERSLRAARQLLDDEEQL TAKTLYMSHRELPAWVSPPDVEKABWLNKIVAQVWPFLGQYMEK LLAETVAPAVRGSNPHLQTFTTRVELGEKPLRI IGVKVHPGQR KEGILLDLNISSVYGDVQTDVEVKKYFCKAGVKGMQLHGVLRVIL EPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD TMIMDSTAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGTIRIHL LAARGLSSKGKYVKGLLEGKSDPYALVRLGTQTFCSRVIDEELN PQWGETYEVMVHEVPGGEIEVEVFDKDPDKDDFLGRMKLDVGRV LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWNWG VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPOLKKGNKENPP MYGLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPVSGELDVQV KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM KLVMRTLYLDSSEICFPTVPGCFGAWDVDSENPGRGSSVDAPPR PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRPLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLNPRWNEVEFVIVTSVPGGELEVEVF				KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPORGSSVDAPPR
VKLKLAGRSFRSHVVREDLNPRWNEVFEVIVTSVPGQELEVEVF DKDLDKDDFLGRKVRLTTVLNSGFLDEWLTLEDVPSGRLHLRL. ERRTPPPTAABLEEVLQVNSLIQTQKSAELAAALLSIYMERAED LPLRKGTKKLSPYATLTVGDSSHKTKTISQTSAPVWDESASFLI RKPHTESLELQVRGEGTGVLGSLSLPLSELLVADQLCLDRWFTL SSGQGVLLRAQLGILVSQHSGVEAKSHSYSHSSSLSEEPELS GGPPHITSSAPEV\RQRLTHVDSPLEAPAGPLGQVKLTLWYSE ERRLVSIVHGCRSLRQNGRDPPDPYVSLLLLPPKNRGTKRRTSQ KKRTLSPEFNERFEWELPLDEAQRRKLDVSVKSNSSFMSREREL LGKVQLDLAETDLSQGVARWYDLMDNKDKGSS 5427 42 3435 ATSSQSLGRADPPRGGTMERSPGEGPSPSPMDQPSAPSDPTDQP PAAHAKPDPGSGGQPAGPGAAGEALAVLTSFGRRLLVLIPVYLA GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLLDDEEQL TAKTLYMSHRELPAWVSFPDVEKAEWLNKIVAQVWPFLGQYMEK LLAETVAPAVRGSNPHLOTFTFTRVELGEKPLRIIGVKVHPGQR KEQILDLNISYVDDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL EPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLDIPGLSSLSD TMIMDSLAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTOTFCSRVIDEELN PQWGETYEVMVHEVPGQEIEVEVFDKDPDKDDFLGRMKLDVGKV LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWWG VSSRPDPPSAAILVYLDRAQDLPWYTSELYPPQLKKGNKEPNP MYGLSIQDVTOESKAYYSTNCPVWEEAFRFFLQDPQSQELDVQV KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLNPRWNEVFEVIVTSVPGQELEVEVFF	1			PCHTTPDSQFGTEHVLRIHVLEAODLIAKDRFLGGLVKGKSDPY
DKDLDKDPFLGRCKVRLTTVLNSGFLDEWLTLEDVPSGRLHLRL ERLTPRPTAABLEEVLQVNSLIQTQKSABLAAALLSIYMERAED LPLRKGTKHLSPYATLTVGDSSHKTKTISQTSAPVMDESASFLI RKPHTESLELQVRGEGTGVLGSLSLPLSELLVADQLCLDRWFTL SSGGGQVLLRAQLGILVSQHSGVEAHSHSYSHSSSSLSEPELS GGPPHITSSAPEV\RQRLTHVDSPLEAPAGPLGQVKLTLWYYSE ERRLVSIVHGCRSLRQNGRDPPDPYVSLLLLPPKNRGTKRRTSQ KKRTLSPEFNERFEWELPLDEAQRRKLDVSVKSNSSFMSREREL LGKVQLDLAETDLSGGVARWYDLMDNKDKGSS 5427 42 3435 ATSSQSLGRADPPRGGTMERSFGEGPSPSPMDQPSAPSDPTDQP PAAHAKPDPGSGGQPAGPGAAGEALAVLTSFGRRLLVLIPVYLA GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLLDDEEQL TAKTLYMSHRELPAWVSFPDVEKAEKLNKIVAQVWPFLGQYMEX LLAETVAPAVRGSNPHLQTFTFRVELGEKPLRIIGVKVHPGQR KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQHGVLRVIL EPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL LAARGLSSKDKYVVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN PQWGETYEVMVHEVPGQEIEVEVFDKDPDKDDFLGRMKLDVGKV LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEGVLQMWMG VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPOLKKGNKEPNP MYQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPGSQELDVQV KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLNPRWMEVFEVIVTSVPGQELEVEVF	i l			VKLKLAGRSFRSHVVREDI.NPRWNEVFRVTVTSVPGOFT.PVPVP
ERLTPRPTAABLEEVLQVNSLIQTOKSAELAAALLSIYMERAED LPIRKGTKHLSPYATLTUGDSSHKTKTISQTSAPVWDESASFLI RKPHTESLELQVRGEGTGVLGSLSLPLSELLVADQLCLDRWFTL SSGQGQVLLRAQLGILVSQHSGVEAHSHSYSHSSSSLSEEPELS GGPPHITSSAPEV\RQRLTHVDSPLEAPAGPLGQVKLTLWYYSE ERKLVSIVHGCRSLRQNGRDPPDPYVSLLLLPDKNRGTKRRTSQ KKRTLSPEFNERFEWELPLDEAQRRKLDVSVKSNSSFMSREREL LGKVOLDLAETDLSGCVARWYDLMDNKDKGSS 42 3435 ATSSQSLGRADPPRGGTMERSPGEGPSPSPMDQPSAPSDPTDQP PAAHAKPDPGSGGGPAGPGAAGEALAVLTSFGRRLLVLIPVYLA GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLLDDEEQL TAKTLYMSHRELPAWVSFPDVEKAEWLNKLVAQVWPFLGQYMEX LLAETVAPAVRGSNPHLQTFTFTRVELGEKPLRIIGVKVHPGQR KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL EPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN PQWGETYEVMVHEVPGQEIEVEVFDKDPDKDDFLGRMKLDVGKV LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQMNWG VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP MVOLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSGELDVQV KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLMPRWNEVFEVIVTSVPGQELEVEVF	1 1			DKDLDKDDFLGRCKVRLTTVLNSGFLDEWLTLRDVDSCDI HI DE
LPLEKGTKHLSPYATLTVGDSSHKTKTISQTSAPVWDESASFLI RKPHTESLELQVRGEGTGYLGSLSLPLEELLVADQLCLDRWFTL SSGGGQVLRRQQLGILVSQHEGVEAHSHSYSHSSSSLSEEPELS GGPPHITSSAPEV\RQRLTHVDSPLEAPAGPLGQVKLTLWYYSE ERKLVSIVHGCRSLRQNGRDPPDYVSLLLLPDKNRGTKRRTSQ KKRTLSPEFNERFEWELPLDEAQRRKLDVSVKSNSSFMSREREL LGKVOLDLAFTDLSQGVARWYDLMDNKDKGSS 5427 42 3435 ATSSQSLGRADPPRGGTMERSPGEGPSPSPMDQPSAPSDPTDQP PAAHAKPDPGSGQPAGPGAAGEALAVLTSFGRRLLVLIPVYLA GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLLDDEEQL TAKTLYMSKRELPAWVSFPDVEKAEWLNKIVAQVWPFLGQYMEK LLAETVAPAVRGSNPHLOTFTFTRVELGEKPLRIIGVKVHPGQR KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL EPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN PQWGETYEVMVHEVPGQEIEVEVFDKDPDKDDFLGRMKLDVGKV LQASVLDDWFPLQGGGGQVHLRLEKLSLLSDAEKLEQVLQWNWG VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVOV KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLNPRWMEVFEVIVTSVPGQELEVEVF] i	i .		EDITOPOTABLE EVI OVNET TOTOVCA DI ARATI CIMIDA DE
RKPHTESLELQVRGEGTGVLGSLSLPLSELLVADQLCLDRWFTL SSGQCQVLLRAQLGILVSQHSGVAHSHSYSHSSSSLSEEPELS GGPPHITSSAPEV\RQRLTHVDSPLEAPAGPLGQVKLTLWYYSE ERKLVSIVHGCRSLRQNGRDPPDPYVSLLLLPDKNRGTKRRTSQ KKRTLSPEFNERFEWELPLDEAQRRKLDVSVKSNSSFMSREREL LGKVQLDLAETTDLSQGVARWYDLMDNKDKGSS 5427 42 3435 ATSSQSLGRADPPRGGTMERSPGEGPSPSPMDQPSAPSDPTDQP PAAHAKPDPGSGQQPAGPGAAGEALAVLTSFGRRLLVLIPVYLA GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLLDDEEQL TAKTLYMSHRELPAWVSFPDVEKAEWLNKIVAQVWPFLGQYMEK LLAETVAPAVRGSNPHLQTFTFTRVELGEKPLRIIGVKVHPGQR KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL ESPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGITRIHL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN PQWGETYEVMVHEVPGQEIEVEVFDKDPDKDDFLGRMKLDVGKV LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWNWG VSSRPDPPSAAILVYYLDRAQDLPMVTSELYPPQLKKGNKEPNP MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV KDDSRALTLGALTLPLARLLTAPELILDOWFQLSSSGPNSRLYM KLVMRILYLDSSEICPFTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQPGTEHVLRIHVLEAQDLIAKDRPLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLNPRWNEVFEVIVTSVPGQELEVEVF		l		I.DI.DYCTYUI CDYATI TUCDCCUVEVCI COMCA NANDON OR -
SSGGQQVLLRAQLGILVSQHSGVEAHSHSYSHSSSLSEEPELS GGPPHITSSAPEV\RQRITHVDSPLEAPAGPLGQVKLTLWYYSE ERKLVSIVHGCRSLRQNGRDPPDYVSLLLLPDKNRGTKRRTSQ KKRTLSPEFNERFEWELPLDEAQRRKLDVSVKSNSSFMSREREL LGKVQLDLAETDLSQGVARWYDLMDNKDKGSS 5427 42 3435 ATSSQSLGRADPPRGGTMERSPGGEPSPSPMDQPSAPSDPTDQP PAAHAKPDPGSGGQPAGPGAAGEALAVLTSFGRRLLVLIPVYLA GAVGLSVGFVLFGLALYLGWRRVDEKERSLRAARQLLDDEEQL TAKTLYMSHRELPAWVSFPDVEKAEWLNKIVAQVWPFLGQYMEK LLAETVAPAVRGSNPHLQTFTFTRVELGEKPLRIIGVKVHPGQR KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL EPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN PQWGETYEVMVHEVPGQEIEVEVFDKDPDKDDFLGRMKLDVGKV LQASVLDDWFPLQGGQGQVHLRLEKLSLLSDAEKLEQVLQWNWG VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLNPRWNEVFEVIVTSVPGQELEVEVF	1 1	1		DEDERICATION OF THE PROPERTY O
GGPPHITSSAPEV\RQRLTHVDSPLEAPAGPLGQVKLTLWYYSE ERKLVSIVHGCRSLRQNGRDPPDPYVSLLLLPDKNRGTKRRTSQ KKRTLSPEFNERFEWELPLDEAQRRKLDVSVKSNSSFMSREREL LGKVQLDLAETDLSGGVARWYDLMDNKDKGSS 5427 42 3435 ATSSQSLGRADPPRGGTMERSPGEGPSPSPMDQPSAPSDPTDQP PAAHAKPDPGSGQQPAGPGAAGEALAVLTSFGRRLLVLIPVYLA GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLLDDEEQL TAKTLYMSHRELPAWVSFPDVEKAEWLNKIVAQVWPFLGGYMEK LLLAETVAPAVRGSNPHLQTFTFTRVELGEKPLRIIGVKVHPGQR KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL EPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELIN PQWGETYEVMVHEVPGQEIEVEVFDKDPDKDDFLGRMKLDVGKV LQASVLDDWFFLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWNWG VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLNPRWNEVFEVIVTSVPGQELEVEVF	, ,	}		CCCOCOLA I DAOI CIT MOSTOSTATIONES PER PROPERTIES DE LA PROPERTIE DE LA PROPERTIE DE LA PROPERTIE DE LA PROPERTIE DE LA PROPERTIE DE LA PROPERTIE DE LA PROPERTIE DE LA PROPERTIE DE LA PROPERTIE DE LA PROPERTIE DE LA PROPE
ERKLVSIVHGCRSLRQNGRDPPDPYVSLLLLPDKNRGTKRRTSQ KKRTLSPEFNERFEWELPLDEAQRRKLDVSVKSNSSFMSREREL LGKVQLDLAETDLSQGVARWYDLMDNKDKGSS ATSSQSLGRADPPRGGTMERSPGEGPSPSPMDQPSAPSDPTDQP PAAHAKPDPGSGQQPAGPGAAGEALAVLTSFGRRLLVLIPVYLA GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLLDDEEQL TAKTLYMSHRELPAWVSFPDVEKAEWLNKIVAQVWPFLGQYMEK LLAETVAPAVRGSNPHLQTFTFTRVELGEKPLRIIGVKVHPGQR KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL EPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN PQWGETYEVMVHEVPGQEIEVEVFDKDPDKDDFLGRMKLDVGKV LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWNWG VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSGPNSRLYM KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQFGTSHVVREDLNPRWNEVFEVIVTSVPGQELEVEVF	1	ĺ		DOGGGGATTERS TO THE CONTROL OF THE C
KKRTLSPEFNERFEWELPLDEAQRRKLDVSVKSNSSFMSREREL LGKVQLDLAETDLSQGVARWYDLMDNKDKGGS ATSSQSLGRADPPRGGTMERSPGEGPSPSDDPTDQP PAAHAKPDPGSGGQPAGPGAAGEALAVLTSFGRRLLVLIPVYLA GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLLDDEEQL TAKTLYMSHRELPAWVSFPDVEKAEWLNKIVAQVWPFLGQYMEK LLAETVAPAVRGSNPHLQTFTFTRVELGEKPLRIIGVKVHPGQR KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL EPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN PQWGETYEVMVHEVPGQEIEVEVFDKDPPKDDFLGRMKLDVGKV LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWNWG VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQPGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLNPRWNEVPEVIVTSVPGQELEVEVF	į į	1		GGPPHITSSAPEV\RQRLTHVDSPLEAPAGPLGQVKLTLWYYSE
LGKVQLDLAETDLSQGVARWYDLMDNKDKGSS 42 3435 ATSSQSLGRADPPRGGTMERSPGEGPSSPMDQPSAPSDPTDQP PAAHAKPDPGSGGQPAGPGAAGEALAVLTSFGRILUVLIPVYLA GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLLDDEEQL TAKTLYMSHRELPAWVSFPDVEKAEWLNKIVAQVWPFLGQYMEK LLAETVAPAVRGSNPHLQTFTFTRVELGEKPLRIIGVKVHPGQR KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL EPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN PQWGETYEVMVHEVPGQEIEVEVFDKDPDKDDFLGRMKLDVGKV LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWNWG VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQPGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLNPRWNEVPEVIVTSVPGQELEVEVF	1	}		EKKLVSIVHGCRSLRQNGRDPPDPYVSLLLLPDKNRGTKRRTSQ
LGKVQLDLAETDLSQGVARWYDLMDNKDKGSS 42 3435 ATSSQSLGRADPPRGGTMERSPGEGPSSPMDQPSAPSDPTDQP PAAHAKPDPGSGGQPAGPGAAGEALAVLTSFGRILUVLIPVYLA GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLLDDEEQL TAKTLYMSHRELPAWVSFPDVEKAEWLNKIVAQVWPFLGQYMEK LLAETVAPAVRGSNPHLQTFTFTRVELGEKPLRIIGVKVHPGQR KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL EPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN PQWGETYEVMVHEVPGQEIEVEVFDKDPDKDDFLGRMKLDVGKV LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWNWG VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQPGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLNPRWNEVPEVIVTSVPGQELEVEVF	1. 1	İ		KKRTLSPEFNERFEWELPLDEAQRRKLDVSVKSNSSFMSREREL
PAAHAKPPPGGGTMERSPGEGFFSTMOPSAPSDPTDQP PAAHAKPDPGSGGQPAGPGAAGEALAVLTSFGRRLLVLIPVYLA GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLLDDEEQL TAKTLYMSHRELPAWVSFPDVEKAEWLNKIVAQVWPFLGQYMEK LLAETVAPAVRGSNPHLQTFTFTRVELGEKPLRIIGVKVHPGQR KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL EPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN PQWGETYEVMVHEVPGQEIEVEVFDKDPPKDDFLGRMKLDVGKV LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWNWG VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLNPRWNEVPEVIVTSVPGQELEVEVF	<u> </u>			LGKVQLDLAETDLSQGVARWYDLMDNKDKGSS
PAAHAKPDPGSGGQPAGPGAAGEALAVLTSFGRRLLVLIPVYLA GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLLDDEEQL TAKTLYMSHRELPAWVSFPDVEKAEWLNKIVAQVWPFLGQYMEK LLAETVAPAVRGSNPHLQTFTFTRVELGEKPLRIIGVKVHPGQR KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL EPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN PQWGETYEVMVHEVPGQEIEVEVFDKDPDKDDFLGRMKLDVGKV LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWNWG VSSRPDPPSAAILVVYLDRAQDLPMYTSELYPPQLKKGNKEPNP MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLNPRWNEVPEVIVTSVPGQELEVEVF	5427	42	3435	ATSSQSLGRADPPRGGTMERSPGEGPSPSPMDQPSAPSDPTDOP
GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLLDDEEQL TAKTLYMSHRELPAWVSFPDVEKAEWLNKIVAQVWPFLGQYMEK LLAETVAPAVRGSNPHLQTFTFTRVELGEKPLRIIGVKVHPGQR KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL EPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN PQWGETYEVMVHEVPGQEIEVEVFDKDPDKDDFLGRMKLDVGKV LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWNWG VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLNPRWNEVPEVIVTSVPGQELEVEVF	1			PAAHAKPDPGSGGQPAGPGAAGEALAVLTSFGRRLLVLTPVYLA
TAKTLYMSHRELPAWVSFPDVEKAEWLNKIVAQVWPFLGQYMEK LLAETVAPAVRGSNPHLQTFTFTRVELGEKPLRIIGVKVHPGQR KEQILLLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL EPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN PQWGETYEVMVHEVPGQEIEVEVFDKDPDKDDFLGRMKLDVGKV LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWNWG VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLNPRWNEVPEVIVTSVPGQELEVEVF	1 1	İ		GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAAROLLDDEFO:
LLAETVAPAVRGSNPHLQTFTFTRVELGEKPLRIIGVKVHPGQR KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL EPLIGDLPFVGAVSMFFIRPTLDINWTGMTNLLDIPGLSSLSD TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN PQWGETYEVMVHEVPGQEIEVEVFDKDPPKDDFLGRMKLDVGKV LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWNWG VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV KDDSRALTLGALTLPARLLTAPELILDQWFQLSSSGPNSRLYM KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLNPRWNEVPEVIVTSVPGQELEVEVF		ţ.	•	TAKTLYMSHRELPAWVSFPDVEKAEWINKTVAOVWDELCOVMEN
KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL EPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN PQWGETYEVMVHEVPGQEIEVEVFDKDPDKDDFLGRMKLDVGKV LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWNWG VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQPGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLNPRWNEVPEVIVTSVPGQELEVEVF	1 1	ļ		LLAETVAPAVRGSNPHLOTFTETPVELGERED DITCURGERGO
EPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN PQWGETYEVMVHEVPGQEIEVEVFDKDPPKDDFLGRMKLDVGKV LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWNWG VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLNPRWNEVFEVIVTSVPGQELEVEVF	1 1	ľ		KEOTI I DI NI SVUCDUO TDUEVUVO CENTROLO TO TO TO TO
TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN PQWGETYEVMVHEVPGQEIEVEVFDKDPDKDDFLGRMKLDVGKV LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWNWG VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQFGTEHVLRTHVLEAQDLIAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLNPRWNEVFEVIVTSVPGQELEVEVF		ļ		EDITCHLDEVCAVCMERTHDDMIDTINGCOMER STATE
LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN PQWGETYEVMVHEVPGQEIEVEVFDKDPDKDDFLGRMKLDVGKV LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWNWG VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQFGTEHVLRTHVLEAQDLIAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLNPRWNEVFEVIVTSVPGQELEVEVF	,			THIMDS IN DELICE DATE FIRE FIRE TO THE TOTAL OF THE TOTAL
PQWGETYEVMVHEVPGQEIEVEVFDKDPDKDDFLGRMKLDVGKV LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWNWG VSSRPDPPSAAILVVYLDRAQDLPMYTSELYPPQLKKGNKEPNP MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLNPRWNEVFEVIVTSVPGQELEVEVF	i i	1		INTELLED THE TAKE TATE AND THE TAKE TAKE THE TAK
LQASVLDDWFPLQGGQQQVHLRLEWLSLLSDAEKLEQVLQWNWG VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLNPRWNEVPEVIVTSVPGQELEVEVF	1 /	1		LAAKGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN
VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQPGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLNPRWNEVPEVIVTSVPGQELEVEVF]			POWGETYEVMVHEVPGQEIEVEVFDKDPDKDDFLGRMKLDVGKV
VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQPGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLNPRWNEVPEVIVTSVPGQELEVEVF	1	1	{	LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWNWG
MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLNPRWNEVFEVIVTSVPGQELEVEVF	} I		j	VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPOLKKGNKEPNP
KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLNPRWNEVFEVIVTSVPGQELEVEVF	, 1			MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLODPOSOFLDVOV
KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLNPRWNEVFEVIVTSVPGQELEVEVF	1	į		KDDSRALTLGALTLPLARLLTAPELTLDOWFOLSSSGDNGDI VM
PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY VKLKLAGRSFRSHVVREDLNPRWNEVFEVIVTSVPGQELEVEVF]	ļ		
VKLKLAGRSFRSHVVREDLNPRWNEVFEVIVTSVPGQELEVEVF] !	1		
DKDLDKDDFLGRCKVRLTTVLNSGFLDEWLTLEDVPSGRLHLRL] [Ĺ		VKI.KI.AGRSEPSKIAIDEDI MEDKIMENERIZINGANDASE ST.
DIGEDRADDF LGRCKVKLTTVLINSGF LDEWLTLEDVPSGRLHLRL				DKDLDKDDET COCKEDT MARK MOSCE SERVENE AT SOCIETIES AND SOC
				D. D. D. D. D. D. C. C. V. K. L. T. V. L. N. S. G. L. D. W. L. L. E. D. V. S. G. K. L. L. L. L. L. L. L. L. L. L. L. L. L.

SEQ	Predicted	Prodict	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptid
NO:	nucleotide	location	
	location	Comment	Torus and Actual Properties and an actual and an actual ac
	corresponding	corresponding	I TO THE CAUCITY I THE ISDICT TO VITAGE.
	to first	to first	D-Deucine, Mamethichine N-X
	amino acid	amino acid	(* - * * Ottoo Defilitaring Deams, - : -
	residue of	residue of	Justine, Tathreonine Valuation
	amino acid	amino acid	""IFYPTOPIAN. Y=Tyrogine V-th-1
		sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
			ERITOPOTA FILEDIA (INSERTION)
	İ	1	ERLTPRPTAAELEEVLQVNSLIQTQKSAELAAALLSIYMERAED
	ł	ł	THE DICKGIRGISPIATETVGOSSHKTKTTCOTCA DITTER
	1	f	1 MILES DELLOVRIGEGICIO (GST. ST. DT. SDT T. DA DOT ST T
	l	1	TO SO SO TENNA OF THE ASSOCIATION OF THE SOURCE OF THE SOU
		ŀ	1 STATE SOME DV (KUKI I HVDS DI FADA ONT COLIVE ME ANDRE
		1	THE TARGET OF THE CASE OF THE PROPERTY OF THE
	1	j	1 1 DE DEMEKEEMET DI ULE DODAL DISCINOTO CENTE
5428	3		1 KDDMWEIDESOGVARWYDI,MDMWD&CCC
	3	1839	SSRSERLSACAIAPPWLVSSRPARPAQLQRPGKMVEDGAEELED
	į.		LVHFSVSELPSRGYGVMEEIRRQGKLCDVTLKIGDHKFSAHRIV
	[LAASIPYFHAMETNOMMECKORETTELEN
	(LAASIPYFHAMFTNDMMECKODEIVMOGMDPSALEALINFAYNG NLAIDOONYOSILMOSEIOYOGMDPSALEALINFAYNG
i			I ************************************
			I TO SEED OF EARLAWAY OF CORDY A DATE OF CORDY
			I X - DODK YOODDLYROU WRODDI WDD A WDWY Y A A
-	'		THE SECOND PROPERTY OF THE PRO
- 1	i		It County of County I A A I I I I CO I A A COUNTY OF A COUNTY
1	ľ	,	
	ļ		
Ī		j	
- 1	1	1	TGQSNL\SSVGDVLTPETDCWTFM\APMACHEGGVGVGCIPLLT
5429	820		
3.23	828	202	RREDALSSEGCLWPSESTVSGNGIPEPQVYAPPRPTDRLAVPPF
ľ	l	j	AQRERFHRFQPTYPYLQHEIDLPPTISLSDGEEPPPYQGPCTLQ
j	1	į.	LRDPEOOLELNRESURADEMENTEDODE
1		}	
5406			T-01.1 C100GGRUEGPPP \ TYSEVTGUVDGCCEOTIOOGGG
5430	441	1507	
- 1	Ĭ	ľ	QKRRKRRKKIMKTIQPKMHNSISWAIFTGLAALCLFQGVPVRS
i	1	The state of the s	THE PARTIES OF THE PROPERTY OF THE PARTY OF
	1	1	THE PER VILLEN CONTROL OF TOMORRAD TO THE TOTAL OF THE PERSON OF THE PER
1	i		
J			~ · · · · · · · · · · · · · · · · · · ·
}	1		
1			
}	1	1	O THE STREET OF
5431			
	2	1312	AAAAPGSRRRRPLPDRPHMAHGYEAPPPPAPRSPAWRARSKPV\
	į	ĺi	PGITINP\TTAEGPSP\TSECACETER CONTROL CO
1	1		LPGITINP\TIAEGPSP\TSEGASEANLVDLOKKLEELELDEQQ
j]		
1	ſ	* -	
- 1	ļ	1 ~	
	1	1 -	CONTROL OF THE PROPERTY OF THE
.]	ľ	•	TOTAL TRAPEREDGITHYSVOSDIWSVCI OF THE ATTORNESS
1	1	1 ~	- MODELLA FORFV VDGERGRUHST SDDDDDDDDDDDDDDDCT
		1	"" TITLE TO THE VICE PERCEPTION OF THE TRANS I
432			AND
-32	2	1312 A	AAAPGSRRRPLPDRPHMAHGYEAPPPPAPRSPAWRARSKPV\
İ	1	, l ī.	PGITINP\TIAFCECD\ MORGA CONTROL PAPRSPAWRARSKPV\
1		· · · · · · · · · · · · · · · · · · ·	PGITINP\TIAEGPSP\TSEGASEANLVDLQKKLEELELDEQQ
- 1		, -·	COLUMN DIVINION OF LKDDDFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF
		Į U.	DIPLICATION OF THE CONTRACTOR
1	1	,	ODIO TOMONINO GOSLOOVI, KEAKRI DEETI COVICTATOR
[ļ	1	THE TOTAL PROPERTY OF THE PROP
1	1	, .	TOTAL STREET AND THE
- 1	į	D	AKELEAI FGRPVVDGEEGEPHS ISPRPRPPGRPVSGHGMDSRP
- 1		A	AIFELLDYIVNEPPPKLPNGVFTPDFQEFVNKCLIKNPAERA
133		DI	KMLTNHTET KROEFFERDER CHEEFFER
	360	1885 SV	KMLTNHTFI KRSEVEEVDFAGWLCKTLRLNQPGTPTRTAV
.33	- 1		
133		150	CHARLE THE THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF T
.33		LF	QEDKVGFEDPLHLCSWRARACPCTWPHC/CTGLLECLGFAGV GWPSLVFVFKNEDYFKDLCGPDAGPIGNATGQADCKAQDERF LIFTLGSFMNNFMTFPTGYIFDRFKTTVARLIAIFFYTTATLI

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
i	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
	sequence	ļ <u>-</u>	\=possible nucleotide insertion)
1		1	IAFTSAGSAVLLFLAMPMLTIGGILFLITNLQIGNLFGQHRSTI
j			ITLYNGAFDSSSAVFLIIKLLYEKGISLR/VLLHLHLCLQYLAC
ŀ		•	STHFPPDAPGAHPIPTAPQLQLWPVPWEWHHKGREG/QQLSMKT
ł	1		GSYSQRSSFQRRKRPQGQGRSRNSAPSGATL/CSRRFAWHLVWL
1	1	ł	SVIQLWHYLFIGTLNSLLTNMAGGDMARVSTYTNAFAFTQFGVL
			CAPWNGLLMDRLKQKYQKEARKTGSSTLAVALCSTVPSLALTSL
	ì	ļ	LCLGFALCASVPILPLQYLTFILQVISRSFLYGSNAAFLTLAFP
		İ	SEHFGKLFGLVMALSAVVSLLQFPIFTLIKGSLQNDPFYVNVMF
5434	66		MLAILLTFFHPFLVYRECRTWKESPSAIA
1 3.33		652	RYAALIISLIQHKLLWRNQHCSRCVIMSPAQSAGLNWLF/GSGK
			HGPFLGCSQYPACDYVRPLKSSADGHIVKVLEGQVCPACGANLV
1			LRQGRFGMFIGCINYPECEHTELIDKPDETAITCPQCRTGHLVQ
1	1		RRSRYGKTFHSCDRYPECQFAINFKPIAGECPECHYPLLIEKKT
5435	4704	1505	AQGVKHFCASKQCGKPVSAE
1 3.33	4704	1597	PGDSSQRLAEMSNAKERKHAKKMRNQPTNVTLSSGFVADRGVKH
	Į .		HSGGEKPFQAQKQEPHPGTSRQRQTRVNPHSLPDPEVNEQSSSK
ì	i		GMFRKKGGWKAGPEGTSQEIPKYITASTFAQARAAEISAMLKAV
1			TQKSSNSLVFQTLPRHMRRRAMSHNVKRLPRRLQEIAQKEAEKA
1			VHQKKEHSKNKCHKARRCHMNRTLEFNRRQKKNIWLETHIWHAK
	1		RPHMVKKWGYCLGERPTVKSHRACYRAMTNRCLLQDLSYYCCLE
1	1		LKGKEEEILKALSGMCNIDTGLTFAAVHCLSGKRQGSLVLYRVN
J	<u>}</u> 1		KYPREMLGPVTFIWKSQRTPGDPSESRQLWIWLHPTLKQDILEE
			TKAACQCVEPIKSAVCIADPLPTPSQEKSQTELPDEKIGKKRKR
1	ì		KDDGENAKPIKKIIGDGTRDPCLPYSWISPTTGIIISDLTMEMN
1	j		RFRLIGPLSHSILTEAIKAASVHTVGEDTEETPHRWWIETCKKP
			DSVSLHCRQEAIFELLGGITSPAEIPAGTILGLTVGDPRINLPQ
1			KKSKALPNPEKCQDNEKVRQLLLEGVPVECTHSFIWNQDICKSV
	·		TENKISDODLNRMRSELLVPGSQLILGPHESKIPILLIQQPGKV
1			TGEDRLGWGSGWDVLLPKGWGMAFWIPFIYRGVRVGGLKESAVH
1			SQYKRSPNVPGDFPDCPAGMLFAEEQAKNLLEKYKRRPPAKRPN
	1	_	YVKLGTLAPFCCPWEQLTQDWESRVQAYEEPSVASSPNGKESDL
			RRSEVPCAPMPKKTHQPSDEVGTSIEHPREAEEVMDAGCQESAG
1	1		PERITDQEASENHVAATGSHLCVLRSRKLLKQLSAWCGPSSEDS
l i	i		RGGRRAPGRGQQGLTREACLSILGHFPRALVWVSLSLLSKGSPE
i i			PHTMICVPAKEDFLQLHEDWHYCGPQESKHSDPFRSKILKQKEK
1 1			KKREKRQKP\GRASSDGPAGEEPVAGQEALTLGLWSGPLPRVTL
1			HCSRTLLGFVTQGDFSMAVGCGEALGFVSLTGLLDMLSSQPAAQ RGLVLLRPPASLQYRFARIAIEV
5436	1781	635	
1 1	_	333	ASDS I PWSEARTTRKLAQRGCQWSLPERMPLVVFCGLPYSGKSR
] [<u> </u>	į.	RAEELRVALAAEGRAVYVVDDAAVLGAEDPAVYGDSAREKALRG ALRASVERRLSRHDVVILDSLNYIKGFRYELY\CLARAARTPLC
1 1	1	I	LUVCUP PCCPI ACROUNCANDADANALIKUFRYELY \CLARARTPLC
; !	1		LVYCVRPGGPIAGPQVAGANENPGRNVSVSWRPRAEEDGRAQAA
1	[{	GSSVLRELHTADSVVNGSAQADVPKELEREESGAAESPALVTPD SEKSAKHGSGAFYSPELLEALTLRFEAPDSRNRWDRPLFTLVGL
j .		ł	EEPLPLAGIRSAL FENDADDUCCTOCODE SCOOTS
1	İ		EEPLPLAGIRSALFENRAPPPHQSTQSQPLASGSFLHQLDQVTS
]]			QVLAGLMEAQKSAVPGDLLTLPGTTEHLRFTRPLTMAELSRLRR QFISYTKMHPNNENLPQLANMFLQYLSQSLH
5437	739	1672	CQEAASEFGGPLHTPAMFLRRLGGWLPRPWGRRKPMRPDPPYPE
] {			PRRVDSSENSGSDWDSAPETMEDVGHPKTKDSGALRVSRAASE
] [PSKEEPOVEOLGSTPMDGT WINDONTGOTTOTTOTTOTTOTTOTTOTTOTTOTTOTTOTTOTTOT
1 1]	PSKEEPQVEQLGSKRMDSLKWDQPISSTQESGRLEAGGASPKLR
1			WDHVDSGGTRPGVSPEGGL\GVPGPGAPLEKPGRREKLLGWLR
[ļ	GEPGAPSRYLGGPEECLQISTNLTLHLLELLASALLALCSRPLR
1 1	j	1	AALDTIGLRGPLGLWLHGLLSFLAALHGLHAVLSLLTAHPLHFA
j i		1	CLFGLLQALVLAVSLREPNGDEAATDWBSEGLEREGEEQRGDPG KGL
5438	2443	1152	
1 !		1112	TKPRKRRHQPASQRQRPWSSDSTGDLLARGKGRKEENKGSDRVS
i i	İ		LAPPSLRRPMMCQSEARQGPELRAAKWLHFPQLALRRRLGQLSC
1		ł	MSRPALKLRSWPLTVLYYLLPFGALRPLSRVGWRPVSRVALYKS
	3	.	VPTRLLSRAWGRLNQVELPHWLRRPVYSLYIWTFGVNMKEAAVE
[1	DLHHYRNLSEFFRRKLKPQARPVCGLHSVISPSDGRILNFGQVK
<u> </u>	<u></u>		NCEVEQVKGVTYSLESFLGPRMCTEDLPFPPAASCDSFKNQLVT

SEO	Predicted		
ID		Predicted end	
NO:	beginning	nucleotide	I Machiguate, Catysteine D-Achartia haza a
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
- 1	to first	amino acid	D-Proline O Cl.
j	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
ł	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	sequence	pedgetice	COUCH, /=possible nucleofide deleti-
ļ	+	 	\=Possible nucleotide insertion\
1	1		REGNELYHCVIYLAPGDYHCFHSPTDWTVSHPRHEDGSIMSUNT
ļ	1	ĺ	GRARWIKE DE CHNERVVLTGDWKHGFFSI.TAVGATI MUGGED TO
ł	l .	J	FUNDERTH SPRHSKGSYNDFSFVTHTNPEGVPMAL BGETTLG (SC
		<u>L</u>	FNLGSTIVLIFEAPKDFNFQLKTGQKIRFGEALGSL
5439	2443	1152	TKPRKRRHQPASQRQRPWSSDSTGDLLARGKGRKEENKGSDRVS
	İ	i	LAPPSLRRPMMCQSEARQGPELRAAKWLHFPQLALRRRLGQLSC
	ĺ	1	MSRPALKLRSWPLTVLYYLLPFGALRPLSRVGWRPVSRVALYKS
1	ł	ì	VPTRIJ.SPANGRI VOVEL DIVIS DE STORMENT SEVENDENTE DE STORMENT DE S
		ì	VPTRLLSRAWGRLNQVELPHWLRRPVYSLYIWTFGVNMKEAAVE
1	ł	j	DLHHYRNLSEFFRRKLKPQARPVCGLHSVISPSDGRILNFGQVK
			NCE VEQUEGOTYSLESFLGPRMCTEDI.PFPPPARSCREETING UM
1	1		REGNELYHCVIYLAPGDYHCFHSPTDWTVSHPDHFDGGIMGIDID
ı	}		GMARWIRELFCHNERVVLTGDWKHGFFGLTDVGATAMGGTDTM
	1 -		TURDUHTNSPRHSKGSYNDFSFVTHTNPEGUDMAI DCBILLO (OG
5440			I PALGSTIVLIFEAUKDENFOLKTCOKIRFCEAT.cet
3440	693	253	EPIPVTPDHRLVTMTHIV\OTFSPVNS\GOPPNVEMLYEEOEVE
1	1		PILGAPHNPAPPMSTVIHIRSETSVPDHVIWST FNTI FMTTGGT
1) .		FIAFAYSVKSRDRKMVGDVTGAQAYASTAKCLNIWALILGIFMT
5441			1 THE TTPVLVVQAOR
3441	2	2054	CRDGGKNGFMVSPMKPLEIKTQCSGPRMDPKICPADPAFFSFIN
,	İ		NSDLWVANIETGEERRLTFCHQGLSNVLDDPKSAGVATFVIQEE
	1		FDRFTGYWWCPTASWEGSEGLKTLRILYEEVDESEVEVIHVPSP
ļ	, ,		ALEERKTDSYRYPRTGSKNPKIALKLAEFQTDSQGKIVSTQEKE
1	!		LVQPFSSLFPKVEYIARAGWTRDGKYAWAMFLDRPQQWLQLVLL
1	1 1		PPALPIPSTENEEQ\RLASARAVPRNVQPYVVYEEVTNVWINVH
1] 1		DIFYPEPOSECEDEL CEL PANECIMO TOTAL CONTROL OF THE CO
ł	1		DIFYPFPQSEGEDELCFLRANECKTGFCHLYKVTAVLKSQGYDW
ł	1		SEPFSPGEGEQSLTNAIWVNEETKLVYFQGTKDTPLEHHLYVVS
	1		YEAAGEIVRLTTPGFSHSCSMSQNFDMFVSHYSSVSTPPCVHVY
			KLSGPDDDPLHKQPRFWASMMEAAKIFHFHTRSDVRLYGMIYKP
	}		HALQPGKKHPTVLFVYGGPQVQLVNNSFKGIKYLRLNTLASLGY
1			AVVVIDGRGSCQRGLRFEGALKNQMGQVEIEDQVEGLQFVAEKY
1 1		1	GFIDLSRVAIHGWSYGGFLSLMGLIHKPQVFKVAIAGAPVTVWM
1 1	i i	ļ	AYDTGYTERYMDVPENNQHGYEAGSVALHVEKLPNEPNRLLILH
		ĺ	GFLDENVHFFHTNFLVSQLIRAGKPYQLQVALPPVSPQIYPNER HSIRCPESGEHYEVTLLHFLQEYL
5442	1	3474	CCORSERREDINGER
1 1	.]		CGQRSRRSPDMPEAKPAAKKAPKGKDAPKGAPKEAPPKEAPAE
	1	- 1	APKEAPPEDQSPTAEEPTGVFLKKPDSVSVETGKDAVVVAKVNG
1 1	}	J	KELPDKPTIKWFKGKWLELGSKSGARFSFKESHNSASNVYTVEL
1 1			MIGRA ADDREST INTERVENTED SCIENT TO THE PROPERTY OF THE PROPER
1 1		l	ESFKRTSEKKSDTAGELDFSGLLKKREVVEEEKKKKKKDDDDLG
1)			IPPEIWELLKGAKKSEYEKIAFQYGITDLRGMLKRLKKAKVEVK
	ł		KSAAFTKKLDPAYQVDRGNKIKLMVEISDPDLTLKWFKNGQEIK
1 1	1	j	PSSKYVFENVGKKRILTINKCTLADDAAYEVAVKDEKCFTELFV
	1	i	ALEF VIII VIPLEUOUVEVGDRVEMAVEVGREGA OVARIMENTO CONTRACTOR
1	1		TREDSFRARIRFREDGKRHILIFSDVVOEDDGDVOVITNICGOGD
1 1	1	L.	ADDI VEDROUEVLODIADLITVKASEOAVEKCEVCDEVIRGISENSIS
l f	ł		NGVEVRYSKKITISHVGRFHKLVTDDVPDFDFGDVTFHDGV77
1 1	1	1	OSTOWED THE TRANSPORT OF THE PROPERTY OF THE P
1	i		VAGNADADDV (SITGEAPSPEAT) WI.KC/ DEVERSOR TO THE
ļ i	1	i	KKVDCSSFV1ESAQREDEGRYTTKVTNDTGEDIZAGTELOTETOTE
1	}		DPPEAVRITSVGEDWAILVWEDDMVDCGKDVTCVT INDVIKKAGO
	ļ		RUMALINE EVETETTYESTKMIEGILVEMPUENTATATA TOUGODOLOG
1	1	i	APPMPIAPISEPLHLIVEDVIDTTTTLKWPDDNDTCACCIDGIE
i i	1	1.4	LVSICLEGSEEWVPANTEPVERCGETVKNII DTCADII DDIAGODA
[1.	LAGKSEPATLAQPVTIRETAEDDKTDI.DDUT.DOTVTDVTQDQT
}		1.	LVVPFQGKPRPQVVWTKGGAPLDTSPVHVPTCDPDTVPFTDAX
<u> </u>	1	1 -	SDSGETELSVQIENMKDTATIR IRVVEKACDDINIAGORIGAD
	}	1 1	VALVEWQAPKDDGNSEIMGYFVOKADKKTMFWFNUVPPNDUMGG
1	i	•	TVSDLIVGNEYYFRVYTENICGLSDSPGVSKNTARILKTGITFK
1	1	ĺ	PPEYKEHDFRMAPKFLTPLIDRVVVAGYSAALNCAVRGHPKPKV
i	ĺ	1	WMKNKMEIREDPKFLITNYQGVLTLNIRRPSPFDAGTYTCRAV
			HELGEALAECKLEVRVPQ

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
}	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine.
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
5443	sequence 66	1000	\=possible nucleotide insertion)
3443	00	1003	SRGQLDAGQSSEQHGGNRQPEQSRSRSSSSSSSPRRSRSAAEPA
		1	MALSMPLNGLKEEDKEPLIELFVKAGSDGESIGNCPFSQRLFMI
1		ł	LWLKGVVFSVTTVDLKRKPADLQNLAPGTHPPFITFNSEVKTDV
1			NKIEEFLEEVLCPPKYLKLSPKHPESNTAGMDIFAKFSAYIKNS RPEANEALERGLLKTLQKLDEYLNSPLPDEIDENSMEDIKFSTR
			KFLDGNEMTLADCNLLPKLHIVKVVAKKYRNFDIPKEMTGIWRY
l			LTNAYSRDEFTNTCPSDKEVEI\AYSDVAKRLHQVKSRLLKEVS
1			FMSSP
5444	2	344	SGPIGVTGAQMAKWLRDYLSFGGRRPPPQPPTPDYTESDILRAY
1			RAQKNLDFEDPY*DSESRLEPDPAGPGDSKNPGDAKYGSPKHRL
1	[IKVEAADMARAKALLGGPGEELEADTEYLDPFDAQPHPAPPDDG
1	ĺ		YMEPYDAQWVMSELPGRGVQLYDTPYEEQDPETADGPPSGQKPR
1			QSRMPQEDERPADEYDQPWEWKKDHISRAFAVOFDSPEWERTPG
			SAKELRRPPPRSPQPAERVDPALPLEKQPWFHGPLNRADAESLL
			SLCKEGSYLVRLSETNPQDCSLSLRSSQGFLHLKFARTRENOVV
ſ			LGQHSGPFPSVPELVLHYSSRPLPVQGAEHLALLYPVVTQTP*Q
	·		*PDWGDRRPNGQVATGLPELWGAEAPSAAAHPGLHRERHPEGLP
1			RAEKPGLRGPLLGLREPLGAGPRGPWGLQEPRRCQVWFSQAPAH
5445	2364	486	QGGGCGYGQSQGPSGRPRGGAGSRH
"	2504	400	ILSRGFLGSVEICIQLPLPASEPVLLLTWARRRWRETRSRREPT TLRAQSVCPWWI*ETRMNRSIPVEVDESEPYPSQLLKPIPEYSP
ĺ			EBESEPPAPNIRNMAPNSLSAPTMLHNSSGDFSQAHSTLKLANH
ł			QRPVSRQVTCLRTQVLEDSEDSFCRRHPGLGKAFPSGCSAVSEP
1			ASESVVGALPAEHQFSFMEKRNQWLVSQLSAASPDTGHDSDKSD
Į.			QSLPNASADSLGGSQEMVQRPQPHRNRAGLDLPTIDTGYDSQPQ
[DVLGIRQLERPLPLTSVCYPQDLPRPLRSREFPQFEPQRYPACA
1	} .		QMLPPNLSPHAPWNYHYHCPGSPDHQVPYGHDYPRAAYQQVIQP
1			ALPGQPLPGASVRGLHPVQKVILNYPSPWDQEERPAQRDCSFPG
1			LPRHQDQPHHQPPNRAGAPGESLECPAELRPQVPQPPSPAAVPR
			PPSNPPARGTLKTSNLPEELRKVFITYSMDTAMEVVKFVNFLLV
1			NGFQTAIDIFEDRIRGIDIIKWMERYLRDKTVMIIVAISPKYKO
1.			DVEGAESQLDEDEHGLHTKYIHRMMQIEFIKQGSMNFRPIPVLF
1			PNAKKEHVPTWLQNTHVYSWPKNKKNILLRLLREEEYVAPPRGP
5446	972	161	LPTLQVVPL
3110	3/2	191	SSWSWCTGRMRKTRLWGLLWMLFVSELRAATKLTEEKYELKEGQ
1 1			TLDVKCDYTLEKFASSQKAWQIIRDGEMPKTLACTERPSKNSHP
1 1			VOVGRIILEDYHDHGLLRVRMVNLQVEDSGLYQCVIYQPPKEPH MLFDRIRLVVTKGFSGTPGSNENSTQNVYKIPPTTTKALCPLYT
1 1			TPRTVTQAPPKSTADVSTPDSEINLTNVTDIIRVPVFNIVILLA
1			GGFLSKSLVFSVLFAVTLRSFVP*AHEPTRMSSDFQPHPSGSCA
			KGGGRR
5447	207	617	MTARTLSLMASLVAYDDSDSEAETEHAGSFNATGQQKDTSGVAR
1 1	1		PPGQDFASGTLDVPKAGAQPTKHGSCEDPGGYRLPLAQLGRSDR
	i		GSCPSQRLQWPGKEPQVTFPIKEPSCSSLWTSHVPASHMPLAAA
]			RFKQVKLSRNFPKSSFHAQSESETVGKNGSSFQKKKCEDCVVPY
1			TPRRLRQRQALSTETGKGKDVEPQGPPAGRAPAPLYVGPGVSEF
į į	ļ		IQPYLNSHYKETTVPRKVLFHLRGHRGPVNTIQWCPVLSKSHML
1			LSTSMDKTFKVWNAVDSGHCLQTYSLHTEAVRAARWAPCGRRIL
, ,	1		SGGFDFALHLTDLETGTQLFSGRSDFRITTLKFHPKDHNIFLCG
			GFSSEMKAWDIRTGKVMRSYKATIQQTLDILFLREGSEFLSSTD
]		ASTRDSADRTIIAWDFRTSAKISNQIFHERFTCPSLALHPREPV
1 1	1	1	FLAQTNGNYLALFSTVWPYRMSRRRRYEGHKVEGYSVGCECSPG
1 1	j		GDLLVTGSADGRVLMYSPRTASRACTLQGHTQACVGTTYHPVLP
j İ	i		SVLATCSWGGDMKIWH*AFHWLSLGEAIGDLAPARGYSGPGRSL KSPSPSKSLLVLLCGRAMFQPATCPWQLPALSK
5448	194	1833	MASKYTDAIVWYQKKIGAYDQQIWEKSVEQREIKGLRNKPKKTA
, ,	. "		HVKPDLIDVDLVRGSAFAKAKPESPWTSLTTKGIVRVVFFPFFF
1 1	ļ		RWWLQVTSKVIFFWLLVLYLLQVAAIVLFCSTSSPHSIPLTEVI
	Ì		GPIWLMLLLGTVHCQIVSTRTPKPPLSTGGKRRKKLRKAAHLEV
[[HREGDGSSTTDNTQEGAVQNHGTSTSHSVGTVFRDLWHAAFFLS
L			GSKKAKNSIDKSTETDNGYVSLDGKKTVKSGEDGIQNHEPQCET

r——			
SEQ	Predicted	Predicted end	Amino poid
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	I WATER CALVERDING DARRAGE A
j	location		1 ordinate Acid, rephenylalaning con.
į		corresponding	Maria Caulie, laisolencine Valverine
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	Sering The Manual Rearginine,
- 1	residue of	amino acid	S-Serine, T-Threonine, V-Valine,
	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- 1	sequence	sequence	Codon, /=possible nucleofide dolot:
	sequence		1 \-possible nucleotide incertion\
			IRPEETAWNTGTLRNGPSKDTQRTITNVSDEVSSEEGPETGYSL
ı		i	RRHVDRTSEGVI. PMPVCUMVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVV
- 1	i	1	RRHVDRTSEGVLRNRKSHHYKKHYPNEDAPKSGTSCSSRCSSSR
1	ŀ	1	ADSCRAKTEDETEDATMEDITHCAECHGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
1	1		VKKEIKDDPFHOSHLPWLHSSHDGLFVIGRITURGANDGWTT
i		Ī	**************************************
	1	1	TDLEQLTAHSASELYVIAFGSNEDVIVLSMVIISFVVRVSLVWI
- 1	1		FFFLLCVAFRTYKOVCIM+TCCCH PND-1011SEVVRVSLVWI
	ŀ	1	FFFLLCVAERTYKQVGIM*TSEGVLRNRKSHHYKKHYPNEDAPK
I	1	ł.	SGTSCSSRCSSRQDSESARPESETEDVLWEDLLHCAECHSSCT
	ì	ŀ	DELD VENDOINPCVKKEYRDDPFHOSHI.DWI.uccupor Director
1	1		T THEORET CARACTERS VILLISGE MARKING HTDGTGVOTEGAN TO THE
1		<u>l</u>	T SOUTH T VERUSUATULEOUT AHSAGELVUTA ECOMERITATE AL-
		1	IISFVVRVSLVWIFFFLLCVAERTYKQVGIM
5449	194	1833	MASKYTDATUWYOKKICAYDOOTU
]		ĺ	MASKYTDAIVWYQKKIGAYDQQIWEKSVEQREIKGLRNKPKKTA
1	-1	,	1 MAREDILLOVDLAKGSAFAKAKPESPWTSI.TTVCTIPITITERPPP
1			I AMMERICAN SKYLF WULLVLYLLOVAA TVI. ECCTCCDIIGTDI GERLE
	j		(OI THEREDUCE VICOLVSTRTPKPPI,STCCVDDDVI DVD X 122
-	1 .		INCEGOGSSIIDNIQEGAVONHGTSTSHSVGTVEDDILTINA NOS -
]	•	GSKKAKNSIDKSTETDNGYVSLDGKKTVKSGEDGIQNHEPQCET
ļ	1 1		IRPEETAWNTGTI PNGBCKDTORDT TOWNS
			IRPEETAWNTGTLRNGPSKDTQRTITNVSDEVSSEEGPETGYSL
	l i		RRHVDRTSEGVLRNRKSHHYKKHYPNEDAPKSGTSCSSRCSSSR
1	1 1		ADDROUGHD TEDATEDATED THE LALE ALCOHOLOGICAL AND THE STATE OF THE STAT
	j j		TARREST TO PER CONTROL OF THE PROPERTY AND THE PROPERTY A
-	1 1	1	*DELOGRAMMENT PGIGYOTEGNAVCE TECHNOLOGICAL
1	1		TELEVITAGE LIVIATES NEDVIVI. CMUTTOE ENTRY CT THE
1	i .	ſ	FFFLLCVAERTYKQVGIM*TSEGVLRNRKSHHYKKHYPNEDA>K
}	1	1	SGTSCSSRCSSRQDSESARPESETEDVLWEDLLHCAECHSSCT
1 .	l i	<u> </u>	SETDVENHOTNEGUVVEVENDER PERSONNENDLEHCAECHSSCT
	i l	1	SETDVENHQINPCVKKEYRDDPFHQSHLPWLHSSHPGLEKISAI
1 :	[i	VWEGNDCKKADMSVLEISGMIMNRVNSHIPGIGYQIFGNAVSLI
1	!	1	DOLLER VERUSUATULEOLTANSASET, VVITAEGENERVITUS GUAR
5450	8136		* TOY A AWADDAMILE LITTCAME LAKUMULM
1	0130	1242	GQQFASFFG*NHPEVTVAMALTD)DLOLOFEMCODERY
]]		ļ	**************************************
	1		LTVVEGWATLSVDGFLNASSAVPGAPLEVPYGLFVGGTGTLGLP
1 1	1	i	YLRGTSRPLRGCLHAATLNGRSLLRPLTPDVHEGCAEEFSASDD
1	i	i i	VALGESGRUST ANERANGERS AND VALGESGRUST ANERANGERS AND VALGESGRUST ANERANGERS AND VALGESCRUST AN
1 1			VALGFSGPHSLAAFPAWGTQDEGTLEFTLTTQSRQAPLAFQAGG
1 1	j		THE PROPERTY OF THE PROPERTY O
1 1	i	1	TAMBLE 15 VDOI PIRTSNRGVI, GVI, FDDCCI I I COI DO I
		1	MAY THE TEAT NASLIGEMENT SUNGOPPET DEAT THE TEATHER THE THE TEATHER THE TEATHER THE TEATHER THE TEATHER THE TEATHER THE THE TEATHER THE THE TEATHER THE THE TEATHER THE THE THE THE THE THE TEATHER THE THE THE THE THE THE THE THE THE THE
1 1		1	**************************************
i l	į	1	PPVFANFTQLLTISPLVVAEGGTAWLEWRHVQPTLDLMEAELRK
1 (1	J	SOVLESVIRGAHYGELET DIT GRORENET CHENENERK
į .		1.	SQVLPSVTRGAHYGELELDILGAQARKMFTLLDVVNRKARFIHD
1 . 1	1	1.	GSEDTSDQLVLEVSVTARVPMPSCLRRGQTYLLPIQVNPVNDPP
1 }	j	1 1	TITE TOO DAY TEEN TOKPLEDEVE ON VDDDCA CECT MEANS
1 [į.	1 '	SOME VERRUGIGEPATEFSCRELEAGGIAVANDCCCDA ON * 1
1	ŀ	,	SUGDENIAS PPATERVVAIRPATOTHPETCT DE ACCOMPTE DE LA
1 1	1	[]	LSVETNAVGQDVSVLFRVTGALQFGELQKHSTGGVEGAEWWATQ
1		1 2	AFHORDVEQGRVRYLSTDPQHHAYDTVENLALEVQVGQEILSNL
1 1	j	<u> </u>	SEPUTION ATUMAT DE LINOVIDADE DE LA LEVQUE LESNI.
į (1 7	SFPVTIQRATVWMLRLEPLHTQNTQQETLTTAHLEATLEEAGPS
1	1	l -	FIFTIEV VVAPRKGNLOLOGTRI SDGOGETODD TO A CDITTOR
1	1	1 -	ACCOMPANIE OF THE PROPERTY OF
1	1	1 -	MVVEGGEGVLSAUHLFVKSINSAGVI.VEIMEDDDI ODI AND -
	f .	1 -	YEAR INVISE INEDLORGE TO CHOOSE THE TOTAL TO THE TOTAL OF THE PROPERTY OF THE
	į	1 •=	SOUTHWEEVRGVERVAIOPVNDHADVOTTCDTEIRIADGGDD
· ·	ĺ	ı	TDDVAFSDADSGFADAQLVLTRKDLLFGSIVAVDEPTRPIYRF
· · · 1	1	ا ا آ	OEDLEKERU FUNCADESTRADILITIES IVAVDEPTRPIYRF
l	-	, -	YEDURARA VIIF VRSGADRGWIOLOVSDGOHON TALL EVON OFF
ì	1	; <u>-</u>	DRVANGSSDVVPOGGOGTIDTAVI,HT.DTMI.DTpccppinngum
1		1.0	OF THE OWN RANGE PARTATS OF THE OWN OF THE OWN OF THE OWN OF THE OWN OF THE OWN OF THE OWN OF THE OWN OF THE OWN OF THE OWN OWN OF THE OWN OWN OF THE OWN OWN OWN OWN OWN OWN OWN OWN OWN OWN
-		1 3	VENUE VILLUATLUVTIALEGDI.ADI.KI.VDUVVTVVIDOODAADA
1	1	(~	RDQUEAAQEAVPPADIVFSVKSDDSAGVIJMUSDCATADEDDS
1			
,	1	L	DPVQSFSQEAVDTGRVI.VI.ucppeanona Total
		1 2	DPVQSFSQEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAPLE VLVELEVLPAAIPLEAQNFSVPEGGSLTLAPPLLRVSGPYFPT

SEO	Predicted	Predicted end	Dmino agid occurre
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1 '	corresponding	to first	Introduction M Mathieurica N Rebysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
İ	residue of		S=Serine, T=Threonine, V=Valine,
1	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	I .	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
}		-	LLGLSLQVLEPPQHGPLQKEDGPQARTLSAFSWRMVEEQLIRYV
1	1	ſ	HDGSETLTDSFVLMANASEMDRQSHPVAFTVTVLPVNDQPPILT
ļ	}	ì	TNTGLOMWEGATAPIPAEALRSTDGDSGSEDLVYTIEQPSNGRV
	1		VLRGAPGTEVRSFTQAQLDGGLVLFSHRGTLDGGFPFRLSDGEH
- {		ł	TSPGHFFRVTAQKQVLLSLKGSQTLTVCPGSVQPLSSQTLRASS
			SAGTDPQLILLYRVVRGPQLGRLFHAQQDSTGEALVNFTQAEVYA
{		ĺ	GNILYEHEMPPEPFWEAHDTLELQLSSPPARDVAATLAVAVSFE
	}		ACCORDIGITATION OF THE PERSON AND TH
	1		AACPQRPSHLWKNKGLWVPEGQRARITVAALDASNLLASVPSPQ
ţ	(RSEHDVLFQVTQFPSRGQLLVSEEPLHAGQPHFLQSQLAAGQLV
1	i		YAHGGGGTQQDGFHFRAHLQGPAGASVAGPQTSEAFAITVRDVN
[ERPPQPQASVPLRLTRGSRAPISRAQLSVVDPDSAPGEIEYEVQ
1	j .		RAPHNGFLSLVGGGLGPVTRFTOADVDSGRLAFVANGSSVAGIF
1			QLSMSDGASPPLPMSLAVDILPSAIEVQLRAPLEVPQALGRSSL
1			SQQQLRVVSDREEPEAAYRLIQGPQYGHLLVGGRPTSAFSOFOT
1	ļ		DOGEVVFAFTNFSSSHDHFRVLALARGVNASAVVNVTVRALLHV
1			WAGGPWPQGATLRLDPTVLDAGELANRTGSVPRFRLLEGPRHGR
1	1		VVRVPRARTEPGGSQLVEQFTQQDLEDGRLGLEVGRPEGRAPGP
İ	1		AGDSLTLELWAQGVPPAVASLDFATEPYNAARPYSVALLSVPEA
ł			ARTEAGKPESSTPTGEPGPMASSPEPAVAKGGFLSFLEANMFSV
	Î l		IIPMCLVLLLALILPLLFYLRKRNKTGKHDVQVLTAKPRNGLA
[[GDTETFRKVEPGQAIPLTAVPGQGPPPGGQPDPELLQFCRTPNP
1			ALKNGOYWV
5451	1	2274	RDSSEQGRTGDTLGRPSACMDALKPPCLWRNHERGKKDRDSCGR
- [22.1	KNSEPGSPHSLEALRDAAPSQGLNFLLLFTKMLFIFNFLFSPLP
	1	:	TRAL TOTI TEGA A TELVI TERROPETE DE L'ENTRE L'ENTRE PER L'ENTRE PE
	[[i	TPALICILTFGAAIFLWLITRPQPVLPLLDLNNQSVGIEGGARK
)	j	GVSQKNNDLTSCCFSDAKTMYEVFQRGLAVSDNGPCLGYRKPNQ
			PYRWLSYKQVSDRAEYLGSCLLHKGYKSSPDQFVGIFAQNRPEW
	1		IISELACYTYSMVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQ
			KALVLIGNVEKGFTPSLKVIILMDPFDDDLKQRGEKSGIEILSL
			YDAENLGKEHFRKPVPPSPEDLSVICFTSGTTGDPKGAMITHQN
1			IVSNAAAFLKCVEHAYEPTPDDVAISYLPLAHMFERIVQAVVYS
i 1			CGARVGFFQGDIRLLADDMKTLKPTLFPAVPRLLNRIYDKVQNE
1		ì	AKTPLKKFLLKLAVSSKFKELQKGIIRHDSFWDKLIFAKIQDSL
)		•	GGRVRVIVTGAAPMSTSVMTFFRAAMGCQVYEAYGQTECTGGCT
1 1	}		FTLPGDWTSGHVGVPLACNYVKLEDVADMNYFTVNNEGEVCIKG
1 1	.]	1	TNVFKGYLKDPEKTQEALDSDGWLHTGDIGRWLPNGTLKIIDRK
			KNIFKLAQGEYIAPEKIENIYNRSQPVLQIFVHGESLRSSLVGV
1 1	1		VVPDTDVLPSFAAKLGVKGSFEELCQNQVVREAILEDLOKIGKE
1	ĺ		SGLKTFEQVKAIFLHPEPFSIENGLLTPTLKAKRGELSKYFRTQ
			IDSLYEHIQD
5452	1833	1138	SRVPSLCLSLSLSPSREPVAGAPGCGTAGPPAMATLWGGLLR
	ł	l	LGSLLSLSCLALSVLLLAQLSDAAKNFEDVRCKCICPPYKENSG
1 1	İ	1	HIYNKNISQKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERSS
])	·]	VTIKVTIIIYLSILGLLLLYMVYLTLVEPILKRRLFGHAQLIQS
1 4	į	[DDDIGDHQPFANAHDVLARSRSRANVLNKVEYAQQRWKLQVQEQ
1 1	ĺ	ł	RKSVFDRHVVLS
5453	111	1520	
1 1	***	1520	PSIPAAVPQSAPPEPHREETVTATATSQVAQQPPAAAAPGEQAV
}	1	i	AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGGSAKE
1	ļ	[PQEERSQQQDDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTVY
1	}	1	KGLDTETTVEVAWCELQDRKLTKSERQRFKEEAEMLKGLQHPNI
j l		ļ	VRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRFKVMKIKVL
1 1	1	ļ	RSWCRQILKGLQFLHTRTPPIIHRDLKCDNIFITGPTGSVKIGD
1	1		LGLATLKRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCM
}		{	LEMATSEYPYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEII
}			EGCIRONKDERYSIKDLLNHAFFQEETGVRVELABEDDGEKIAI
[]			KLWLRIEDIKKLKGKYKDNEAIEFSFDLERNVPEDVAQEMVESG
1 1	}		YVCEGDHKTMAKAIKDRVSLIKRKREQRQL*
5454	111	1520	DC1D97/DCVDDBBhbbbhhbbhhbbhhbbhhbbhhbhbhbhbhbhbhbh
		2320	PSIPAAVPQSAPPEPHREETVTATATSQVAQQPPAAAAPGEQAV
1 1]		AGPAPSTVPGSTSKDRPVSQPSLVGSKEEPPPARSGSGGGSAKE
1	1		PQEERSQQQDDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTVY
L			KGLDTETTVEVAWCELQDRKLTKSERQRFKEEAEMLKGLQHPNI

Descripting processing incleaning and action action processing to first amino acid annivo acid amino acid annivo a		SEQ	Predicted	Predicted end	
No: nucleotide location corresponding corresponding corresponding corresponding corresponding anino acid anino acid anino acid anino acid anino acid anino acid sequence seque		ID			
Cocation		NO:			I M-Manage Cetysteine D-Aconstia and a
corresponding to first smino acid aniro acid aniro acid aniro acid aniro acid aniro acid sequence sequ		ł	location		(Sideamic Acid, F=Phenylalaning C. Ci
to first amino acid arito acid residue of residue of residue of amino acid anino acid acid acid acid acid acid acid acid		ł .		toffesponding	I henrectaine, imisolencine Valuaina
amino acid residue of amino acid sequence Seq		İ	to first		L=Leucine, M=Methionine, N-lengyngine
residue of amino acid sequence Sequence		i			Parcoline, Q=Glutamine, R=Arginine
amino acid sequence Codo, /-possible nucleotide deletion, Vpossible nucleotide insertion Forest and the codo, /-possible nucleotide insertion Forest and		ļ			S=Serine, T=Threonine V-Valine
Sequence Veryossesty value insertion: UPDOWS AND IN SECULAR INSERTION INSERTION OF SERVICE OF SER		1		1	W=Tryptophan, Y=Tvrosine Y=Unknown + or
VRPTUSSEETYWERKKCTLUTPEURSCHLANTLANFRYMKIKUL RSWCROLLAGUCPHITETPEITHRDLKCONIFITETPETSWERKER LEGATERITYSECONAGUITREVTSGWERMINITETRATISTUS AND LEGATERITYSECONAGUITREVTSGWERASFOKWAIFEWERKER LEGATERITYSECONAGUITREVTSGWERASFOKWAIFEWERKER LEGATERITYSECONAGUITREVTSGWERASFOKWAIFEWERKER LEGATERITYSECONAGUITREVTSGWERASFOKWAIFEWERKER LEGATERITYSECONAGUITREVTSGWERASFOKWAIFEWERG WWGKGKAVLENDAWUITGONESGUERGEWERG WWGKGKAVLENDAWUITGONESGUERGEWERG WWGKGKAVLENDAWUITGONESGUERGEWERG WWGKGKAVLENDAWUITGONESGUERGEWERGEWERG WWGKGKAVLENDAWUITGONESGUERGEWERGEWERGEWERGE WWGKGKAVLENDAWUITGONESGUERGEWERGEWERGEWERGE WWGKGKAVLENDAWUITGONESGUERGEWERGEWERGEWERGE WWGKGKAVLENDAWUITGONESGUERGEWERGEWERGEWERGE WWGKGKAVLENDAWUITGONESGUERGEWERGEWERGEWERGEWERGEWERGE WWGKGKAVLENDAWUITGONESGUERGEWERGEWERGE WWGKGKAVLENDAWUITGONESGUERGEWERGEWERGEWERGEWERGEWERGE WWGKGKAVLENDAWUITGONESGUERGEWERGEWERGEWERGEWERGEWERGEWERGEWERG		ļ		sequence	Codon, /=possible nucleofide deletion
VRYPSSESTYMERKELUVETELMTSSTILTUTELMTEKUMER TOTTETSSKEED LGIATLERASPARSVIGTPEFMAPEMTEKUDEKUNT ITTETTSSKEED LGIATLERASPARSVIGTPEFMAPEMTEKUDEKUNT ITTETTSSKEED LGIATLERASPARSVIGTPEFMAPEMTEKUDEKUNDTVATEVEKUT EGCICROKKOERYSIKOLLMIAFFOGETGYMVELAEEDDOGKINT VEGEDRYMINGKYKUNGAL TESFFOLERWYSEDVAGENVESG VEGEDRYMINGKYKUNGAL TESFFOLERWYSEDVAGENVESG VEGEDRYMINGKYKUNGAL TESFFOLERWYSEDVAGENVESG VEGEDRYMINGKYKUNGAL TESFFOLERWYSEDVAGENVESG VEGEDRYMINGKYKUNGAL TESFFOLERWYSEDVAGENVESG VEGEDRYMINGKYKUNGAL TESFFOLERWYSEDVAGENVESG VEGEDRYMINGKYKUNGAL TESFFOLERWYSEDVAGENVESG VEGEDRYMINGKYGGRIVAL TOSGLOGKOLT VARAGENIA OPERATIONAL GALEELITEELTASHAT VARAGET TANTICKOKKYANGAKUNLORGI GALEELITEELTASHAT VARAGET TANTICKOKKYANGAKUNLORGI GALEELITEELTASHAT VARAGET TANTICKOKKYANGAKUNLORGI GALEELITEELTASHAT VARAGET TANTICKOKKYANGAKUNLORGI COPTYDIIVUNGA SYNCTIMENIA ON TANDICKOKKYANGAKUNLORGI COPTYDIIVUNGA SYNCTIMENIA ON TANDICKOKKYANGAKATA TANDICKOKKYANGAKATA TANDICKOKKYANGAKATA TANDICKOK			sequence		\=possible nucleotide incertion\
ALGAMATANA DE JAHITET PI LINDIACONI FITTS PTGS YKIGD LEMASSI YP SSCONA QUI YR VYSCOVERA PRYPER VENE THE VENE TI BGCIENT PY SSCONA QUI YR VYSCOVERA PROMITE YE VENE TI BGCIENT PY SSCONA QUI YR VYSCOVERA PROMITE YE VENE TI KALDATEDI LE SA KOLLIMAR PE GESTLERNYE BUNADEN EN PER LERNYE BUNADEN LE STEDLERNYE BUNADEN EN PER LERNYE BUNADEN EN PER LERNYE BUNADEN EN PER LERNYE BUNADEN EN PER LERNYE BUNADEN EN PER LERNYE BUNADEN EN PER LERNYE BUNADEN EN PER LERNYE BUNADEN EN PER LERNYE BUNADEN EN PER LERNYE BUNADEN EN PER LERNYE BUNADEN EN PER LERNYE BUNADEN EN PER LERNYE BUNADEN EN PER LERNYE BUNADEN EN PER LERNYE BUNADEN EN PER LA SERVE BUNADEN EN PER		})		VRFYDSWESTVKGKKCIVLVTELMTSCTI VTVI VDEVIN
LEMASTEY PYSECONAGO Y RATEVISIONED STATEVIDES DEVISION AS ENCISION DEVISION AS A VIRVISION PROVED THE RESET OF THE PROPERTY OF		İ		1	RSWCRQILKGLOFLHTRTPPITHPDLYCDNIPHTGCCC
EGCTENMORERY SI ROLLANDAP (CERTIFORM CONTROLLAR EDGERATA) KUMENTED I KALKIKAK KUNKALEFSTBLENNYEEUVAGEMVESG VICEDERMAN I KONSULKKRERGORU. LTWISPATTRESI-FRUKAMEPITETTALI ELLIFEGLISVEGILFRILD WINGKALIKANAN VITGATSELGKEGAKUPYAGGKUNLCGANG GALEELI RELTASHARI KOTTAKYATIKATSEGKUNLCGANG GALEELI RELTASHARI KYOTTAKYATOKUNLGANGKUNLCGANG GALEELI RELTASHARI KYOTTAKYATOKUNLGANGKUNLCGANG GALEELI RELTASHARI KYOTTAKYATOKUNLGANGKUNLCGANG GALEELI RELTASHARI KYOTTAKYATOKUNLGANGKUNLCGANG GALEELI RELTASHARI KYOTTAKYATOKUNLGANGKUNLCGANG GALEELI RELTASHARI KYOTTAKYATOKUNLGANGKUNLCGANG GALEELI RELTASHARI KYOTTAKYATOKUNLGANGKUNLCGANG GALEELI RELTASHARI KYOTTAKYATOKUNLGANGKUNLCGANG GALEELI RELTASHARI KYOTTAKYATOKUNLGANGKUNLGANG GALEELI RELTASHARI KYOTTAKYATOKUNLGANGKUNLGANG GALEELI RELTASHARI KYOTTAKYATOKUNLGANGKUNLGAN		l	}	1	LGLATLKRASFAKSVIGTDEEMAREMATERIA
S455 1359 377 LIMIESTED IKKINGKY KUNEAL PESSPELERING VANGEMESE STEDERING AGENT SENDERING STED		ĺ	i	į.	LEMATSEYPYSECONA A OLYPPUTCOWER OF THE ENDES VDVYAFGMCM
S455 1359 377 LTWSPATRRSIPVEVAMPETETALIPLIFEGLIVEGIFRILD WROKAYLINARALIFRORGIU- WROKAYLINARALIFROYSILKERKRORGOU- GALESLIRELTASHARKVOTHKYTLUTEDITSGAIVAAABIL COFGVUDILVINALSISTIGUMSITEMTUDDEWISINVEGIFRILD RALLIPBMIRRROGHIVAISSIGGKMSIPFESAYAASKHATQAF DOLARBERGYISTEVTUISPGVITHTUISVANITHTUDDEWISINVEGIFVAVAABIL COFGVUDILVINALSISTIGUMSITEMTUDDEWISINVEGIFVAVAABIL AALLIPBMIRRROGHIVAISSIGGKMSIPFESAYAASKHATQAF DOLARBERGYISTEVTUISPGVITHTUISVANITHTUDDEWISINVARDAFI LACARS PVEVAQOVLAAVGKKKOVILADILDSLAVULETLAD DOLARBERGYISTEVTUISPGVITHTUISVANITATADAF DOLARBERGYISTEVTUISPGVITHTUISVANITATADAF DOLARBERGYISTEVTUISPGVITHTUISVANITATADAF DOLARBERGYISTEVTUISPGVITHTUISVANITATADAF DOLARBERGYISTEVTUISPGVITHTUISVANITATADAF DOLARBERGYISTEVTUISPGVITHTUISVANITATADA DOLARBERGYISTEVTUISPGAAGETEVTYSTAPAAC TURAMPORAS DILEVKKRIISLIKKPILARSPUISPGAAG REPUBAADUKOOLODIAABEKKRIKRITTISHRYESITTVOTOGGTIA OKOKKICOPROSTAATATIOKAKYPAIVAVKSITSVAVPIMAAGA REPUBAADUKOOLODIAABEKKRIKRITTISHRYESITTVOTOGGTIA OKOKKICOPROSTAATATIOKAKYPAIVAVKSITSVAVPIMAAGA REPUBAADUKOOLODIAABEKKRIKRITTISHRYESITTVOTOGGTIA OKOKKICOPROSTAATATIOKAKYPAIVAKANITAOLOPISSAGAA REPUBAADUKOOLODIAABEKKRIKASUULETTADAGAA DAAGAOOLODIAABEKKRIKAAULETTAAAAA MINOSALOOPIVATAA REPUBAADUKOOLODIAABEKKRIKAAULET GEKRISTIVATAA REPUBAADUKOOLODIAABEKKRIKAAULET GEKRISTIVATAA REPUBAADUKOOLODIAABEKKRIKAAULET AARAMAANAANAA REPUBAADUKAA REPUBAADUKAANAA REP			(1	EGCIRONKDERYSIKDIINWAERORUMA
1359 377 11879 PATRIESIP, PKYRAMIP TISTAIL ILPLIFOCLS VIGIL PRILLA WURKCAYLERNAVVITOATS GLIGECAKVIYAAGAKULOGRINA GLIELLIR ELTASHATE VOTH PHYLVITED TO TAVAAAABEI LOCFGEY VDI LVNINAGISYRGTI MDTTUVUKKWISTINYTS PVALT KALLIPSIN IRROGHI VAI SI LOGKMIST PEVANASKIATOAFF DELRABHEQYSE EVIVI S PGYHTHILS VAI ATTAGGES GRYGWDTT TAGGES EVEXAPOVLAAV VAKKKAVI LABULPSIAVYLRTLAPO LEKRAMI VAI TAGGES EVEXAPOVLAAV VAKKKAVI LABULPSIAVYLRTLAPO LEKRAMI VAI TAGGES EVEXAPOVLAAV VAKKKAVI LABULPSIAVYLRTLAPO LEKRAMI VAI TAGGES EVEXAPOVLAAV VAKKKAVI LABULPSIAVYLRTLAPO LEKRAMI VAI TAGGES EVEXAPOVLAAV VAKKKAVI LABULPSIAVYLRTLAPO LEKRAMI VAI TAGGES EVEXAPOVLAAV VAI TAGGES EVEXAPOVLAAV VAI TAGGES EVEXAPOVLAAV VAI TAGGES EVEXAPOVLAAV VAI TAGGES EVEXAPOVLA VAI TAGGES EVEXAPO		Ì		1	KLWLRIEDIKKI KCKYVDNEA I DEGERA PROVELAEEDDGEKIAI
LIMYSPATRSLIPKYKAMDETISTALIFILIFOCLGVEGIFRILD WINGKALKRAVVVITAGIGLIKECKAVARAGKILULCORNO GALEELIRELTASHATKVOTHEPILVTFOLTESGA VAAAAGELIL COFGYVOLIVANAGIS SYRGTI INDTIVULVIKEN INYPOPVALI KALLPSHIKROGHIVAISSIOGKMSI PERSAVAASKHATOAFP DCHARAMGVEGI EUVII SEVJIHTMISUKWI INYPOPVALI KALLPSHIKROGHIVAISSIOGKMSI PERSAVAASKHATOAFP DCHARAMGVEGI EUVII SEVJIHTMISUKWI INYPOPVALIT TAQOGSPVEVAQDULAAVOKKKKUVI LADLLPSLAVVIRTLARD LIPSIMASBARRERKSKINS TEVAMPOR SPLLEVKORI LEKKPEL KARSADENLESSRI LKRRDI OKEDGLEPEKKRTRGLGATTKITTSHERVESLTY VOOTOGGTTA OKVSKKTGSROSPLLEVKORI LEKKPEL KARSADOLPLSSRI LKRRDI OKEDGLEPEKKRTRGLGATTKITTSHERVESLTY VOOTOGGTTA OKVSKKTGSROSPLLEVKORI LEKKPEL KARSADOLPLSSRI LKRRDI OKEDGLEPEKKRTRGLGATTKITTSHERVESLTY VOOTOGGTTA OKVSKKTGSROSPLLEVKORI LEKKPEL KARSADOLPLSSRI LKRRDI OKEDGLEPEKKRTRGLGATTKITTSHERVESLTY VOOTOGGTTA OKVSKKTGSROSPLLEVKORI LEKKPEL KARSADOLPLSSRI LKRRDI OKEDGLEPEKKRTRGLGATTKITTSHERVESLTY VOOTOGGTTA OKVSKKTGSROSPLLEVKORI LEKKPEL KARSADOLPEKGATTSHE ALSSQAEVARADOLKGGLOCH SEKROLE OKOPOLOGOLDOL OKOPOLOGOLDOL OKUSKATORPHON PERSON LEKKROLI OKOPOLOGOLOGOLOGOLOR OLD OLD OLD OLD OLD OLD OLD OLD OLD OLD	1			1	YVCEGDHKTMAKATKDRUGI TITTUTTER TOTAL TOTAL
GALEGILRY STRATEVOTHEPT LITERIOLISCA IVAAAABAIL CCFGYVDILVNINAGISYRGTIMDTTUPUKRWIETNYFGPVALT KALIPSNIRRGGHIVAISTGGMEN TEYNAASKATQAFF DCLAREMEQYSIETVIS GGYMETTUPUKRYWETNYFGPVALT AGGRSEVSVAQOULAAVCKKKOVI LABALIPSLAVYLRTLADO LEFSLANSRAKKERKSKINS CAGGIVARGAVULYPASRAGERTEVYGSPAPSLELKISPGACC TEVUMDOCRS PLEEVKGNIELKRPLIKAPSOLPLOSSILKREPD OKUSKKTGGRCSTA LATGLKOKKYPAVPUKSGTSGVPMAGG KKPSKRPANDLKGGLCDINABLKKCERETIOLONGOLODOLO DAQQVKALGTERTTLEGGILAKVGAOAECGGOELKIRLACVLEL EERISTYGGOLVOELCKROVELGERRGIKMOSLEKERELOTSER ALSSSGAEVASLROETVAQAALLITEEERHIGLEMERRHIHNOL GELKGNIRVYCRVERVELVEGETPFOLLLEFORGGOEDOLEGLI IR ALRILESVAGELSGGOWTYSFVASVVEIYWETVROLLATGTRK GOGGCEIKRAGPOSSELTVINASVYVEIXWETTOLLATGTRK ARRELLELSGERGGORTTSPOGGCOSTATGTRAGGAR DEVERREWETTTOLTVASSPYPPVVCGARCGROCHOLLOCK REALLLISAGELTTTOLTVASSPYTHOTYSGCATTAGRAGGAR EEGELATTILITYEVDUSSELTVANASVEHOLOCK REALLLISAGRAGGATTGTOGGARGATGTAGAR EEGELATTILITYEVDUSSELTVANATGTAGGELERETGTATATGTE GORGANDEN KANAMATAGARGELETGTANATGTAGAR EEGELATTATTILITYEVDUSSELTATATAGARGATGTAGAA ASLOGGCOGGAGTTGTOGARTSPOGATTARKAGAARGAA BERKGRYBAGGALTTKAAAAGGEL		5455	1359	377	LTMVCDATDVCI DVIVAMDET TOO
GENERAL RECORD TO LIVENAGI SY ROTI MDTIVUNE AWE INYEPOPALT ALLES SHIRROGHIVA IS SIGGIMS I PERSA VAS KHATQAFE DELAR MENGYET ETVIT SHOY HITMIS WATADAREIL ALLES SHIRROGHIVA IS SIGGIMS I PERSA VAS KHATQAFE DELAR MENGYET ETVIT SHOY HITMIS WATADOS RY VANDUT TAQORS PVEVAQOV LANVOKKKOVI LADLIPSLAVILRILADO I FISHANSARAKERKS KNY SHOY HITMIS WATADOS SHOW			1	1	WYPGKAYLPNAMMUTTESTALLPLLFGCLGVFGLFRLLQ
TALLESNIKERGHIVAISSIQEMEINERAYARKHATOAFF DELRAEMEQYE TEVTVISPGYIHTMLSWNAITAAGREYGWDTT TAQERS VEVAQDULABAWGKKKUDU LADLEPSLAVYLRTLAPC LFFSLMABRAREREKSKNS COAGLIVAAWGKKUDU LADLEPSLAVYLRTLAPC LFFSLMABRAREREKSKNS COAGLIVAAWGKKUDU LADLEPSLAVYLRTLAPC LFFSLMABRAREREKSKNS ORDEROGEPEKKERGLATTKITTSHEVSTATFSGACT TEVDMDPQRSPLLEVKONIELKRPLIKAPSOLPLEGSELKRRDD MEDGLEPEKKERGLATTKITTSHEVSLTTVPOTCOGTTA OKVSKKTGERCSTAIATGLKNOKPVPAVPUVKSGTGAVP PMAGG KKPSKRPAMDLKGGLCULANELKGERERTOTLDGENOOLODOUG DAQQUVKALGTERTTLEGHLAKVOAOABGCGOELKURACVUEL EERILSTOGELOVELGKKOVVELGEERRENGOLERCHRACVUEL LEGRISTOGELOVELGKKOVVELGEERRENGOLERCHRACVUEL LEGRISTOGELOVELGKKOVVELGERRENGOLERCHRACVUEL LEGRISTOGELOVELGKKOVVELGEERRENGOLERCHRACVUEL LEGRISTOGELOVELGKKOVVELGEERRENGOLERCHRACVUEL LEGRISTOGELOVELGKKOVVELGEERRENGOLERCHRACVELG LEGRISTOGELOVELGKKOVVELGEERRENGOLERCHRACVELG LEGRISTOGELOVELGKKOVVELGEERRENGOLERCHRACVELG LEGRISTOGELOVELGKKOVVELGEERRENGOLERCHRACVELG LEGRISTOGELOVELGKKOVVELGEERRENGOLERCHRACVERG ALKILESVAOELSGOGNTISFVASVVEVGEKKUNDERGESDEPTREL SLESSDERRGTLSGAPAPPTRUBGEGGESDEPTREL ALKILESVAOELSGOGNTISFVASVVEVGEKKUNDLAG SERLEDGILAPPGRESSOLEVEVYBERGAPKANTITERG OGGEKEIRRADGEBELTVINARVVEVGEKKUNDLAG SERLEDGILAPPGRESSOLEVEVYBERGAPKANTITERG OGGEKEIRRADGEBELTVINARVVEVGEKKUNDLAG SERLEDGILAPPGRESSOLEVEVYBENGERSKALCGAPLSIVDLAG SERLEDGILAPPGRESSVEVETARVEVGEKKUNDLAGENSLEPTRENSLERF ASKVEBSULFOTAGOSRAWKKTOPLOCVCVCVCVCVCVCVCVCVV VVPNOKLTYLLONSLGGSAKOMAFVINARVVEVGEKSKULDLAGE SERLEDGILAPPGRESSVEFTARVAKTORT VARIAV ASKMENTAVKORGAVAGATORARVEVGERSSLEDPLKGTFRA ASKVEBSULFOTAGOSRAWKKTOPLOCVCVCVCVCVCVCVCVV VRVNOKLTYLLONSLGGSAKOMAFVINGERSSLEDPLKGTFRA ASKVEBSULFOTAGORRAVCKRALVERNINGSFLANGERSLADPLKGTFRA ASKVEBSULFOTAGORRAVCKRALVERNINGSFLANGERSLADPLKGTFRA ASKVEBSULFOTAGORRAVCKRALVERNINGTSFLANGERSLADPLKGTFRA ASKVEBSULFOTAGORRAVCKRALVERNINGTSFLANGERSLADPLKGTFRA ASKVEBSULFOTAGORRAVCKRALVERNINGTSFLANGERSLADPLKGARV ARBEITACHGGERSALVERNINGTSFLANGERSLADPLKGARV ARBEITACHGGERSALVERNINGTSFLANGERSLADPLKGARV ARBEITACHGGERSALVERNINGTSFLANGERSLADPLKGARV ARBEITACHGGERSALVERNINGTSFLANGERSLADPLA			1		GALEEL TREE TO SULTIFICATE GLICKE CAKVEYAAGAKLVLCGRNG
Delrarency et evyt spoy i this want tadoes rowmott tagers vera double and tagers vera double and tagers vera double and tagers vera double and tagers vera double and tagers vera double and tagers vera double and tagers vera double and tagers vera double and tagers vera double and tagers vera double and tagers vera double and tagers vera double and tagers vera double and tagers vera double and tagers vera double and tagers and	- 1		1	1	OCECYMPILIPRIA CONTRACTOR OF THE PROPERTY OF TH
Delrarency et evyt spoy i this want tadoes rowmott tagers vera double and tagers vera double and tagers vera double and tagers vera double and tagers vera double and tagers vera double and tagers vera double and tagers vera double and tagers vera double and tagers vera double and tagers vera double and tagers vera double and tagers vera double and tagers vera double and tagers vera double and tagers vera double and tagers and	- 1		1	1	VALIBOATION OF THE PROPERTY OF
5456 2 2332 CGRGIVANGAGYLINDIASORIGUNDEL TAGGER PVEVAGOVIANGKKENDY LADILPS LAVVLETLAPE LFSLMASRARERKSKNS CGRGIVANGAGVIVLTYBERASGERTRYPGSPAPSSLPINSPGAGG TEVDMDPGRSPLLEVKENIELKRPLI KAPSOLPLEGSELKREPD ONEDGLEPERKERTGLGATTKITTSHRVESITTVPGTGGTTA OKVSKKTGERCSTALATGLKNOKPYPAVPVOKSGETGGYPPMAGG KKPSKRPAMDLKGGLCULNAELKGERETOTILDGENOCLODOLR DAQQUVALGTERTILEGHLAKVOAOABGGGOELKURLAGVLEI EERLSTDGELOVELOKKOVELGERERGOLEEKERILDODOLR ALGSSOAEVASLRGETVAOAALLTEREERLHGLEBERRRHINGL GELKGINTVPCRVEPVLPGGPTPPPGLGOEDEVEEIA ALGSSOAEVASLRGETVAOAALLTEREERLHGLEBERRRHINGL GELKGINTVPCRVEPVLPGGPTPPDGLOEDEVLEGIALTER ALRILFSVAOELSGOGWTSFVASVATTMEGGGESDDPTRL SLESSBERGGTLGGAPAPPTRUBES PDRVFPPGGGODEVEEIA MINVOSALDSPYDCTFANGOTGSKATT PINGEGGEBOLEDLEGLIFR ALRILFSVAOELSGOGWTSFVASVATVENTUREVBLATATGRE OGGEKIR RRADGGGEBLITVTNARVFVSCEKKUDLAG SERLDBGLADFYDETATARVFVSCEKKUDLAGGAGSGLOPLSKUDLAG SERLDBGLADFYDETATARVFVSCEKKUDLAGGAGSGLOPLSKUDLAG SERLDBGLADFYDETATARVFVSCEKKUDLAGGAGSAGVAFVNIBLEBERWSESLINDLAG SERLDBGLADFGBERRLTSTGATANSVENTUREFENSLEFTERSTGLAF ANKWESVLIVLANSLGGAAGMAFVNIBLEBERWSELGGAPKANTGER ANKWESVLIVLANSLGGAAGMAFVNIBLEBERWSELGGAPKANTGER ANKWESVLIVLANSLGGAAGMAFVNIBLEBERWSELGGAFMANTGET TAGGGAAATODPAARFOVOKHSKOELSSI HIGGSKLOPLKSTPA ANKWESVLOFTOKTORAGORRIKKTDDPLCVCVCVCVCVCVCVCVCVVCVV VRYMSKLITILLSKKOMLDHFGATHHOVYSREGELLREKRIGVFGI TSVDFHISSEGLIFFGASSBJFHCROGGARSSLAPLFKVIGTERSLYSGLI VNK APHDEYFOYCTHESGGHERILTYLGHPTOVSRESELLIRERKRIGVFGI TSVDFHISSEGLIFFGASSBJFHCROGGNEVSPENGEVSPMK PLEIKTGCSGPRMDFKICFADPAFFSFINNSDAWANTETGEER RITFCHGGLISNVLDDPKSAGVAFFVIGEFRSVSCELVPMK PLEIKTGCSGPRMDFKICFADPAFFSFINNSDAWANTETGEER RITFCHGGLISNVLDDPKSAGVAFFVIGEFRSVSGLEFALEVEV PARAGTTRDEKVAKARLBERGTDGOKKVSTORDFWSPEGGECVPMK PLEIKTGCSGPRMDFKICFADPAFFSFINNSDAWANTETGEER ARAGTTRDEKVAKARLBERGTDGOKKVSTORDFWSPEGGESCHPKV RKSALLLLASFGTDGOKKVSTORDFWSPEGGESCHPKV RKSALLLLASFGTDGOKKVSTORDFSSELLGERGALETAL ARAGTTRDEKVAKARLBERGGVARAFTULAUTRTGEER ALGCGSCOPCECANCGOWGGGKCHGALLOCG SGRORDFALGERKTVAGAGGSGREGELLGENGAGNT LEGENGSGARTALTHENTARAGGARAFTHLASGOLEFALDER LEGENGTAGSSPCOKENTALTERSAGRASGTALLDEKRINNVEI G					AND POWIERROGHIVAISSIOGENSTOPPS AVAICULATION TO
2 2332 CGAGIVAGGALAVGKKKRVTLADLISSLAVILRILAGO DEFENMASRARKERKINS CGAGIVAGGALVALUTYAGRAGERTEVFGSPAFSILPINSPAGG TIVMDDCRSPILEVKKINGLGATTKITTSHERVESLTVPDTOGOTTA OXYSKKYGPRCSTALATOLIKONGVPEVKKTGGLGATTKITTSHERVESLTTVPDTOGOTTA OXYSKKYGPRCSTALATOLIKONGVPEVKKGTGEKRYPD QHEDGLEPEKKTRGLGATTKITTSHERVESLTTVPDTOGOTTA OXYSKKYGPRCSTALATOLIKONGVPEVVEVKGGTGEVAPPMAGE KKPSKRPAMDLKGQLOLIMAELKECREPTOTLODENQOLOPOLR KKPSKRPAMDLKGQLOLIMAELKECREPTOTLODENQOLOPOLR KKPSKRPAMDLKGQLOLIMAELKECREPTOTLODENQOLOPOLR KKPSKRPAMDLKGQLOLIMAELKECREPTOTLODENQOLOPOLR KKPSKRPAMDLKGQLOLIMAELKECREPTOTLODENQOLOPOLR KKPSKRPAMDLKGQLOLIMAELKECREPTOTLODENQOLOPOLR KKPSKRPAMDLKGQLOLIMAELKECREPTOTLODENQOLOPOLR KKPSKRPAMDLKGQLOLIMAELKECREPTOTLODENQOLOPOLR ALKELDSVORTHAGAPATPHORESTORYPPGGGODEVFESIA MINOSALDGYPYCLTFAVGOTGSGKTTTMEGGGGDDCLYESIA MINOSALDGYPYCLTFAVGOTGSGKTTTMEGGGGDDCLYESIA MINOSALDGYPYCLTFAVGOTGSGKTTTMEGGGGDDCLYEGIAR ALKELDSVAPUSCLGSGAKMFVNISPIGGGGDDLKGLTPK ALKELDSALGDGGRERILETCALANSISSTGLVIMALSINKES VPYRINSKLTYLLQNSLGGSAKMFVNISPIGGGSDLFILLDAGN AVARTAQNBERSSRSHSVFQLOISGERSSGGLGCAPLSLVDLAG SERLDPENJLGTAGSGNKWKTDDLCCVCVCVCVCVCVCVCVCVCVCVCVCVCVCVCVCVCV	- 1			ł	DCDRAEMEQYELEVIVISPGYIHTMI.SVMATTADGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
2 2332 CGGUVAAGAVULVYPASRAGERTRVPGSPAFSSLPINSPGACG TEVDMDPCRSPpLEVKGNIELKRPLIKAPSOLPLSGSRLKRRPD QREDGLEPEKKETRGLGATTKITISRPVSLTVTVPOTQGOTTA OKVSKKTGPRCSTATATGLKNOKKVPAPVPVKKSGTSGVPPMAGG KKPSKRPADILKGQLCDLINAELKREPPVSLTTVPQTGGOTTA OKVSKKTGPRCSTATATGLKNOKKVPAPVPVKKSGTSGVPPMAGG KKPSKRPADILKGQLCDLINAELKREPPVSLTTVPQDGOTTA OKVSKKTGPRCSTATATGLKNOKKVPAPVPVKKSGTSGVPPMAGG KKPSKRPADILKGQLCDLINAELKREPPTSLTDGENOGLGEKGRRLOTGEA ALGOSOLFVPCTFATGGTGSCKTFTMEGGGESPPTRL GERLSTTGEGLVOELKKOVELGEERRGLKGLGEEKGERLOTGEA ALSSSOAEVASLRQETVAQAALLTSPGGGGSPPPTRL SLSRSDERRGTLSGAPAPPTRHDFSDRVFPPGSGGDPDPTRL SLSRSDERRGTLSGAPAPPTRHDFSDRVFPPGSGGDPDPTRL ALGUSTAVGLSGGAGTTSPTASTGTGSCKTFTMEGGGGSPPPTRL ALGUSTAVGLSGGGGTTSPTASTTGTSGGGGSPPTRL OGGECFIRRAGPGSEELTVTNARYVPVSCEREVDALLHLARGTRK OGGECFIRRAGPGSEELTVTNARYVPVSCEREVDALLHLARGTRK OGGECFIRRAGPGSEELTVTNARYVPVSCEREVDALLHLARGTRK OGGECFIRRAGPGSEELTVTNARYVPSGERSKGLCCAPLSLVDLAG SEELDPGLALGPGREELLRFTOAINSSLSTLGLVINALENKESH VPFNSKLTYLLOSLGGSAKMLMFVSLPLEREVSSELINGLKT AVARTAGNESSSENSVFOLOSGGSSKOLTSPLSVESLUNGLENG SEELDPGLALGPGREELLRFTAGANSKNKTDPDLCVCVCVCVCVCVCVCVCVCVCVCVCVCVCVCVCVCVCV	- 1				TAGGREEVE VAQUIVLAAVGKKKDVT LADILIDGI AUVI DOT TOO
OREOGEPEKKET RGLGATTKITTSHERVESLTTVEDTOGGOTTA OKVSKKTGPRCSTATATGLKNOKEVPANPVOKKSGTSGVPMAGG KKPSKRFADRLKGGCDLINABLKRETROTLDGENGOLDDOLA KKPSKRFADRLKGGCDLINABLKRETROTLDGENGOLDDOLA DAQQVKALGTERTTLEGHLAKVQAQABGGOGELKALRACVLEL BERLSTGGELVGELKGKVEVELGEBERGLEMERREHDEL QELKGNITVPCZWRFVLFGEBTPPPGLLLFPSGGGFSDPFPRL SLSSSDERGGTLSGAPAPPTRHDESTDRVFPGSGGOPSDPFPRL SLSSSDERGGTLSGAPAPPTRHDESTDRVFPGSGGOPSDPFPRL SLSSSDERGGTLSGAPAPPTRHDESTDRVFPGSGGOPSDPFPRL ALRHLFSVAQELSGGGGTTSFVASVYETYMETVEDLLAGTTEKG QGECKEIRRAGFGSEELTVTNARYVPVSCEREVDALLHLARGNR AVARTAGNERSSREHSVYGLOISGESKNINGSLSVDLAG SERLDPGLALGGGERRHERTOAINSLSTLGLVINALSNIKSH VPFNSKLTYLLQNSLGGSAKHIMFVSLPERENVSSEINSLEYSH ASKVEPSULFGTAGSNRKWETDDLCVCVCVCVCVCVCVCVCVCVCVCV VPFNSKLTYLLGNSGGSAKHIMFVSLPERENVSSEINSLFF ASKVEPSULFGTAGSNRKWETDDLCVCVCVCVCVCVCVCVCVCVCVCV SAMYRYKGGRVAGGCTGMRACPGRISPLERERGGERAATTGTF TADRGDAAATDDPAAFGVQKHSMDGIRSIHGSGAERMATTGTF TADRGDAAATDDPAAFGVQKHSMDGIRSIHGSGAERMATTGTF TADRGDAAATDDPAAFGVQKHSMDGIRSIHGSGAERMATTGTF TADRGDAAATDDPAAFGVQKHSMDGIRSIHGSGAERMATTGTF TASTDFHSESGLFLFQASNSLFHCRDGGKNGFNVSGEDGCVSPMK PELIKTGCSGFRNDFRICFADPAFFSINSLLWANIETGEER RIJFCHGGLSNVLDDPKSAGWATFVIGEERDLFFTGVMCPTASW ESSELLKILILEVEDESEVEVINDSPRALEFRTDSVRYPPT GSKNPKIALKLAFFQTDSGGKIVSTOEKELVOPPSSLFPKVEVI ARGMTRDGKYAMAMPLDRPOQWLQLVLLDFPLLFTFSTEMEGGA SALCGSCPOECPAVCGVRGHORLDQCS FVFGLEFDOMEPAQFSATMSAPSEEEYARLWAGDEKELTOMAEV VRKNLEGLOTELKGLENVLUTNTOSENERLASVQRLIKE INGNVEI QRGRLRDDIKGYKFFERARLLDQYSELERENTSLKOVSVLRONO VEFFELKHEIKHEERTFKINGLAAFVGLAVELEKROUKLOFFELEUTER LKTREGONSLAKELSHMSINDSFYTSLLWSLLOFFSDAA EPPNDAAALVUNFFEGGIAKLPLDLNKTSTPKREGLAFPSPSLVS DLLSEMSLUTGTELKGLENGLAKLDLAFBRODAELLSVORGLIKE INGNVEI GERCHTTENLSAKRLDASKERGTALDNEKONGSHEDG DYFKUINIBELGTELKVQLOMMERKEKAGLLATLOPTOKOLDHROF SLSEQGEKVTRITENLSAKRLDASKERGTALDNEKDROSHEDG DYFKUININGPELLACKVRAVAAPAGERGLAKLAFLERREAD HABEKGRYBERGQALTEKVSLLEKARSROPRELLARLEKSLKKVS DVAGETGGSLSVAGDELVTSSELLAHLHCMCMNOMETPRRYML DYVREGGGGAGRTSPGGRTSPEARRSPILLPRGLAARGRA	ſ	5456	2	2222	DEFSORMANCERKSKNS
OREOGEPEKKET RGLGATTKITTSHERVESLTTVEDTOGGOTTA OKVSKKTGPRCSTATATGLKNOKEVPANPVOKKSGTSGVPMAGG KKPSKRFADRLKGGCDLINABLKRETROTLDGENGOLDDOLA KKPSKRFADRLKGGCDLINABLKRETROTLDGENGOLDDOLA DAQQVKALGTERTTLEGHLAKVQAQABGGOGELKALRACVLEL BERLSTGGELVGELKGKVEVELGEBERGLEMERREHDEL QELKGNITVPCZWRFVLFGEBTPPPGLLLFPSGGGFSDPFPRL SLSSSDERGGTLSGAPAPPTRHDESTDRVFPGSGGOPSDPFPRL SLSSSDERGGTLSGAPAPPTRHDESTDRVFPGSGGOPSDPFPRL SLSSSDERGGTLSGAPAPPTRHDESTDRVFPGSGGOPSDPFPRL ALRHLFSVAQELSGGGGTTSFVASVYETYMETVEDLLAGTTEKG QGECKEIRRAGFGSEELTVTNARYVPVSCEREVDALLHLARGNR AVARTAGNERSSREHSVYGLOISGESKNINGSLSVDLAG SERLDPGLALGGGERRHERTOAINSLSTLGLVINALSNIKSH VPFNSKLTYLLQNSLGGSAKHIMFVSLPERENVSSEINSLEYSH ASKVEPSULFGTAGSNRKWETDDLCVCVCVCVCVCVCVCVCVCVCVCV VPFNSKLTYLLGNSGGSAKHIMFVSLPERENVSSEINSLFF ASKVEPSULFGTAGSNRKWETDDLCVCVCVCVCVCVCVCVCVCVCVCV SAMYRYKGGRVAGGCTGMRACPGRISPLERERGGERAATTGTF TADRGDAAATDDPAAFGVQKHSMDGIRSIHGSGAERMATTGTF TADRGDAAATDDPAAFGVQKHSMDGIRSIHGSGAERMATTGTF TADRGDAAATDDPAAFGVQKHSMDGIRSIHGSGAERMATTGTF TADRGDAAATDDPAAFGVQKHSMDGIRSIHGSGAERMATTGTF TASTDFHSESGLFLFQASNSLFHCRDGGKNGFNVSGEDGCVSPMK PELIKTGCSGFRNDFRICFADPAFFSINSLLWANIETGEER RIJFCHGGLSNVLDDPKSAGWATFVIGEERDLFFTGVMCPTASW ESSELLKILILEVEDESEVEVINDSPRALEFRTDSVRYPPT GSKNPKIALKLAFFQTDSGGKIVSTOEKELVOPPSSLFPKVEVI ARGMTRDGKYAMAMPLDRPOQWLQLVLLDFPLLFTFSTEMEGGA SALCGSCPOECPAVCGVRGHORLDQCS FVFGLEFDOMEPAQFSATMSAPSEEEYARLWAGDEKELTOMAEV VRKNLEGLOTELKGLENVLUTNTOSENERLASVQRLIKE INGNVEI QRGRLRDDIKGYKFFERARLLDQYSELERENTSLKOVSVLRONO VEFFELKHEIKHEERTFKINGLAAFVGLAVELEKROUKLOFFELEUTER LKTREGONSLAKELSHMSINDSFYTSLLWSLLOFFSDAA EPPNDAAALVUNFFEGGIAKLPLDLNKTSTPKREGLAFPSPSLVS DLLSEMSLUTGTELKGLENGLAKLDLAFBRODAELLSVORGLIKE INGNVEI GERCHTTENLSAKRLDASKERGTALDNEKONGSHEDG DYFKUINIBELGTELKVQLOMMERKEKAGLLATLOPTOKOLDHROF SLSEQGEKVTRITENLSAKRLDASKERGTALDNEKDROSHEDG DYFKUININGPELLACKVRAVAAPAGERGLAKLAFLERREAD HABEKGRYBERGQALTEKVSLLEKARSROPRELLARLEKSLKKVS DVAGETGGSLSVAGDELVTSSELLAHLHCMCMNOMETPRRYML DYVREGGGGAGRTSPGGRTSPEARRSPILLPRGLAARGRA			}	2332	CGAGLVAAGAVLVLYPASRAGERTRVPGSPAPSSLPLHSPGACG
OKVSKKTOPRCSTALATGIKNOK PVPAVPUNKSSTSUVPMAGS KKPSKRAWDLKGQLCDLMAELKRCRERTOTLDQENQQLQDOLR KKPSKRAWDLKGQLCDLMAELKRCRERTOTLDQENQQLQDLOR DAQQUVKALGTETTTLEGHLAKOADEOGGQIKAULRACVUELL EERLSTQEGLVQELQKKQVELQEERRGLMSQLEEKERRLOTSEA ALSSSOAEVASLKQETVAQAALITEERERLHQLEMERRKHINQL QELKGNIRVPCRVRPVLGEPTPPPGLLLPFSGGGESDPPTRL SLSSDERROTLSGAPAPTRHDBSFDRVPPGSGGDEVFESIA MLVQSALDGYPVCIFAYQOTGSKTPTMEGGGGDDLGELIPR ALRRILFSVAQELSGGWTYSFVASYVELYMSTVRDLLATGTRKG GGGCEIRRAGPGSEELTVTMARTAVPVSCEKEVDALIHLARONR AVARTAQNBESSRISIVSVOLOISGEHSSRGLQCGAPLSLVDLAG SERLIDGELALGGGERERLEFTGANSLSLCTLGLVVDLAG SERLIDGELALGGGERERLEFTGANSLSLCTLGLVVDLAG SERLIDGELALGGGERERLEFTGANSLSLCTLGLVVDLAG SERLIDGELALGGGERERLEFTGANSLSLCTLGLVVDLAG SERLIDGELALGGGERERLEFTGANSLSLCTLGLVVDLAG SERLIDGELALGGGERERLEFTGANSLSLCTLGVVDLAGVRGS VPYWNSKLTYLLONSLCGSAMMLMFWISPLEENVSSELNSLRF ASKVERSVLTGTAGANRXWKTDASLSCTLGLVVDLAGVRGVENG SERLIDGELALGGERERLEFTGANSLSCTLGVVCVCVCVCVCVCVCVCVCVCVCVCVCVCVCVCVCVCV			í	1	I TEVENDEURS PLLEVKGNIELKRPI, TKAPSOLDT SCERT KRAPA
KKPSKRPAWDLKGK_CDLMABELKRCRERTGTLDQENQOLQDOLR DAQQUKALSTRETTLEGILAKVQAQABGGGGLKMLRACVLEI ERRLSTQEGIVOEQLKKQVELGEKERGLMSQLEKKERRLGTSEA ALSSSQAEVASLKQETVAQAALLTEREERLHGLEMERRRLHNQL GELKGNTRVPCRYRPVLPGEPTPPFGLLLPFSGPGGPSDPTRIA SLSSDBERGTLSGAPAPTHDESFDRVPPFGGGDEVPPEIA MLVQSALDGYPVCIFAYQGTGSGKTFTMEGGGGDPUFEIA MLVQSALDGYPVCIFAYQGTGSGKTFTMEGGGGDPUFEIA MLVQSALDGYPVCIFAYQGTGSGKTFTMEGGGGDPUFEIA ALRRIHSFVAQELSGGWTYSFVASYVEIYMETVTDLATGTRKG QGGCEIRRAGPGSEELTVTNARYVPVSCKEVDALLHLARQNR AVARATAQNERSSRSISVPQLOLGSESSRGLQCGAPLSLVDLAG SERLDPGLALGGEREBLRETQAINSSLSTLGLVTMALSNRESH VPVRNSKLTYLLJONSLGGSAKMLMFVNIJSHEBENVSBSLINSIR ASKVEPSVLFGTAGSNRKWKTDPDLCVCVCVCVCVCVCVCVV PVRNSKLTYLLJONSLGGSAKMLMFVNIJSHEBENVSBSLINSIR ASKVEPSVLFGTAGSNRKWKTDPDLCVCVCVCVCVCVCVCVV PVPRNSKLTYLLJONSLGGSAKMLMFVNIJSHEBENVSBSLINSIR ASKVEPSVLFGTAGSNRKWKTDRDLCVCVCVCVCVCVCVCVV PVPRNSKLTYLLJONSLGGSAKMLMFVNIJSHEBENVSBSLINSIR ASKVEPSVLFGTAGSNRKWKTOSBRGSFLINSIGAERMATTGTP TADRGBAAATDDPAARFCVQKHSVBGLRSILHGSRKVSGLIVNK APHDFQFFVQKTDESGPHSHRLYYLGNPYGSREAGSHAMTTGTP TADRGBAAATDDPAARFCVQKHSVBGLRSILHGSRKVSGLIVNK APHDFQFFVQKTDESGPHSHRLYYLGNPYGSRENGSLIVSETPKKV RKSALLLLSNKQMLDHPQAPFFSFINNSLWWANI ERIGERE FITFCHGGLSNKUDDPKSAGVAFTUGSEFDLEFURWCTFASW EGSEGLKTLRILYEEVDESEVEVIHVPSPALEERKTDSYRYPRT GKRPKIALKLARFQTDSQGKIVSTGLEVPFSSLFPKVEVI ARAGTTDGXVAMAMFLDRPQGWLQLVLLPPALFISTENBEGQA ASLCOSCPOECPAVCSVRGGHQRLDQCS FVPGIREFQWEFRQFSATTSASPEEEETARLVMEAQPEWIRREV KKLSHELAETTREKIQAAPYGLAVLEEKHOLKLQFFELBVDYEA IRSEMEGLKEAFGQAATTNIKKVASCTSPKRGLABLETL QRGHLARDIKYSKYRPRALLQDYSELEFENILQKVGSVLIRONQ VEFEGLKHEIKHEETTEYLNSQLEDAITLKEISRGLEBALET LKTERGQKNSLKRELSHYMSINDSFYTSHLHVSLDGLKSSDDAA BENNDJABALVNOFERINGGLAKLPGGSREELILQKALSSTLGRABAEQ VEFEGLKHEIKHEETTEYLNSQLEDAITLKEISRGLEEALET LKTERGQKNSLKRELSHYMSINDSFYTSHLHVSLDGLKSSDDAA BENNDJABALVNOFERINGGLAKLPGASKDOTALDNEKDROSHDG DYSEVOLINGPEILACKYNDAVARGERERGCLLATLQDTGKOLEHTRG SLSGOGKVTRITERHISALRRILAGALLATLQDTGKOLDKSSDDA DAGGGGSSPSPGSSLSJENDSPRAGELARLLEKELKVS DVAGETGGSLSVAQDEDUTTSEELLANLYHHVCMCNNFTANNVILL DYYREGGGGAGRTSFGGRTSP	- 1		}		ZHEDGILEFERRRIRGLGATTKTTTSHDDWDGTTTWDOWGGOWN
DAQQVRALCTETTLEGHLAXVQAQABGGGGELKMIRACVIEL EERLSTQEGIVQELQKKQVELQEERRGLMSQLEEKERRLOTSEA ALSSSQAEVASLKQETVAQAALTEERERLHGLEMERRIHNQL QELKGNIRVPCRVRPVLPGEPTPPPGLLLPFSGPGGPSDPPTRL SLSRSDERRGTLSGAPAPPTRHDESFDRVSPPGSGDEVFESIA MLVQSALDGYPVCIFAYGGTGSKIFTMEGGPGGPDELGIPR ALRHIFSVAQELSGGGWTISFVASYVEIYMETVRDLLATGTRKG QGGGCEIRRAGPGSEELTVTNATVYVSCKEVDALLHLARQNR AVARTAQNERSSRSISVFOLQISGEHSSRGLOCGAPLSLVDLAG SERLIDPGLALGPGERERLETQAINSLSTLGLVIMALSNRESH VPYRNSKLTYLLQNSLGSAGMUMFVNISPLEENVSSEINSLRF ASKVBESVLFGTAGSNRKWKTDDPLCVVCVCVCVCVCVCVCVV MSMYRVRGGRVAGGFIGWRAPPCFRAIX DDFVERRRYTTTCLVRSPPRVPVCGHACSWWGGSLDPLKGTPA LESSAELMRRVKVKLRLDKENTGSWRSSINSGAERMATTGTP TADRCDAAATDDPAARROVQKHSWDGLRSIHGGERKYSGLIVNK APHDFCFVOKTDESGPHSHLVYLGMPVGSRNSLLYSEIPKKV REALLLLSNKQMDJHFQATPHGVVSRSEBLLERERRLGYFGI TSYDFHSBSGLFLRQASNSLFHCRDGGKNGFWVSPGPGCVSPWK PLEIKTOCGSGPMDPKCTPADAPSFINNSDLWVANIETGERE RLIFCHGGLSNVLDDPKSAGVATFVIQEEFDRFTGYWGCTASW EGSEGLKTLRILVEEVDESEVEVIRVPSPALEERKTDSVRYPRT GKRPKIALKLAEPCTDSQOKTVSTQEKELOOPPSSLFPKVEVI ARAGMTRDGXVANAMFLDRPQOWLQLVLLPALFIPSTENEGOA ASLCQSCPGCEPAVGVAGGGGRGERGESELSIGSASKEQYY VRKVLELQTELKQLKRVLINTTOSENERLASVQELKEINQNVEI QRGRLERDDIKEYKFRARALLOVSELEEPNISLQKVEINIGNOUVEI QRGRLERDDIKEYKFRARALLOVSELEEPNISLGKALKSTURVEI DLISELNISETICKLKQOLMOMEREKAGLLATLODTOKOLHTRG SLENGGOKVNTRITERLSALRILONGTSTKKREGADAA EPNNDABALVNGFERGGGLAKLPLONKTSTKKREGADAA EPNNDABALVNGFERGGGLAKLPLONKTSTKKREGADAA EPNNDABALVNGFERGGGLAKLPLONKTSTKKREGADAAPPSDLVS DLLSELNISETICKLKQOLMOMEREKAGLLATLODTOKOLHTRG SLENGGOKVNTRITERLSALRILONGTSTKKREGADAAPPSDLVS DLLSELNISETICKLKQOLMOMEREKAGLLATLODTOKOLHTRG SLENGGOKVNTRITERLSALRILANGTHRANDRINGREDAA HABEKGRYBERGGGSKYGLIBLSALRILANGTHRANDRINGREPNINGL DVYENDINGPETLACKYNVAVARAGGELRECLLARLEKLKKVS DVAGETGGSLSVAQDELVTTSEELLANLYHHVSLOCHREPORVML DVYENGGGGAGRTSFGGRTSFELLANLYHHVSLCCHREPORM	-		-	1	VKVSKKIGPRCSTALATGLKNOKPVPAVDVOVCCTCCVPDVA CO
ERRESTOGGLVGELQKRQUSLGEERRRILMOLDEKERRILGTERA ALSSSQAEVASLRGETVAQAALLTEREERIHGLEMERRILHNQL QELKGNITRVECTVRPULPGETPP GALLLFPSGPGGPSDPFTRL SLSKSDERGTLSGAPAPPTRHDFS FDRUFPPGSGODEVFEIA MLVQSALDGYPVCIFAYGOTGSGKTFTMSGGGGGDPGLGGLIPR ALRHLFSVAQELSGQGWTTS FVASYVETVRETVRDLLATGTRKG QGGCEL RRAGPGSEELTVTNARYVPVSCEKEVDALLHLARQNR AVARTAQNERS SSRSHSVFGLSGEHSSRGLOCGAPISLVDLAG SERLDPGLALGPGEPBRLRETQAINSSLSTLGLVIMALSNKESH VPYMSKLTYLLONSLGGSAKMIKTVDPLCVCVCVCVCVCVVVV MYMYRVRGGRVAGGFIGWRAPCPRAIX 5457 2 1540 DDFVERRRITTCLVRSPPHVVCGHACSNNGGSLDPLKGTPA ASKVEPSVLFGTAQSNRWKTDPDLCVCVCVCVCVCVCVVV MYMYRVRGGRVAGGFIGWRAPCPRAIX ASKVEPSVLFGTAQSNRWKTDPDLCVCVCVCVCVCVVVV MYMYRVRGGRVAGGFIGWRAPCPRAIX ASKVEPSVLFGTAQSNRWKTDPDLCVCVCVCVCVCVVVV MYMYRVRGGRVAGGFIGWRAPCPRAIX ASKVEPSVLFGTAQSNRWKTDPDLCVCVCVCVCVCVVVV MYMYRVRGGRVAGGFIGWRAPCPRAIX ASKVEPSVLFGTAQSNRWKTDPDLCVCVCVCVCVCVVVV MYMYRVRGGRVAGGFIGWRAPCPRAIX ASKVEPSVLFGTAQSNRWKTDPDLCVCVCVCVCVCVVVV MYMYRVRGGNVAGAMACHOLKTGNRGSLDPLKGTPA ASKVEPSVLFGTAQSNSLFHVVCGHACSNNGGSLDPLKGTPA ASKVEPSVLFGTAQSNSLFHVVCGHACSNNGGSLDPLKGTPA ASKVEPSVLFGTAQSNSLFHVVCGHACSNNGGSLDPLKGTPA ASKVEPSVLFGTAQSNSLFHVVCGHACSNNGGSLDPLKGTPA ASKVEPSVLFGTAQSNSLFHVVKSTGSMRGSFINSGARMATTGTP TADRCDAAATDDPAAFFGVCHSWGGRSLDPLKGTPKVFGI TADRCDAAATDVGSGRMDFLKTGTAGRACHALTGRETPKVVFGI TSVDFHSESGLFLPQASNSLFHCRDGKNNGGWSPGGCVSPMK PLEIKTQCSGRMDPKCPADPAFFSFINSDLWVANIETGEER RITFCHQGLSNVLDDPKSAGQMATFVLGEEFDRTGWWCPTASW EGSECLKTLRILYEEVUDSEVEVIHVPSPALEERKTDSVRYPT ARAGTTRDGKVAMAMFLDPQOWLQLVLLPPALFTSTTSMEGOA EGSECLKTLRILYEEVUDSEVEVIHVPSPALEERKTDSVRYPT ARAGTTRDGKVAMAMFLDRPQOWLQLVLLPPALFTSTTSMEGOA ASLQSCPOECPAVCGVRGGHQRLDQCS FVPGLREERFQAATHRKVSQLEDAIRLKGLRPGDEAV KRLSHELAETTREIQAAEGGLAULBEKHOLKLQFFELEVDYEA IRSEMCLKEAFGQAHTHHKVTSQLEDAIRLKGLAPPGDEAV VEPGCLKHEIKRLEETEVINSGLEDAIRLKGLAPPGDAVA VEPGCLKHEIKRLEETEVINSGLEDAIRLKGLAPPGDAVA BENNDAAAALNDAAATVINGSFTSTHAGGGLAPPGLARF LKTERGCNSLRRGCHGGALGCKARGTALDBEKDRDHEDG DYSEVDINGPEILACKYHOVABAGGERREGLKARGTHEAREAQ HABEKGRYEAEGGATTERVSLLEKARGORGLLARLEKELKKVS DVAGETQGSLSVAGOLLVTFSELANLHHVCMCNNETPRNYML DYYREGGGGGGGRTSFEARGRAPILLPRINGLARLE	- 1		1	ļ	1 KRESKREAWDLKGULCDLNAELKRCREDTOTT DOUMOG OF CE
ALSSSQAEVASLRQETVAQAALLITEEERLHOEL QELGGNITVFCRVEPVLFGEPTEPPEGLLEFPESGGESDPPTRI ALSSSDRRGTTSGAPAPPTRHDFS DRWFPPGSGGDEVFEETA MLVQSALDGYPVCIFAYGQTGSGKTFTMEGGFGGPDCLFEGIPR ALRHLFSVAQELSGCWTTSFVASYVETVRETVRDLLATGTRKG QGGCETRRAGPGSSELTVTNARYVPVSCEKEVDALLHLARGNR AVARTAQNERSSRSHSVFQLOISGENSRGLGCGAPLSLVDLAG SERLDPGLALGGPGEFRELRETVNARYVVSCEKEVDALLHLARGNR AVARTAQNERSSRSHSVFQLOISGENSGLGCGAPLSLVDLAG SERLDPGLALGGPGEFRELRETVNARYVVSCEKEVDALLHLARGNR AVARTAQNERSSRSHSVFQLOISGENSGLGUTAMANSLSTELSTVALAG SERLDPGLALGGGENFURTVATURINGSTLGLVIMALSNKESH VPYRNSKLTYLLONSLGGSAKMLMFVNISPLEEWVSSLINSLRF ASKVEPSVLFGTAQSNRKWKTDPDLCVCVCVCVCVCVCVCVCVV MSMYRVGGRVAGGCFIGWRAPCPFAIX DDFVERRRWTRTTCLVRSPPHVPVGGHACSNNGGSLDPLKGTPA ASKVEPSVLFGTAQSNRKWKTLDDLKSTGSRSFSTINSEGAERMATTGTP TADRGDAAATDDPAARFOVQKHSWGSRSFSINSEGAERMATTGTP TADRGDAAATDDPAARFOVQKHSWGSRSFSINSEGAERMATTGTP TADRGDAAATDDPAARFOVQKHSWGSRSFSINSEGAERMATTGTP TASTDFHSSGGLFLFQASNSLFHCRDGGRNGFMVSPGGFGCVSPMK PLEIKTQCSGGRMPKICPADPAFFSINNSULWANIETGEER RLTFCHGGLSNVLDDPKSAGVATFVIOEEPDRFTGVWCCPTASW EGSECLKTLRILYEEVDESEVELVHSPALEERKTLGVFGI ARAGWTRDGKYAWMMFLDRPQOWLOLVLLPPALFIPSTENEGOA ASLCQSCPQECPAVCGNUGGHOLDCS FYPGLREFOWSPAQPSATMSAPSEEEFYARLWEAQPEWLRAEV KRLSHLALEFTREKIQAAEYGLAVLEEKHOLKLQFEELEVDYEA IRSEMECLKEAFGGAHTNHKVAADCESEEESLIGSASKEQY VRKVLELOTELKQLRNVLTINTOSENERLLSVAQELKEINQNVEI ORGELRDIKKYKFRERALLODYSSLEENNISLOKOVSVLRONO VEPECLKHEIKRILEEFTPYLNSQLEDAIRLSVAQELKEINQNVEI DLLSEINISSIGKLKQLRNVFEHGGLAKLPLDNKTSTPKKEGLAPSPSBLVS DLLSEINISSIGKLKQLKNOMMRREKRGLLATLODTOKOLEHTRG SLSEGGEKVTRITBINSALRRILDANSTPKKEGLAPPSPSLVS DLLSEINISSIGKLKQCHMMRREKRGLLATLODTOKOLEHTRG SLSEGGEKVTRITBINSALRRILDANSTPKKEGLAPPSPSLVS DLASEMISSIGKLKQCHMMRREKRGLLATLODTOKOLEHTRG SLSEGGEKVTRITBINSALRRILDANSTPKKEGLAPPSPSLVS DLASEMISSIGKLKQCHMMRREKRGLLATLODTOKOLEHTRG SLSEGGEKVTRITBINSALRRILDANSTPKKEGLAPPSPSLVS DVAGETGSLSVAQDELVFRISELANLWHHVCMNTTPRKKUL DYYREGGGGAGRTSPGAGRTSPEARGRSPILLPRGLARLEGRA			1	į	DAGGG TERT TERGHLARVOADAFOGOOFT VAIT DAGGG
GELKONIKVEGUNPAULGGETTPPGLILTPSGEGGEDPTRIA GELKONIKVEGUNPAULGGETTPPGLILTPSGEGGEDPTRIA SLSKSDERGTLSGAPAPPTHDESFFREVPPGSGODEVPEETA MLVQSALDGYPVCTPAVGTGSGKTPTMGGGGGDEVPEETA ALRILFSVAQELSGQWTYSFVASYVETYMEGGGGDEVLEGI PR ALRILFSVAQELSGQWTYSFVASYVETYMEGGGDEDLEGI PR ALRILFSVAQELSGQWTYSFVASYVETYMEGGGGDEDLEGI PR ALRILFSVAQELSGQWTYSFVASYVETYMEGGGDEDLEGI PR AVARTAQNERSSRSHSVYDLQISGEMSKGLQCCAPLSLVDLAG SERLDPGLALGPGERERLRETQAINSLSTLGLVIMALSNKESH VPYMNSKLTYLLONSLGSAKMIMFVNISSLETLGLVIMALSNKESH VPYMNSKLTYLLONSLGSAKMIMFVNISSLESTLGVIMALSNKESH ASKVEPSVLFGTAGNSKWKTDDPLCVCVCVCVCVCVCVCVCVCVCVCVCVCVCVCVCVCVCV	- 1		1		1 - FILES I VEGTO V VETOKKO V ELOPER RELIGIOR OF THE PROPERTY
SLSRSDERGTLSGAPAP PTRHDESFDRYPPGSGOPSPETRI SLSRSDERGTLSGAPAP PTRHDESFDRYPPGSGOPSPETRI MLVQSALDGYPVCTFAYQOTGSGKTYPPGSGOPSPETRI ALRHLSFVAQDELSGQGMTYTSPVASYVETYMETVRDLLATGTRKG QGGEGTRRAQDGSGGETTYSPVASYVETYMETVRDLLATGTRKG QGGEGTRRAQDGSGELTVTNARYVPVSCKEVDALLHLARQNR AVARTAQNERSSRSHSVFQLQISGHSRGLQCGAPLSLVDLAG SEBLDGGLALGPGERELRETQAINSLISTIGLVYMALSNKESH VPYRNSKLTYLLONSLGGSAKMLMFWISPLEENVSSELNSLRP ASKVEPSVLRGTAGNSRKWATDPDLCVCVCVCVCVCVCVCVCV MSMYRVBGGRVAGGCFIGWRAPCPRAIX DDFVERRRWTRTCLVRSPPHVPVCGHACSWNGGSLDPLKGTPA LIRSABRLMRKVKLKLRLDKENTGSWRSFSLNSEGARRMATTGTP TADRGDAAATDDPAARFOVQKHSWDGLRSITHGSRXYSGLIVNK APHDFGFVQKTDESGPHSRLYVLGMPYGSRENSLLYSEIPKCV RKSALLLLGWKQMLDHFQATPHHGVYSREELLIRERKRLGVFGI TSYDFHSESGLELFQASNSLFHCRDGKNGFWVSPGPGCVSPMK PLEIKTQCSGPMDPKICPADPAFFSFINNSLWVANIETIGER RLTFCHQGLSNVLDDPKSAGVATFV1QEEFDRFTGYWCPTASW EGSGCKTKLTLYBEVDGESVEVIHVPSPALEERKTDSYRYPRT GSKNPKLALKLAFFQTDSQGKIVSTQEKELVQPFSSLFPKVEYI ARAGWTRDGKYAWAMFLDRPQQWLGVLVLLPPALFIPSTENEGOA ASLOGSCPGCPAVGSVRGRHORLDOCS FVPGGREPQMEPAGPSATMSAPSGEEFVARLVMEAQPEWLRAEV KRLSHLALGTELKQLRNVLTHTYGSENBELASVAQELKEINGNVEI IRSEMEQLKEAFGQAHTMHKVAADGESREESLIQESASKQYY VRKVLELQTELKQLRNVLTHTYGSENBELASVAQELKEINGNVEI LKTRERGKNSLRKELSHYMSIDGVSELDERITSLQKGVSVLRQNO VEFFGLKHEIKRLEETTELMOASKERGTALDHKORSUFLOCH VEFFGLKHEIKRLEETTELMOASKERGTALDHKORSUFLOR VEFFGLKHEIKRLEETTELMOASKERGTALDHCKDFSDDAA EPNNDAEALVNGFEHGGLAKLPLDNKTSTPKEGLAPPSSPLVS DLLSELMISSICKLKQOLMOMERSKAGALATLODTKOLEETRG SLSSQOKVTRITTENLSALAKRLQASKERGTALDNEKDRAFEDG DYYEVDINGPEILACKXHVANAPAGGELREQLKALRSTHEAREAQ HAEEKGRYEAGGALTEKVSLLERASGORELLARLEKELKKVS DVAGETQGSLSVAQDELVTTSEELAMLYHMVCNNETTPRIVML DYYREGGGGGRTSPGGGTSPFRENGREPILLPKGLLAPPEAGRA DGGGSSSSPSPGSSLSPBLLEDPBERMYNILLALLALLALLALLALLALLALLALLALLALLALLALLA	- 1				AUGGGVASTROETVAOAALI,TEREEDI.UGI.EMERREET
MINOSALDGYPOTTAYOUGSKTFTMEGGGGDEVFEEIA MINOSALDGYPOTTAYOUGSKTFTMEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	ſ		i i		AND CONTRACTOR AREA TO PROPERTY AND A STREET OF THE PROPERTY AND A STREET
ALRILISVAÇCI SAÇGUTTS FVASYVE I YNETVROLLATOTRIC QGGCE I RRAGPGSEELTVINARY VP VSCEKEVDALLHTARONR AVARTAQNERS SRISVO TO ISGEMS SRICLOCGAPL SI LVDLAG SERLDPOLALGPGERERLETQA INSISTICLU VINALSNKESH VPYNNSKLTYLLONSLGGSAKMIMFVNI SPLEENVSESLNSLEP ASKVEPSVLFOTAGSINKKTDPDLCVCVCVCVCVCVCVCVCV MSMYVRGGRVAGGCF I GWRAPCPRAIK DDFVERRRWITTTCLVRSPPHVPVGHACSNWGGSLDPLKGTPA KLEASARLMRKVKKLRLDKENT GSWRS FSLNSEGAERMATTGTP TADRGDAAATDD PAARFOVQKHSWDGLRS I HIGSKXYSGLI VNK APHDFQFVQKTDESGPHSHLIVYLGMPYGSRENSLLYSEI PKKV RKEALLLLSWKQNLDHPQATPHHGVYSREELLLERKRLGVFGI TSYDFHSESGLIFLPQASNSLFHCROGKNGFWSPGPGCVSFMK PLEIKTQCSGPRMDPKICPADPAFFSF I INNSDLWANTETGER RLTFCHQGISNVLDDPKSAGVATFVI (DEFDRFTGYWRCPTASW EGSEGLKTLRILYEEVDESEVEVI VP SPALEERKTDSYRYPRT GSKNPKI ALKLAEFGYDSQKI VSTQEKELVQPFSSLFPKVEYI ARAGWTRDGKYAWAMFLDRPQOMLQULVLLPPALFI PSTENEEOA ASLOGSCPGCPSVCGVRGGHQRIDQCS FVPGGREPOMPAGPGSTANDASPSEEEFYARLVMEAQPEWLRAEV KRLSHELAETTREK (QAAEYGLAVLEEKHCLKUFFELEUV)FA IRSEMEQLKEAFGQAHTNIKKVAADGESRESSI (DESASKEQYY VRKVLELOTEIKKQLRWTINTSONENELASVAQBLKE INQNVEI QRGRLRDDIKEYKRPEARLLQDYSELEENISLQKOVSVLRQNQ VEPFGLKHEI KRLEEETEYLINS (LEDAI RLIKETSERQLEERALET LKTEREOKNSLEKELSHWIS INDSFYTSHIHVSLODGLKFSDDAA EPNNDAEALVNGFEIGGIAKL PLDNKTSTPKKEGLAP PSPSLVS DLLSELMI SEI OKLKQOLMQMEERERGGLATTLOTTKOOLEPHTRG SLSEQQEKVTRITTENLSALRILQASKEROTALDNEKDRISCHDAH EPNDAEALVNGFEIGGIAKL PLDNKTSTPKKEGLAP PSPSLVS DLLSELMI SEI OKLKQOLMQMEERERGGLATALTLOTTKOOLEPHTRG SLSEQQEKVTRITTENLSALRILQASKEROTALDNEKDRISCHDAH EPNDAEALVNGFEIGGIAKL PLDNKTSTPKKEGLAP PSPSLVS DLLSELMI SEI OKLKQOLMQMEERERGGLATALTLOTTKOOLEPHTRG SLSEQQEKVTRITTENLSALRILQASKEROTALDNEKDRISCHDAH EPNDAEALVNGFEIGGIAKL PLDNKTSTPKKEGLAP PSPSLVS DLYSEQGEGAGRTSPEARGRSPILLPKGLLARLEKELKKVS DVAGETQGSLSVAQDELVTFSEELLANLHHVCMCNNETTNEVML DYYREGGGGAGRTSPEGRSPILLPKGLLARERAGA HAERGRYEAFFGGAT TEARRAGRSPILLPKGLLARERAGA DGGTGDSSPSPGSSLEPSTEDBERDWIN VALLALLBREAGRA DGGTGDSSPSPGSSLEPSTEDBERDWIN VALLALLBREAGRA DGGTGDSSPSPGSSLEPSTEDBERDWIN VALLALLBREAGRA DGGTGDSSPSPGSSLEPSTEDBERDWIN VALLALLBREAGRA	-]]		DESASDERRGTLSGAPAPPTRHDFSFDRVFDDGGGGDEVDDGG
CGGCET RRAGPGSEELTVTNARYVPVSCEKEVDALHLARQUR AVARTAONERSERSHSVFOLOTSGERSSRGLOCGAPLSLVDLAG SERLDPGLALGPGERERLETQAINSSISTLGLVTMALSNKESH VPYRNSKLTYLLONSLGGSAKMLMFVN1SPLEENVSESINSLEP ASKVEPSVLFGTAGSNKRWKTDPDLCVCVCVCVCVCVCVVP MSMYRVRGGRVAGGGFTGWRAPCPPALIK DPFVERRRWTRTTCLVRSPPHVFVCGHACSWNGGSLDPLKGTPA LLRSAERLMRKVKLRLDKENTGSWRSFSLNSEGAERMATTGTP TADRGDAAATDDPAARFQVQKHSUBGLRSJTHGRKYSGLIVNK APHDFQFVQKTDESGPHSHRLYYLGMPYGSRENSLLYSEIPKKV RKRALLLLENKQMLDHFQATPHHOVYSREEBLLERRKRLGVFGI TSYDFHSESGLFLFQASNSLFHCRDGGKNGFWSFGFGCVSFMK PLEIKTQCSGPRMDPKLCPADPAFFSFINNSDLWVANIETGEER RITFCHGGISNVLDDPKSAGVATFVIQEFPDFTTYWWCPTASW EGSEGLKTLRILYEEVDESEVEVIHVPSPALEERKTDSYRYPRT GSKNPKIALKLAEFGTDSQGKIVSTQEKELVOPPSSLFPKVEYI ARAGMTRDGKYAMAMFLDRPQQMLGVLLLLPALFIPSTENEEQA ASLCOSCPGCPAVCGVRGGHQRLDQCS FVPGLREPQWEPAQPSATMSAPSEEEEYARLVMEAQPEWLRAEV KRLSHELAETTREKIQAAFYGLAVLEEKHOLKLQFEELEUVYEA LRSEMEQLKEAFGQAHTNIKKVAADGESREESIQESASKEQYY VRKVLELOTELKQLRWITUTOSENERLASVAQELKEINGNVEI QRGRLRDDIKEYKPREARLLQDYSELEEMISLQKOVSVLRQNO VEPEGLKHEIKRLEETETYLNSQLEDAIRLKEISERQLEEALET LKTEREOKNSLRKELSHWISIDSFYTSHLWYSLDGLKFSDDAA EPNNDAEALVNGFEIGGLAKLPLDNKTSTPKKEGLAPPSPSLVS DLLSELNISEIQKLKQOLMQMEERKAGLLATLQDTQKOLEHTRG SLESQEKVTRLTENLSALRILQASKERGTABLDRLEKELKKVS DVAGETQGSLSVAQDELVTFSEELANLATLADTGKOLEHTRG SLESQEKVTRLTTENLELQASKERGTABLREKRISHENG HAERGKYERGAGGAGRTSFEGRAGLARLLARLKELKELKKVS DVAGETQGSLSVAQDELVTFSEELANLHHVCMCNNETTNRVML DYYREGGGGGRRTSFEGRSTSFEARGRSPILLPKGLLAPEAGRA DGGTGDSSPSPGSSLESPLEDRERDMYNLYNLIALLARDEAU	ı		! [MINUSALDGIPVCIFAYGOTGSGKTFTMFGGDGCDDOX BOX TOD
AVARTAOMERSSRESVFOLOISGEHSSRELOCGAPLSLVDLAG SERLDPGLALGGERERLETOAINSSLSTIGLVIMALSNKESH VPYRNSKLTYLLQNSLGGSAKMEMFVBIISPLEEBVSESINSLEF ASKVEPSVLFGTAGSNRKWKTDDLCVCVCVCVCVCVCVCVCV PSSKLTYLLQNSLGGSAKMEMFVBIISPLEEBVSESINSLEF ASKVEPSVLFGTAGSNRKWKTDDLCVCVCVCVCVCVCVCVCVCV MSMYRVRGGRVAGGGFIGWRAPCPRAIX DDFVERRRWTRTTCLVRSPPHVPVCGHACSWNGGSLDPLKGTPA LLRSAERLMRKVKKLRLDKENTGSWRSFSLNSEGAERMATTGTP TADRGDAAATDDPAARFOVGKHSWDGLRSIIHGSRXYSGLIVNK APHDFGPVOKTDESSPHSHRLYYLGMPYGSRENSLIVSEIPKKV RKSALLLLSWKQMLDHFQATPHHGVYSREELLRERKRILGVFGI TSYDFHSESGLFLFQASNSLFHCRDGGKNGFMVSPGFGCVSPMK PLEIKTYGCSGPRMPKICPADPAFFSFINNSDLWVANIETGEER RLTFCRGGLSNVLDDPKSAGVATFVIQEEFDRFTGYWWCPTASW EGSELKTLRILVEEVDESEVVIHVPSPALEERKTDSYRYPRT GSKNPKIALKLABFOTDSOGRIVSTQEKELVOPFSSLFPKVEYI ARAGTTROKYAMAMFLDRPQOWLQLVLLPPALFIPSTENEEQA ASLCOSCPOECPAVCCVVRGORDLOCS FVPGLREPQWEPAQPSATMSAPSEEEEYARLVMEAQPEWLRAEV KRLSHELABTTREKIQAAEYGLAVLEEKHQLKLQFEELEVDYEA IRSEMEQLKEAFGAATTHKKVAALGEGSREESLIQESASKEOTY VRKVLELQTELKQLKRNULTHTOGSENERLASVAQELKEINGNVEI QRGRLRDDIKEVKFREARLLQDYSELLEENISLOKGVSVLRONQ VEFFGLKHEIKRLEBETEYLNSGLEDAIRLKEISERQLEEALET LKTEREOKNSLRKELSHYMSINDSFYTSHLHVSLOUKPSDDAA EPNNDAEALVNGFEHGGLAKIPLDNKTSTPKKEGLAPPSPSLVS DLLSELNISEICKLKOLMOMEREKKAGLLATLQDTCKOCLEHTEG SLSEQQEKVTRLTENLSALRRLQASKERGTALDDREKDRDSHEDG DYYEVDINGPEILACKYHVAZARGEELREQLKALRSTHEAREAQ HAREKGRYRAERGOALTEKVSLLEKASROORSELLARLERLEKKVS DVAGETQGSLSVAQDELVTFSEELARLYHVCMNETPNRVML DYYREGGGGAGRTSPGGRTSPERARGRSFILLAPLERLEKKVS DVAGETGGSLSVAQDELVTFSEELARLYHVCMNETPNRVML DYYREGGGGAGRTSPGGRTSPERARGRSPILLAPLERLEKKVS	- 1		1		ADMID SVAULLSGOGWTYS FVASYVET VNETVED I A MODELL
SERLDPGLALGPGERERLETQAINSSLSTIGLVIMALSNKESH VPYNNSKLTYLLONSSLSTIGLVIMALSNKESH VPYNNSKLTYLLONSSLSTIGLVIMALSNKESH ASKVEPSVLFGTAQSNRKWKTDDLCVCVCVCVCVCVCVCVCVV MSMYRVRGGRVAGGGFIGWRAPCPRAIX DFYERRWITSTCLVRSPPHVPVCGHACSWNGGSLDPLKGTPA LLRSAERLWRKVKKLRLDKENTGSWRSFSINSEGAERMATTGTP TADRGDAAATDDPAARFOVOKHSWDGLRSI IHGSRKYSGLIVNK APHDFOPVOKTDESGPHSHRLYYLGMPYGSRENSLLYSEIPKKV RKEALLLLSWKQMLDHFQATTPHGVVSREEELLRERKRLGVFGI TSYDFHSESGLFIFQASNSLFHCRDGGKNOFMVSPGPGCVSPMK PLEIKTOCSGPRMDPKICPADPAFFSFINNSDLWVANIETGEER RLIFCHQGLSNVLDDPKSAGVATFVIQEEFDRFTGYWWCPTASW ESSEGLKTLRILYEEVDESEVEVIHVSPALEERKTDSYRYPRT GSKNPKIALKLAEFQTDSQGKIVSTQEKELVQPFSSLFPKVEYI ARAGWTRDGKYAWAMFLDRPQOWLQLVLLPPALFIPSTENEEQA ASLCOSCPOECPAVCGVGGGGORLDOCS FVPGGREPQWEPAQPSATMSAPSEEEYARLVMEAQPEWLRAEV KRLSHELAETTREKIQAEVGLAVLEEKHQLKLQFFELEUDYEA IRSEMEQLKEAFGQAHTNHKKVAADGESREESLIQESASKEQYY VRKVLELQTELKQLRNVLTNTQSENERLASVAQELKEINONVEI QRGRLRDDIKEYKFREARLLQDYSELEEENISLQKQVSVLRQNQ VEFSGLKHEIKTRLEEETEYLNSQLEDAIRLKEISERQLEEALET LKTEREQKNSLRKELSHYMSINDSFYTSHLHYSLDGLKFSDDAA EPNNDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS DLLSEINISETGKLKQOLMOMEREKAGLATLQDTQKQLEHTRG SLSSQQEKVTRLTENLSALRRLQASKERQTALDNEKDRDSHEDO DYYEVDINGPEILACKYHVAVARAGGELREQLKALRSTHEAREAQ HAREKGRYEAREGQALTEKVSLEKARSTHEAREAQ DYAGETGGSLSVAQDELVTFSEELARLIYHHVCMNNETPNRVML DYYGEGGGGAGRTSPGGRTSPERARGRSPILLPRGLLAKKVS DVAGETGGSLSVAQDELVTFSEELARLIYHHVCMNNETPNRVML DGYGGGSSPGSSLISPSPGSLSPERARGRSPILLPRGLLARPEAGRA DGGTGDSSPGSSLSPSLSDPREBRYNYMLUL HIDDOWNEN	-		1		200ECETRIAGEGSEELTVINARVVDVGCERDVDALLITE ADAM
SERDIPGIALGYGERERICRTQAINSSLSTIGIVIMALSNKESH VPYNNSKLTYILOPLGGAAMINFWNISPLEENVSESLINSLRF ASKVEPSULFGTAQSNRKWKTDPDLCVCVCVCVCVCVCVCVCVCVCVCVCVCVCVCVCVCVCV			1 1		1 AVARIAQNERSSKSHSVFOLOISGEHSSDGI.OCCADI GI IDI A
ASKVEPSVLFGTAQSRKWKTDPULCVCVCVCVCVCVCVP ASKVEPSVLFGTAQSRKWKTDPULCVCVCVCVCVCVCVCVVP MSMYRVRGGRVAGGCFIGWRAPCPRAIX DDFVERRWIRTTCLVRSPPHVPVCHACSWNGGSLDPLKGTPA LIRSABELMRRVKKIRLDKENTGSWRSFSLNSEGAERMATTGTP TADRGDAAATDDPAARFQVQKHSWDGLRSI IHGSRXYSGLIVNK APHDFQFVQKTDESGPHSHRLYYLGMPYGSRENSLLYSEIPKKV RKEALLLLSWKQMLDHFQATPHHQVYSREEELLRERKRLGVFGI TSYDFHSESGLFLFQASNSLFHCRDGGKNGFWVSPGPGCVSPMK PLEIKTQCSGPRMDPKICPADPAFFSFINNSLWVANIETGEER RILFCHGGLSNVLDBYSAGVATFVIQEEFDRFTGYWWCPTASW EGSEGLKTLRILYEEVDESEVEVIHVPSPALEERKTDSYRPPRT GSKNPKIALKLAEFQTDSGGKIVSTQEKELVQPFSSLFPKVEYI ARAGWTRDGKYAWAMFLDRPQQWLQLVLLPPALFITSTENEEQA ASLCQSCPQECPAVCGVRGGHQRLDQCS FVPGLREPQWEPAQPSATMSAPSEEEFYARLVMEAQPEWLRAEV KRLSHELAETTREKIQAAEYGLAVLEEKHQLKLOFFEELEVDYEA IRSEMEQLKEAFGQAHTMHKKVAADGESREESLIGESASKEQYY VRKVLELOTELKQLKNVLTNTOSENERLASVAQELKEINQNVEI QRGRLRDDIKEYKFFEARLLQDYSELEERIISLQKQVSVLRQNO VEPEGLKHEIKRLEEFTEYLNSQLEDAIRLKEISERQLEEALET LKTEREQKNSLRKELSHYMSINDSFYTSHLHVSLDGLKFSDDAA EPNNDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS DLISELNISEIQKLKQOLMOMMEREKGGLLATLQOTQKOLEHRG SLEEQGEVTRITENLSALRRLQASKERQTALDNEKDRDSHEDG DYYEVDINGPEILACKYHVANAEAGELREQLKALRSTHEAREAQ HABEKGRYEABEQALTEKVSLLEKASRQDRELLARLEKELKKVS DVAGETGGSLSVAQDELVTFSEELANLYHHVCMCNNETPNRVML DYYREGQGGAGRTSFGGRTSFEARGRSSILLPKGLLAPLERGRA	1		1		SERBUPGUALGPGERERLRETOAINSSI,STICTIVINAL OVER THE
5457 2 1540 DFFARGER/BACKWRTDDLCVCVCVCVCVCVCVCVP MSMYRVRGGCVAGCETIGWRAPCPRAIX DDFVERRWRTTTCLVRSPPHVPVCGRACSWNGGSLDPLKGTPA LLRSAERLMRKVKKLRLDKENTGSWRSFSINSEGAERMATTGTP TADRGDAAATDDDAARFQVQKHSWDGLRSI IIGSRKYSGLIVNK APHDFQFVQKTDESGPHSHRLYYLGMPYGSRENSLIYSEIPKKV RKEALLLLSWKGMLDHFQATPHHGVYSREEELLRERKRLGVFGI TSYDFHSESGLFLFQASNSLFHCRDGKNGFMVSPGPGCVSPMK PLEIKTQCSGPRMDFKICPADPAFFSFINNSDLWWANIETGEER RLIFCHQGLSNVLDDPKSAGVATFVIQEEFDRFTGYWMCPTASW EGSEGLKLTRILYEEVDESEVEVIHVPSPALEERKTDSVRYPRT GSKNPKIALKLAEFQTDSQCKIVSTQEKELVQPFSSLFPKVEYI ARAGWTRDGKYAWAMFLDRPQQWLQLVLLDPALFIPSTENEEQA ASLCOSCPOECPAVCGVRGCHQRLDQCS FVPGIREPQWREPAQPSATMSAPSEEEYARLVMEAQPEWLRAEV KRLSHELAETTREKIQAAEYGLAVLEEKKQLKLQFEELBEVDYEA IRSEMEQLKEAFGQAHTNHKKVAADGESREESLIQESASKEQYY VRKVLELQTELKQLRNVLINTQSENERLASVAQBLKEINONVEI QRGRLRDDIKEYKFREARILQDYSELEEENISLQKQVSVLRQNQ VEFEGLKHEIKRLEETEYLNSQLEDAIRKEISERQLEEALET LKTEREQKNSLRKELSHYMSINDSFYTSHLHVSLDGLKFSDDAA EPNDDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS DLLSELNISEICKLKQOLMQMEREKAGLLATLQDTOKQLEHTRG SLSEQQEKVTRITENLSALRRLQASKERQTALDNEKDRDSHEDG DYSEVDINGPEILACKVHVAVAEAGELREQLKALRSTHEAREAQ HAEEKGRYEAEGQALTEKVSLLBKASRQDREGLLARLEKELKKVS DVAGETGGSLSVAQDELVTPSEELANLYHHVCMNNETPNRVML DYYREGQGGAGRTSPGGRTSPEARGRRSPILLPKGLLAPEAGRA DGGTGDSSPSPGSSLPSRLEBREDRNIVYNLIALHDEVHUNG	- [1		VFIRMS ADJULIONSLIGGSAKMI MEUNITEDI PENINGTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTO
2 1540 DDFVERRWIRTTCLVRSPPHVPVGHACSWNGGSLDFLKGTPA LIRSAERLMRKVKKLRLDKENTGSWRSFSLNSEGAERMATTGTP TADRGDAAATDDPAARFOVQKHSWDGLRSI HGSRXYSGLI VNK APHDFQFVQKTDESGPHSHRLYYLGMPYGSRENSLLYSEI PKKV RKEALLLLSWKQMLDHFQATPHHOVYSREEELLRERKRLGVFGI TSYDFHSESGLFLFQASNSLFHCRDGGKNGFMVSPGPGCVSPMK PLEIKTQCSGFMDPKICPADPAFFSFINNSDLWVANLETGEER RLTFCHQGLSNVLDDPRSAGVATFVIQEEFDRFTGYWCCPTASW ECSEGLKTLRILYEEVDESEVEUHVPSPALEERKTDSYRYPRT GSKNPKIALKLAEFQTDSQGKIVSTQEKELVQPFSSLFPKVEYI ARAGWTRDGKXAWAMFLDRPQQWLQLVLLPPALFIPSTENEEQA ASLCQSCPQECPAVCGVRGGHORLDQCS FVPGLREPQWEPAQPSATMSAPSEEEFYARLVMEAQPEWLRAEV KRLSHELAETTREKIQAEYGLAVLEEKHQLKLQFEELEVDYEA IRSEMEQLKEAFGQAHTNHKKVAADGESREESLIQESASKEQYY VRKVELLQTELKQLENVLITHTQSENERLLASVAQELKEINQNVEI QRGKLRDDIKKPKPREARLLQDYSELEEENISLQKOVSVLRQNQ VEFEGLKHEIKRLEEETEYLNSQLEDAIRKEISERQLEEALET LKTEREQKNSLRKELSHYMSINDSFYTSHLHYSLDGLKFSDDAA EPNNDAEALVNGFBEIGGLAKLPLDNKTSTPKKEGLAPPSPSLVS DLLSELNISEIQKLKQQLMQMEREKAGLATLQDTQKQLEHTRG SLSEQQEKVTRLTENLSALRRLQASKERQTALDNEKDRDSHEDG DYYEUDINGPEILACKYHVAVAREAGELRECLKARSTHEAREAQ HABEKGRYEAEGQALTEKVSLLEKASRQDRELLARLEKELKKVS DVAGETQGSLSVAQDELVTFSEELANLYHHVCMCNNETENRVML DYYREGQGGGRTSPGGRTSPEARGRSFILLPRGLLAPEAGRA	- }				NORVEESVERGTAQSNRKWKTDPDLCVCVCVCVCVCVCVCVCVCVCVCVCVCVCVCVCVCVCV
DDFVERRWIRTTCLVRSPPHVPVCGHACSWNGGSLDPLKGTPA LLRSAERLMRKVKKLRLDKENTGSWRSFSLINSGAERMATTGTP TADRGDAAATDDPAARFOVQKHSNDGLRSITHGSRXYSGLIVNK APHDFQFVQKTDESGPHSHRLYYLGMPYGSRENSLYSEIJPKKV RKEALLLLSWKQMLDHFQATPHHGVYSREEELLREKKRLGVFGI TSYDFHSESGLFLFQASNSLFHCRDGGKNGFMVSPGPGCVSPMK RLTFCHGGLSNVLDDPKSAGVATFVIQEEFDRFTGYWWCPTASW EGSGLKTLRILYEEVDESEVEVIHVPSPALEERKTDSYRYPRT GSKNPKIALKLAEFQTDSQGKIVSTQEKELVOPFSSLFPKVEYI ARAGWTRDGKVAMAMFLDRPQQWLQLVLLPPALFIPSTENEEQA ASLCQSCPDECPAVCSVRGGHQRLDQCS FVPGGLREPQMEPAQPSATMSAPSEEEEYARLVMEAQPEWLRAEV KRLSHELAETTREKIQAAEYGLAVLEEKHOLKLQFEELEVDYEA IRSEMEQLKEAFGQAHTNHKKVAADGESREESLIQESASKEQYY VRKVLELQTELKQLRNVLTNTQSENERLASVQELKEINQNVEI QRGRLRDDIKEYKFREARLLQDYSELBEENISLQKOVSVLRQNQ VEFFGLKHEIKRLEEETEYLNSQLEDAIRLKEISERQLEEALET LKTEREQKNSLRKELSHYMSINDSFTTSHLHVSLDGLKFSDDAA EPNNDAEAIVNGFEHGGLAKIPLDNKTSTPKKEGLAPPSPSLVS DLLSELNISEIQKLKQQLMQMEREKAGLLATLQDTQKOLEHTRG SLSEQQEKVTRLTENLSALRRLQAKERGTALDNEKDRDSHEDG DYYEVDINOPEILACKYHVAVAEAGELREQLKALRSTHEAREAQ HAEEKGRYEAEGQALTEKVSLLEKASROORELLARLEKELKKVS DVAGETQGSLSVAQDELVTFSEELANLYHHVCMCNNETENRVML DYYREGQGGAGRTSPGGRTSPEARGRSPILLPRGLLAPEAGRA DGGTGDSSPSPSGSLPSPLSDPBERDWIN VAN LALLBONWIME	\vdash	5457			"DITE VEGGE VAGGE L'EWRAPEPRA - V
TADRGDAAATDDPAARFOVQKHSWDGLRSI HGSRKYSGLIVNK APHDFQFVQKTDESGPHSHRLYYLGMPYGSRENSLLYSEIPKKV RKEALLLLSWKQMLDHFQATPHHGVYSREEELLRERKRLGVFGI TSYDFHSESGLFLFQASNSLFHCRDGGKNGFWVSPGFGCVSPMK PLEIKTQCSGFRMDPKICPADPAFFSFINNSDLWVANIETGEER RLTFCHQGLSNVLDDPKSAGVATFVIQEEFDRFTGYWWCPTASW EGSEGLKTLRILYEVDESEVEVIHVPSPALEERKTDSYRYPRT GSKNPKIALKLAEFQTDSQGKIVSTQEKELVQPFSSLFPKVEYI ARAGWTRDGKYAWAMFLDRPQQWLQLVLLPPALFIPSTENEEQA ASLCQSCPQECPAVCGVRGGHQRLDQCS FVPGLREPQWBPAQPSATMSAPSEEEEYARLVMEAQPEWLRAEV KRLSHELAETTREKIQAAEYGLAVLEEKHQLKLQFFEELEVDYEA IRSEMEQLKEAFGQAHTNHKKVAADGESREESLIQESASKEQYY VRKVLELQTELKQLRNVLINTOSENERLASVAQELKEINQNWEI QRGRLRDDIKEYKFREARLLQDYSELEEENISLQKQVSVLRQNQ VEFEGLKHEIKRLEESTEYLNSQLEDAIRLKEISERQLEEALET LKTEREQKNSLRKELSHYMSINDSFYTSHLHVSLDGLKFSDDAA EPNNDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS DLLSELNISEICKLKQOLMQMEREKAGLLATLQDTQKQLEHTRG SLSEQQEKVTRLTENLSALRRLQASKERQTALDNEKDRDSHEDG DYYEVDINOPETLACKYHVAVAEAGELREQLKALRSTHEAREAQ HAEEKGRYEAEGGALTEKVSLLEKASRQDRELLARLEKELKKVS DVAGETQGSLSVAQDELVTFSEELANLYHHVCMCNNETPNRVML DYYREGQGGAGRTSPGRTSPGARGRSFILLPKGLARPAGARA	1	,	-	1540	DDFVERRRWTRTTCLVRSPPHVPVCGHACSWNCCGLDDLVGTG
APHDFQFVQKTDESGPHSHLYYLGMPYGSRENSLLYSEIPKW RKEALLLLSWKQMLDHFQATPHHOVYSREEEILLRERKRIGVFGI TSYDFHSESGIFLFQASNSLFHCRDGGKNGFMVSPGPGCVSPMK PLEIKTQCSGPMDPKICPADPAFFSFINNSDLWVANIETGEER RLTFCHQGLSNVLDDPKSAGWATFVIQEEFDRFTGYWWCPTASW EGSEGLKTLRILYEEVDESEVEVIHVPSPALEERKTDSYRYPRT GSKNPKLALKLAEFQTDSQGKIVSTQEKELVQPFSSLFPKVEYI ARAGWTRDGKYAWAMFLDRPQQWLQLVLLPPALFIPSTENEEQA ASLCQSCPQECPAVCGVRGGHQRLDQCS FVPGLREPQWEPAQPSATMSAPSEEEEYARLVMEAQPEWLRAEV KRLSHELAETTREKIQAAEYGLAVLEEKHQLKLQFEELEVDYEA IRSEMEQLKEAFGQAHTNHKKVAADGESREESLIGEASKEQYY VRKVLELQTELKQLRNVLTNTOSENERLASVAQBLKEINQNVEI QRGRIRDDIKEYKFREARLLQDYSELEENISLQKQVSVLRQNQ VEFEGLKHEIKRLEEETEYLNSQLEDAIRLKEISERQLEEALET LKKTEREQKNEJKKELSHYMSINDSFYTSHLHVSLDGLKFSDDAA EPNNDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS DLLSELNISEIQKLKQOLMQMEREKAGLLATLQDTQKQLEHTRG SLSEQCEKVTRLTEBNSALRRLQASKERQTALDNEKDRDSHEDG DYYEVDINGPEILACKYHVAVAAEAGELREQLKALRSTHEAREAQ HAEEKGRYEAEGQALTEKVSLLEKASRQDRELLARLEKELKKVS DVAGETQGSLSVAQDELVTFSEELANLYHHVCMCNNETPNRVML DYYREGGGGAGRTSPEGRTSPEARGRSPILLPKGLLARLEKELKKVS DVAGETQGSLSVAQDELVTFSEELANLYHHVCMCNNETPNRVML DYYREGGGGAGRTSPEGRTSPEARGRSPILLPKGLLAPEAGRA	İ				I DERSAERLMRKVKKLRLDKENTGSWRSFSINSEGAEDMARDS I
REALLLISWKQMLDHFQATPHHGVYSREELLRERKRLIGVFGI TSYDFHSESGLFLFQASNSLFHCRDGGKNGFMVSPGPGCVSPMK PLEIKTQCSGPRMDPKICPADPAFFSFINNSDLWVANIETGEER RLTFCHQGLSNVLDDPKSAGVATFVIQEEFDRFTGYWWCPTASW ESSEGLKTLRILYEEVDESEVEVIHVPSPALEERKTDSYRYPRT GSKNPKIALKLAEFQTDSQGKIVSTQEKELVQPFSSLFPKVEYI ARAGWTRDGKYAWAMFLDRPQQWLQLVLLPPALFIPSTENEEQA ASLCQSCPQECPAVCGVRGGHQRLDQCS FVPGLREPQWEPAQPSATMSAPSEEEFYARLVMEAQPEWLRAEV KRLSHELAETTREKIQAAEYGLAVLEEKHQLKLQFEELEVDYEA IRSEMEQLKEAFGQAHTNHKKVAADGESREESLIQESASKEQYY VRKVLELQTELKQLRNVLTNTQSENERLASVAQELKEINQNVEI QRGRLRDDIKKYKFREARLLQDYSELEEENISLQKQVSVLRQNQ VEFEGLKHEIKRLEEETEYLNSQLEDAIRLKEISERQLEBALET LKTEREQKNSLRKELSHYMSINDSFYTSHLHVSLDGLKFSDDAA EPNNDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS DLLSELNISEIQKLKQOLMQMEREKAGLLATLQDTQKQLEHTRG SLESQQEKVTRLTENLSALRRLQASKERQTALDNEKDRDSHEDG DYYEVDINGPEILACKYHVAVAEAGELREQLKALRSTHEAREAQ HAEEKGRYEAEGQALTEKVSLLEKASRQDRELLARLEKELKKVS DVAGETQGSLSVAQDELVTFSEELANLYHHVCMCNNETPNRVML DYYREGGGGAGRTSPGGRTSPEARGRRSPTLLPKGLLAPEAGRA DYYREGGGGAGRTSPGGRTSPEARGRRSPTLLPKGLLAPEAGRA	-		1		I ADAGDAAA TUDPAARFOVOKHSWIGI. PGTTUGGDYVGGI TIDIG
TSYDFHSESGLFLFQASNSLFHCRDGKNGFMYSPGPGCVSPMK PLEIKTQCSGPRMDPKTCPADPAFFSFINNSDLWANIETGEER RLTFCHQGLSNVLDDPKSAGVATFVIQEEFDRFTGYWWCPTASW EGSEGLKTLRILYEEVDESEVEVIHVPSPALEERKTDSYRYPRT GSKNPKIALKLAEFQTDSQGKIVSTQEKELVQPFSSLFPKVEYI ARAGWTRDGKYAWAMFLDRPQQWLQLVLLPPALFIPSTENEEQA ASLCQSCPQECPAVCGVRGGHQRLDQCS FVPGLREPQWEPAQPSATMSAPSEEEEYARLVMEAQPEWLRAEV KRLSHELAETTREKIQAAEYGLAVLEEKHQLKLQFEELEVDYEA IRSEMEQLKEAFGQAHTNHKKVAADGESREESLIQESASKEQYY VRKVLELQTELKQLRNVLTNTQSENRELASVAQELKEINQNVEI QRGRLRDDIKEYKPREARLLQDYSELEEENISLQKQVSVLRQNQ VEFEGLKHEIKRLEEETEYLNSQLEDAIRLKEISERQLEEALET LKTEREQKNSLRKELSHYMSINDSFYTSHLHVSLDGLKFSDDAA EPNNDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS DLLSELNISEIQKLKQOLMQMEREKAGLLATLQDTQKQLEHTRG SLSEQQEKVTRLTENLSALRRLQASKERQTALDNEKDRBHEDG DYYEVDINGPEILACKYHVAVAEAGERERQLKALRSTHEAREAQ HAEEKGRYEAEGQALTEKVSLLEKASRQDRELLARLEKELKKVS DVAGETQGSLSVAQDELVTFSEELANLYHHVCMCNNETPNRVML DYYREGQGGAGRTSPEGRTSPEARGRRSPILLBPGLLAPEAGRA DGGTGDSSFSPGSSLPSPLSDPRPERMYNIN LALLBOUNNE	1				AFRICA OF VOKTDESGPHSHRI.VYT.GMPVGGDPNCT TVGDTDTTT
PLEIKTQCSGPRMDPKICPADPAFFSFINNSDLWVANIETGEER RLTFCHQGLSNVLDDPKSAGVATTVIQEEFDRFTGYWWCPTASW EGSEGLKTLRILYEEVDESEVEVIHVPSPALEERKTDSVRYPRT GSKNPKIALKLAEFQTDSQGKIVSTQEKELVQPFSSLFPKVEYI ARAGWTRDGKYAWAMFLDRPQQWLQVLLDPPALFIPSTENEEQA ASLQQSCPQECPAVCGVRGGHQRLDQCS FVPGLREPQWEPAQPSATMSAPSEEEEVARLVMEAQPEWLRAEV KRLSHELAETTREKIQAAEYGLAVLEEKHQLKLQFEELEVDYEA IRSEMEQLKEAFGQAHINHKKVAADGESREESLIQESASKEQYY VRKVLELQTELKQLRNVLITTQSENERLASVAQELKEINQNVEI QRGRLRDDIKEYKFREARLLQDYSELEEENISLQKQVSVLRQNQ VEPEGLKHEIKRLEEETEYLNSQLEDAIRLKEISERQLEEALET LKTEREQKNSLRKELSHYMSINDSFYTSHLHVSLDGLKFSDDAA EPNNDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS DLLSELNISEIQKLKQQLMQMEREKAGLLATLQDTOKQLEHTRG SLSEQQEKVTRITENLSALRRLQASKERQTALDNEKDRDSHEDG DYYEVDINGPEILACKYHVAVAEAGELREQLKALRSTHEAREAQ HAEEKGRYEAEGQALTEKVSLLEKASRQDRELLARLEKELKKVS DVAGETQGSLSVAQDELVTFSEELANLYHHVCMCNNETPNRVML DYYREGQGGAGRTSPGGRTSPEARRRSPILLPKGLLAPEAGRA DGGTGDSSSSPGSSLPSPLEDBRREDWNIYNLIALIDDOLWING	1	- 1	1	i	REALDED SWAQMEDHFOATPHHGVYSREEELL PERVELOUNGE
RLIFCHQGLSNVLDDPKSAGVATFVIQEEFDRFTGYWCCPTASW EGSEGLKTLRILYEEVDESEVEVIHVPSPALEERKTDSYRYPRT GSKNPKIALKLAEFQTDSQGKIVSTQEKELVQPFSSLFPKVEYI ARAGWTRDGKYAWAMFLDRPQQWLQLVLLPPALFIPSTENEEQA ASLCQSCPQECPAVCGVRGGHQRLDQCS FVPGLREPQWEPAQPSATMSAPSEEEEYARLVMEAQPEWLRAEV KRLSHELAETTREKIQAAEYGLAVLEEKHQLKLQFEELEVDYEA IRSEMEQLKEAFGQAHTNHKKVAADGESREESLIQESASKEQYY VRKVLELQTELKQLRNVLTNTQSENERLASVAQBLKEINQOVEI QRGRLRDDIKEYKFREARLLQDYSELEEENISLQKQVSVLRQNQ VEFEGLKHEIKRLEEETEYLNSQLEDAIRLKEISERQLEEALET LKTEREQKNSLRKELSHYMSINDSFYTSHLHVSLDGLKFSDDAA EPNNDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS DLLSELNISEIQKLKQQLMQMEREKAGLLATLQDTQKQLEHTRG SLSEQQEKVTRLTENLSALRRLQASKERQTALDNEKDRDSHEDG DYYEVDINGPEILACKYHVAVAEAGELREQLKALRSTHEAREAQ HAEEKGRYEAEGQALTEKVSLLEKASRQDRELLARLEKELKKVS DVAGETQGSLSVAQDELVTFSEELANLYHHVCMCNNETPNRVML DYYREGQGGAGRTSPEGRTSPEARGRRSPILLPKGLLAPEAGRA DGGTGDSSPSPGSSLPSPLSDPRREDMYNULLILIDDOWNUNG	1	J	1		101DF NSESGLE LE QASNSLEHCRDGGKNGFM/GDCDCG/GDCG
EGSEGLKTLRILYEEVDESEVEVIHVPSPALEERKTDSYRYPRT GSKNPKIALKLAEFQTDSQGKIVSTQEKELVQPFSSLFPKVEYI ARAGWTRDGKYAWAMFLDRPQQWLQLVLLPPALFIPSTENEEQA ASLCQSCPQECPAVCGVRGGHQRLDQCS FVPGLREFQWEPAQPSATMSAPSEEEEYARLVMEAQPEWLRAEV KRLSHELAETTREKIQAAEYGLAVLEEKHQLKLQFEELEVDYEA IRSEMEQLKEAFGQAHTNHKKVAADGESREESLIQESASKEQYY VRKVLELQTELKQLRNVLTNTQSENERLASVAQELKEINQNVEI QRGRLRDDIKEYKFREARLLQDYSELEEENISLQKQVSVLRQNQ VEFEGLKHEIKRLEEETEYLNSQLEDAIRLKEISERQLEEALET LKTEREQKNSLRKELSHYMSINDSFYTSHLHVSLDGLKFSDDAA EPNNDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS DLLSELNISEIQKLKQQLMQMEREKAGLLATLQDTQKQLEHTRG SLSEQQEKVTRLTENLSALRRLQASKERQTALDNEKDRDSHEDG DYYEVDINGPEILACKYHVAVAEAGELREQLKALRSTHEAREAQ HAEEKGRYEAEGQALTEKVSLLEKASRQDRELLARLEKELKKVS DVAGETQGSLSVAQDELVTFSEELANLYHHVCMCNNETPNRVML DYYREGQGGAGRTSPGGRTSPEARGRRSPILLPRGLLAPEAGRA DGGTGDSSPSPGSSLPSPLSDPRREDMNIVNLIALHDENDENLIC		1	- 1	í	FDEINIQUESCERMUPKICPADPAFFSFTNNSDLWUNNIERGESS
GSKPKITERLEYDESEVEVIHVPSPALEERKTDSYRYPRT GSKNPKIALKLAEFQTDSQGKIVSTQEKELVQPFSSLFPKVEYI ARAGWTRDGKYAWAMFLDRPQQWLQLVLLPPALFIPSTENEEQA ASLCQSCPQECPAVCGVRGGHQRLDQCS FVPGLREPQWEPAQPSATMSAPSEEEYARLVMEAQPEWLRAEV KRLSHELAETTREKIQAAEYGLAVLEEKHQLKLQFEELEVDYEA IRSEMEQLKEAFGQAHTNHKKVAADGESREESLIQESASKEQYY VRKVLELQTELKQLRNVLTNTQSENERLASVAQELKEINQNVEI QRGRLRDDIKEYKFEARLLQDYSELEENISLQKQVSVLRQNQ VEFFGLKHEIKRLEEETEYLNSQLEDAIRLKEISERQLEEALET LKTEREQKNSLRKELSHYMSINDSFYTSHLHVSLDGLKFSDDAA EPNNDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS DLLSELNISEIQKLKQQLMQMEREKAGLLATLQDTQKQLEHTRG SLSEQQEKVTRLTENLSALRRLQASKERQTALDNEKDRDSHEDG DYYEVDINGPEILACKYHVAVAEAGELREQLKALRSTHEAREAQ HAEEKGRYFAEGQALTEKVSLLEKASRQDRELLARLEKELKKVS DVAGETQGSLSVAQDELVTFSEELANLYHHVCMCNNETPNRVML DYYREGQGGAGRTSPGGRTSPEARGRRSPILLPKGLLAPEAGRA DGGTGDSSPSPGSSLPSPLSDPRREDWNIVNLALIALDEAGRA	1	,	ţ	i	KDIF CROGLONVLDDDPKSAGVATEVIOEREDDEMCVWJODEN OF
5458 6642 4022 FVPGLREPQWEPAQPSATMSAPSEEEYARIVMEAQPEWLRAEV KRLSHELAETTREKIQAAEYGLAVLEEKHOLKLQFEELEVDYEA IRSEMEQLKEAFGQAHTNHKKVAADGESREESLIQESASKEQYY VRKVLELQTELKQLRNVLTNTQSENERLASVAQELKEINQNVEI QRGRLRDDIKEYKFREARLLQDYSELEEENISLQKQVSVLRQNQ VEFEGLKHEIKRLEEETEYLNSQLEDAIRLKEISERQLEEALET LKTEREQKNSLRKELSHYMSINDSFYTSHLHVSLDGLKFSDDAA EPNNDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS DLLSELNISEIQKLKQOLMQMEREKAGLLATLQDTQKQLEHTRG SLSEQQEKVTRLTENLSALRRLQASKERQTALDNEKDRDSHEDG DYYEVDINGPEILACKYHVAVAEAGELREQLKALRSTHEAREAQ HAEEKGRYFAEGQALTEKVSLLEKASRQDRELLARLEKELKKVS DVAGETQGSLSVAQDELVTFSEELANLYHHVCMCNNETPNRVML DYYREGGGGAGRTSPGGRTSPEARGRRSPILLPRGLLAPEAGRA DGGTGDSSPSPGSSLPSPLSDPRREDMNIVNLIALIBLEDGUNG		ł	1	ſ	EGGEGERICKILIEEVDESEVEVIHVDQDAI FEDVEDOVENESE
ASLCQSCPQECPAVCGVRGGHQRLDQCS FVPGLREPQWEPAQPSATMSAPSEEEYARLVMEAQPEWLRAEV KRLSHELAETTREKIQAAEYGLAVLEEKHQLKLQFEELEVDYEA IRSEMEQLKEAFGQAHTNHKKVAADGESREESLIQESASKEQYY VRKVLELQTELKQLRNVLTNTQSENERLASVAQELKEINQNVEI QRGRLRDDIKEYKFREARLLQDYSELEEENISLQKQVSVLRQNQ VEFEGLKHEIKRLEEETEYLNSQLEDAIRLKEISERQLEEALET LKTEREQKNSLRKELSHYMSINDSFYTSHLHVSLDGLKFSDDAA EPNNDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS DLLSELNISEIQKLKQQLMQMEREKAGLLATLQDTQKQLEHTRG SLSEQQEKVTRLTENLSALRRLQASKERQTALDNEKDRDSHEDG DYYEVDINGPEILACKYHVAVAEAGELREQLKALRSTHEAREAQ HAEEKGRYEAEGQALTEKVSLLEKASRQDRELLARLEKELKKVS DVAGETQGSLSVAQDELVTFSEELANLYHHVCMCNNETPNRVML DYYREGGGGAGRTSPGGRTSPEARGRRSPILLPKGLLAPEAGRA DGGTGDSSPSPGSSLPSPLSDPRREDNNIVNLLALHDENDEN		1	1	•	GSIGN FRIADKLAEFOTDSOGKTVSTOFKFI MODERAL PRIMERS
5458 6642 4022 FVPGLREPQWEPAQPSATMSAPSEEEYARLVMEAQPEWLRAEV KRLSHELAETTREKIQAAEYGLAVLEEKHQLKLQFEELEVDYEA IRSEMEQLKEAFGQAHTNHKKVAADGESREESLIQESASKEQYY VRKVLELQTELKQLRNVLTNTQSENERLASVAQELKEINQNVEI QRGRLRDDIKEYKFREARLLQDYSELEEENISLQKQVSVLRONQ VEPEGLKHEIKRLEEETEYLNSQLEDAIRLKEISERQLEEALET LKTEREQKNSLRKELSHYMSINDSFYTSHLHVSLDGLKFSDDAA EPNNDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS DLLSELNISEIQKLKQOLMQMEREKAGLLATLQDTQKQLEHTRG SLSEQQEKVTRLTENLSALRRLQASKERQTALDNEKDRDSHEDG DYYEVDINGPEILACKYHVAVAEAGELREQLKALRSTHEAREAQ HAEEKGRYEAEGQALTEKVSLLEKASRQDRELLARLEKELKKVS DVAGETQGSLSVAQDELVTFSEELANLYHHVCMCNNETPNRVML DYYREGGGGAGRTSPGGRTSPEARGRRSPILLPRGLLAPEAGRA DGGTGDSSPSPGSSLPSPLSDPRREDWNIVNLIALHEDENHUNG]		ĺ	ļ	ANGULTADGRIAWAME LORPOOWIGI, VI, I, DDAT, ET DETENDED .
FVPGLREPQWEPAQPSATMSAPSEEEEYARLVMEAQPEWLRAEV KRLSHELAETTREKIQAAEYGLAVLEEKHQLKLQFEELEVDYEA IRSEMEQLKEAFGQAHTNHKKVAADGESREESLIQESASKEQYY VRKVLELQTELKQLRNVLTNTQSENERLLASVAQELKEINQNVEI QRGRLRDDIKEYKFREARLLQDYSELEEENISLQKQVSVLRQNQ VEFECLKHEIKRLEEETEYLNSQLEDAIRLKEISERQLEEALET LKTEREQKNSLRKELSHYMSINDSFYTSHLHVSLDGLKFSDDAA EPNNDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS DLLSELNISEIQKLKQQLMQMEREKAGLLATLQDTQKQLEHTRG SLSEQQEKVTRLTENLSALRRLQASKERQTALDNEKDRDSHEDG DYYEVDINGPEILACKYHVAVAEAGELREQLKALRSTHEAREAQ HAEEKGRYEAEGQALTEKVSLLEKASRQDRELLARLEKELKKVS DVAGETQGSLSVAQDELVTFSEELANLYHHVCMCNNETPNRVML DYYREGQGGAGRTSPGGRTSPEARGRRSPILLPKGLLAPEAGRA DGGTGDSSPSPGSSLPSPLSDPRREDNNIVNLALIALDEAGRA	-	5458	CCAS		ASICOSCPOECPAVCGVRGGHORLDOCS
IRSEMEQLKEAFGQAHTNHKKVAADGESREESLIQESASKEQYY VRKVLELQTELKQLRNVLTNTQSENERLASVAQELKEINQNVEI QRGRURDDIKEYKFREARLLQDYSELEEENISLQKQVSVLRONQ VEPEGLKHEIKRLEEETEYLNSQLEDAIRLKEISERQLEEALET LKTEREQKNSLRKELSHYMSINDSFYTSHLHVSLDGLKFSDDAA EPNNDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS DLLSELNISEICKLKQQLMQMEREKAGLLATLQDTQKQLEHTRG SLSEQQEKVTRLTENLSALRRLQASKERQTALDNEKDRDSHEDG DYYEVDINGPEILACKYHVAVAEAGELREQLKALRSTHEAREAQ HAEEKGRYEAEGQALTEKVSLLEKASRQDRELLARLEKELKKVS DVAGETQGSLSVAQDELVTFSEELANLYHHVCMCNNETPNRVML DYYREGQGGAGRTSPGGRTSPEARGRRSPILLPKGLLAPEAGRA DGGTGDSSPSPGSSLPSPLSDPRREDNNIVNLIALIDENGHER			6642	4022	FVPGLREPQWEPAQPSATMSAPSEEEEYAPLAMPAQDEWLDAR
VRKVLELQTELKQLRNVLTNTQSENERLASVAQELKEINQNVEI QRGRLRDDIKEYKFREARLLQDYSELEEENISLQKQVSVLRQNQ VEFECLKHEIKRLEEETEYLNSQLEDAIRLKEISERQLEEALET LKTEREQKNSLRKELSHYMSINDSFYTSHLHVSLDGLKFSDDAA EPNNDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS DLLSELNISEIQKLKQQLMQMEREKAGLLATLQDTQKQLEHTRG SLSEQQEKVTRLTENLSALRRLQASKERQTALDNEKDRDSHEDG DYYEVDINGPEILACKYHVAVAEAGELREQLKALRSTHEAREAQ HAEEKGRYEAEGQALTEKVSLLEKASRQDRELLARLEKELKKVS DVAGETQGSLSVAQDELVTFSEELANLYHHVCMCNNETPNRVML DYYREGQGGAGRTSPGGRTSPEARGRRSPILLPKGLLAPEAGRA DGGTGDSSPSPGSSLPSPLSDPRREDNNIVNLIALIBDENGUR		ļ	f		KRLSHELAETTREKIOAAEYGLAVLEEKHOLKLOEBELTIKE
QRGRLRDDIKEYKFEARLLQDYSELEENISLQKOVSVLRQNQ VEFEGLKHEIKRLEEETEYLNSQLEDAIRLKEISERQLEEALET LKTEREQKNSLRKELSHYMSINDSFYTSHLHVSLDGLKFSDDAA EPNNDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS DLLSELNISEIQKLKQQLMQMEREKAGLLATLQDTOKQLEHTRG SLSEQQEKVTRLTENLSALRRLQASKERQTALDNEKDRDSHEDG DYYEVDINGPEILACKYHVAVAEAGELREQLKALRSTHEAREAQ HAEEKGRYFAEGGALTEKVSLLEKASRQDRELLARLEKELKKVS DVAGETQGSLSVAQDELVTFSEELANLYHHVCMCNNETPNRVML DYYREGQGGAGRTSPGGRTSPEARGRRSPILLPKGLLAPEAGRA DGGTGDSSPSPGSSLPSPLSDPRREDWNIYNLALALBEAGRA	1	- 1	J	ĺ	IRSEMEQLKEAFGOAHTNHKKVAADGESPEEGLTOEGAGKTOOM
VEFEGLKHEIKRLEEETEYLNSQLEDAIRLKEISERQLEEALET LKTEREQKNSLRKELSHYMSINDSFYTSHLHVSLDGLKFSDDAA EPNNDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS DLLSELNISEIQKLKQQLMQMEREKAGLLATLQDTQKQLEHTRG SLSEQQEKVTRLTENLSALRRLQASKERQTALDNEKDRDSHEDG DYYEVDINGPEILACKYHVAVAEAGELREQLKALRSTHEAREAQ HAEEKGRYFAEGQALTEKVSLLEKASRQDRELLARLEKELKKVS DVAGETQGSLSVAQDELVTFSEELANLYHHVCMCNHETPNRVML DYYREGQGGAGRTSPGGRTSPEARGRRSPILLPKGLLAPEAGRA DGGTGDSSPSPGSSLPSPLSDPRREDWNIVNLIALHDENGHAR			1	[VRKVLELQTELKOLRNVLTNTOSENERI ASVAORI VETNOVIT
LKTERGKNSLRKELSHYMSINDSFYTSHLHVSLDGLKFSDDAA EPNNDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS DLLSELNISEIQKLKQOLMQMEREKAGLLATLQDTQKQLEHTRG SLSEQQEKVTRLTENLSALRRLQASKERQTALDNEKDRDSHEDG DYYEVDINGPEILACKYHVAVAEAGELREQLKALRSTHEAREAQ HAEEKGRYFAEGQALTEKVSLLEKASRQDRELLARLEKELKKVS DVAGETQGSLSVAQDELVTFSEELANLYHHVCMCNNETPNRVML DYYREGQGGAGRTSPGGRTSPEARGRRSPILLPKGLLAPEAGRA DGGTGDSSPSPGSSLPSPLSDPRREDMNIVMLIALHEDENKIR	1		1		QRGRLRDDIKEYKFREARLLODYSELFERNISLOVOUSHI DOWN
EPNNDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS DLLSELNISEIQKLKQQLMQMEREKAGLLATLQDTQKQLEHTRG SLSEQQEKVTRLTENLSALRRLQASKERQTALDNEKDRDSHEDG DYYEVDINGPEILACKYHVAVAEAGELREQLKALRSTHEAREAQ HAEEKGRYEAEGQALTEKVSLLEKASRQDRELLARLEKELKKVS DVAGETQGSLSVAQDELVTFSEELANLYHHVCMCNNETPNRVML DYYREGQGGAGRTSPGGRTSPEARGRRSPILLPRGLLAPEAGRA DGGTGDSSPSPGSSLPSPLSDPRREDMNIVNLIALLEDENGRA		i	I	1	VEFEGLKHEIKRLEEETEVINSOLEDATRI VETORDOLEDATRI
DLISEINISEIQKLKQLKOLKORTPKKEGLAPPSPSLVS DLLSELNISEIQKLKQLKQKAGLLATLQDTQKQLEHTRG SLSEQQEKVTRLTENLSALRRLQASKERQTALDNEKDRDSHEDG DYYEVDINGPEILACKYHVAVAEAGELREQLKALRSTHEAREAQ HAEEKGRYEAEGQALTEKVSLLEKASRQDRELLARLEKELKKVS DVAGETQGSLSVAQDELVTFSEELANLYHHVCMCNNETPNRVML DYYREGQGGAGRTSPGGRTSPEARGRRSPILLPKGLLAPEAGRA DGGTGDSSPSPGSSLPSPLSDPRREDWNIYNLALLALDOLKULA	1	ì		1	LKTEREOKNSLRKELSHYMSINDSEUMOUT BROTESEKQLEEALET
SLISEQUEKVTRLTENLSALRRLQASKERQTALDNEKDRDSHEDG SLSEQQEKVTRLTENLSALRRLQASKERQTALDNEKDRDSHEDG DYYEVDINGPEILACKYHVAVAEAGELREQLKALRSTHEAREAQ HAEEKGRYEAEGQALTEKVSLLEKASRQDRELLARLEKELKKVS DVAGETQGSLSVAQDELVTFSEELANLYHHVCMCNNETPNRVML DYYREGQGGAGRTSPGGRTSPEARGRRSPILLPKGLLAPEAGRA DGGTGDSSPSPGSSLPSPLSDPRREDWNIYNLALLADENGRA	1	1		i	EPNNDAEALVNGFEHGGLAKI.DI.DNVTGTDVVDGV.
DYYEVDINGPEILACKYHVAVAÆAGELREQLKALRSTHEAREAQ HAFEKGRYEAEGQALTEKVSLLEKASRQDRELLARLEKELKKVS DVAGETQGSLSVAQDELVTFSEELANLYHHVCMCNNETPNRVML DYYREGQGGAGRTSPGGRTSPEARGRRSPILLPKGLLAPEAGRA DGGTGDSSPSPGSSLPSPLSDPRREDWNIVNLIALLEDOLKUL		1	İ	į	DLLSELNISEIOKI, KOOLMOMEREVACI, PROCESSIONAL
HAEEKGRYEAEGQALTEKVSLLEKASRQDRELLARLEKELKKVS DVAGETQGSLSVAQDELVTFSEELANLYHHVCMCNNETPNRVML DYYREGQGGAGRTSPGGRTSPEARGRRSPILLPKGLLAPEAGRA DGGTGDSSPSPGSSLPSPLSDPRREDWNLYNLIALLEDOLWUR	1		•	1	SLSEOOEKVTRI TENI SALBEI CARREDON TO THE STATE OF THE SALBEIGH STATE OF THE SALBEIGH
DVAGETQGSLSVAQDELVTFSEELANLYHHVCMCNNETPNRVML DYYREGQGGAGRTSPGGRTSPEARGRRSPILLPKGLLAPEAGRA DGGTGDSSPSPGSSLPSPLSDPRREDMNIVMLIAILDENGRA	1	1			DYYEVDINGPETLACKYRIANA DA CONTRACTOR DE LA CRYTERIA DE CONTRACTOR DE LA CRYTERIA DE CONTRACTOR DE CON
DYYREGOGGAGRTSPGGRTSPERARGRRSPILLPRGLIAPEAGRA DGGTGDSSPSPGSSLPSPLSDPRREDMNIVALIALIBEAGRA DGGTGDSSPSPGSSLPSPLSDPRREDMNIVALIALIBEAGRA	1	- 1	1]	HAEEKGRYEAFGOALTENGOTTON
DITREGUGGAGRTSPEGRRSPILLPKGLLAPEAGRA DGGTGDSSPSPGSSLPSPLSDPRREPMNIYNLTALIBDOLUMI		1	1	f ;	DVAGETOGSLSVAODELUTT
DOGIGOSSESPECIALISTED OF THE PROPERTY OF	1]	}	J;	DYVREGOGGA CPTC PGC PTC PTC PTC PTC PTC PTC PTC PTC PTC PT
DOGIGOSSESPECIALISTED OF THE PROPERTY OF		1	1	1 *	DIIREGUGGAGKTSPGGRTSPEARGPRSPTLLDVGLLADERGD
ASSACTIBLISKURIASQELGPAVDKDKEALMEEILKLKSLLSTK				1 '	DGG1GD33F3FGSSLPSPLSDPRREDMNTVNLTATTRDGTMT 0
				L	THE TANGET OF THE PAYOR DE LA CONTRACTOR

SEO	Predicted	1 Bar 1 2 2 2	
ID	beginning	Predicted end	Amino acid segment containing signal peptide
NO:		nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
MO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
[corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
l l	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1 - 4	\=possible nucleotide insertion)
—	 	 	PROTEST DOWN (ANY CORPORATION)
	1 .		REQITTLRTVLKANKQTAEVALANLKSKYENEKAMVTETMMKLR
ì	Ī	1	NELKALKEDAATFSSLRAMFATRCDEYITQLDEMQRQLAAAEDE
i	1	1	KKTLNSLLRMAIQQKLALTQRLELLELDHEQTRRGRAKAAPKTK
	<u> </u>	<u></u>	PATPSVSHTCACASDRAEGTGLANQVFCSEKHSIYCD
5459	316	1262	RGGHRLSGMASNFNDIVKQGYVRIRSRRLGIYQRCWLVFKKASS
Ĭ	1	ì	KGPKRLEKFSDERAAYFRCYHKVTELNNVKNVARLPKSTKKHAI
ļ			GIYFNDDTSKTFACESDLEADEWCKVLQMECVGTRINDISLGEP
	1	1	DLLATGVEREQSERFNVYLMPSPNLGCYMGECALQITYEYICLW
	1	1	DVQNPRVKLISWPLSALRRYGRDTTWFTFEAGRMCETGEGLFIF
[Í	1	OTDDCCATVOVIDICARIA TO TO TOTAL TO STATE OF THE STATE OF
	1		QTRDGEAIYQKVHSAALAIAEQHERLLQSVKNSMLQMKMSERAA
i	ĺ	[SLSTMVPLPRSAYWQHITRQHSTGQLYRLQDVSSPLKLHRTETF
5450	ļ <u>.</u>		PAYRSEH
5460	45	2097	RPGCRAGELSTGSRARERVRNRVSAPCGQDSRRCDPEVLRGRSP
1		!	GLGLAEMPSCGACTCGAAAVRLITSSLASAORGISGGRIHMSVL
1 .	[GRLGTFETQILQRAPLRSFTETPAYFASKDGISKDGSGDGNKKS
ļ	J	}	ASEGSSKKSGSGNSGKGGNQLRCPKCGDLCTHVETFVSSTRFVK
1		[CEKCHHFFVVLSEADSKKSIIKEPESAAEAVKLAFQQKPPPPPK
1	l .	ļ	KIYNYLDKYVVGQSFAKKVLSVAVYNHYKRIYNNIPANLRQQAE
1			VEKQTSLTPRELEIRREDEYRFTKLLQIAGISPHGNALGASMQ
]		COMMODIBOEVECCER DECURPTIVE DECURPTIVE DECURPTIVE
1	ļ ·		QQVNQQIPQEKRGGEVLDSSHDDIKLEKSNILLLGPTGSGKTLL
ļ	}		AQTLAKCLDVPFAICDCTTLTQAGYVGEDIESVIAKLLQDANYN
•	1		VEKAQQGIVFLDEVDKIGSVPGIHQLRDVGGEGVQQGLLKLLEG
1	}		TIVNVPEKNSRKLRGETVQVDTTNILFVASGAFNGLDRIISRRK
į.	i i		NEKYLGFGTPSNLGKGRRAAAAADLANRSGESNTHQDIEEKDRL
1	1		LRHVEARDLIEFGMIPEFVGRLPVVVPLHSLDEKTLVQILTEPR
	1		NAVIPQYQALFSMDKCELNVTEDALKAIARLALERKTGARGLRS
ì	}		IMEKLLLEPMFEVPNSDIVCVEVDKEVVEGKKEPGYIRAPTKES
	i		SEEEYDSGVEEEGWPRQADAANS
5461	1481	160	INPPPPPKSPCGRARKWRRRRRPGAPEAAVMELPSGPGPERLFD
			SHRLPGDCFLLLVLLLYAPVGFCLLVLRLFLGIHVFLVSCALPD
Ì	1 1		CHI DEFINITION OF THE PERSON THE PROPERTY OF THE PERSON
1	1		SVLRRFVVRTMCAVLGLVARQEDSGLRDHSVRVLISNHVTPFDH
1	1 1		NIVNLLTTCSTPLLNSPPSFVCWSRGFMEMNGRGELVESLKRFC
	1		ASTRLPPTPLLLFPEEEATNGREGLLRFSSWPFSIQDVVQPLTL
1	1 . 1		QVQRPLVSVTVSDASWVSELLWSLFVPFTVYQVRWLRPVHRQLG
	·		EANEEFALRVQQLVAKELGQTGTRLTPADKAEHMKRORHPRLRP
ł	i i		QSAQSSFPPSPGPSPDVQLATLAQRVKEVLPHVPLGVIORDLAK
1			TGCVDLTITNLLEGAVAFMPEDITKGTQSLPTASASKFPSSGPV
<u>{</u>	j l		TPQPTALTFAKSSWARQESLQERKQALYEYARRRFTERRAQEAD
5462	663	3353	KIKEROMSANNSPPSAOKSVLPTAIPAVLPAASPCSSPKTGLSA
1	l i		RLSNGSFSAPSLTNSRGSVHTVSFLLQIGLTRESVTIEAQELSL
	ļ		SAVKDLVCSIVYQKFPECGFFGMYDKILLFRHDMNSENILQLIT
1	1		CARETUREDIVIDUE CARACTERISTE CONTRACTOR CONTR
1			SADEIHEGDLVEVVLSALATVEDFQIRPHTLYVHSYKAPTFCDY
1	ſ		CGEMLWGLVRQGLKCEGCGLNYHKRCAFKIPNNCSGVRKRRLSN
J	.		VSLPGPGLSVPRPLQPEYVALPSEESHVHQEPSKRIPSWSGRPI
1	[1		WMEKMVMCRVKVPHTFAVHSYTRPTICQYCKRLLKGLFRQGMQC
}	l		KDCKFNCHKRCASKVPRDCLGEVTFNGEPSSLGTDTDIPMDIDN
			NDINSDSSRGLDDTEEPSPPEDKMFFLDPSDLDVERDEEAVKTI
]	l I		SPSTSNNIPLMRVVQSIKHTKRKSSTMVKEGWMVHYTSRDNLRK
		i	RHYWRLDSKCLTLFQNESGSKYYKEIPLSEILRISSPRDFTNIS
	1		OGSNDHCEETTTDTMIVELCEUTICECCUTICE TENTS
	1	į	QGSNPHCFEIITDTMVYFVGENNGDSSHNPVLAATGVGLDVAQS
	, i		WEKAIRQALMPVTPQASVCTSPGQGKDHKDLSTSISVSNCQIQE
1	1		NVDISTVYQIFADEVLGSGQFGIVYGGKHRKTGRDVAIKVIDKM
]	! !		RFPTKQESQLRNEVAILQNLHHPGIVNLECMFETPERVFVVMEK
;	1	ĺ	LHGDMLEMILSSEKSRLPERITKFMVTQILVALRNLHFKNIVHC
j l	i	İ	DLKPENVLLASAEPFPQVKLCDFGFARIIGEKSFRRSVVGTPAY
} [{	ĺ	LAPEVLRSKGYNRSLDMWSVGVIIYVSLSGTFPFNEDEDINDQI
) 1		Į.	QNAAFMYPPNPWREISGEAIDLINNLLQVKMRKRYSVDKSLSHP
1 1	ſ	ſ	
]			WLQDYQTWLDLREFETRIGERYITHESDDARWEIHAYTHNLVYP
5463	237	1010	KHFIMAPNPDDMEEDP
1 }		1012	LLSVTMTTSRCSHLPEVLPDCTSSAAPVVKTVEDCGSLVNGQPQ
		1	YVMQVSAKDGQLLSTVVRTLATQSPFNDRPMCRICHEGSSQEDL

SEO	Predicted	I Beeck at 1	
ID	beginning	Predicted end	
NO:	nucleotide	nucleotide	A=Alanine, C=CVSteine, D=Aspartic hold =
1	location	location	Giutamic Acid, F=Phenvlalanine G-Clicking
J	corresponding	corresponding	H=H1Stldine, I=Isoleucine, K=Ivsine
	to first	to first	L=Leucine, M=Methionine, N=Asparagine
İ	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine
1	residue of	residue of	S=Serine, T=Threonine, V=Valine
i	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, Y=Unknown + 54
		sequence	(codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
			LSPCECTGTLGTIHRSCLEHWLSSSNTSYCELCHEREAUERVOR
	}	1	PLVEWLRNPGPQHEKRTLFGDMVCFI,FITPI,ATTSGWLCI BCAN
1 .	1	1	DHLHFSSRLEAVGLIALTVALFTIYLFWTLVSFRYHCRLYNEWR
		1	RTNQRVILLIPKSVNVPSNQPSLLGLHSVKRNSKETVV
5464	195	677	SPSMNPRKKVDLKLIIVGAIGVGKTSLLHQYVHKTFYEEYQTTL
ļ	1]	GASILSKIIILGDTTLKLQIWDTGGQERVRSMVSTFYKGSDGCI
ł	1		LAFDVTDLESFEALDIWRGDVLAKIVPMEQSYPMVLLGNKIDLA
	1		DRKYQSILENHLTESIKLSPDQSRSRCC
5465	5278	3348	KCDDDBALDMADEN ECDANONIA
	1		KGDPREFIRVHREALECDYVSAHLHEWIDLIFGYKQQGPAAVEA
- [Į.	ĺ	VNVFHHLFYEGQVDIYNINDPLKETATIGFINNFGQIPKQLFKK
1			PHPPKRVRSRLNGDNAGISVLPGSTSDKIFFHHLDNLRPSLTPV
			KELKEPVGQIVCTDKGILAVEQNKVLIPPTWNKTFAWGYADLSC
1			RLGTYESDKAMTVYECLSEWGQILCAICPNPKLVITGGTSTVVC
J	<u> </u>		WEMGTSKEKAKTVTLKOALLGHTDTVTCATASIAVHITUGGED
	i i		DRTCIIWDLNKLSFLTQLRGHRAPVSALCINELTGDIVSCAGTY
·	1		IHVWSINGNPIVSVNTFTGRSQQIICCCMSEMNEWDTQNVIVTG
1	!		HSDGVVRFWRMEFLQVPETPAPEPAEVLEMOEDCPEAGIGOERG
1	[DEDSSDSEADEQSISODPKDTPSOPSSTSHRPRAASCRATAAUC
1	1 1		TDSGSDDSRRWSDQLSLDEKDGFIFVNYSEGOTPAHLOGDLSUD
ļ	ļ		HPNPIEVRNYSRLKPGYRWEROLVFRSKI,TMHTAFDRKDNAUEA
	1		EVTALGISKDHSRILVGDSRGRVFSWSVSDOPGRSAADUWVKDE
	i i		GGDSCSGCSVRFSLTERRHHCRNCGOLFCOKCSRFOSFIKBLKI
5466	3		SSPVKVCQNCYYNLQHERGSEDGPRNC
3100	1 3 1	992	HACAHASAHASGRLVRWWRKRRSVMGIQTSPVLLASLGVGLVTL
ľ	}		LGLAVGSYLVRRSRRPQVTLLDPNEKYI.I.RIJ.DKTTVQHNTVDB
}			REALPTAHRTLGLPVGKHIYLSTRIDGSLVIRPVTPVTSDPDCC
1	1		YVDLVIKVYLKGVHPKFPEGGKMSOYLDSI,KVGDIA/FFPGDCCI
1 1	·		LTYTGKGHFNIQPNKKSPPEPRVAKKLGMIAGGTGTTPMLOLTP
1	İ		ALDROPEDPTQCFLDFANOTEKDIIDREDLEELOADVDNDEVIN
	1		FTEDHPPKDWAYSKGFVTADMIREHLPAPGDDVIALCGPPDMX
FACT			QLACHPNLDKLGYSQKMRFTY
5467	2103	4	GEALRVGTRGCRRDLPDPQARIFIQKKDLEEDESVTAAHLKSRG
1	1		RSPRKIDQFCNSSNMVHGSVTFRDVAIDFSQEEWECLQPDQRTL
1 1	1		YRDVMLENYSHLISLAGSSISKPDVITLLEQEKEPWMVVRKETS
) i	1		RRYPDLELKYGPEKVSPENDTSEVNLPKQVIKQISTTLGIEAFY
1 [FRNDSEYRQFEGLQGYQEGNINQKMISYEKLPTHTPHASLICNT
1 1	1		HKPYECKECGKYFSCGSNLIQHQSIHTGEKPYKCKECGKAFQLH
1	1		IQLTRHQKFHTGEKTFECKECGKAFNLPTQLNRHKNIHTVKKLF
1 1			ECKECGKSFNRSSNLTQHQSIHAGVKPYQCKECGKAFNRGSNLI
1 1	1		QHQKIHSNEKPFVCKECGMAFRYHYQLIEHCQIHTGEKPFECKE
	ļ	ĺ	CGKAFTLLTKLVRHQKIHTGEKPFECRECGKAFSLLNQLNRHKN
1	ļ		IHTGEKPFECKECGKSFNRSSNLVQHQSIHAGIKPYECKECGKG
1 1	1		FNRGAHLIQHQKIHSNEKPFVCRECEMAFRYHCQLIEHSRIHTG
] [DKPFECQDCGKAFNRGSSLVQHQS1HTGEKPYECKECGKAFRLY
1		İ	LOLSOHOKTHTGEKPECKECGKAFRLY
1]	LQLSQHQKTHTGEKPFECKECGKFFRRGSNLNQHRSIHTGKKPF
			ECKECGKAFRLHMHLIRHQKLHTGEKPFECKECGKAFRLHMQLI
5468	225	2976	RHQKLHTGEKPFECKECGKVFSLPTQLNRHKNIHTGEKAS
1 1	1	~2,0	SFLTDLFQSLAQLENLCKQLYETTDTTTRLQAEKALVEFTNSPD
]	1		CLSKCQLLLERGSSSYSQLLAATCLTKLVSRTNNPLPLEQRIDI
1 (.	1	i	RNYVLNYLATRPKLATFVTQALIQLYARITKLGWFDCQKDDYVF
1 1	[}	RNATTDVTRFLQDSVEYCIIGVTILSQLTNEINQVSATAFLIEA
]	Ì		DTTHPLTKHRKIASSFRDSSLFDIFTLSCNLLKOASGKNININD
[Í	1	ESQHGLLMQLLKLTHNCLNFDFIGTSTDESSDDLCTVOTPTSWP
į ,		J	SAFLDSSTLQLSTIGRCEYEKTCALLVOLFDOSAOSYOELLOSA
]]		İ	SASPMDIAVQEGRLTWLVYIIGAVIGGRVSFASTDEODAMDGEL
		ļ	VCRVLQLMNLTDSRLAQAGNEKLELAMLSFFEOPRKTYTGDOVG
1	}		KSSKLYRRLSEVLGLNDETMVLSVFIGKIITNLKYWGPCPDTTE
]			KTLQLLNDLSIGYSSVRKLVKLSAVOFMLNNHTSRHFSELGINN
ſ		į.	QSNLTDMRCRTTFYTALGRLLMVDLGEDEDOYEOFMI.DI.TAARE
	1		AVAQMESTNSFNEQEAKRTLVGLVRDLRGIAFAFNAKTSPMMIR
L			EWIYPSYMPILQRAIELWYHDPACTTPVLKLMAELVHNRSQRLQ
			- Indiana Market Control of the Cont

SEQ	Predicted	I modified and	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
ĺ	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
	1		FDVSSPNGILLFRETSKMITMYGNRILTLGEVPKDQVYALKLKG
	1		ISICFSMLKAALSGSYVNFGVFRLYGDDALDNALQTFIKLLLSI
ł	1		PHSDLLDYPKLSQSYYSLLEVLTQDHMNFIASLEPHVIMYILSS
ļ.		1	ISEGLTALDTMVCTGCCSCLDHIVTYLFKQLSRSTKKRTTPLNQ
1			ESDRFLHIMQQHPEMIQQMLSTVLNIIIFEDCRNQWSMSRPLLG
		1	LILLNEKYFSDLRNSIVNSQPPEKQOAMHLCFENLMEGIERNI.
	<u> </u>	l	TKNRDRFTQNLSAFRREVNDSMKNSTYGVNSNDMMS
5469	134	2653	DQEFETSLVPWHLPMGWLCSGLLFPVSCLVLLOVASSGNMKVLO
	1	İ	EPTCVSDYMSISTCEWKMNGPTNCSTELRLLYOLVFLLSEAHTC
1	{	1	VPENNGGAGCVCHLLMDDVVSADNYTLDLWAGOOLLWKGSEKPS
i	ľ		EHVKPRAPGNLTVHTNVSDTLLLTWSNPYPPDNYLYNHI,TYAUN
ļ		}	IWSENDPADFRIYNVTYLEPSLRIAASTLKSGISYRARVRAWAQ
J			CYNTTWSEWSPSTKWHNSYREPFEQHLLLGVSVSCIVILAVCLL
}	<u> </u>		CYVSITKIKKEWWDQIPNPARSRLVAIIIQDAQGSQWEKRSRGQ
			EPAKCPHWKNCLTKLLPCFLEHNMKRDEDPHKAAKEMPFQGSGK
ł	į		SAWCPVEISKTVLWPESISVVRCVELFEAPVECEEEEEVEEEKG SFCASPESSRDDFQEGREGIVARLTESLFLDLLGEENGGFCQQD
			MGESCLLPPSGSTSAHMPWDEFPSAGPKEAPPWGKEQPLHLEPS
1			PPASPTQSPDNLTCTETPLVIAGNPAYRSFSNSLSQSPCPRELG
			PDPLLARHLEEVEPEMPCVPQLSEPTTVPQPEPETWEQILRRNV
1	}		LQHGAAAAPVSAPTSGYQEFVHAVEQGGTQASAVVGLGPPGEAG
1			YKAFSSLLASSAVSPEKCGFGASSGEEGYKPFODLIPGCPGDPA
			PVPVPLFTFGLDREPPRSPQSSHLPSSSPEHLGLEPGEKVEDMP
ſ			KPPLPQEQATDPLVDSLGSGIVYSALTCHLCGHI,KOCHGOEDGG
1			QTPVMASPCCGCCCGDRASPPTTPLRAPDPSPGGVPLFASLCDA
1			SLAPSGISEKSKSSSSFHPAPGNAQSSSQTPKIVNFVSVGPTYM
5470	17		RVS
	- ′	1418	TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF
			KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY
			SFLVGCASISDVIAQVVPVAILLHSHLECREPLLIPILSLYMGA
	i		LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA
1 1			LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP
1 1			YGWLTEIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA
1	j		LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF
1 1	•]		PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLDVI.
l i			GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKOKKKMENESAT
5471			EGEDSAMTDMPPTEEVTDIVEMREENE
34/1	1868	658	RSSAPPGPQRAAAATAAAAAGVEMAAAAAQGGGGGEPRRTEGV
			GPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVR
1	Ĭ		KTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILR
ļ f			ASTLEAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR
1 1	ł	:	GLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHD
]])		HTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSL
ļ l	1		PSKTKVAWAKLFPKSDSKALDLLDRMLTFNPNKRITVEEALAHP
[[ì		YLEQYYDPTDEPVAEEPFTFAMELDDLPKERLKELIFQETARFO
L	ł		PGVLEAP
5472	1469	753	LYVMARYLSDEEVAVSIDRLCKANGRSPSIPFGTVRIPGRARVR
j	1		DPQALWIFGYGSLVWRPDFAYSDSRVGFVRGYSRRFWQGDTFHR
] [ľ	GSDKMPGRVVTLLEDHEGCTWGVAYQVQGEQVSKALKYLNVREA
			VLGGYDTKEVTFYPQDAPDQPLKALAYVATPONPGYLGPAPEEA
]	1		IATQILACRGFSGHNLEYLLRVRDVMQLCGPQAQDEHLAAIVDA
 		<u> </u>	VGTMLPCFCPTEQALALV
5473	3	2119	FMNVKLLIQDLEDIEQRVPVMDAQYKIITKTAHLITKESPQEEG
[1		KEMFATMSKLKEQLTKVKECYSPLLYESQOLLIPLBELEKOMTS
			FYDSLGKINEIITVLEREAQSSALFKOKHOELLACOENCKKTLT
	ľ		LIEKGSQSVQKFVTLSNVLKHFDQTRLQROIADIHVAFQSMVKK
	į		TGDWKKHVETNSRLMKKFEESRAELEKVLRIAQEGLEEKGDPEE
	į	}	LLRRHTEFFSQLDQRVLNAFLKACDELTDILPEQEQQGLQEAVR
			KLHKQWKDLQGEAPYHLLHLKIDVEKNRFLASAEECRTELDRET

SEQ	Predicted	Predicted end	
	beginning	nucleotide	
NO:	nucleotide	location	
}	location	corresponding	1 CTCCMILL ACIG. FEPDANTI STANIGE A AS .
ĺ	corresponding	to first	**-**+3C+U+DE, = \$0 Anaina
	to first		1 Ucucine, Mamerbionine Manager
	amino acid	amino acid	*~F-O-LINE, O-GINEAmina D-A
	residue of	residue of	1 Descripe, Tathreonine Wattoling
	residue or	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
		T	KLMPOEGGERTINEUDURGERTION)
•	1	J	KLMPQEGSEKIIKEHRVFFSDKGPHHLCEKRLQLIEELCVKLPV
	1 :		1 NOT TRUITED TO TOUR TENED TO THE TENED TO
	[j	1 ~ CONTOINDIOUNGIKGEAIDTAMBREATURATURATURA
	ł	}	1 2 1 2 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1
			1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -
]	TARE THE SEPTEMBLUCK LAKE SAKKEDVA OA AAAAAAAA
	Į.	1	1 ************************************
	1	Į.	YLFQTGSSHERFLSFSSLESLESELEQTKEFSKRTESIAVQAEN
	1	ł	LVKEASETDLEDONKOLLGGGNEGTESTAVQAEN
	}		LVKEASEIPLGPQNKQLLQQQAKSIKEQVKKLEDTLEEEYVIDK
5474	2	780	1 -
	i -	780	TPDVRQLQASRRGIAVASWCSPRWFAGEEMAFVKSGWLLRQSTI
			THE TAXABLE PARTIES AND THE PROPERTY OF THE PARTIES
			T ADOMEST AREA DOMESTICATION OF THE COMPANY OF THE
		1	LODSRTNTAYVGSAVMTDETSVVSSPPPYTAYAAPAPEVGRTLS
			LQQAYGYGPYGGAYPPGTQVVYAANGQAYAVPYQYPYAGLYGQQ
			PANOVIIRERYPDNDCDLALCATIATION
5475	2	506	PANQVIIRERYRDNDSDLALGMLAGAATGMALGSLFWVF
j			ARGWLESLSLTCQTTPPPSSPCLLHSPETFIHTMPPNLTGYYRF
			I VOSIGNADI I DUALNI SLAVEKTALI.I. IZDDVA ZDVO
- 1			1 ACC VOLD VOVER RECORDS VICED VCCORTUMIZED PROFESSIONS
5476	192		1 TANGUMU DEGENUT PRI TANDA MADAMA
	-52	1457	SDSMSLLDCFCTSRTOVRSLDDFKOCEmcTrovs
	j		1 - 2 1 0 0 D V D C S IN V SHIEL () VET RECEPTIVE TO THE TRANSPORT TO THE
			VTIKITNLENCNEERLKALQKAVILSHFFRHPNITTYWTVFTVG
	- 1		SWLWVISPEMAYGRAGOLI PRISTRE
- 1	. 1		SWLWVISPFMAYGSASQLLRTYFPEGMSETLIRNIJFGAVRGLN YLHONGCIHRSIYASHIIICON
1	1		
			I
1			
í	ľ		I -xz pvicebyooppout Alekkimkeedubett of t business-
5477	3		1 ~~+ + + + + + + + + + + + + + + + + +
	٠ ا	1044	RGNSRLRYSHEDELOLPRIPELERTCHOLL DRUGGE
- 1	- 1		VQEKVFKGLDLLEKAAEMLSQLDLFSRNEDLEEIASTDLKYLLV
1	j.	ĺ	PAFQGALTMKQVNPSKRLDHLQRAREHFINYLTQCHCYHVAEFE
l l		1	LDETMING A FARMAN OF THE LOCAL THE LAYER TO THE TOTAL THE PROPERTY OF THE PROP
1		ł	
			HRLSAMKSAVESGOADDERVEEVYLLULORUSTATA
			HRLSAMKSAVESQADDERVREYYLLHLQRWIDISLEEIESIDQ EIKILRERDSSREASTSNSSDOFDDDV DEVLOORD
			HRLSAMKSAVESGQADDERVREYYLLHLQRWIDISLEEIESIDQ EIKILRERDSSREASTSNSSRQERPPVKPFILTRMAQAKVFGA GYPSLPTMTVSDWYEOHRKVGALDDOGLAVARDAGA
5478	2		HRLSAMKSAVESGADDERVREYYLLHLQRWIDISLEEIESIDQ EIKILRERDSSREASTSNSSRQERPPVKPFILTRNMAQAKVFGA GYPSLPTMTVSDWYEQHRKYGALPDQGIAKAAPEEFRKAAQQQE EQEEKEEEDDEOTLHRAREWDDWKDTHDEGYCNDOWYK
5478	2	835	HRLSAMKSAVESGQADDERVREYYLLHLQRWIDISLEEIESIDQ EIKILRERDSSREASTSNSSRQERPPVKPFILTRNMAQAKVFGA GYPSLPTMTVSDWYEQHRKYGALPDQGIAKAAPEEFRKAAQQQE EQEEKEEEDDEQTLHRAREWDDWKDTHPRGYGNGOMG
5478	2	835	HRLSAMKSAVESGQADDERVREYYLLHLQRWIDISLEEIESIDQ EIKILRERDSSREASTSNSSRQERPPVKPFILTRNMAQAKVFGA GYPSLPTMTVSDWYEQHRKYGALPDQGIAKAAPEEFRKAAQQQE EQEEKEEEDDEQTLHRAREWDDWKDTHPRGYGNRQNMG KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFYTASDDKT VKVWATHROKFLFSLSCHTNWYGGAYEGDPGANTASTORY
5478	2		HRLSAMKSAVESGQADDERVREYYLLHLQRWIDISLEETESIDQ EIKILRERDSSREASTSNSSRQERPPVKPFILTRNMAQAKVFGA GYPSLPTMTVSDWYEQHRKYGALPDQGIAKAAPEEFRKAAQQQE EQEEKEEEDDEQTLHRAREWDDWKDTHPRGYGNRQNMG KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDERDCCTGIALAR
5478	2		HRLSAMKSAVESGQADDERVREYYLLHLQRWIDISLEEIESIDQ EIKILRERDSSREASTSNSSRQERPPVKPFILTRNMAQAKVFGA GYPSLPTMTVSDWYEQHRKYGALPDQGIAKAAPEEFRKAAQQQE EQEEKEEEDDEQTLHRAREWDDWKDTHPRGYGNRQNMG KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFPRCCTGIALARGE
5478	2		HRLSAMKSAVESGQADDERVREYYLLHLQRWIDISLEEIESIDQ EIKILRERDSSREASTSNSSRQERPPVKPFILTRNMAQAKVFGA GYPSLPTMTVSDWYEQHRKYGALPDQGIAKAAPEEFRKAAQQQE EQEEKEEEDDEQTLHRAREWDDWKDTHPRGYGNRQNMG KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLGHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLOHYCLHSAAVGLSFHDGONYL
5478	2		HRLSAMKSAVESGQADDERVREYYLLHLQRWIDISLEEIESIDQ EIKILRERDSSREASTSNSSRQERPPVKPFILTRNMAQAKVFGA GYPSLPTMTVSDWYEQHRKYGALPDQGIAKAAPEEFRKAAQQQE EQEEKEEEDDEQTLHRAREWDDWKDTHPRGYGNRQNMG KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHOGPATTVAFSPTGEVEAGGGDTY
5478	2		HRLSAMKSAVESGQADERVREYYLLHLQRWIDISLEEIESIDQ EIKILRERDSSREASTSNSSRQERPPVKPFILTRNMAQAKVFGA GYPSLPTMTVSDWYEQHRKYGALPDQGIAKAAPEEFRKAAQQQE EQEEKEEEDDEQTLHRAREWDDWKDTHPRGYGNRQNMG KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEDBLTLEDBLY
			HRLSAMKSAVESGQADDERVREYYLLHLQRWIDISLEEIESIDQ EIKILRERDSSREASTSNSSRQERPPVKPFILTRNMAQAKVFGA GYPSLPTMTVSDWYEQHRKYGALPDQGIAKAAPEEFRKAAQQQE EQEEKEEEDDEQTLHRAREWDDWKDTHPRGYGNRQNMG KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGGSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP
	2	835	HRLSAMKSAVESGQADDERVREYYLLHLQRWIDISLEEIESIDQ EIKLIRERDSSREASTSNSSRQERPPVKPFILTRNMAQAKVFGA GYPSLPTMTVSDWYEQHRKYGALPDQGIAKAAPEEFRKAAQQQE EQEEKEEEDDEQTLHRAREWDDWKDTHPRGYGNRQNMG KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP
5478		835	HRLSAMKSAVESGQADDERVREYYLLHLQRWIDISLEETESIDQ EIKILRERDSSREASTSNSSRQERPPVKPFILTRNMAQAKVFGA GYPSLPTMTVSDWYEQHRKYGALPDQGIAKAAPEEFRKAAQQQE EQEEKEEEDDEQTLHRAREWDDWKDTHPRGYGNRQNMG KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVFRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSOHINWVPCAKFS DDGNITMS
		835	HRLSAMKSAVESGQADDERVREYYLLHLQRWIDISLEEIESIDQ EIKILRERDSSREASTSNSSRQERPPVKPFILTRNMAQAKVFGA GYPSLPTMTVSDWYEQHRKYGALPDQGIAKAAPEEFRKAAQQQE EQEEKEEEDDEQTLHRAREWDDWKDTHPRGYGNRQNMG KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFURSCTIANAGNDRTVK
		835	HRLSAMKSAVESGQADDERVREYYLLHLQRWIDISLEEIESIDQ EIKILRERDSSREASTSNSSRQERPPVKPFILTRNMAQAKVFGA GYPSLPTMTVSDWYEQHRKYGALPDQGIAKAAPEEFRKAAQQQE EQEEKEEEDDEQTLHRAREWDDWKDTHPRGYGNRQNMG KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFURSCTIANAGNDRTVK
		835	HRLSAMKSAVESGQADDERVREYYLLHLQRWIDISLEEIESIDQ EIKILRERDSSREASTSNSSRQERPPVKPFILTRNMAQAKVFGA GYPSLPTMTVSDWYEQHRKYGALPDQGIAKAAPEEFRKAAQQQE EQEEKEEEDDEQTLHRAREWDDWKDTHPRGYGNRQNMG KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASDSTCIAAAGMDNTVKVW
		835	HRLSAMKSAVESGQADDERVREYYLLHLQRWIDISLEETESIDQ EIKILRERDSSREASTSNSSRQERPPVKPFILTRNMAQAKVIGA GYPSLPTMTVSDWYEQHRKYGALPPQGIAKAAPEEFRKAAQQE EOEEKEEEDDEQTLHRAREWDDWKDTHPRGYGNRQNMG KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSGHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQWWWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSPTGRYFASGGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL
		835	HRLSAMKSAVESGQADDERVREYYLLHLQRWIDISLEETESIDQ EIKILRERDSSREASTSNSSRQERPPVKPFILTRNMAQAKVIGA GYPSLPTMTVSDWYEQHRKYGALPDQGIAKAAPEEFRKAAQQE EOEEKEEEDDEQTLHRAREWDDWKDTHPRGYGNRQNMG KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSGHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQWWWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQWWWKSNF DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQWMWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKIKOR
	2	835	HRLSAMKSAVESGQADDERVREYYLLHLQRWIDISLEEIESIDQ EIKILRERDSSREASTSNSSRQERPPVKPFILTRNMAQAKVFGA GYPSLPTMTVSDWYEQHRKYGALPDQGIAKAAPEEFRKAAQQQE EQEEKEEEDDEQTLHRAREWDDWKDTHPRGYGNRQNMG KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP
5479		835 1952	HRLSAMKSAVESGQADDERVREYYLLHLQRWIDISLEEIESIDQ EIKILRERDSSREASTSNSSRQERPPVKPFILTRNMAQAKVFGA GYPSLPTMTVSDWYEQHRKYGALPDQGIAKAAPEEFRKAAQQQE EQEEKEEEDDEQTLHRAREWDDWKDTHPRGYGNRQNMG KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQWWWKSNF DIGDHGEVTKVFRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKTV VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQWWWKSNF DIGDHGEVTKVFRPPATLASSMGNLTVSILEQRLTLEEDKLKQC DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP LSTERMEEEELVKGRLOATTDKDVIOEETGOVDVASSEN
5479	2	1952	HRLSAMKSAVESGQADDERWYKYKLIGRYKQKKELE HRLSAMKSAVESGQADDERVREYYLLHLQRWIDISLEEIESIDQ EIKILRERDSSREASTSNSSRQERPPVKPFILTRNMAQAKVFGA GYPSLPTMTVSDWYEQHRKYGALPPQGIAKAAPEEFRKAAQQQE EQEEKEEEDDEQTLHRAREWDDWKDTHPRGYGNRQNMG KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAPSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKOC LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAPSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP LSLTSRMEEAELVKGRLQAITDKRKIQEEISQKRLKIEEDKLKH
5479	2	1952	HRLSAMKSAVESGQADDERWYKYKLIEEDKLKH HRLSAMKSAVESGQADDERVREYYLLHLQRWIDISLEEISIDQ EIKILRERDSSREASTSNSSRQERPPVKPFILTRNMAQAKVFGA GYPSLPTMTVSDWYEQHRKYGALPDQGIAKAAPEEFRKAAQQQE EQEEKEEEDDEQTLHRAREWDDWKDTHPRGYGNRQNMG KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKUDL MEGRLLYTLHGHQGPATTVAPSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP LSLTSRMEEAELVKGRLQAITDKRKIQEEISQKRLKIEEDKLKH DHLKKKALREKWLLDGISSGKROREMMVNONGORDUNGTER
5479	2	1952	HRLSAMKSAVESGQADDERVREYYLLHLQRWIDISLEEIESIDQ EIKILRERDSSREASTSNSSRQERPPVKPFILTRNMAQAKVFGA GYPSLPTMTVSDWYEQHRKYGALPDQGIAKAAPEEFRKAAQQQE EQEEKEEDDEOTLHRAREWDDWKDTHPRGYGNRQNMG KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAPSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP LENQQLIMQRATP LENGGLIMQRATP LLSLTSRMEEAELVKGRLQAITDKRKIQEEISQKRLKIEEDKLKH DHLKKKALREKWLLDGISSGKEQEEMKKQNQQDQDHQIQVLEQSI
5479	2	1952 I	HRLSAMKSAVESGQADDERVREYYLLHLQRWIDISLEEIESIDQ EIKILRERDSSREASTSNSSRQERPPVKPFILTRNMAQAKVFGA GYPSLPTMTVSDWYEQHRKYGALPDQGIAKAAPEEFRKAAQQQE EQEEKEEEDDEQTLHRAREWDDWKDTHPRGYGNRQNMG KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP LSLTSRMEEAELVKGRLQAITDKRKIQEEISQKRLKIEEDKLKH QLHKKKALREKWLLDGISSGKEQEEMKKQNQQDQHQIQVLEQSI LRLEKEIQDLEKAELQISTKEEAILKKLKSIERTTEDIIRSVKV
5479	2	1952 I	HRLSAMKSAVESGQADDERVREYYLLHLQRWIDISLEEIESIDQ EIKILRERDSSREASTSNSSRQERPPVKPFILTRNMAQAKVFGA GYPSLPTMTVSDWYEQHRKYGALPDQGIAKAAPEEFRKAAQQQE EQEEKEEDDEQTLHRAREWDDWKDTHPRGYGNRQNMG KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP LSLTSRMEEAELVKGRLQAITDKRKIQEEISQKRLKIEEDKLKH QHLKKKALREKWLLDGISSGKEQEEMKKQNQQDQHQIQVLEQSI LRLEKEIQDLEKAELQISTKEEAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSSIPLDERMEKET
5479	2	1952 I	HRLSAMKSAVESGQADDERVREYYLLHLQRWIDISLEEIESIDQ EIKILRERDSSREASTSNSSRQERPPVKPFILTRNMAQAKVFGA GYPSLPTMTVSDWYEQHRKYGALPDCGIAKAAPEEFRKAAQQE EQEEKEEEDDEQTLHRAREWDDWKDTHPRGYGNRQNMG KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAPSRTGEYFASGGSDEQVMVWKSNF DURTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAPSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP LSLTSRMEEAELVKGRLQAITDKRKIQEEISQKRLKIEEDKLKH QHLKKKALREKWILDGISSGKEQEEMKKQNQQDQHQIQVLEQSI LRLEKEIQDLEKAELQISTKEEAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEQNR CALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ
5479	2	1952 1	HRLSAMKSAVESGQADDERVREYYLLHLQRWIDISLEEIESIDQ EIKILRERDSSREASTSMSSRQERPPVKPFILTRNMAQAKVFGA GYPSLPTMTVSDWYEQHRKYGALPDQGIAKAAPEEFRKAAQQQE EQEEKEEEDDEQTLHRAREWDDWKDTHPRGYGNRQNMG KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAPSRTGEYFASGGSDEQVMVWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP LSLTSRMEEAELVKGRLQAITDKRKIQEEISQKRLKIEEDKLKH DLSLTSRMEEAELVKGRLQAITDKRKIQEEISQKRLKIEEDKLKH CRIEKEIQDLEKAELQISTKEEAILKKLKSIERTTEDIIRSVKV

SEO	I Decedi - t - d		
ID	Predicted beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ì	sequence	sequence	Codon, /=possible nucleotide deletion,
	bequence	 	\=possible nucleotide insertion)
	1	1	LMTPWEESNVMQDKDAPSPKPRLSPRETIFGKSEHQNSSPTCQE
1		1	DEEDVRYNIVHSLPPDINDTEPVTMIFMGYQQAEDSEEDKKFLT
1	İ		GYDGIIHAELVVIDDEEEEDEGEAEKPSYHPIAPHSQVYQPAKP
5481	3	1422	TPLPRKRSEASPHEKHKS
1	1 ,	1442	NSPGSVCLCQCVCPSLLHCLPPLLLLLPLLLHESPQPPALRV
i	1		VATSSDRNFMNKHQKPVLTGQRFKTRKRDEKEKFEPTVFRDTLV
1		ļ	QGLNEAGDDLEAVAKFLDSTGSRLDYRRYADTLFDILVAGSMLA
1	1		PGGTRIDDGDKTKMTNHCVFSANEDHETIRNYAQVFNKLIRRYK
1	İ	l	YLEKAFEDEMKKLLLFLKAFSETEQTKLAMLSGILLGNGTLPAT
)			ILTSLFTDSLVKEGIAASFAVKLFKAWMAEKDANSVTSSLRKAN
			LDKRLLELFPVNRQSVDHFAKYFTDAGLKELSDFLRVQQSLGTR
}	ĺ		KELQKELQERLSQECPIKEVVLYVKEEMKRNDLPETAVIGLLWT CIMNAVEWNKKEELVAEQALKHLKQYAPLLAVFSSQGQSELILL
]		j	QKVQEYCYDNIHFMKAFQKIVVLFYKADVLSEEAILKWYKEAHV
			AKGKSVFLDQMKKFVEWLQNAEEESESEGEEN
5482	1492	528	THVVMTGMCYAPHQVLSYINGVTTSKPGVSLVYSMPSRNLSLRL
}-			EGLQEKDSGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPS
1			CRLQGVPHVGANVTLSCQSPRSKPAVQYQWDRQLPSFQTFFAPA
1			LDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGP
			GAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDA
[IAPRTLPWPKSSDTISKNGTLSSVTSARALRPPHGPPRPGALTP
1			TPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSGLSRMGAVP
			VMVPAQSQAGSLV
5483	1	788	FFFFKGCRAGRGNESDYRKLEEMHQRFLVSERSKDDLQLRLTRA
! :		•	ENRIKQLETDSSEEISRYQEMIQKLQNVLESERENCGLVSEQRL
1			KLQQENKQLRKETESLRKIALEAQKKAKVKISTMEHEFSIKERG
[]			FEVQLREMEDSNRNSIVELRHLLATQQKAANRWKEETKKLTESA
1			FIRINNLKSELSRQKLHTQELLSOLEMANEKVAENEKLILEHOE
		·	KANRLQRRLSQAEERAASASQQLSVITVQRRKAASLMNLENI
5484	3	1997	IMADMEDLFGSDADSEAERKDSDSGSDSDSDOENAASGSNASGS
1 1			ESDQDERGDSGQPSNKELFGDDSEDEGASHHSGSDNHSERSDNR
			SEASERSDHEDNDPSDVDQHSGSEAPNDDEDEGHRSDGGSHHSE
1 1			AEGSEKAHSDDEKWGREDKSDQSDDEKIQNSDDEERAGGSDEDK
1 1	}		LQNSDDDEKMQNTDDEERPQLSDDERQQLSEEEKANSDDERPVA
1			SDNDDEKQNSDDEEQPQLSDEEKMQNSDDERPQASDEEHRHSDD
1 1			EEEQDHKSESARGSDSEDEVLRMKRKNAIASDSEADSDTEVPKD
)	j		NSGTMDLFGGADDISSGSDGEDKPPTPGQPVDENGLPQDQQEEE
l· 1			PIPETRIEVEIPKVNTDLGNDLYFVKLPNFLSVEPRPFDPQYYE
i i	. 1	· ·	DEFEDEEMLDEEGRTRLKLKVENTIRWRIRRDEEGNEIKESNAR
j j			IVKWSDGSMSLHLGNEVFDVYKAPLQGDHNHLFIRQGTGLQGQA
[1			VFKTKLTFRPHSTDSATHRKMTLSLADRCSKTQKIRILPMAGRD
1 1	1		PECQRTEMIKKEEERLRASIRRESQQRRMREKQHQRGLSASYLE
1	1		PDRYDEEEEGEESISLAAIKNRYKGGIREERARIYSSDSDEGSE
			EDKAQRLLKAKKLTSDEVRPNLFNSRGLSCTQEPTALNEELTDQ
5485	161	1074	AGTN
		10/4	KRKILSSMMDSEAHEKRPPILTSSKQDISPHITNVGEMKHYLCG
	(CCAAFNNVAITFPIQKVLFRQQLYGIKTRDAILQLRRDGFRNLY
! !	1		RGILPPLMQKTTTLALMFGLYEDLSCLLHKHVSAPEFATSGVAA
ŀ	}	i	VLAGTTEAIFTPLERVQTLLQDHKHHDKFTNTYQAFKALKCHGI
	l	ľ	GEYYRGLVPILFRNGLSNVLFFGLRGPIKEHLPTATTHSAHLVN
		ļ	DFICGGLLGAMLGFLFFPINVVKTRIQSQIGGEFQSFPKVFQKI
5486	1404	142	WLERDRKLINLFRGAHLNYHRSLISWGIINATYEFLLKVI
		146	IPGSTISWSPAAARGLSVCRCCRLHPASAMDLFGDLPEPERSPR
1)		PAAGKEAQKGPLLFDDLPPASSTDSGSGGPLLFDDLPPASSGDS
l			GSLATS I SOMVKTEGKGAKRKTSEEEKNGSEELVEKKVCKASSV
	1		IFGLKGYVAERKGEREEMQDAHVILNDITEECRPPSSLITRVSY FAVEDGHGGIPASYFA ANN HOW TRYPPGOVER OF THE PROPERTY OF THE PROPER
- 1			FAVFDGHGGIRASKFAAQNLHQNLIRKFPKGDVISVEKTVKRCL
1			LDTFKHTDEEFLKQASSQKPAWKDGSTATCVLAVDNILYIANLG
- 1			DSRAILCRYNEBSOKHAALSLSKEHNPTQYEERMRIQKAGGNVR
·~			DGRVLGVLEVSRSIGDGQYKRCGVTSVPDIRRCQLTPNDRFILL

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Ĩ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
- [amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +-Ston
İ	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
			ACDGLFKVFTPEEAVNFILSCLEDEKIOTREGKSAADARVEAAC
5487			NRLANKAVQRGSADNVTVMVVRIGH
3407	535	182	AVSLEQIRGLQTPAPVPLPLQPCPSNCDMERVTLALLLLAGLTA
İ			LEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGK
5488	1072		CKCKSSQKQHSPVPEKAIPLITPGSATTC
1 3.00	10/2	259	AMAASGEPQRQWQEEVAAVVVVGSCMTDLVSLTSRLPKTGETIH
İ		ľ	GHKFFIGFGGKGANQCVQAARLGAMTSMVCKVGKDSFGNDYIEN
- 1	1	j	LKQNDISTEFTYQTKDAATGTASIIVNNEGQNIIVIVAGANLLL
ļ	}		NTEDLRAAANVISRAKVMVCQLEITPATSLEALTMARRSGVKTL
		1	FNPAPAIADLDPQFYTLSDVFCCNESEAEILTGLTVGSAADAGE
1	}]	AALVLLKRGCQVVIITLGAEGCVVLSQTEPEPKHIPTEKVKAVD
5489	81	893	TTVSFKI
		333	GKGPVAAFIDQSNIFLTDPKIFLGQWREEPKMPLLLLGETEPLK
1			LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVLGGV
J			LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFKELD
1			IAGDEDNRRWMRENVPGEKKPQNGIPLPPQIFNEEQYCGDFDSF FSAKEENIIYSFLGLAPPPDSKGSEKAZEGGETEAQKEGSEDVG
			NLPEAQEKNEBEGETATEETEEIAMEGAEGEAEEEEETAEGEEP
			GEDEDS
5490	81	893	GKGPVAAFIDQSNIFLTDPKIFLGQWREEPKMPLLLLGETEPLK
1 1			LERDCRSPVEPWAAASPDLA_ACLCHCQDLSSGAFPNRGVLGGV
1			LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFKELD
			IAGDEDNRRWMRENVPGEKKPQNGIPLPPQIFNEEQYCGDFDSF
1 1			FSAKEENIIYSFLGLAPPPDSKGSEKAEEGGETEAQKEGSEDVG
1 1	į		NLPEAQEKNEEEGETATEETEEIAMEGAEGEAEEEEETAEGEEP
F400			[GEDBDS
5491	204	1194	GSAPRLSLGPTGAQARDPDWWARPPSRPYTQSKEDRPDTEGRSE
1 1			QGDMASSFLPAGAITGDSGGELSSGDDSGEVEFPHSDFTFFTCC
			LAELFEKAAAHLQGLIQVASREOLLYLYARYKOVKVGNCNTDVD
1 1		1	SFFDFEGKQKWEAWKALGDSSPSOAMOEYIAVVKKI.DPGWNDOI
1 1			PEKKGKEANTGFGGPVISSLYHEETIREEDKNIFDYCPFNNIDU
1			TTKAIKSKNVDVNVKDEEGRALLHWACDRGHKELVTVLLOUPAD
1			INCQUINEGQTALHYASACEFLDIVELLLOSGADPTLRDODGGT.P
5492	3	1896	EEVIGCKTVSLVLQRHTTGKA
1	•	7030	ASKNPLSAVCTTGIMSSLAVRDPAMDRSLRSVFVGNIPYEATEE
1		1	QLKDIFSEVGSVVSFRLVYDRETGKPKGYGFCEYQDQETALSAM
i i	ľ		RNLNGREFSGRALRVDNAASEKNKEELKSLGPAAPIIDSPYGDP
1 1			IDPEDAPESITRAVASLPPEQMFELMKQMKLCVQNSHQEARNML
1			LONPOLAYALLQAQVVMRIMDPEIALKILHRKIHVTPLIPGKSQ
1	ł		SVSVSGPGPGPGLCPGPNVLLNQQNPPAPQPQHLARRPVKDI
, ,		J	PPLMQTPIQGGIPAPGPIPAAVPGAGPGSLTPGGAMQPQLGMPG VGPVPLFPGQVQMGPPRAPARA
		1	VGPVPLERGQVQMSDPRAPIPRGPVTPGGLPPRGLLGDAPNDPR GGTLLSVTGPVPDGVI CDPVVCDPVCD
1		1	GGTLLSVTGEVEPRGYLGPPHQGPPMHHASGHDTRGPSSHEMRG GPLGDPRLLIGEPRGPMIDOPGLIMMCGGGRAPOTA
1		1	GPLGDPRLLIGEPRGPMIDQRGLPMDGRGGRDSRAMETRAMETE VLETRYMERRGMETCAMETRCMEARGARGARGARGARGARGARGARGARGARGARGARGARGA
}			VLETRVMERRGMETCAMETRGMEARGMDARGLEMRGPVPSSRGP MTGGIQGPGPINIGAGGPPQGPRQVPGISGVGNPGAGMQGTGIQ
1 1		1	GTGMQGAGIQGGGMQGAGIQGVSIQGGGIQGGGIQGASKQGGSQ
1 1	İ	1	PSSFSPGQSQVTPQDQEKAALIMQVLQLTADQIAMLPPEQRQSI
<u> </u>			LILKEQIQKSTGAS
5493	1	1876	RAPMMTKAVPEEPRKPGRLTQALNSPLTWEHVWICVPGGTPDCL
1 1	1	1	TDTFRVKRPHLRRSASNGHVPGTPVYREKEDMYDEIIELKKSLH
] [1		VQKSDVDLMRTKLRRLEEENSRKDRQIEQLLDPSRGTDFVRTLA
	.		EKRPDASWVINGLKQRILKLEQQCKEKDGTISKLQTDMKTTNLE
			EMRIAMETYYEEVHRLQTLLASSETTGKKPLGEKKTGAKRQKKM
			GSALLSLSRSVQELTEENQSLKEDLDRVLSTSPTISKTQGYVEW
1		Ì	SKPRLLRRIVELEKKLSVMESSKSHAAEPVRSHPPACLASSSAL
		1	HRQPRGDRNKDHERLRGAVRDLKEERTALQEQLLQRDLEVKQLL
		İ	QAKADLEKBLECAREGEEERREREEVLREEIQTLTSKLQELQEM
			KKEEKEDCPEVPHKAQELPAPTPSSRHCEQDWPPDSSEGLPRP
		1.	RSPCSDGRRDAAARVLQAQWKVYKHKKKKAVLDEAAVVLQAAFR
			TARADALVA TARARARA VIOLA PROPERTY VI

Predicted

Predicted end

SEO

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	I PERMITTED LECVICEINE DENOMINES DESTRE
1	location	corresponding	June Acid, Faphenwalaning C-Classic
1	corresponding	to first	1 "-" Location Laisoleucina V-7
- 1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
- [amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
L	sequence		Codon, /=possible nucleofide dolories
			\=possible nucleotide insertion) QKIHTH
5499	324	926	
1	1	1	GFGQIGRGHKITTYPFSPRKSGRKGMAQSQGWVKRYIKAFCKGF
- 1	1	ļ	FVAVPVAVTFLDRVACVARVEGASMQPSLNPGGSQSSDVVLLNH
ł	1		WKVRNFEVHRGDIVSLVSPKNPEQKIIKRVIALEGDIVRTIGHK
j	}	i	NRYVKVPRGHIWVEGDHHGHSFDSNSFGPVSLGLLHAHATHILW
5500	1978	1286	PPERWQKLESVLPPERLPVQREEE
		1	KPDWRLQNLPPRLYLWRSSRFGFGHLKKRLQMDFKIEHTWDGFP
J		Ī	VKHEPVFIRLNPGDRGVMMDISAPFFRDPPAPLGEPGKPFNELW
	1	1	DYEVVEAFFLNDITEQYLEVELCPHGQHLVLLLSGRRNVWKQEL
1	1	j	PLSFRVSRGETKWEGKAYLPWSYFPPNVTKFNSFAIHGSKDKRS
			YEALYPVPQHBLQQGQKPDFHCLEYFKSFNFNTLLGEEWKQPS DLWLIEKCDI
5501	2927	2226	CPRDVCADVADCVCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
1			CRPPVSARVAPGHQGAVGGSGRRPARVEVVDAAARPSSRPFSLP
Ļ			1 MATERIALISKULDWERSDEWKEEMEI, TI. VCI. OVECVERSTRATIVE
1	f	1	SGQFSEDMIPTVGFNMRKVTKGNVTIKIWDIGGQPRFRSMWERY
Į.	į.		CRGVNAIVYMIDAADREKIEASRNELHNLLDKPQLQGIPVLVLG
		1	NKRDLPNALDEKQLIEKMNLSAIQDREICCYSISCKEKDNIDIT
5502	3	824	
i			NSAFPVWVPERTALLTCPLGAAPGSSREAPGIAGPPNSTAMSKL
-	}		GKFFKGGGSSKSRAAPSPQEALVRLRETEEMLGKKQEYLENRIQ
ł	1	i .	REIALAKKHGTQNKRAALQALKRKKRFEKQLTQIDGTLSTIEFQ
J			REALENSHTNTEVLRNMGFAAKAMKSVHENMDLNKIDDLMQEIT
1			EQQDIAQEISEAFSQRVGFGDDFDEDELMAELEELEQEELNKKM TNIRLPNVPSSI.PAOPNPVDCMCGTP
			TNIRLPNVPSSSLPAQPNRKPGMSSTARRSRAASSQRAEEEDDD IKQLAAWAT
5503	216.	654	
i l	1		KGVRRRGRVRSDSEDSHLGYFKMSFLLPKLTSKKEVDQAIKSTA EKVLVLRFGRDEDPVCLQLDDILSKTSSDLSKMAAIYLVDVDQT
}	l j		AVYTQYFDISYIPSTVFFFNGQHMKVDYGGEDPALRSIKAVRRT
			SPAGTLGEKPVNS
5504	58	3563	QLSFSFQAPVTFDDITVYLLQEEWVLLSQQQKELCGSNKLVAPL
1 1		j	GPTVANPELFRKFGRGPEPWLGSVQGQRSLLEHHPGKKQMGYMG
			EMEVQGPTRESGQSLPPQKKAYLSHLSTGSGHIEGDWAGRNRKL
1 1		i	LKPRSIQKSWFVQFPWLIMNEEQTALFCSACREYPSIRDKRSRL
1 1	j		IEGYTGPFKVETLKYHAKSKAHMFCVNALAARDPIWAARFRSIR
1 1	Ì	[DPPGDVLASPEPLFTADCPIFYPPGPLGGFDSMAELLPSSRAEL
1 1	ı		EDPGGDGAIPAMYLDCISDLRQKEITDGIHSSSDINILYNDAVE
]]		i i	DCIQUESAEGUSEEVPVVFEELPVVFEDVAIVVETPPERIOR DES
]		1	VICEDIAD VIKMIN LELLASI GPAAAKDDI. TOVI EDDAA DISTERNAL
1 1	ı	Į.	O' MONGREPOWANIVAVREADTOASAADERT TOCCOURAGE I
]		4	COSSICEEGDGPRRIKRTYRPRSTORGWFCOFDWIVIDDIADWY
()	•		+ CONCIDENTIAL PROPERTY AND THE PROPERTY OF TH
1 1	1	· · · · · · · · · · · · · · · · · · ·	TIVE TO THE PRIME OF THE PRIME TO THE PRIME
]	1	i ·	Presidence of the property of
	1	Į	VRISPCVSVLLDSSTDASEOACVGTVTRVRVOMEUVEGVEGT 1
1	1	1 .	DISEARDGIFETIVSALDELDIPERKPGWDZGIGTDGGDAF G
	j	1.	GGTA THE GEAT LOTTE AND COST DESIGNATION OF THE STATE OF
1			The voice of the contract of t
,		()	ALL VERE IUSSNERUNELOEGAADI. FOR TIDI VIDI MANDINI S. C
		l i	RRTLHALLVSWPALARHLORVAEAGGOTGHPAKGNIKIMBGEWE
			RRTLHALLVSWPALARHLQRVAEAGGQIGHRAKGMLKLMRGFHF VKFCHFLLDFLSIYRPLSEVCOKETVLITEVNATICRAYUAN
			RRTLHALLVSWPALARHLQEGAAPLEQEIIRLKDLNAVRWVASR RRTLHALLVSWPALARHLQRVAEAGGQIGHRAKGMIKLMRGFHF VKFCHFLLDFLSIYRPLSEVCQKEIVLITEVNATLGRAYVALES LRHQAGPKEEEFNASFKDGRLHGICLDKLEVAROBEOADD
			TATUTATE 1055.NKRLNELQEGAAPLEQEIIRLKDLNAVRWVASR RRTLHALLVSWPALARHLQRVAEAGGQIGHRAKGMLKLMRGFHF VKFCHFLLDFLSIYRPLSEVCQKEIVLITEVNATLGRAYVALES LRHQAGPKEEFNASFKDGRLHGICLDKLEVAEQFFQADRERTV LTGIEYLQQRFDADRPPOLKNMEVFDTMAMBGGIELA
			TATUTATE 1055.NKRLNELQEGAPLEQEIIRLKDLNAVRWVASR RRTLHALLVSWPALARHLQRVAEAGGQIGHRAKGMLKLMRGFHF VKFCHFLLDFLSIYRPLSEVCQKEIVLITEVNATLGRAYVALES LRHQAGPKEEFNASFKDGRLHGICLDKLEVAEQRFQADRERTV LTGIEYLQQRFDADRPPQLKNMEVFDTMAWPSGIELASFGNDDI LNLARYFECSLPTGYSEEALLEFWLGLKTTAOHLBESMGNDDI
			RATUPAT 1055.NKRLNELQEGAPLEQEIIRLKDLNAVRWVASR RRTLHALLVSWPALARHLQRVAEAGGQIGHRAKGMLKLMRGFHF VKFCHFLLDFLSIYRPLSEVCQKEIVLITEVNATLGRAYVALES LRHQAGPKEEFNASFKDGRLHGICLDKLEVAEQRFQADRERTV LTGIEYLQQRFDADRPPQLKNMEVFDTMAWPSGIELASFGNDDI LNLARYFECSLPTGYSEEALLEEWLGLKTIAQHLPFSMLCKNAL AQHCRFPLLSKLMAVVVCVPISTSCCFEGEKAMNEIDTDERDRYK
·		1 1 1 1 2 8	RATUPAT 1055.WKRLNELQEGAPLEQEIIRLKDLNAVRWVASR RRTLHALLVSWPALARHLQRVAEAGGQIGHRAKGMLKLMRGFHF VKFCHFLLDFLSIYRPLSEVCQKEIVLITEVNATLGRAYVALES LRHQAGPKEEFNASFKDGRLHGICLDKLEVAEQRFQADRERTV LTGIEYLQQRFDADRPPQLKNMEVFDTMAWPSGIELASFGNDDI LNLARYFECSLPTGYSEEALLEEWLGLKTIAQHLPFSMLCKNAL AQHCRFPLLSKLMAVVVCVPISTSCCERGFKAMNRIRTDERTKL SNEVLNMLMMTAVNGVAVTEYDDDD TOWN TESCRE
			RRTTHALLVSWPALARHLQEGAAPLEQEIIRLKDLNAVRWVASR RRTTHALLVSWPALARHLQRVAEAGGQIGHRAKGMLKLMRGFHF VKFCHFLLDFLSIYRPLSEVCQKEIVLITEVNATLGRAYVALES LRHQAGPKEEEFNASFKDGRLHGICLDKLEVAEQRFQADRERTV LTGIEYLQQRFDADRPPQLKNMEVFDTMAWPSGIELASFGNDDI LMLARYFECSLPTGYSEEALLEEWLGLKTIAQHLPFSMLCKNAL AQHCRFPLLSKLMAVVVCVPISTSCCERGFKAMNRIRTDERTKL LNGVPARSPASARLRKEEMGALVUFFDBTOVBILLSSGRFSHVYT
		I I I S C C	RRTTHALLVSWPALARHLQEGAAPLEQEIIRLKDLNAVRWVASR RRTTHALLVSWPALARHLQRVAEAGGQIGHRAKGMIKLMRGFHF VKFCHFLLDFLSIYRPLSEVCQKEIVLITEVNATLGRAYVALES LRHQAGPKEEEFNASFKDGRLHGICLDKLEVAEQRFQADRERTV LTGIEYLQQRFDADRPPQLKNMEVFDTMAWPSGIELASFGNDDI LNLARYFECSLPTGYSEEALLEEWLGLKTIAQHLPFSMLCKNAL AQHCRFPLLSKLMAVVVCVPISTSCCERGFKAMNRIRTDERTKL SNEVLNMLMMTAVNGVAVTEYDPQPAIQHWYLTSSGRRFSHVYT ZAQVPARSPASARLRKEEMGALYVEEPRTQKPPILPSREAAEVL LDCIMEPPERLLYPHTSOEAPGMS
5505	3312	1219 N	RRTLHALLVSWPALARHLQEGAAPLEQEIIRLKDLNAVRWVASR RRTLHALLVSWPALARHLQRVAEAGGQIGHRAKGMLKLMRGFHF VKFCHFLLDFLSIYRPLSEVCQKEIVLITEVNATLGRAYVALES LRHQAGPKEEEFNASFKDGRLHGICLDKLEVAEQRFQADRERTV LTGIEYLQQRFDADRPPQLKNMEVFDTMAWPSGIELASFGNDDI LNLARYFECSLPTGYSEEALLEEWLGLKTIAQHLPFSMLCKNAL AQHCRFPLLSKLMAVVCVPISTSCCERGFKAMNRIRTDERTKL SNEVLNMLMMTAVNGVAVTEYDPQPAIQHWYLTSSGRRFSHVYT CAQVPARSPASARLRKEEMGALYVEEPRTQKPPILPSREAAEVL CDCIMEPPERLLYPHTSQEAPGMS
5505	3312	1219 N	RRTLHALLVSWPALARHLQEGAAPLEQEIIRLKDLNAVRWVASR RRTLHALLVSWPALARHLQRVAEAGGQIGHRAKGMLKLMRGFHF VKFCHFLLDFLSIYRPLSEVCQKEIVLITEVNATLGRAYVALES LRHQAGPKEEFNASFKDGRLHGICLDKLEVAEQRFQADRERTV LTGIEYLQQRFDADRPPQLKNMEVFDTMAWPSGIELASFGNDDI LNLARYFECSLPTGYSEEALLEEWLGLKTIAQHLPFSMLCKNAL AQHCRFPLLSKLMAVVVCVPISTSCCERGFKAMNRIRTDERTKL SINEVLNMLMMTAVNGVAVTEYDPQPAIQHWYLTSSGRRFSHVYT CAQVPARSPASARLKEEMGALYVEEPRTQKPPILPSREAAEVL DCIMEPPERLLYPHTSQEAPGMS ICSPRSLSAAKMSNRNNKLPSNLPQLQNLIKRDPPAYIEEFLQ
5505	3312	1219 N	RATUPAT 1055.4KRLNELQEGAAPLEQEIIRLKDLNAVRWVASR RRTLHALLVSWPALARHLQRVAEAGGQIGHRAKGMLKLMRGFHF VKFCHFLLDFLSIYRPLSEVCQKEIVLITEVNATLGRAYVALES LRHQAGPKEEFNASFKDGRLHGICLDKLEVAEQFFQADRERTV LTGIEYLQQRFDADRPPQLKNMEVFDTMAWPSGIELASFGNDDI LNLARYFECSLPTGYSEEALLEEWLGLKTIAQHLPFSMLCKNAL AQHCRFPLLSKLMAVVVCVPISTSCCERGFKAMNRIRTDERTKL SINEVLNMLMMTAVNGVAVTEYDPQPAIQHWYLTSSGRRFSHVYT CAQVPARSPASARLRKEEMGALYVEEPRTQKPPILPSREAAEVL DCIMEPPERLLYPHTSQEAPGMS ICSPRSLSAAKMSNRNNKLPSNLPQLQNLIKRDPPAYIEEFLQ LYNHYKSNVEIFKLQPNKPSKELAELVMFMAQISHCYPEYLSNF QEVKDLLSCNHTVLDPDIRMTECKALILLENKNINNELPRINN
5505	3312	1219 N	RRTLHALLVSWPALARHLQEGAAPLEQEIIRLKDLNAVRWVASR RRTLHALLVSWPALARHLQRVAEAGGQIGHRAKGMLKLMRGFHF VKFCHFLLDFLSIYRPLSEVCQKEIVLITEVNATLGRAYVALES LRHQAGPKEEEFNASFKDGRLHGICLDKLEVAEQRFQADRERTV LTGIEYLQQRFDADRPPQLKNMEVFDTMAWPSGIELASFGNDDI LNLARYFECSLPTGYSEEALLEEWLGLKTIAQHLPFSMLCKNAL AQHCRFPLLSKLMAVVCVPISTSCCERGFKAMNRIRTDERTKL SNEVLNMLMMTAVNGVAVTEYDPQPAIQHWYLTSSGRRFSHVYT CAQVPARSPASARLRKEEMGALYVEEPRTQKPPILPSREAAEVL CDCIMEPPERLLYPHTSQEAPGMS

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
-	location	corresponding	H=Histidine, I=Isoleucine, K=Lvsine
\	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion,
-	sequence	 	\=possible nucleotide insertion)
1		}	YTMLRDSNATAAKMSLDVMIELYRRNIWNDAKTVNVITTACFSK VTKILVAALTFFLGKDEDEKQDSDSESEDDGPTARDLLVQYATG
1			KKSSKNKKKLEKAMKVLKKHRKKKKPEVFNFSAIHLIHDPQDFA
ŀ	1	{	EKLLKQLECCKERFEVKMMLMNLISRLVGIHELFLFNFYPFLQR
	1	}	FLQPHQREVTKILLFAAQASHHLVPPEIIQSLLMTVANNFVTDK
			NSGEVMTVGINAIKEITARCPLAMTEELLQDLAQYKTHKDKNVM
1	Ì		MSARTLIHLFRTLNPQMLQKKFRGKPTEASIEARVQEYGELDAK
ļ	}		DYIPGAEVLEVEKEENAENDEDGWESTSLSEEEDADGEWIDVOH
İ			SSDEEQQEISKKLNSMPMEERKAKAAAISTSRVLTOEDFOKIRM
İ		į.	AQMRKELDAAPGKSQKRKYIEIDSDEEPRGELLSLRDTERLHKK
ļ)	PKSDKETRLATAMAGKTDRKEFVRKKTKTNPFSSSTNKEKKKOK
5506			NFMMMRYSQNVRSKNKRSFREKQLALRDALLKKKKRMK
3306	1	1531	FRGDLCGQRGGSAPGEGGSSAWPAPAHPLPEREREALCPGRS
1	[CSGGGGETPGTTPVWSPLEGGGDEELRPNPYVRFPYRWWAVVV
1			LAAFPSLGAGGETPEAPPESWTQLWFFRFVVNAAGYASFMVPGY LLVQYFRRKNYLETGRGLCFPLVKACVFGNEPKASDEVPLAPRT
[(EAAETTPMWQALKLLFCATGLQVSYLTWGVLQERVMTRSYGATA
1	. 1		TSPGERFTDSQFLVLMNRVLALIVAGLSCVLCKQPRHGAPMYRY
1			SFASLSNVLSSWCQYEALKFVSFPTQVLAKASKVIPVMLMGKLV
			SRRSYEHWEYLTATLISIGVSMFLLSSGPEPRSSPATTLSGLTL
1			LAGYIAFDSFTSNWQDALFAYKMSSVOMMFGVNFFSCLFTVGSL
1			LEQGALLEGTRFMGRHSEFAAHALLLSICSACGOLFIFYTIGOF
	•		GAAVFTIIMTLRQAFAILLSCLLYGHTVTVVGGLGVAVVFAALL
5507	3704		LRVYARGRLKQRGKKAVPVESPVQKV
3307	3/04	1271	PRGTRRCRPAGRASRRARRRPPCPGPAAPGSLEIGGFGTAAGKK
1	•		VAVADVQFGPMRFHQDQLQVLLVFTKEDNQCNGFCRACEKAGFK
1			CTVTKEAQAVLACFLDKHHDIIIIDHRNPRQLDAEALCRSIRSS KLSENTVIVGVVRRVDREELSVMPFISAGFTRRYVENPNIMACY
}			NELLQLEFGEVRSQLKLRACNSVFTALENSEDALEITSEDRFIQ
1			YANPAFETTMGYQSGELIGKELGEVPINEKKADLLDTINSCIRI
1			GKEWQGIYYAKKKNGDNIQQNVKIIPVIGQGGKIRHYVSIIRVC
}	J		NGNNKAEKISBCVQSDTHTDNQTGKHKDRRKGSLDVKAVASRAT
			EVSSQRRHSSMARIHSMTIEAPITKVINIINAAQESSPMPVTEA
1			LDRVLEILRTTELYSPQFGAKDDDPHANDLVGGLMSDGLRRLSG
1 5			NEYVLSTKNTQNVSSNIITPISLDDVPPRIARAMENEEYWDFDI
1			FELEAATHNRPLIYLGLKMFARFGICEFLHCSESTLRSWLQIIE
			ANYHSSNPYHNSTHSADVLHATAYFLSKERIKETLDPIDEVAAL
. }			IAATIHDVDHPGRTNSFLCNAGSELAILYNDTAVLESHHAALAF QLTTGDDKCNIFKNMERNDYRTLRQGIIDMVLATEMTKHFEHVN
			KPVNSINKPLATLEENGETDKNQEVINTMLRTPENRTLIKRMLI
1			KCADVSNPCRPLQYCIEWAARISEEYFSQTDEEKQQGLPVVMPV
1	}		FDRNTCSIPKSQISFIDYFITDMFDAWDAFVDLPDLMQHLDNNF
			KYWKGLDEMKLRNLRPPPB
5508	1151	691	LSSVFSRRSASMFAVGCSMGPFLHYWYLSLDRLFPASGLRGFPN
1 1	1	ı	VLKKVLVDQLVASPLLGVWYFLGLGCLEGOTVGESCOELREKFW
	İ		EFYKADWCVWPAAQFVNFLFVPPQFRVTYINGLTLGWDTYLSYL
- <u></u>			KYRSPVPLTPPGCVALDTRAD
5509	1238	619	RKSRGCQNALSASGPAAAAAAIMVRKLKFHEQKLLKQVDFLNWE
1	İ		VTDHNLHELRVLRRYRLQRREDYTRYNQLSRAVRELARRLRDLP
1 1	1		ERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRRR
} }			LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM
5510	96	1105	EDFVTWVDSSKIKRHVLEYNEERDDFDLEA
~~~	20	1195	PAGAHLSSGSSEPLVEPGRGRVGARVKGERGLQASGSAPGRSKM
1 1	ļ	ļ	AEGERQPPPDSSEEAPPATQNFIIPKKEIHTVPDMGKWKRSQAY
<u> </u>		ļ	ADYIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTLDRWID
[ . [	1		ETPPVDQPSRFGNKAYRTWYAKLDEEAENLVATVVPTHLAAAVP
]		J	EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI
1			WGSSQLIDHPYLEPRHFVDE KAVNENHKDYMFLECILFITEMKT
		İ	GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF
			KFGSLLPIHPVTSG

The bestinding in unlocated and nucleotic decision. Cocation control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control c		SEO	Predicted	,	
Sol: nucleotide location corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding amino acid residue of amino acid asiquence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequen		_ ~	beginning		
Corresponding   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Cof			nucleotide		
COTRESPONDING to first amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid		1			1 Caucanite Acid, rephantistancia, a sa
to first anino acid residue of sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence		]			o jamabolulie, leisolencina Vitaria
residue of anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid acid acid acid acid acid acid acid			to first		Debeucing, Namethioning Nadomass
residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence		1			refloring, Oscillamine Dalvers
amino acid sequence  Codo, /-possible nucleotide deletion, sequence  Codo, /-possible nucleotide insertion)  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980  1980		1		amino acid	Sectine, TeThreonine Vevaline
Sequence		j			W=ITYPtophan, Y=Tyrosine V=II=
SS11   276		Ĺ		Jeduciice	I access / abossible uncleutide desert
TVLOQV IE DOSKYCI ENGLYS TOORTWINK INNELLTIK HERSTI IONF VALKSELIFSGLPOKK IVVERSINNAKK PIVE HERSTI IONF VALKSELIFSGLPOKK IVVERSINNAKK PIVE HERSTI IONF VALKSELIG PROJECTION OF THE PROVINCE AND THE PROVINCE AND THE PROVINCE PROVINCE AND THE PROVINCE PROVINCE AND THE PROVINCE PROVINCE PROPERTY OF THE PROVINCE PROVINCE PROPERTY OF THE PROVINCE PROPERTY OF THE PROVINCE PROPERTY OF THE PROVINCE PROPERTY OF THE PROVINCE PROPERTY OF THE PROVINCE PROPERTY OF THE PROVINCE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF		5511	276	1980	1 /-POBSIDIE NUCLEOFIDE incertion)
TVLOQV IE DOSKYCI ENGLYS TOORTWINK INNELLTIK HERSTI IONF VALKSELIFSGLPOKK IVVERSINNAKK PIVE HERSTI IONF VALKSELIFSGLPOKK IVVERSINNAKK PIVE HERSTI IONF VALKSELIG PROJECTION OF THE PROVINCE AND THE PROVINCE AND THE PROVINCE PROVINCE AND THE PROVINCE PROVINCE AND THE PROVINCE PROVINCE PROPERTY OF THE PROVINCE PROVINCE PROPERTY OF THE PROVINCE PROPERTY OF THE PROVINCE PROPERTY OF THE PROVINCE PROPERTY OF THE PROVINCE PROPERTY OF THE PROVINCE PROPERTY OF THE PROVINCE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF		1	· ·		HSPROIOVOAKELARKER
FEYERLIGAND FOR LEFTY YOUNG READING SWARAGEFFOR LE LEGOVALS LINE SET IN YYKELGY FEYERSES FIRE SORULLUS SCHOLLER SET IN YYKELGY FEYERSES FIRE SORULLUS SCHOLLER SET IN YYKELGY FEYERSES FIRE SORULLUS SCHOLLER SET IN YYKELGY FEYERSES FIRE SORULLUS SCHOLLER FIRE THE YYKELGY FEYERSES FIRE SORULLUS SCHOLLER FIRE THE YOUNG COUNTY ON THE YOUNG SORULLUS SCHOLLER FIRE THE YOUNG COUNTY ON THE YOUNG SORULLUS SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SORULLUS SCHOLLER FIRE YOUNG SCHOLLER FOR YOUNG SORULLUS SCHOLLER FIRE YOUNG SCHOLLER FOR YOUNG SORULLUS SCHOLLER FOR YOUNG SORULLUS SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SORULLUS SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHOLLER FOR YOUNG SCHO		}			
LIGNOVALSILMOKT NOT AV UNERALDOK YORKYSGESFYRE SONULLILE KICILLKTI KGTAVVDLGGMGPFORLE SONULLILE KICILLKTI KGTAVVDLGGMGPOSI ICT VMRSDGT SLYATFIDLADA I BURLEK KICILLKTI KGTAVVDLGGMGPOSI ICT VMRSDGT SLYATFIDLADA I BURLEK KICILLKTI KGTAVVDLGGMGPOSI ICT VMRSDGT SLYATFIDLADA I BURLEK KICILLKTI KGTAVVDLGGMGPOSI ICT VMRSDGT SLYATFIDLADA I BURLEK KICILLKT KGTAVVDLGGMGPOSI ICT VMRSDGT VASICULLUL KURCH KOM MASIKTYKEL MURDEV VOR GUNDEN FOR VOR SUCKESPEVE VILLEHLIG KOM KOM MASIKTYKEL MURDEV THARLISLEST FEGOTYLINDER KOM KOM VOR SONUL THARLISLEST FEGOTYLINDER KOM KOM VOR SONUL THARLISLEST FEGOTYLINDER KOM KOM VOR SONUL THARLISLEST FEGOTYLINDER KOM KOM VOR SONUL THARLISLEST FEGOTYLINDER KOM KOM VOR SONUL THARLISLEST FEGOTYLINDER KOM KOM VOR SONUL THARLISLEST FEGOTYLINDER KOM KOM VOR SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL THARLISLES AND SONUL TH		ł	1		HLESTITCHETANI YEAL CHOSEN STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STAT
SOEPULKILEE KGILLKII KOTAVULGENGOPES I CTWRREDGT SULARIDLAG HURKTAFOTH I YOTOKGOKKHPOOVPOULKI MSTWARDE CAHUP FOVUCGMKTREDUTHI YOTOKGOKKHPOOVPOULKI MSTWARDE CHUP FOVUCGMKTREDUTHI JOTKGLILISUKFSWOR WSTAKTELARIPORTAEKUGAALIIODPKGLILISUKFSWOR VOSHOVPLOVTHARIHESLEETFECTUNDENTACLGEPGS VSILGHLIAFDEVLIKSSODPOPHIVSYLLITISHAAVAHKII OTKOSP PEVAOARIHIEKAKASVIANAMKIIDHONTACLGEPGS VSILGHLIAFDEVLIKSSODPOPHIVSYLLITISHAAVAHKII OTKOSP PEVAOARIHIEKAKASVIANAMKIIDHONTACLGEPGS VSILGHLIAFDEVLIKSSODPOPHIVSYLLITISHAAVAHKII OTKOSP PEVAOARIHIEKASSODPOPHIVSYLLITISHAAVAHKII OTKOSP PEVAOARIHIEKASSODPOPHIVSYLLITISHAAVAHKII OTKOSP PEVAOARIHIEKASSODPOPHIVSYLLITISHAAVAHKII OTKOSP PEVAOARIHIEKASSODPOPHIVSYLLITISHAAVAHKII OTKOSP PEVAOARIHIEKASSODPOPHIVSYLTISHAAVAHKII OTKOSP PEVAOARIHIEKASSODPOPHIVSYLTISHAAVAHKIIL OTKOSP PEVAOARIHIEKASSODPOPHIVSYLTISHAAVAHKIIL OTKOSP PEVAOARIHIEKASSODPOPHIVSYLTISHAAVAHKIIL OTKOSP PEVAOARIHIEKASSODPOPHIVSSOPPPEPSSPPS PSTARGOPSSRDTMSDSEESSODROLKIVVIGGASKATSITTC PAOATISMOKYLOHOMINISHAAVATAAAVAHAA OTKOSP PEVAOARIHIIN TERPEKIHER CORSCIVUKADIVANINOEPMS TOPUAALMAKIILOEMINITISHEMIHTEN SSPEPPEPSSPPS PSTARGOPSSRDTMSDSEESSODROLKIVVIGGASKATSITTC PAOATISMOKYLOHOMINISHAAVATAAVATAAVAHAA OTKOSP PAOATISMOKYLOHOMINISHAAVATAAVATAAVAHAA OTKOSP PAOATISMOKYLOHOMINISHAAVATAAVATAAVAA OTKOSP PAOATISMOKYLOHOMINISHAAVATAAVAA OTKOSP PAOATISMOKYLOHOMINISHAAVATAAAA OTKOSP PAOATISMOKYLOHOMINISHAAVATAAAA OTKOSP PAOATISMOKYLOHOMINISHAAVAANAAVAAAAAAAAAAAAAAAAAAAAAAAAAAAAA		1	1		FGYEEKLOSNPLOHLEFTATION FOR THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE
SLYATEDLAAAIDAMENYEPOTMYTYTEKKENGOVETLENVINSIPOLICATION MSIKTYKELINPORTHEWOLOALIIO (DYKOLLISDYKEFSWOR MSIKTYKELINPORTHEWOLAALIIO (DYKOLLISDYKEFSWOR MSIKTYKELINPORTHEWOLAALIIO (DYKOLLISDYKEFSWOR VOORGOTSUPIOTHARLHSLEETEGCYIINDOTHACIOPEGS VOORGOTSUPIOTHARLHSLEETEGCYIINDOTHACIOPEGS VOORGOTSUPIOTHARLHSLEETEGCYIINDOTHACIOPEGS VOORGOTSUPIOTHARLHSLEETEGCYIINDOTHACIOPEGS VOORGOTSUPIOTHARKUSULANGMELIGITPUCRM DPSILLTITYTOSVULULUKKNINSKREPITOODEAKYPIOLI IEKKISHNTRYFEFGLPSDHVULGKUNTVOLLAKIINELUP RAYTPVSSDDORGVULI KIYFKNINPOYPEGGKMTQY.EBNM IGETIFFROPRGRIPYIIGFGGLGI PPOTSEPKKTLAHLGMIA GGTGIFFMOLIIRITKYDESPRIPSBERTMSLIFTOODEAKYPIOLIBINK IGETIFFROPRGRIPYIIGFGGLGI PPOTSEPKKTLAHLGMIA GGTGIFFMOLIIRITKYDESPRIPSBERTMSLIFTOODEASKITCHITO FANDETSGGYKOTTIGDFPLICTAAIMENLEKIGYTUNGENGELDIVERELE EIAATHEDOPPLICTAAIMENLEKIGYTUNGENGSCHITOTE POTSEGGEGSEDMINSSEESEGOROLKUTOSSESPPPEPESPS PPTSRGGOSSDTMINSSEESEGOROLKUTOSSESPPPEPESPS PPTSRGGOSSDTMINSSEESEGOROLKUTOSSASKITCHITO FANDETSGGYKOTTIGDFPRRITIDGGNAVTLOIDUNGTIG GKMIDKYIYGAGGAULVUTTINNOSFENLEBWATTUNKOSPENE TOPLUALUGNKIDLEHMATIKERISCHOPTSKIRTVIKOSPRIPSE FORMINGAGGAULVUTTINNOSFENLEBWATTUNKOSPENE TOPLUALUGNKIDLEHMATIKERISCORVARAITUNGEMS SYPLEFGKVARABILGIALUKHASI EOSGRVAKAAITUNGEMS PRINSPRSSINGAUO  SYPLEFGKVARABILGIALUKHASI EOSGRVAKAAITUNGEMS FUNGSMINGLIGHHATYNY PFGILLOVAJOLIVUTUNGEMS FUNGSMINGLIGHHATYNY PFGILLOVAJOLIVUTUNGEMS FUNGSMINGLIGHANSTAVUTUNGATAITUNGEMPSITATUNGEMS FUNGSMINGLIGHANSTAVUTUNGATAITUNGEMPSITATUNGEMPSITATUNGEMPSITATUNGEMPSITATUNGEMPSITATUNGEMPSITATUNGEMPSITATUNGEMPSITATUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAITUNGATAIT			İ		LGDVQALSLWOKFRDLSTEEVIDAVKELGIBLE
MSINDRERCOHUP FOVOCAMETRIONTHOLISIOLISION MASIETT RELEVISION STUDIES AND MASIETT RELEVISION STUDIES AND MASIETT RELEVISION STUDIES AND MASIETT RELEVISION STUDIES AND MASIETT RELEVISION STUDIES AND MASIETT RELEVISION STUDIES AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT REPRESENTATION AND MASIETT R		1	1		SQEVLKLLESKGLLLKTIKGTAVUDI SCNAPDAST
MASINTTKELKRIPGETAERWGLAALIOVERSIMDE VOOSRODTSUPLYTHARLISILEETTGGYLINDFRACLGEPGG VIORSREDTSUPLYTHARLISILEETTGGYLINDFRACLGEPGG VIORSPEVAGRARHICKSOPPOPRINTSYLLTISHAAVARKIT OTKOS PEVAGRARHICKSOPPOPRINTSYLLTISHAAVARKIT OTKOS PEVAGRARHICKSOPPOPRINTSYLLTISHAAVARKIT OTKOS PEVAGRARHICKSOPPOPRINTSYLLTISHAAVARKIT OTKOS PEVAGRARHICKSOPPOPRINTSYLLTISHAAVARKIT OTKOS PEVAGRARHICKSOPPOPRINTSYLLTISHAAVARKIT OTKOS PEVAGRARHICKSOPPOPRINTSYLLTISHAAVARKIT OTKOS PEVAGRARHICKSOPPOPRINTSYLLTISHAAVARKIT OTKOS PEVAGRARHICKSOPPOPRINTSYLLTISHAAVARKIT OTKOS PEVAGRARHICKSOPPOPRINTSYLLTISHAAVARKIT OTKOS PEVAGRARHICKSOPPOPRINTSHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISHAAVARTITISH		i	1		T SECTION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF T
VPOSRCDTOVPLOTHARLISLEETEGGYINDFITACLOEPOS VSILOHILARIDEVLYKSCOPOPRHIVSYLLTISHANAJAKKI JCKOS PEVAGARHILAKAVASVLANDENTACLOEPOS VSILOHILARIDEVLYKSCOPOPRHIVSYLLTISHANAJAKKI JCKOS PEVAGARHILAKAVASVLANDELIGITPVCRM DPSLLITITYTSVTULVLKSKNISRREEPITIODPEKKYLDI IEKKISHITARFREEDESDHVLLGUSTVOKTAM RAYPVSSDDDREVDLI IKIYFKNVHOOYPEGGRATOY-ZENK RAYPVSSDDDREVDLI IKIYFKNVHOOYPEGGRATOY-ZENK RAYPVSSDDDREVDLI IKIYFKNVHOOYPEGGRATOY-ZENK RAYPVSSDDDREVDLI IKIYFKNVHOOYPEGGRATOY-ZENK RAYPVSSDDDREVDLI IKIYFKNVHOOYPEGGRATOY-ZENK RAYPVSSDDDREVDLI IKIYFKNVHOOYPEGGRATOY-ZENK RAYPVSSDDREVERGREENESSERTERSGERNYLJESSPPPEPSSPP EARATHDOPOLNAVINIDELINE PICHWXSCHYADRIKEHLDPPAK STLLLVCGPPELIOTAAHNNLEKKYTOMIFTY PPTSRCGPOSRDINKSDEEESDROLKIVVLGOGASCKYSLITIC FARSTERSKYKOTIGLIPFIRI I'LLPERINVTLQUESSPPPEPSSPPE PPTSRCGPOSRDINKSDEEESDROLKIVVLGOGASCKYSLITIC CAMBERY YNGAPKYTOOR PICHWATAVIVLOOGASCKYSLITIC CAMBERY YNGAPKYTOOR PICHWATAVIVLOOGASCKYSLITIC CAMBERY YNGAPKYTOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATAVIVLOOR PICHWATA		1			1 SWEET CONVEYED WITH THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE STORE OF THE
VSILOHELBRPDEVIKSSOPPOPRHIVSYLLITISHAANVAHKI OKOS PPEVAGRAHHLKAVRSVIANOMKILGITEVCEM DESLLITITITYTVTUVULVUKSMINSKEPETIOOPEAKVELD. IEKKISHTRAFREGLPSDHVLGLPVGNYVQLLAKIDMEKUL RAYPPVSSDDRGVPULI IKI YKNVIVPKORGMYNOVLENNK IGETIFFRGPRGRJFYIGMIGHIGI PROTTEPKKTLADHLGWIA GGTGITHMQLIRHITURDSDETRISLI HANOTEEDILWKKELE ELARTHPOOFDLWTLDRPPIGWKYSGCPYTJADHLGWIA GGTGITHMQLIRHITURDSDETRISLI HANOTEEDILWKKELE ELARTHPOOFDLWTLDRPPIGWKYSGCPYTJADHLGWIA GGTGITHMQLIRHITURDSDETRISLI HANOTEEDILWKKELE ELARTHPOOFDLWTLDRPPIGWKYSGCPYTJADHIGWIA GGTGITHMQLIRHITURDSDETRISLI HANOTEEDILWKKELE ELARTHPOOFDLWTLDRPPIGWKYSGCPYTJADHIGWIA GGTGITHMQLIRHITURDSDETRISLI HANOTEEDILWKKELE ELARTHPOOFDLWTLDRPPIGWKYSGCPYTJADHIGWIA GTATIPHPOOFDLWTLDRPPIGWKYSGCPYTJADHIGWIA GTATIPHPOOFDLWTLDRPPIGWKYSGCPYTJADHIGWIA GTATIPHPOOFDLWTLDRPPIGWKYSGCPYTJADHIGWIA GTATIPHPOOFDLWKYSGCPYTJADHIGWHA FARAFICH GOORGACHTURG GARAFTICH GARAGKATALTIC GKMLDKYJYGAGCVULVYDITIN YGGFENLEDBYTJVKKVSGESE TOPUVALVGNGIDHERTIT TREPHLHFOCONGESSHIYARAT DSVPLCPGKWAABILGITURGMALTURVILGIDHIGOTIG GKMLDKYJYGAGCVULVADIVANTQEPMS TOPUVALVGNGIDHIGWTT TREPHLATIC GOORGACHT TOPUVALVGNGIDHIGWTT TREPHLATIC GOORGACHT TOPUVALVGNGIDHIGWT TREPHLATIC GOORGACHT TOPUVALVGNGIDHIGWT TREPHLATIC GOORGACHT TOPUVALVGNGIDHIGWT TOPUVALVGNGIDHIGWT TREPHLATIC GOORGACHT TOPUVALVGNGIDHIGWT TOPUVALVGNGIDHIGWT TOPUVALVGNGIDHIGWT TOPUVALVGNGIDHIGHT TOPUTAL TOPUTAL TOPUTAL TREPHLATIC GOORGACHT TOPUVALVGNGIDHIGHT TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPUTAL TOPU		ł			1
120 1015 DPEVAGRELLERAVRSVLANGKLIGITPVCMS DPSILLTITYTYTVTUTUTUTUTUTUTUTUTUTUTUTUTUTUTUTUTU		1	İ		1 '- YOU OF LOT THAK THE TERRORY MOTION OF
120 1015   DPSLLTTTVTGVTUVLVLKSMISKRREPTTLODPEKYPLD.   IBKEKLSHNTRERREGLSSDHVLGLPUNDYVOLLAKINDELTV   RAYTPVSSDDRGFVDLIKITYTEMPLYPEGGKMOTV-EIMK   IGETIFFRGFRGFLFYHGPGRGLGIRPDGTSEPKKTLADHLGMIA   GGTGITHM_QLIRHITKOPSDETRIGHERDYSEPKKTLADHLGMIA   GGTGITHM_QLIRHITKOPSDETRIGHERDYSEPKKTLADHLGMIA   GGTGITHM_QLIRHITKOPSDETRIGHERDYSEPKKTLADHLGMIA   GGTGITHM_QLIRHITKOPSDETRIGHERDYSEPKKTLADHLGMIA   STLLLVGGPPHLOTAAHPRILEKLIFLADHLGFMIA   STLLLVGGPPHLOTAAHPRILEKLIFLADHLGFMIA   FAMRLPSGSFRTPFAGASTFGGSCENTVLFSSSPPFPEPSSPPS   PPTSRGGPGSRDTMBSEERSQNDRLKLVVLIGDGASGKTSLITTC   FAGETGKQYKQTTGLDFPLRRITLPGRILNTVLIGDGASGKTSLITTC   FAGETGKQYKQTTGLDFPLRRITLPGRILNTVLIGDGASGKTSLITTC   FAGETGKQYKQTTGLDFPLRRITLPGRILNTVLIGDGASGKTSLITTC   FAGETGKQYKQTTGLDFPLRRITLPGRILNTVLIGGGASGKTSLITTC   FAGETGKQYKQTTGLDFPLRRITLPGRILNTVLIGGGASGKTSLITTC   FAGETGKQYKQTTGLDFPLRRITLPGRILNTVLIGGGASGKTSLITTC   FAGETGKQYKQTTGLDFPLRRITLPGRILNTVLIGGGASGKTSLITTC   FAGETGKQYKQTGLDFPLRRITLPGRILNTVLIGGASGKTSLITTC   FAGETGKQYKQTGLDFPLRRITLPGRILNTVLIGGASGKTSLITTC   GYMULKYMAGRASGASGLADGTFFFICHTURLIVLVVLIGGASGKTSLITTC   TYMPPRSSMCANQ   VINEYSMIGHTS GGGATGALDGTTKSLIKKYLCKKOKRT   CTIGSTLTFYLETELLGTTLVGMALATGGAGGFGFTCHLMLND   YKQGHMOLLOWHHFTMYFFFGLLGVADLICFTISSLPSUKKOKRT   CTIGSTLTFYLETELLGTTLVGMALATGGAGGFTGCHLMLND   YKQGHMOLLOWHHFTMYFFFGLLGVADLICFTISSLPSUKKOKRT   GYMULKYMAGRGSGSEEMB   TYMPGRGGASTGFTTMVLGGTSMLPGGGAFTGWLVKSRCLLGAPF   FVELVERGLDFDGASGLADGTGTTMVLGGTSMLPGGAFTGWLVKSRCLLGAPF   FEVENSULLAPSHLMALLTLGINSAMVLDGGTSHELDFGUNTATLDSLIT   GOTED TRIKLGHLANDVLGGTSMLPGGAFTGGALQDILGSSVGKE   YNDTGGALDFJGGMALHKGLETQLLGCTVDTSVAKGGSLBSWMG   SVPEGVLEDIKATGTVSDLKGGIKGALGAKRNIDGNNERPSPPP   NDYSPLBGERTLIHTDPAKNCVANLGGAIFGGALQDILGSSVGKE   YNDTGGALGGNTGGSVTGSTTMDLEGGTMATHTSTTKL   KAMMRYDGTGFSPRKSFTASSFLFFRHALLLITLALLGFFTWAG   KAMMRYDGTGFTRFVTGSFGMATGAGAGAGAGA   KAMMRYDGTGFTRFVTGSFGMATGSFGMATGGAAGAGAGAGAAGA   KAMMRYDGTGFTRFVTGSFGMATGSFGMATGGAAGAGAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA		1	- 1	•	I TO SEE THE VERY PROPERTY OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF T
I IEKKEISHMTRERFERSLESDHULGVENOTYOLLAKINDELVY RAYTPVSSDDDRGFVDLIIKTYFRNYHEQYERGKMTQY-ZENNK IGETIFFERGRGRIPYHIGPNOTHOTYSELKALINDELVY RAYTPVSSDDDRGFVDLIIKTYFRNYHEQYERGKMTQY-ZENNK IGETIFFERGRGRIPYHIGPNOTHOTYSERVERTADHIGMIA GGTGITFMLQLIRHITKOPSDRTRMSLIFANOTEDIILVRKELE EIARTHEQOFDLWTYLDRPPIGMENSEGFVTADMIKEHLPPPAK STLLLVGPPPPLIQTAAHPRILEKLGYTQDMIFTY ARMELPSGBFTPPBGASTFRGSCENTLYSSSPPPFEPSSFPS PPTSRGGPGSRDTMSDGEESQORGCKIVVLGDCASGKTSLTTC FAGSTFCKQYKQTIGLDFFLRRITLDGGLNVTLQIMDIGGOTIG GKMLDKYIVGAGGVLLVVDITKYQSTELBEWITVVKKYGESS TOPLVALVONKIDLEHMRITKDEKHLRYCOGNFSSHFYSAKTG DSVFLCFGCVARALIGKKINAGEIBESGGRVVKADIVNYNGEPMS TOPLVALVONKIDLEHMRITKDEKHLRYCOGNFSSHFYSAKTG DSVFLCFGCVARALIGKKINAGEIBESGGRVVKADIVNYNGEPMS RTVMPPRSSMGAVQ VNRFSHMONFGGBALDGTFFFIIGLMCTKSILXVICKGKRF TYMPPRSSMGAVQ VNRFSHMONFGGBALDGTFFFIIGLMCTKSILXVICKGKRF CYLGSKTLFYR_EILEGITIVCMALTGMGEQPIPCOFHLMLYD YRGGHMONLLGWHIFTMYPFFGLLGSGGFFAUVIDLGDAF TKGGFAGFTGFRATVILLELLESSILLLQGSMFFGIGFVLYPSGGPAWDIM DHENILFITICFCWHYAVTIVIVGMNYAFITHULKSRLKRLCSS EVELLKANEREOSSEEM FVRLVGRGDCDPLLSVULTTMPLYEGLGSGGFKTAVVIDLGEAP TKGGFAGFTGFRCIIBSVIKRAGMPREVRUVQYNINTEELLYSVL KEFIHILFYRHLLVUPRDFRRVVIIESUCPSIPFETLTFULFFYL FEVDSVLLAPSHIMALLTIGINSAMVLDCGYBESUVLPIVEGIP VLNCHGALPLIGGGALHFGKALHKELEFOLLEGVTDTSVAKEGSLFSVMG SVPEGVLEDIKARTCFVSDLKRGLKIQAKTOLAKFNIDGNNERVSPPP NUTYELDGERILHHLISSITENSVVEILIGSLGCGGFGVATAVILIDSL ICCFIDTRKGLARNLVVIGGTSMLPGFHIRILARIEKTULERSVMG SVPEGVLEDIKARTCFVSDLKRGLKIQAKTOLAKFNIDGNNERVSPPP NUTYELDGERILHHLISSITENSVVEILIGHLILTIALLGGPTWAG KMAGFGGGKYFSTTEDUHBITGLRVSVGLLLVKSVVVLLGDSW DVKLGALGHTGFTUNGESFGMMTPGAFLGRWMYTKSCN YFYGKLDGGISSAFPSGGGOVLVGTYGOPLIGIKSIGFFWNY YFYGKLDGGISSAFPSGGGOVLVGTYGOPLIGIKSIGFFWNY YFYGKLDGGISSAFPSGGGOVLVGTYGOPLIGIKSIGFFWNY YFYGKLDGGISSAFPSGGGOVLVGTYGOPLIGIKSIGFFWNY TDGTSDLJKLGALSVKEDAKTOOLDEKFONEKK  5517 246 499 SEIVVAMRTDSSKWTDUESGVANFASSARAGRRNALPDIOSSAA TGGTSVAMRTDSSKWTDUESGVANFASSARAGRRNALPDIOSSAA FLETVANGWFGGFTAVKKURCHTVOLARDENPTHREGEGMA PLKTVANGWFGGFTVAVKMUKKTFTVLSANLFOKDENTINGENDEPT HIMBSNMPDGFFAVKKPDCYYSIGRENNYGOLDLWRNPDDAFRY HUMPSGROFTVANKKKURKTFTVLSANL		5512	120	1015	T TO THE TOTAL PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE
RATTPVSSDDDRGFQDLIKITYTERWHEGYEGKGMOTY-ERMK IGETIFFRGRGRLFYHIGPGRLGIRPOTSEPKKTLADHLGMIA GGTGITHMQLIRHTKHOSPGRTRANGLIFENOTEGILVRKELE ELARTHPDOFDLWYTLDRPPIGKKYSGFVTADMIKEHLPPAK STLILUCGPPPLIOTAAHPRILEKLYDDNIFTY  2 837 ARWRLPSDSFRTPFAGAETPGRGSCRNTLFSSSPPPFEFSSFPS PTSRGGOGRDTMSDSEESGORGLKIVVLIGDASGKTSLITTC FAQETFGKQYKQTIGLDFFLRRITLDGRLANTUQUBLGGOTIG GKMLDKYIVGAGGVLLVYDLTRYQSFENLEBWITVVKKYSEESE TOPLVALVONKIDLEHMRTIKPEKHLRPCQENGFSSHPYSAKTG DSVFLCFGKVAAELLGIKLNKABIEGSGRVVKADIVNYNQEPMS RTVNPRSSMCAVQ VNRPSSIMGNFRGHALPGTFFFIIGLWGTKSILKYICKKQRRT CYLGSKTLFYR-EILBGITVCMALTGMAGFOIPGCOPHLMLYD YKQGHNOLLGHHIFTNYFFFIIGLWGTKSILKYICKKQRRT CYLGSKTLFYR-EILBGITVCMALTGMAGFOIPGCOPHLMLYD YKQGHNOLLGHHIFTNYFFFIIGLWGTKSILKYICKKQRRT CYLGSKTLFYR-EILBGITVCMALTGMAGFOIPGCOPHLMLYD YKQGHNOLLGHHIFTNYFFFIIGLWGTKSILKYICKKQRRT CYLGSKTLFYR-EILBGITVCMALTGMAGFIICHVVPFLGGLOGGGGFADUM MENALPTVAFFIFYNNTHGRENLDIFFIIGLWGTKSILKYICKKQRRT CYLGSKTLFYR-EILBGITTVCMALTGMAGFIICHVVPFLGGLOGGGGFADUM MENALPTVAFFIFYNNTHGRENLDIFFIIGLWGTKSILKYICKKGRRT CYLGSGGGGGGFGFCITGSVLILGGGGGGGFATVVTDGLAFFI EFLVRNNVLLBLIRSSILLLGGGSWFFOIGFVLYPPSGGPADUM DHENILPTICFCCHHAVYIVTVCMNYAFITHUVKSRLKRLCSS EVGLLKNAREROSSEEBM TKCGFAGGTGGFCITISVV KRAGPKPVGVVQYNINTEELYSYL KEFHILLYFRILLVNPRDERVVI IESVLCPSHFRETLITVLFKY FEVESVLLAPSHLMALLTGINSAMVLDGCYSEFRETVLTVLFKY VLNCKGALPJLGGKALHKELETQLLEGCTVDTSVAKEGSLPSWG SVEGVLEDIKARTCFVSDLKKRGLKTOAAKNTDIGNNERPSPPP NDTPLLDGEKIHHLGSTRDSVVCEITGALQDILGSSVSKE YNNGTGRIPDMGSLNNPPLEMMPDVCKTOPPLMKLAFSTFK KRALGTTKFRIHTPBARANCVAMIGGTALQDILGSVSKE YNNGTGRIPDMGSLNNPPLEMMPDVCKTOPPLMKLAFSTFK KRALGTTKFRIHTPBARANCVAMIGGTALQDILGSVSKE YNNGTGRIPDMGSLNNPPLEMMPDVCKTOPPLMKLAFSTFK NSERPFGAGGFYPSTTEDUTHTIGLKVSVGLLLVKSVQVKLGDSW DVKLGALGGNTGVTLQGGFYTFKVCHOFATROMYTKSCD YFYGKLDGGISSAPPSGGGULVGTYQOYQLLGIKSIGFFMNY PLEPTTTEPPVNLTYSANSPVGR SETYVAMRTDSSKMTDVESGVANFASSARAGERRALPDIOSSAA TOGTSDLAKAGAGAVASVPPDAGFORDER FLYVANNHGDETVGRELLHLIDVILVALGHROPDAFRY PLEPTYTEPPVNLTYSANSPVGR PLYVANNHGDETVGRELLHLIDVILVALGHROPDAFRY HREFERDAR HTMPSNBCOPTYGENTYNDOLDRAFPCHORDER HTMPSNBCOPTYGENTYNDOLDRAFPCHORDER HTMPSNBCH				1013	DESIGNET I TV TGV TV LVI VI KOMMODDDED TOV ODDES
TOPTIFERGREFYIGGENTOTERMENTAMENTAMENT GOTGITFMOLINETRODSORTRINGLIFANOTEEDILVRELE BIANTHPOQPILMETROPSORTRINGLIFANOTEEDILVRELE BIANTHPOQPILMENTAMENTOR POTORENS SOFTAMBLIFANOTEEDILVRELE BIANTHPOQPILMENTAMENTOR POTORENS SOFTAMBLIFANOTEEDILVRELE BIANTHPOQPILMENTAMENTOR POTORENS SOFTAMBLE BEINTHPOPPA  STILLVCGPPPLIOTAMHENLEKIGYTOMIFTY  ARMENPSDSPRIPEPPAGATFTEGENETRYSSESPPEPESFPE PPTSRGOPGSRDTMSDSEESQDROLKIVVLGDGAGGKTSLITC GOMBEN FOR PROSECUTION OF THE TARGET PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION OF THE PROSECUTION		İ			1 TORGETS THE LERGINS POR THE LEGISLATION TO THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF
GOTGITPMQLINETINGPSIGRINGINEPOTESPKKTLADHLGMIA GOTGITPMQLINETINGPSIGRINGINEPOTESPKKTLADHLGMIA ETARTHPDQPDLMYTLDRPPIGWKYSSGFYADMINEHHPPPAK STLLLUGPPPILOTAAHHRUEKLGYYQDMIFTY FRIEDRICH ARWELPSDSPRIPPAGAETPGRGSGRYLPSSSPPPEPSSPPS PPTSRGOPGSRPTMSDSEESEGOKIVLYSGSSPPPEPSSPPS PPTSRGOPGSRPTMSDSEESEGOKIVLYGGGSGRYSTLTC FAQETFGKQYKQTIGLDFFLRRITLPGNLNVTLQUMDIGGOTIG GKMLDKYIYGAQGVLLVYDTINYGSFFINEDWYTVVKKVSEESE TOPLVALVGNKIDLEHMETINFERHLRFCQENGFSSHYSAKTG DSVFLCFQKVAAELIGIIKNKAEIGOSQRVVKADIVNYNQEPMS TONPPRSSMCAVQ VNRFSWIMGNFFGHALPGTFFFIIGLMWCTKSILKYICKKORFT CYLGSKTLFYRE_EILEGITIVGMALTGMAGGOFIPCOPHLMLYD YKGGHNNOLLIGHHETMYFFFGLLGVADILCTIISSLPVGLTKL MLSNALFVEAFIFTWHTHGREMLDIFVHLULVVFLTGLVAFL EFLVRNINVLLELLRSSLILLGGSWFFOIGFVLYPPSGGPAMDIM DHENILFLTICFCHHYAVTIVIVGMMYAFITWLVKSRIKRLCSS EVGLIKNAERSOESEBEM TKGGFAGSTGFRCIIPSVIKRAGMYPVWAVQYNIMTEELLYSVL KEFIHILVFRILLVNPRDRRVVIISSVLCPSHPRETLTRVLFKY FEVBSVLLAPSHLMAALLTIGIISAGMYRPVWAVQYNIMTEELLYSVL KEFIHILVFRILLVNPRDRRVVIISSVLCPSHPRETLTRVLFKY FEVBSVLLAPSHLMAALLTIGIISAGMYRPURVAVQYNIMTEELLYSVL KERIHILVFRILLVNPRDRRVVIISSVLCPSHPRETLTRVLFKY FEVBSVLLAPSHLMAALLTIGIISAGMYRPURVAVGNATLIIDSL IOCSIDTRKGLARNIVVIGGTSMLDGFIHRILAEIRYLVEKKY VNDTYSLDGGKLHRILESTOLLEQCTVDTSVAKEGSIPSVMG SVPEGVLEDIKARTCFVSDLKAGKIQAAKRNIJGSNERPSPPP NDYSPLDGGKITSTTETTPHAARACVAMALGGAIFGALDDILGSRSVEKE YNNOTGRIPDWCSLNNPPLEMMFDVGXTOPPLMKRAPSTEK  SSS16 3 735 NREPPGAGGGSPFRSPTASSFYMFAGAGAGAGE IKAMMRYPGTTRPVTGSSPGMHRPERMLLLLIALLGGPTWAG MYMGGGKYFSTTEDTPHAALTTVAVFAGAFLGMWYMYTSKDR VYFYGKLDGGISSAYPSGEGOVLVGIYGGYOLLGIKSIGFEMNY PLEPFTTEPPVNLITYSANSPVGR SETYVANRTDSSKMTDVESGVANFASSARAGRRNALPDIGSSAA TGALYSARTTDEPVNLITYSANSPVGR SETYVANRTDSSKMTDVESGVANFASSARAGRRNALPDIGSSAA TGALYSARTTDEPVNLITYSANSPVGR PLEPTYTEPPVNLITYSANSPVGR PLEPTYTEPPVNLITYSANSPVGR PLEPTYTHEPPVNLITYSANSPVGR PLEPTYTHEPPVNLITYSANSPVGR PLEPTYVANRTDSSKMTDVESGVANFASSARAGRRNALPDIGSSAA TGALYSARTDPSSKMTDVESGVANFASSARAGRRNALPDIGSSAA TGALYSARTDPSSKMTDVESGVANFASSARAGRRNALPDIGSSAA THIMPSMPDGFEAVAKKDCYYSIGRENNOYDLNRNPPDAFFY NAVNGRGPTVAMKWILKTEFTVLASALHGGALVASYPFDMOVQA TGALYSARLTPDDDVFTYNLKKGGECKN		}			1 -411 11 VSSDDDRGFVDLL1KTVFKNVHDAVDRGGVVMATT
STLILVCGPPPLIQTAAHNILEKIGTYOMI FITY  ARWELPSDSFRIPPAGAFTGRGSCRNYLPSSSPPEPSSPPS PPTSRGOPGSFUTMSDSEESEGDROLKLIVLLGDGASGKTSLITC PAGETGKQYKQTIGLDFFLRRITLDGGLINVTLQIWDIGGTIG GKMLDKYIYGAGQULLVYDLTVASFENLEWYTVVKKVSEESE TOPLVALVGRKIDLEHMRTIKPEKHLRCQGEGSSHIVSAKTG DSVPLCPGKVAABILGIKLNKABIBOSGRVVKADIUWYNOEPMS PTWPPRSSMCAVQ  VREPSHIMENFRGHALPGTFFFIIGLWECTKSILKYICKKGKRF CYLGSKALPTLE-BLEEGTIVUMALTGMAEGOFIPCPHIMLYD YKGGHNOLLGHHHFMYFFFLLGVADILCFTISSLPVSIITEL MESNALFVERFFYWHTIGGRUDIFVWOLLVLVVEUTIGLVAFL EFLVRINVLLELLIRSSLILLQGSWFFQIGFVLYPPSGGPAWDLM MESNALFVERFFYWHTIGGRUDIFVWOLLVLVVEUTIGLVAFL EFLVRINVLLELLIRSSLILLQGSWFFQIGFVLYPPSGGPAWDLM DHEN LLFITICCHWYAVTIVIVGMYAFTIWLVKGRIKKICGS EVGLIKNABREGESEEM FVELVGRGDCDPLLSVCLTTMPLYEGLGSGEKTAVVIDLGEAP KKGFAGFIGFRCIIPSVIKAGMPKPVRVQVINTEBLLYSYL KKFIHILVFRHLLVMPRDRRVVIESVLCPSHFREFLTRVLFKY FEVPSVLLAPSHLMALITIGIAMAVLDCGYRESLVLPIYRGIP VLNCKGALPLGGKALHRELETOLLEQCTVDTSVAKEQSLPSVMG SVPEGVLEDIKARTCFVSDLKRGLKIOAAKFNIDGANEPSPPP NVDYPLDGEKILHILGSIRDSVVEILFFCDNEGSVATLILDSL IQCPIDTRKGLABRILVVIGGTSMLEGGLIRGLAGGAFGALOGAGGS KKALGTTEFIHTPPAKANCVAGGAIFGALGATGALOGLIGGSVSKE YNDTGRIDDWCSLINKPPLEMPDVGKTYOPLMKRAPSTEK  SSS16 3 735 NEREPGAGGGGPFRKSPTASSFLFPWFLASSFWGAGGAGES IKAMWRVPGTTRRVTGESGGMHRPDAMILLLGITLALLGGFPWAG MYGFGGKYFSTTEDYDHEITGLKVSVCUKLGDSW DVKLGALGGNTQEVTLQFGGFYTKVVAFQAFLERGMWYTSKDR YFYFKLDGGISSAYPSGGGVLVGIYGQYQLLGIKSIGFFWNY PLEEPTTEPPVNLTYSANSPVG  SEIYVAMRTDSSKMTDVESGVANFASSARGRRNALPDIQGSAA TDGTSSDLPLKLEALSVKEDAK VEKKTYDOLLEKFONDERK THMPSNWSVTHLUSGKSVKGRNLAWVLVVGRFPKEHRIGIP EFKYVANMINGDETVGRELLLHIJVLYSDKOPDETINLINGTR IHMPSNWFLOFETVARMKLKTETFULSANLLVUVGRFPKEHRIGIP EFKYVANMINGDETVGRELLLHIJVLYSDKOPDETTINLINGTR IHMPSNWFLOFETVARMKLKTETFULSANLLUNGGRENEFN			1		1 ~ CETTE ENGERGRAPTING PONIGTO DO OTO DO DEVENTE SESSE
2 637 ARWELPESPRIPPAGAETPEGGSCRNYLPSSPPPEPSSFPS PPTSRGGPGSRDTMSDSEESQDRQLKVVLGDGASGKTSLTTC FAQAFTEKQVYGVTIGLDF FLRRITLPGKLINVTLQIWDIGGQTIG GKMLDKYIYGAQGYLLUYDITKYQSFENLEDWYTVVKKVSEESE TOPLVALVORK INLEMMRTIKPEKHLRFQCENGFSSHFVSAKIG DSVPLCPGKVAAEILGIKLINKAEIEOSQRVVALADIVNYNQEPMS RTVNPPRSSMCAVQ VNRPSWIMMFRGHALPGTFFFIIGLWWCTKSILKYICKKQKRT CYLGSKILFYR_BILBGTIVGMALTGWGBOPIPCCPHLMLYD YKQGHNOLLIGWHFHTMY FFOJGFVLTYPESGPAWDIM MLSNALFVERFIF YNNTHGREMLDIFYNQLLUVAFLICHVAFL EFLVENNVLLELLRSSLILLQGSWFFFOJGFVLTYPESGPAWDIM DHENILFTICTCHWYAATTIVTOMNYAFTHWUKSKLKRLCSS EVGLLKNAEREGESBEEM  5515 1572 260 FVELVGRGGDGPLLSVCLTTMPLVEGIGSGGEKTAVVIDLGEAF TKCGFAGETGPRCIIFSVIKRAGMPKDVRVVQVNINTEBLYSYL KEFIHLLYPRHLAUNPRDRRVVILESVLCPSHFRETLITAVLFKY FEVDSVLLAPSHLMALLILGINSAMVLDCGVRESJUPLTYFEGIF VLNCWGALPLGGKALHKELETOLLEQCTVUTSVAKEOSLPSVMG SVPBGVLEDIKARTCFYSDLKACHYOAGATHALAEILVEKYK KKALGTKTFRIHTDPAKANCVAWLGGAIFGALQDILGSRSVSKE YNOTGRIPDWGSLNNPPLEMMPDUCKTOPPIMKRAFSTEK KKALGTKTFRIHTDPAKANCVAWLGGAIFGALQDILGSRSVSKE YNOTGRIPDWGSLNNPPLEMMPDUCKTOPPIMKRAFSTEK IKAMWRVGTTRRPVTGESFGMRPDRAMLLLTLALLGGPTWAG MYGPGGGKYFSTEDYDHEITGARVSVGLLLKSVOKULGDSW DVKLGALGGGNOEVTLOPGEYTTKVFVAFQAFLRMWMYTSKDR YFYSGLLDGGISSAYPSGEGOVLUGTVGCYGLLGIKSIGFEMNY PLEEPTTEPPVNLTYSANSPUCR  5517 246 499 SEIYVANMTDSEKMTDVESGVANFASSARAGRRNALPDIGSSAA TDGTSSLPJKLERALSVKEDAKSKEKTTODQLERFONEKE  SEIYVANMTDGFLMKLSVKTORLSKETTODULERFINLINSTR PLEEPTTEPPVNLTYSANSPUCR SEIYVANMTGDETVRLSGKSVKKGRNLWVLVGGFFKEHIGIP FFKYVANMHGDETVGRELLLILIPTVTSDKOPDETVNLTNSTR IHMPSNMPDGFEAVKKPDCYSTGRENTOVLDERFONEKE IHMPSNMPDGFEAVKKPDCYSTGRENTOVLDERFONEFNILDTSTR IHMPSNMPDGFEAVKKPDCYSTGRENTOVLDERFONEFNILDTSTR IHMPSNMPDGFEAVKKPDCYSTGRENTOVLDERFONEFNILDTSTR IHMPSNMPDGFEAVKKPDCYSTGRENTOVLDERFONEFNILDTSTR IHMPSNMPDGFEAVKKPDCYSTGRENTOVLDURNFPDAFFY INVSRGPETVANWKALKTETTLYLSANLENGGALVASYPFDMCVQA TGGALYSSSTPDDDFOTGRENTATTSARRPNMKGGDECKNMNFN		ł	1	•	EIARTHPDOEDLWYTI DERDIGHTENSLIFANQTEEDILVRKELE
ARWENDSPRIPPAGAGTTGRGSCRYUFSSSPPPEPSSFPE PRISAGOPGSPUMSDSEESERDODQLKIVULOGASGKTSLITTC FAQRTFGKQYKOTIGLDFFLRRITLPGNLNVTLQIWDIGGTIG GKMLDKYIYGAGQGULLVYDITRYQSFFBLEDWYTVVKKVSEESE TOPLVALVGNKIDLEHMRTIKPEKHLRCCORGFSSHFVSAKTG DSVFLCPGKVAAEILGIKLNKAEIBOSGRVVKADIVNYNOEPMS RTWNPRSSMCAWQ  VNRPSNIMGNFRGHALPGTFFFIIGLWGTKSILKYICKKÖKRT CYLGSKTLFYR_EILEGITIVGMALIGMAEGOFFPCGPHLMLYD YKGGHNOLLGWHFFTMYFFFILGLWGTKSILKYICKKÖKRT CYLGSKTLFYR_EILEGITIVGMALIGMAEGOFFPCGPHLMLYD YKGGHNOLLGWHFFTMYFFFILGLWGTKSILKYICKKÖKRT CYLGSKTLFYR_EILEGITIVGMALIGMAEGOFFPCGPHLMLYD YKGGHNOLLGWHFFTMYFFFILGLWGTKSILKYICKKÖKRT CYLGSKTLFYR_EILEGITIVGMALIGMAEGOFFPGCPHLMLYD YKGGHNOLLGWHFFTMYFFFILGLWGTKSILKYICKKÖKRT CYLGSKTLFYR_EILEGITIVGMALIGMAEGOFFPGEPHLMLYD MLSNALLFVEAFFTYNHTHGREMLDIFFYNGLITVLVFFILSLPVSLITKL MLSNALLFVEAFFTYNHTHGREMLDIFFYNGLITVLVFFILSLPVSLITKL MLSNALLFVEAFFTYNHTHGREMLDIFTYNLVKSTLKRLCSS EVGLUKNABREGESEEM  5515  1572  260  FVRLUCRGGCDPLLSVCLTTMPLYEGIGSGGEKTAVVIDLGEAF TKCGPAGFTGPFCITFSULVETTWLVKSTLKRLCSS EVGLUKNABREGESEEM  FVRLUCRGGCDPLLSVCLTTMPLYEGIGSGGEKTAVVIDLGEAF TKCGPAGFTGPFCITFSULVETSULVETSULVETYLFYY FEVPSVLLAPSHLMALLTLGINSAMVLDCGYRSSLVLPIYEGIP VLNCUGALPLGGKALHRELETOLLEGVTUTSVAKEGSLPSVMG SYPEGVLEDIKARTCFVSDLKRGLWKOARKFUNDGNNEEPSPPP NUDYPLDGEKILHILGSIRDSVVEILFCDNEEGSLPSVMG SYPEGVLEDIKARTCFVSDLKRGLWKOARKFUNDGNNEEPSPPP NUDYPLDGEKILHILGSIRDSVVEILFCDNEEGSFWAGAGGAGES IKAMPUPGTTRFPVTGESPGMHRPEAMLLUTLALLGGFTWAG KMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSVOVKLGDSW DVKLGALGGHTOEVTLOPGEYITKVEVAFOAFLGMWMYTSKDR YFYERKLDGGISSANFSSGGOVLUTAGYQVOLLGIKSVOVGKODSW DVKLGALGGHTOEVTLOPGEYITKVEVAFOAFLGMWMYTSKDR YFYERKLDGGISSANFSSGSANFASSARGRRNALFDIGSSAA TDGTSDLPKLERALSVRCDAKSKDEKTTODGLERFONMEE  SETVAMMTDSSKMTDVESGVANFASSARGRRNALFDIGSSAA TDGTSDLPKLERALSVRCDAKSKDEKTTODGLERFONMEE FLKTVANNSSGPTANTMGDELTWALDFRYHRGEGMEA FLKTVANNSSVTHLBSIGKSVKGDRILWVLVGRFFREHEIGIF EFFXVANNMGGDETVGRELLHLIDTYLTSDCKOPETTNILNSTR HIMPSMPDGFEAVKKRDCYSTSGRENINGLOLDRNFPDAFEY IHMPSMPDGFEAVKKRDCYSTSGRENINGCOLUNNFFN					STLILVCGPPPLTOTA A HPMI BYL CYCOPY
FAQETFCKQYKQTIGLDFPIRRITLPENIAVTLQIMDIGGOTIG GKMLDKXIYGAQGYLLYYDTTNYQSFENLEDWYTVVKKVSEESE TOPLVALVGKINLDEHMRITPEKHLRFCQENEFSSHFVSAKTG DSVPLCPQKVAAEILGIKLNKABIEGSGRVVKADIVNYVQEPMS RTVMPPRSSMCAVQ VNRPSHIMGHFRGHALPGTFFFIIGLMWCTKSILKYICKKQKRT CYLGSKXLFYRLEILEGITIVCMALTGMAGEQFIPCCPHLMLYD YKQGHNOLLGWHFFTMY FFFGIGLWCTKSILKYICKKQKRT CYLGSKXLFYRLEILEGITIVCMALTGMAGEQFIPCCPHLMLYD YKQGHNOLLGWHFFTMY FFFGIGLWCTKSILKYICKKQKRT CYLGSKXLFYRLEILEGITIVCMALTGMAGEQFIPCCPHLMLYD HENLIFLTICCCWHYAVTIVIVGMYAFGIGFVLYPPSGGBAWDLM DHENLIFLTICCCWHYAVTIVIVGMYAFGIGFVLYPPSGGBAWDLM DHENLIFLTICCCWHYAVTIVIVGMYAFGIGFVLYPPSGGBAWDLM DHENLIFLTICCCWHYAVTIVIVGMYAFGIGFVLYPPSGGBAWDLM DHENLIFLTICCCWHYAVTIVIVGMYAFGIGFVLYPPSGGBAWDLM COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER COMMANDER CO		2213	2	837	ARWRLPSDSPRIPPAGAETPGPGGCPAVI PGGGGG
GKMLDKYI YGAQGYLLVYI TYGAFENLEDWI TVUKKYSEESE TQPLVALVGRKI DLEHMRTI KPEKHLEFCCENGFSSHFVSAKTG DSVPLCPGKVAAELLGI KLNKAE I EOSGRVVRADI VNYNQEPPS RTVMPPRSSMCAVQ VNRPSWIMGNFREHALPGTFFFI I GLWWCTKSI LKYICKKÖKRT CYLGSKTLFYR_EI LEGITU TVGMALTGWAGEQF I PCCPHILMLYD YKGGHNOLLGWHHFTMYFFFGLLGWDTLKYI CKKÖKRT CYLGSKTLFYR_EI LEGITU CMALTGWAGEQF I PCCPHILMLYD YKGGHNOLLGWHHFTMYFFFGLLGWDLI LCFTI SSLPVSLTKL MESMALFVER FI FYNNTHERMLD I FYHQLLVLVVPLITCLVAFL EFLVRNNVLLELLRSSLI LLQGSWFFQ I GFVLYVPSGGPAWDLM DHEN LIFLT FCWHYAVTI VIGMWYAFITWLVKSRLKRLCSS EVGLLKNARREGESEERM TKCGPAGETGPECI FSVY KRAGMPKPVUVYNINTEELYSYL KEFIHLLYFRHLLVMPRDRRVVI LESCYCTTMPLYEKY FEVPSVLLAPSHLMALLTIG INSAMVLDCGYRESLVLPI YEGIP VINCKGALPLIGKGALHKELETQLLEGCTVDTSVAKCOSLPSVMG SVPEGVLEDI KARTCFVSDLKRGLKI QAAKTNI DGNNER! PSPPP NDVPYLDGEK KLHHLIGSTROVEL ILFG CHTVDTSVAKCOSLPSVMG SVPEGVLEDI KARTCFVSDLKRGLKI QAAKTNI DGNNER! PSPPP NDVPYLDGEK KLHHLIGSTROVEL ILFG CHTVETSVAKCOSLPSVMG SVPEGVLEDI KARTCFVSDLKRGLKI QAAKTNI DGNNER! PSPPP NDVPYLDGEK KLHHLIGSTROVEL ILFG CHTVETSVAKCOSLPSVMG SVPEGVLEDI KARTCFVSDLKRGLKI QAAKTNI DGNNER! PSPPP NDVPYLDGEK KLHHLIGSTROPPOVET INFOLMER PSPPP NDVPYLDGEK KLHHLIGSTROPPOVET INFOLMER PSPPP NDVPYLDGEK KLHHLIGSTROPPOVET INFOLMER PSPPP NDVPYLDGEK KLHHLIGSTROPPOVET INFOLMER PSPPP NDVPYLDGEK KLHHLIGSTROPPOVET INFOLMER PSPPP NDVPYLDGEK KLHHLIGSTROPPOVET INFOLMER PSPPP NDVPYLDGEK KLHHLIGSTROPPOVET INFOLMER PSPPP NDVPYLDGEK KLHHLIGT INFOLMER PSPPP NDVPLGGEKYFTTED PDWCSLNNPPLEMRPOWET INFOLMER PSPPP NDVPLGGEKYFTTED PDWCSLNNPPLEMR PSRFWMYTSKDR YFYFGKLDGGISSAPPSGEGOVLUG I YGQYQLLG I KS I GFEMMY PLEEPTTEPPVNLTYSANSPVGR  5517 246 499 SETVANMTYDGSTROPPOSSKMTDVESGVANFASSARAGRRNALPDI QSSAA TDGTSDLPLKLRALSVEDAKERDEKTTODQLEK POMEEK DAMADAWVRAWDLINMFPCLWLGLIGL VAN DLFRINGEGMEA FLKTVAQNY SSYTHLISI GERNYNQ YLD VLROFF PKER I GI P EFKYVANNHGDET VGRELLLILLI DYLVTSDGKDPET INI NSTR I HIMPSMN PGFEAVKRPDCYYSI GRENN NQUDLINNFPDAEY NNVSRQPETVANWILKTET FVIJSANLHGGLVAN SYP FDNGQOA TGALYSRSLTPODD VG YLAHTY ASRNPMKRGDECKNIKMFPN		ļ	j		
TOPLVALVGRKIDLEHMETIKPGKHLRFCOENGFSSHYVSAKTG DSVELCPOKVAAELIGIKLNKAEIEOSORVVKADIVNYNOEPMS RTVNPPRSSMCAVQ RTVNPPRSSMCAVQ VNRPSWIMGNFRGHALPGTFFFIIGLWWCTKSILKYICKKOKRT CYLGSKTLFYRLSGITIVUGMALTGWAGEOFIPCOPHLMLYD YKQGHNNOLLGWHIFINYFFFGLLGVADILCFTISSLPVSLTKL MLSNALFVEAFIFYNHTHGREMLDIFVHOLLVLVUYFLTGLVAFIL EFLVRNNVLLELLRSSLILLQGSWFFQIGFVLYPPSGOPAWDLM DHENILFLTICFCWHYAVTIVIVGMYNAFITWLVKSRLKKRLCSS EVGLLKNAEREOSSEEM  5515 1572 260 FVRLVGRGDOPLISVCLTTWPLYGGLGSGGEKTAVVIDLGEAP TKCGPAGETGPRCIIPSVIKRAGMPKPVRVVQYNINTEELYSYL KEFIHILYFRHLLVNPRDRRVVIIESVLCPSHFFETTIRVJFKY FEVPSVLLAPSHIMALITGINSAMVLDCGYRESLVLPIYKGIP VLNCKGALPLGRALHKELETOLLEQCTVDTSVAKEQSLPSVMG SVPPGVLEDIKARTCFVSDLKKGLKTOAAFRINGANEREPSPP NUDYPLDGEKILHILGSIRDSVVEILFGEODNERGSVATLILDSL IOOPIDTRKQLAENLAVIGGTSMLPGFHRILLARIRVLVEKPKY KKALGTKTFIHTPPAKNVANLGGAI FGALQDILGSRSVSKE YYNOTGRIPDMCSLANNPPLEMMFDVGKTQPPIMKRAFSTEK  TKAMRVPGTTRRPVTGESPGMHRPEAMLLUTLALLGGFTWAG MKGPGGGKYPSTTEDYDHEITGLRVSVGLLLVKSVQVKLGDSW DVKKGALGROTOEVTLQPGEYTTKVFVAFQAFLRGMYMTISKDR YFYRGKLDGQISSAYPSGEGGVLVGIYGGYOLGIKS IGFEMNY PLEEPTTEPPUNLTYSANSPVGR  5517 246 499 SEIYVAMTDSSKMTDVESGVANFASSARAGRRNALPDIQSSAA TDGTSDLPLKLEALSVKEDAKENDEKTODQLEKRONEEK DAWADAWVRAWDLNMDFPCLWLGLLPLIVAALDDRYHRGGGMEA TDGTSDLPLKLEALSVKEDAKENDEKTODQLEKRONEEK PLKTVAQNYSSVTHLHSIGKSVKGRNLAWLVVGRPRPKEHRIGIP EFKYVANMHGDETVGRSLLLHLIDYLVTSDGKDPEITNLINSTR NNVSRQPETVAVMWELKTETVLSANLHGGALVASYPPROMGOA TGALYSSSTPDDDVFCYLAHTYASRNPNMKKGDECKNKMMTPN	ĺ		1		1 CAN TROUT TOTAL BUILDING THE POST VALUE AND AND AND AND AND AND AND AND AND AND
DSYFICPOKVAAELIGIKINKREIEGSGRVVKADIVNYNOEPMS RTVNPPRSSMCAVQ RTVNPPRSSMCAVQ VRRPSWIMGNFRGHALPGTFFFIIGLWCTKSILKYICKKOKRT CYLGSKTLFYR_EILEGITIVGMALTGWAGEGFIPCCPHLMLYD YKGGHNOLLGWHHFINYFFFGLGVADILCFTISSLPVSLTKL MISNALFVEAFIFYNTHFGREMLDIFVHOLLVLVVFLTGLVAFL EFLVRNNVLLELLRSSLILLQGSWFFGGFVLYPPSGGPAWDLM DHENILFLTICFCWHYAVTTVIVGMYAFITWLVKSRLKRLCSS EVGLLKNAREGEGSEEMT EVGLLKNAREGEGSEEMT TKGGFAGFTGRCIIPSVIKRAGMPKPVRVVQYNINTEELYSYL KEFIHILYPRHLLVNPRGRVVIIESVLCPSHFPETLTRVLFKY FFVPSSVLLAPSHIMALLTIGINSAWLDCGYRESLVLPIYRGIP VILNCWGALPLGGKALHKELETQLLECTVDITSVAKEGSLPSVMG SVPEGVLEDIKARTCFVSDLKRGLKTQAAKFNIDGNBERPSPPP NVDYPLDGEKILHILGSINDSVVELIFEQDNERGSVATLILDSL IOCPIDTKGLAENLVUIGGTSMLPGFLHRLLAEIRYLVEKPKY KKALGTKFFRIHTPPAKANCVAWLGGAIFGALQDILGSRSVSKE YYNQTGRIPDMCSLNNPPLEMMFDUKTQPFLMKRAFSTEK KMYGPGGGKYFSTTEDYNHEITGLKSVGLLLUKSVOVKLGDSW KMYGPGGGKYFSTTEDYNHEITGLKSVGLLLUKSVOVKLGDSW KMYGPGGGKYFSTTEDYNHEITGLKSVGLLLUKSVOVKLGDSW TYFYGKLDGGISSAYPSGEGOVLVGIYGQYQLLGIKSIGFEMNY PLEEPTTEPPVNLTYSANSPVG SEIYVAMRTDSSKMTDVESGVANFASSARAGRNALPDIQSSAA TDGTSDLPLKLEALSVKEDAKEKDEKTTODQLEKPONEEK DAWADAWTARADLINMFPCLAEGGENYNGYLVGRPFKERRIGIP EFKYVANMHGDETVGRELLLHLIDJAVASDCREICH IHHMSNNIPDGFEAVKKEDCYYSIGRNYNGYDLNRNFPDAFERY NNVSRQPETVAVMKWLKTETFVLSANLENGGALVASYFPDNGVQA TGALMSRSLTPDDDVFQYLAHTVASRNPNMKKGDECKNKMNFPN GTVNGYSWYTLAHTGRANDLWMFPCLAERGRUNGNYFPDNGVQA TGALMSRSLTPDDDVFQYLAHTVASRNPNMKKGDECKNKMMFPN			1		
S514 1295 449 VNRPSMIMGNPRGHALPGTFFF IGLWWCTKSILKYICKKQKRT VNGPWMMGNPRGHALPGTFFF IGLWWCTKSILKYICKKQKRT VKGGHWNOLLGWHHFTMYFFFGLIGVADILCFTISSLPVSLTYKL MLSNALFVEAFIFYNHTHGRENDIFFPGLIVLVYFTJGLVAFL EFLVRNNVLLELLRSSLILLQGSWFFDGFVLYPPSGGPAWDLM DHENILFLTICFCHHYAVTIVIVGMNYAFITWUKKSRLKRLCSS EVGLLKNAREROESEERM  5515 1572 260 FVRLVGRGDCDPLLSVCLTTMPLYEGLGSGGKTAVVIDLGEAP TKCGFAGETOPRCIIPSVIKRGKGSGGKTAVVIDLGEAP TKCGFAGETOPRCIIPSVIKRGKGKQAKFNIDGNNERPSPPP VLNCWGALPLGGKALHKELETOLLEQCTVDTSVAKEGSLPSVMG SVFEGVLEDIKARTCFSULKGGKACHKELETOLLEQCTVDTSVAKEGSLPSVMG SVFEGVLEDIKARTCFSULKGGKACAFKNIDGNNERPSPPP NVDYPLDGEKILHILGSIRDSVVEILFFCDMERGSVATLILDSL IOCPIDTRKQLAENLVVIGGTSMLFGFHRILAEIRYLVEKPKY KKALGTKTFRIHTPPAKANCVAWLGGAFFANDGNNERPSPPP NVDYPLDGEKILHILGSIRDSVVEILFFCDMERGSVATLILDSL IOCPIDTRKQLAENLVVIGGTSMLFGFHRILAEIRYLVEKPKY YNNOTGRIPDWGSLNNPPLEMMPDVGKTOPPLMKRAFSTEK XKALGTKTFRIHTPPAKANCVAWLGGAFFGAOGAGCS KKALGTKTFRIHTPPAKANCVAWLGGAFFGAWATLLLGSPTWAG KKALGTKOPTINGPOFFTASFLFPWRFLASSFFWGAGGAGCS KKALGTKOPTINGPOFFTASFLFPWRFLASSFFWGAGGAGCS KMYGPGGKYFSTTEDYDHEITGLRVSVGLLLVKSVQVKLGDSW DVKLGALGGNTQEVTLOGEVITKVFVAFQAFLRGMWYTSKDR VFYFGKLDGQISSAYPSQEGQVLVGTYGQYQLLCHKSIGFEMNY PLEEPTTEPPVNLTYSANSPVGR  5517 246 499 SEIYVAWRTDSSKMTDVESGVANFASSARAGRRNALPDIQSSAA TDGTSDLPLKLEALSVKEDAKEXDEKTTODQLEKPQNEEK  5518 3 1375 DAWADAWYRWDLSWSVTHLHSIGKSVKGRNLAVVLVVKGFPKEHRIGIP EFKYVANMHGDETVGRELLLHLIDYLVTSDGKDPEITNLINSTR HIMPSSNDPOFFRAVKKPDCYYSIGRENNYQDVLNNRFPDAFEY NNVSRQPETVAVMWLKKTETFVLSANLHGGALVASYFPDMCVQA TGALMSRSLTPDDDVFQYLAHTYSANPPMKKGDECKNAMFPN	Į		}		1 -5 - 5 1 TO A ON WITH THE WINK I. I K DE KAHI DE COENCE DOCUMENT - 1
VNRPSWIMGNPRGHALPGTFFFIIGLWWCTKSILKYICKKQRRT CYLGSKTLFYRLEILEGITIVCMALTGMAGEQFIPCCPHLMLYD YKGGHNOLLGWHFTMYFFFGLLGVADILCFTISSLPVSLTKKL MLSNALFVEAFIFYNHTHGRENLDIFVHQLIVLVYFLTGLVAFL EFLVRNNVLLEILRSSLILLQGWFFOIGFYLYPPSGGPAWDLM DEBNILFTITCFCHHYAVTIVIVGMYYAFITWDVKSRLKRLCSS EVGLIKNAEREQESEEM  FVRLVGRGDCDPLLSVCLTTWPLYEGIGSGGEKTAVVIDLGEAP KEFIHLLYFRHLLVNPRDRRVVIIESVLCPSHFRETLTRVLFKY FEVPSVLLAPSHHMALITLGINSAWVLDCGYRESLVLPIYEGIP VLNCGGAJETGPRCIIPSVIKRAGMPKPVRVVQYNINTEELYSYL KEFIHLLYFRHLLVNPRDRRVVIIESVLCPSHFRETLTRVLFKY FEVPSVLLAPSHHMALITLGINSAWVLDCGYRESLVLPIYEGIP VLNCGGAJETGPRCIIPSCTVDTSVAKEQSLPSVMG SVPEGVLEDIKARTCFVSDLKRGLKIQAAKFNIDGNNERPSPPP NVDYPLDGEKILHILGSIRDSVVEILFFCQDUEEGSVATLILDSL IQCIDTRKQLAENLVVIGGTSMLPGFHRILAEIRYLVEKPKY KKALGTKTFRIHTPPAKANCVANLGGAIFGALQDILGSRSVSKE YYNOTGRI PDWCSLNNPPLEMMFDVGKTQPPLMKRAFSTEK KKALGTKTFRIHTPPAKANCVANLGGAIFGALQDILGSRSVSKE YYNOTGRI PDWCSLNNPPLEMMFDVGKTQPPLMKRAFSTEK KKALGTKTFRINTPPAKANCVANLGGAIFGALQDILGSRSVSKE YYNOTGRI PDWCSLNNPPLEMMFDVGKTQPPLMKRAFSTEK KKALGTKTFRIHTPPAKANCVANLGGAIFGALQDILGSRSVSKE YKNOTGGGKYFSTTEDYDHEITGLRVSVGLLVKSVQVKLGDSW DVKLGALGGNTQEVTLQFGEYTIKVFVAFQAFLKRGMVMYTSKDR YFYFGKLDGQISSAYPSQEGQVLVGIYGQYQLLGIKSIGFENNY PLEEPTTEPPVNLTYSANSPVGR  5517 246 499 SEIYVAMRTDSSKMTDVESGVANFASSARAGRRNALPDIQSSAA TDGTSDLPLKLEALSVKEDAKERDEKTTODOLEKPONEEK DAWADAWVANDLINMDFFCLWLGLLDFLVAALDFNYHRQEGMEA FLKTVAQNYSSVTHLHSIGKSVKGRNLWVLVVGRFREHRIGIP EFKYVANMHGDETVGRSLLLHLLDYLVTSDGKOPEITNLINSTR IHMPSNNPOGFEAVKWDCYYSIGRENVNQYDLNRNFPDAFEY NNVSRQPETVAVMWKKTETEVLSANLHGGALVASYFDNAVQA TGALMSRSLTPDDDVFQVAMKKGDECKNONNFPN	Į				1 -0 Tot Arragottottrokakikosobininabitanin
CYIGSKTLFYRLEILEGITIVGMALTGMAGEOFIPGCPHIMLYD YKGGHMNOLLGWHHFTMYFFGLLGVADILCFTISSLPVSITKL MLSNALFVEAFIFYNHTHGRENLDIFYHOLLVLVVFFIGLVAFL EFLVRNNVLLELLESSILLLQGSWFFOLGFVLYPPSGGPAWDLM DEBNIFFLTICFCWHYAVTIVIVGMNYAFITWLVKSRLKRLCSS EVGLLKNARERGESEEBM  5515 1572 260 FVRLVGRGDCDFLLSVCHTTMPLYEGLGSGGEKTAVVIDLGEAF TKCGFAGETGPRCTIPSVIKRAGMPKPVRVVQYNINTEELYSYL KEFIHILYFRHLLVNPRDRRVVIESVLCPSHFRETLTRVLFKY FEVPSVLLAPSHLMALTLIGINSAMVLDCGYRESVLPIYYEGIP VLNCWGALPLGGKALHKELETOLLEQCTVDTSVAKEOSLESVMG SVPEGVLEDIKARTCFVSDLKGGKIQAAKFNIDGMNERPSPPP NVDYPLDGEKILHILGSIRDSVVEILFEQDNEFQSVATLILDSL IOCPIDTRKQLAENLVVIGGTSMLPGFHRLLAEIRYLVEKPKY KKALGTKFRIHTPPAKANCVAMLGGAIFGALQDLIGSRSVSKE YYNGTGRIPDMCSLNNPPLEMMPPVGKTOPPIMKRAFSTEK KKALGTKFRIHTPPAKANCVAMLGGAIFGALQDLIGSRSVSKE YYNGTGRIPDMCSLNNPPLEMMPPVGKTOPPIMKRAFSTEK  S516 3 735 NSREPPQAGFGPSPRKSPTASSFLFFWRPLASSFWMGAGGAQES IKAMWRVPGTTRRPVTGESPGMHRPEAMLLLITLALLGGPTWAG KMYSPGGKYSTTEDYDHEITGLRVSVGLLLVKSVQVKLGDSW DVKLGALGGNTQEVTLQPGGYITKVFVAFQAFLRGMWYTSKDR YFYFGKLDGQISSAYPSGEGOVLVGTYGQYQLLGIKSIGFEWNY PLEEPTTEPPVNLTTSANSPVGR  5517 246 499 SEIYVANRTDSSKMTDVESGVANFASSARAGRRNALPDIQSSAA TDGTSDLPIKLEALSVKEDAKKEDEKTTQDQLEKPQNEEK FLKTVAONYSSVTHLHSIGKSVKGRNLWVLVVGFPKEHRIGIP EFKYVANMHGDETVGRELLHHLIDVLVTSDGKOPEITNLINSTR IHIMPSINDPGFFEAVKDCYYSIGRENVNQVDLNRNFPDAFEY NNVSRQPETVAVMKWLKTETFVLSANLHGGALVASYFFDNGVQA GÖTNGYSWYPLOGGMODNNYTWAGOGETURLEIGENEN	1	5514	1295	449	1 1112 - 1100111011011
MISNALFVEAFTFYNNTHGREMLDIFFIGLUVAVFLTGLVAFL EFLVRNAVLLELLRSSLILLQGSWFFQIGFVLYPPSGGPAWDLM DHENILFLTICFCWHYAVTIVIVGMWYAFTTWLVKSRLKRLCSS EWGLLKNAERROESEEBM  FWELVGRGCDPLLSVCLTTMPLYEGLGSGGEKTAVVIDLGEAF TKCGFAGETGPRCIIFSVIKRAGMPRPVRVVQYNINTEELYSYL KEFIHLLYFRHLLAVBPRDRRVVI IESVLCPSHFRETLTRVLFKX FEVPSVLLAPSHLMALLTLGINSAMVLDCGYRESLVLPIYEGIP VLNCWGALPLIGGKALHKBLETQLLEQCTVDTSVAKEQSLPSVMG SVPEGVLEDIKARTCFVSDLKRGLKIQAAKFNIDGNNERPSPPP NVDYPLDGEKILHILGSIRDSVVEILFEQDNERQSVATLILDSL IQCPIDTRFCFVSDLKRGLKIQAAKFNIDGNNERPSPPP NVDYPLDGEKILHILGSIRDSVVEILFEQDNERQSVATLILDSL IQCPIDTRFDAKANCVAMLGGAIFGALQDILGSRSVSKE YYNQTGRIPDWCSLNNPPLEMMPDVGKTQPPLMKRAFSTEK KKALGTKTFRIHTPPAKANCVAMLGGAIFGALQDILGSRSVSKE YYNQTGRIPDWCSLNNPPLEMMPDVGKTQPPLMKRAFSTEK NSREPFQAGFGPSPRKSPTASSFLFPWRPLASSFWMGAQGAQES IKAMWRVPGTTRRYDTGSPGMHRPEAMLLLITLALLGGPTWAG KMYGPGGGKYFSTTEDVDHEITGLRVSVGLLLVKSVQVKLGDSW DVKLGALGGNTQSVTLQFGEYITKVFVAFQAFLRGMVMYTSKDR YFFGKLDGQISSAYPSQEGQVLVGIYGQYQLLGIKSIGFEMNY PLEEPTTEPPVNLTYSANSPVGR  5517 246 499 SEIYVANRTDSSKMTDVESGVANFASSARAGRRNALPDIQSSAA TDGTSDLPLKLEALSVCBAKEKDEKTTODQLEKPONEEK TDGTSDLPLKLEALSVCBAKEKDEKTTODQLEKPONEEK FLKTVAQNYSSVTHLHSIGKSVKGRNLWVLVVGRFPKEHRIGIP EPKYVANMHGDETVGRELLHLIDTLJVTSDGKDPBITNLINSTR IHIMPSNNPDQFFAVKKPDCYYSIGRENYNQVDLNRNPPDAFFEY NNVSRQPETVAVMKWLKTETFVLSANLHGGALVASYPFPDNGVQA TGALYSRSLTPDDDVFQYLJAHTYASRNPNMKKGDECKNKMNFPN GVYNGSVWYPLOGGMDDYNYUMAOCRELUK LGCEWNM	- 1		1		CYLGSKTLEYPERTIFCATIVONS
EFLVRNAVLEBLIRSSIILLQGSWFFQIGFVLYPPSGGPAWDLM DHENIJELICFCWHYAVTIVIVGMYAFITWLVKSRLKRLCSS EVGLLKNAEREGESEEEM FVRLVGRGCDPPLSVGLTTMPLYEGLGSCGEKTAVVIDLGEAF FVRLVGRGCDPPLSVGLTTMPLYEGLGSCGEKTAVVIDLGEAF TKCGFAGETGPRCIIPSVIKRAGMPKPVRVQYNINTEELYSYL KEFIHLLYFRILLVMPRDRPVIIESVLCPSHFRETLTRVLFKX PEVPSVLLAPSHLMALTLIGINSAMVLDCGYRESLVLPIYEGIP VLNCWGALPLGGKALHKELETQLLEQCTVDTSVAKEQSLPSVMG SVPEGVLEDIKARTCFVSDLKRGLKIQAKFNIDGNEERPSPPP NVDYPLDGEKILHILGSIRDSVVEILFEQDNERGSVATLILDSL IQCPIDTRKQLAERLVVIGGTSKMLDGFLHRILABIRYLVEKPKY KKALGTKTFRIHTPPAKANCVAWLGGAIFGALQDILGSRSVSKE YYNQTGRIPDWCSLNNPPLEMMFDVGKTQPPLMKRAFSTEK NSREPPQAGFGGBSPRKSPTASSFLFPWRPLASSFWMGAQGAQES IKAMWRVPGTTRRPVTGESPGMRRPEAMLLLUTLALLGGPTWAG KMYGPGGGKYFSTTEDYPHEITGLRVSVGLLLVKSVQVKLGDSW DVKLGALGGNTQEVTLQPGEYITKVFVAFQAFLRGMVMYTSKDR YFYFGKLDGQISSAYPSQEGQVLUGIYGQYQLLGIKSIGFEWNY PLEEPTTEPPVNLTYSANSPVGR  5517 246 499 SEIYVAMTDSKMTDVESGVANFASSARAGRRNALPDIQSSAA TDGTSDLPLKLEALSVKEDAKEKDEKTTOQQLEKPQNEEK FLKTVAQNYSSVTHLMSIGKSVKGRNLWVLVVGRFPKEHRIGIP EFKYVANMHGDETVGRELLHLIDTLLVTSDCKDPEITNLINSTR IHMPSNNPDGFFAVKKPDCYYSIGRENYNQVLNRNPPDAFEY NNVSRQPETVAVMKWLKTETFVLSANLHGGALVASYFPDNGVQA TGALYSRSLTPDDDVFQYLJAHTYASRNPNMKKGDECKNKMNFPN GVTNGYSWYPLOGGMDDYNY WAROCPELINE LECCHWNN	-		1 1		YKQGHWNOLLGWHHFTMYFFFGLICWADIAGEOFIPGCPHLMLYD
DHENILFLTICFCWHYAVTIVIVGMNYAFITWLVKSRLKRLCSS EVGLLKANEREOESEEEM  FVRLVGRGDCDPLLSVCLTTMPLYEGLGSGEEKTAVVIDLGEAP TKCGFAGETGPRCIIPSVIKRAGMPKPVRVVQYNINTEELYSVI KEFIHILYFRHLLVNPRDRRVVIIESVLCPSHFRETUTRVLFKY PEVPSVILAPSHLMALLTIGINSAMVLDCGYRESLVLPIYEGIP VINCWGALPLGEKALHKLESTOLLEQCTVDTSVAKEGSLPSVMG SVPEGVLEDIKARTCFVSDLKRGLKIQAAKRNIDGMREPPSPPP NVDYPLDGEKILHILGSIRDSVVEILFEQDNEEGSVATLILDSL ICCPIDTRKGLAENLVVIGGTSMLPGFLHRLLAEIRYLVEKKKY YNNOTGRIPDWCSLNNPPLEMMFDVGKTQPPLMKRAPSTEK KKALGTKTFRIHTPPAKANCVAWLGGAIFGALQDILGSRSVSKE YYNQTGRIPDWCSLNNPPLEMMFDVGKTQPPLMKRAPSTEK NGREPPQAGFGPSPRKSPTASSFLFFWRPLASSFWGAGAGES KMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSVQVKLGDSW DVKLGALGGNTQSVTLQGEYITKVFVAFQAFLRGWMYTSKDR YFYRGKLDGGISSAYPSQEGQVLVGIYGQVQLLGIKSIGFEWNY PLEEPTTEPPVNLTYSANSPVGR  5517 246 499 SEIYVAMRTDSSKNTDVESGVANFASSARAGRNALPDIQSSAA TDGTSDLPLKLEALSVKEDAKETTQDGLEKPQNEEK TDGTSDLPLKLEALSVKEDAKETTQDGLEKPQNEEK FLKTVAQNYSSVTHLHSIGKSVKGRNLWVLVVGRFPKEHRIGIP EFKYVANMHGDETVGRELLHHILDYLVTSDGKDPEITMLINSTR HIMPSNNPDGFEAVKKPDCYYSIGRENNNQYDLNRNPPDAFEY NNVSRQPETVAVMKWLKTETFVLSANLHGGALVASYPFDNGVQA TGALYSRSLTPDDDVFGYLAHTYASRNPNMKKGDECKNKMNFPN	1		}		1 ADDI ADDI TE INH THISKEMI DI EMINOTI AND ASSESSMENT
ENGLLKNAEREOESEEMM  FVRLVGRGDCDPLLSVCLTTMPLYEGLGSGEKTAVVIDLGEAP TKCGFAGETGPRCIIFSVIKRAGMPKPVRVVQYNINTEELYSYL KEFIHLLYRRHLLVNPRDRRVVIIESVICCPSHFRETTLTRVLFKY PEVPSVLLAPSHLMALLTLGINSAMVLDCGYRESLVLPIYEGIP VINCMGALPLGGKALHKELETQLLEQCTVDTSVAKEGSLPSVMG SVPEGVLEDIKARTCFVSDLKRGLKTQAAKFNIDGNNERPSPPP NVDYPLDGEKILHILGSIRDSVVEILFEQDNEEQSVATLILDSL IOCFIDTRKQLAENLVVIGGTSMLPGFLHRILAEIRYLVEKPKY KKALGTKFFRIHTPPAKANCVAWLGGAIFGALQDILGSRSVSKE YYNQTGRIPDWCSLNNPPLEMMFDVGKTQPPLMKRAFSTEK  S516  3  735  NSREPPQAGFGPSPRKSPTASSFLFFWRPLASSFWMGAQGAQES IKAMWRVPGTTRRPVTGESPGMHRPEAMLLLLTLALLGGFTWAG KMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSVQVKLGDSW DVKLGALGGNTQCVTLQPGGYITKVFVAFQAFLRGMVWTYSKDR YFYFGKLDGQISSAYPSQEGQVLVGIYGGYQLLGIKSIGFEMNY PLEEPTTEPPVNLTYSANSPVGR  5517  246  499  SEIYVAMRTDSSKMTDVESGVANFASSARAGRRNALPDIQSSAA TDGTSDLPLKLEALSVKEDAKEADEKTTODQLEKFQNEEK FLKTVAQNYSSVTHLHSIGKSVKGRNLWVLVVGRFPKEHRIGIP FFKYVANMHGDETVGRELLLHLIDYLVTSDGKDPEITMLINSTR IHIMPSNNPDGFFAVKKPDCYYSIGRENYNQYDLNRNFPDAFEY NNVSRQPETVAMMKULKTETFVLSANLEGGALVASYFFDNGVQA TGALYSRSLTPDDDVFCYVARTGGALVASYFFDNGVQA TGALYSRSLTPDDDVFCYLAHTYASRNPNMKKGDECKNKMNFPN	1		j l		T TO THE TOTAL PROPERTY AND THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK TH
Total   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furly   Furl	1		l ' (	•	T TO THE TOP CHILD IN THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF
TKCGFAGETGPRCIIPSVIKRAGMPKPVRVQVNINTEELSYSIL KEFIHILYFRHLLVNPRDRRVVI IESVLCPSHFEETLTRVLFKY FEVPSVILAPSHLMALLTLGINSAMVLDCGYRESLVLPIYEGIP VINCWGALPLGGKALHKELETQLLEQCTVDTSVAKEQSLPSVMG SVPEGVLEDIKARTCFVSDLKRGLKIQAAKFNIDGNNERPSPPP NVDYPLDGEKILHILGSIRDSVVEILFEQDNERGSVATLILDSL IQCPIDTRKQLAENLVVIGGTSMLFGFLHRLLAEIRYLVEKPKY KKALGFKFRHTPPPAKANCVAWLGGAIFGALQDILGSRSVSKE YYNQTGRIPDWCSLNNPPLEMMPDVGKTQPPLMKRAFSTEK NSREPPQAGFGPSPRKSPTASSFLFPWRPLASSFWMGAQCAQES IKAMWRVPGTTRRPVTGESPGMHRPEAMLLLUTLALLGGPTWAG KMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSVQVKLGDSW DVKLGALGGNTQEVTLQPGEYITKVFVAFQAFLRGMVMYTSKDR YFYFGKLDGGISSAYPSQEGQVLVGIYGQYQLLGIKSIGFEWNY PLEEPTTEPPVNLTYSANSPVGR  5517 246 499 SEIYVAMRTDSKMTDVESGVANFASSARAGRRNALPDIQSSAA TDGTSDLPLKLEALSVKEDAKEKDEKTTODQLEKPQNEEK DAWADAWVRAWDLNMDFPCLWLGLLLPLVAALDFNYHRQEGMEA FLKTVAQNYSSVTHLHSIGKSVKGRNLWVLVVGRFPKEHRIGIP EFKYVANMHGDETVGRELLLHLIDYLVTSDGKDPEITNLINSTR IHIMPSMNPDGFEAVKKPDCYYSIGRENYNQYDLNRNFPDAFEY NNVSRQPETVAVMKWLKTETFVLSANLEGGALVASYPFDNGVQA TGALYSRSLTPDDVFQYLAHTYASRNPNMKKGDECKNKNNFPN GVYNGYSWYPLQGGMODYNYIMACGETTLE	Γ	5515	1572	260	1
KEFIHLLYFRHLUNDRDRRVVI LESVLCPSHFRETLTRVLFKY FEVPSVLLAPSHLMALLTLGINSAMVLDCGYRESLVLP1YEGIP VINCWGALPLGGKALHKELETQLLEQCTVDTSVAKEQSIPSVMG SVPEGVLEDIKARTCFVSDLKRGLKIQAAKRNIDGNNERPSPPP NVDYPLDGEKILHILGSIRDSVVEILFEQDNEEQSVATLILDSL IQCPIDTRKQLAENLVVIGGTSMLPGFLHRILAEIRYLVEKPKY KKALGTKTFRIHTPPAKANCVAWLGGAIFGALQDILGSRSVSKE YYNQTGRIPDWCSLNNPPLEMMFDVGKTQPPLMKRAFSTEK  NSREPPQAGFGPSPRKSPTASSFLFPWRPLASSFWMGAQGAQES IKAMWRVPGTTRRPVTGESPGMHRPEAMLLLTLALLGGFTWAG KMYGFGGGKYFSTTEDYDHEITGLRVSVGLLLVKSVQVKLGDSW DVKLGALGGNTQEVTLQPGEYITKVFVAFQAFLRGMVMYTSKDR YFYFGKLDGQISSAYPSQEGQVLVGIYGQYQLLGIKSIGFEWNY PLEEPTTEPPVNLTYSANSPVGR  5517 246 499 SEIYVAMRTDSSKMTDVESGVANFASSARAGRRNALPDIQSSAA TDGTSDLPLKLEALSVKEDAKEKDEKTTQDQLEKPQNEEK DAWADAWVRAWDLNMPFPCLWLGLLLDLVAALDFNYHRQEGMEA FLKTVAQNYSSVTHLHSIGKSVKGRNLWLVVGFPKEHRIGIP EFKYVAMMHGDETVGRELLLHLIDYLVTSDGKDPEITNLINSTR IHIMPSNNPDGFEAVKKPDCYYSIGRENYNQVDLNRNFPDAFEY NNVSRQPETVAVMKWLKTETFVLSANLHGGALVASYPFDNGVQA TGALYSRSLTPDDDVFQYLAHTYASRNPNMKKGDECKNKMNFPN	ı			200	TYCCEAGURGE CONTROL OF THE TYCCEAGURGE CONTROL OF THE TYCCEAGURGE CONTROL OF THE TYCCEAGURGE CONTROL OF THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE THE TYCE
FEVPSVLLAPSHLMALLTLGINSAMVLDCGYRESLVLPIYEGIP VLNCWGALPLGGKALHKELETQLLEQCTVDTSVAKEQSLPSVMG SVPEGVLEDIKARTCFVSDLKRGLKIQAAKFNIDGANERPSPPPP NVDYPLDGEKILHILGSIRDSVVEILFEQDNEEQSVATLILDSL IQCPIDTRKQLAENLVVIGGTSMLEGFLHRILAEIRYLVEKPKY KKALGTKTFRIHTPPAKANCVAWLGGAIFGALQDILGSRSVSKE YYNQTGRIPDWCSLNNPPLEMMFDVGKTQPPLMKRAFSTEK YYNQTGRIPDWCSLNNPPLEMMFDVGKTQPPLMKRAFSTEK NSREPPQAGFGPSPRKSPTASSFLFPWRPLASSFWMGAQGAQES IKAMWRVPGTTRRPVTGESPGMHRPEAMLLLLTLALLGGPTWAG KMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSVQVKLGDSW DVKLGALGGNTQEVTLQPGEYITKVFVAFQAFLRGMVMYTSKDR YFYFGKLDGQISSAYPSQEGQVLVGIYGQYQLLGIKSIGFEWNY PLEEPTTEPPVNLTYSANSPVGR  5517 246 499 SEIYVAMRTDSSKMTDVESGVANFASSARAGRRNALPDIQSSAA TDGTSDLPLKLEALSVKEDAKEKTTQDQLEKPQNEEK DAWADAWVRAWDLNMDFPCLWLGLLLPLVAALDFNYHRQEGMEA FLKTVAQNYSSVTHLHSIGKSVKGRNLWVLVVGRFFKEHRIGIP EFKYVANMHGDETVGRELLLHLIDYLVTSDGKDPEITILLINSTR IHIMPSNNPPGFEAVKKPDCYYSIGRENYNQYDLNRNFPDAFEY NNVSRQPETVAVMKWLKTETFVLSANLHGGALVASYPFDNGVQA TGALYSRSLTPDDDVFQYLAHTYASRNPNMKKGDECKNKMNFPN GVTNGYSWYPLOGGMODYNYIWAOCREITERLEGGEND	}		í , , , , , , , , , , , , , , , , , , ,		TREGIAGE IGERCITES VIKRACMDEDIDIRIOIDITES TO THE TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL
SVPEGVLEDIKARTCFVSDLKRGLKIQAAKFNIDGNNERPSPPP NVDYPLDGEKILHILGSIRDSVVEILFEQDNEEQSVATLILDSL IQCPIDTRKQLAENLVVIGGTSMLPGFLHRLLAEIRYLVEKPKY KKALGTKTFRIHTPPAKANCVAWLGGAIFGALQDILGSRSVSKE YYNQTGRIPDWCSLNNPPLEMMFDVGKTQPPLMKRAFSTEK  SS16  3  735  NSREPPPQAGFGPSPRKSPTASSFLFPWRPLASSFWMGAQGAQES IKMWRVPGTTRRPVTGESPGMHRPEAMLLLLTLALLGGPTWAG KMYGPGGGKYFSTTEDYDHEITGLRVSVGLLVKSVQVKLGDSW DVKLGALGGNTQEVTLQPGEYITKVFVAFQAFLRGMVMYTSKDR YFYFGKLDGQISSAYPSQEGQVLVGIYGQYQLLGIKSIGFEWNY PLEEPTTEPPVNLTYSANSPVGR  SEIYVAMRTDSSKMTDVESGVANFASSARAGRRNALPDIQSSAA TDGTSDLPLKLEALSVKEDAKEKDEKTTQDQLEKPQNEEK  TDGTSDLPLKLEALSVKEDAKEKDEKTTQDQLEKPQNEEK FLKTVAQNYSSVTHLHSIGKSVKGRNLWVLVVGRFFKEHRIGIP EFKYVANMHGDETVGRELLLHLIDYLVTSDGKDPEITNLINSTR IHIMPSNNPDGFEAVKKPDCYYSIGRENYNQYDLNRNFPDAFEY NNVSRQPETVAVMKWLKTETFVLSANLHGGALVASYPFDNGVQA TGALYSRSLTPDDDVFQYLAHTYASRNPNMKKGDECKNKMNFPN GVTNGYSWYPLQGGMODYNYIWAACCELITTETGOWND	ł		j		1 THE DEPTH OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPER
NVDYPLDGEKILHILGSIRDSVVEILFEQDNEEQSVATLILDSL IQCPIDTRKQLAENLVVIGGTSMLPGFLHRLLAEIRYLVEKPKY KKALGTKTFRIHTPPAKANCVAWLGGAIFGALQDILGSRSVSKE YYNQTGRIPDWCSLNNPPLEMMFDVGKTQPPLMKRAFSTEK  SFREPPQAGFGPSPRKSPTASSFLFPWRPLASSFWMGAQGAQES IKAWMRVPGTTRRPVTGESPGMHRPEAMLLLLTLALLGGFTWAG KMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSVQVKLGDSW DVKLGALGGNTQEVTLQPGEYITKVFVAFQAFLRGMVMYTSKDR YFYFGKLDGQISSAYPSQEGQVLVGIYGQYQLLGIKSIGFEWNY PLEEPTTEPPVNLTYSANSPVGR  5517 246 499 SEIYVAMRTDSSKMTDVESGVANFASSARAGRRNALPDIQSSAA TDGTSDLPPLKLEALSVKEDAKEKDEKTTQDQLEKPQNEEK TDGTSDLPPLKLEALSVKEDAKEKDEKTTQDQLEKPQNEEK FLKTVAQNYSSVTHLHSIGKSVKGRNLWVLVVGRFPKEHRIGIP EFKYVANMHGDETVGRELLLHLIDYLVTSDGKDPEITNLINSTR IHIMPSNIPPDGFEAVKKPDCYYSIGRENYNQYDLNRNFPDAFEY NNVSRQPETVAVMKWLKTETFVLSANLHGGALVASYPFDNGVQA TGGLYSRSLTPDDDVFQYLAHTYASRNPNMKKGDECKNKMNFPN GVTNGYSWYPLOGGMODYNYLWACCERTTLELGGCHMMMFPN	1				VINCWGALPIGGKALHKELETOLLEGGYRESLVLPIYEGIP
IOCPIDTRKQLAENLVVIGGTSMLPGFLHRILAEIRYLVEKPKY KKALGTKTFRIHTPPAKANCVAWLGGAIFGALQDILGSRSVSKE YYNQTGRIPDWCSLNNPPLEMMFDVGKTQPPLMKRAFSTEK YYNQTGRIPDWCSLNNPPLEMMFDVGKTQPPLMKRAFSTEK NSREPPQAGFGPSPRKSPTASSFLFPWRPLASSFWMGAQGAQES IKAMWRVPGTTRRPVTGESPGMHRPEAMLLLLTLALLGGFTWAG KMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSVQVKLGDSW DVKLGALGGNTQEVTLQFGGYITKVFVAFQAFLRGMVMYTSKDR YFYFGKLDGQISSAYPSQEGQVLVGIYGQYQLLGIKSIGFEWNY PLEEPTTEPPVNLTYSANSPVGR  5517 246 499 SEIYVAMRTDSSKMTDVESGVANFASSARAGRRNALPDIQSSAA TDGTSDLPLKLEALSVKEDAKEKDEKTTQDQLEKPQNEEK DAWADAWVRAWDLNMDFPCLWLGLLLPLVAALDFNYHRQEGMEA FLKTVAQNYSSVTHLHSIGKSVKGRNLWVLVVGRFPKEHRIGIP EFKYVANMHGDETVGRELLLHLIDYLVTSDGKDPEITNLINSTR IHMPSNNPDGFEAVKKPDCYYSIGRENYNQYDLNRNFPDAFEY NNVSRQPETVAVMKWLKTETFVLSANLHGGALVASYPFDNGVQA TGGALYSRSLTPDDDVFQYLAHTYASRNPNMKKGDECKNKMNFPN GVTNGYSWYPLOGGMODYNYLWAOCRETTALEIGGCKNKMNFPN			· · · · · · · · · · · · · · · · · · ·		1 ~ · · · · · · · · · · · · · · · · · ·
KKALGTKTFRIHTPPAKANCVAWLGGAIFGALQDILGSRSVSKE YYNQTGRIPDWCSLNNPPLEMMPDVGKTQPPLMKRAFSTEK YYNQTGRIPDWCSLNNPPLEMMPDVGKTQPPLMKRAFSTEK NSREPPQAGFGPSPRKSPTASSFLFPWRPLASSFWMGAQGAQES IKAMWRVPGTTRRPVTGESPGMHRPEAMLLLLTLALLGGFTWAG KMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSVQVKLGDSW DVKLGALGGNTQEVTLQFGGYITKVFVAFQAFLRGMVMYTSKDR YFYFGKLDGQISSAYPSQEGQVLVGIYGQYQLLGIKSIGFEWNY PLEEPTTEPPVNLTYSANSPVGR  5517 246 499 SEIYVAMRTDSSKMTDVESGVANFASSARAGRRNALPDIQSSAA TDGTSDLPLKLEALSVKEDAKEKDEKTTQDQLEKPQNEEK FLKTVAQNYSSVTHLHSIGKSVKGRNLWVLVVGRFPKEHRIGIP EFKYVANMHGDETVGRELLLHLIDYLVTSDGKDPEITNLINSTR IHMPSNNPDGFEAVKKPDCYYSIGRENYNQYDLNRNFPDAFEY NNVSRQPETVAVMKWLKTETFVLSANLHGGALVASYPFDNGVQA TGGALYRSSLTPDDDVFQYLAHTYASRNPMKKGDECKNKMNFPN GVTNGYSWYPLOGGMODYNYIWAOCRETTALEIGGCKNKMNFPN		)	j		I TO TE ADDIENTINGS INDSVIVETT, PEODMEROOVER TO THE
TOGTSDLPLKLEALSVKEDAKENDELLULVAALDENVHREGEA  3 735 SEPPOAGFGPSPRKSPTASSFLFPWRPLASSFWMGAQGAGES IKAMWRVPGTTRRPVTGESFGMHRPEAMLLLLLLGGPTWAG KMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSVQVKLGDSW DVKLGALGGNTQEVTLQPGEYITKVFVAFQAFLRGMYMYTSKDR YFYFGKLDGQISSAVPSQEGQVLVGIYGQYQLLGIKSIGFEWNY PLEEPTTEPPVNLTYSANSPVGR  5517 246 499 SEIYVAMRTDSSKMTDVESGVANFASSARAGRRNALPDIQSSAA TDGTSDLPLKLEALSVKEDAKEXDEKTTQDQLEKPQNEEK TDGTSDLPLKLEALSVKEDAKEXDEKTTQDQLEKPQNEEK FLKTVAQNYSSVTHLHSIGKSVKGRNLWLVVGRFPKEHRIGIP EFKYVANMHGDETVGRELLLHLIDYLVTSDGKDPEITNLINSTR IHIMPSNNPDGFEAVKKPDCYYSIGRENYNQYDLNRNFPDAFEY NNVSRQPETVAVMKWLKTETFVLSANLHGGALVASYPFDNGVQA TGGALYSRSLTPDDDVFQYLAHTYASRNPMKKGDECKNKMNFPN GVTNGYSWYPLOGGMODYNYIWAOCRETTALELGGCKNKMNFPN			Í		
S516 3 735 NSREPPQAGFGPSPRKSPTASSFLFPWRPLASSFWGAQGAQES IKAMWRVPGTTRRPVTGESPGMHRPEAMLLLLTLALLGGFTWAG KMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSVQVKLGDSW DVKLGALGGNTQEVTLQPGEYITKVFVAFQAFLRGMYMYTSKDR YFYFGKLDGQISSAYPSQEGQVLVGIYGQYQLLGIKSIGFEWNY PLEEPTTEPPVNLTYSANSPVGR  5517 246 499 SEIYVAMRTDSKMTDVESGVANFASSARAGRRNALPDIQSSAA TDGTSDLPLKLEALSVKEDAKEKDEKTTQQLEKPQNEEK TDGTSDLPLKLEALSVKEDAKEKDEKTTQQLEKPQNEEK FLKTVAQNYSSVTHLHSIGKSVKGRNLWVLVVGRFPKEHRIGIP EFKYVANMHGDETVGRELLLHLIDYLVTSDGKDPEITNLINSTR IHIMPSNNPDGFEAVKKPDCYYSIGRENYNQYDLNRNFPDAFEY NNVSRQPETVAVMKWLKTETFVLSANLHGGALVASYPFDNGVQA TGGLYSRSLTPDDDVFQYLAHTYASRNPNMKKGDECKNKMNFPN GVTNGYSWYPLOGGMODYNYIWACCETTLELGGCKNMNFPN		1	1		I WE WELL THE TERMINE VANIED AT THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AND THE TERMINE AN
IKAMWRVPGTTRRPVTGESPGMHRPEAMLLLLTLALLGGFTWAG KMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSVQVKLGDSW DVKLGALGGNTQEVTLQPGEYITKVFVAFQAFLRGMVMYTSKDR YFYFGKLDGQISSAYPSQEGQVLVGIYGQYQLLGIKSIGFEWNY PLEEPTTEPPVNLTYSANSPVGR  5517 246 499 SEIYVAMRTDSKMTDVESGVANFASSARAGRRNALPDIQSSAA TDGTSDLPLKLEALSVKEDAKEKDEKTTQDQLEKPQNEEK TDGTSDLPLKLEALSVKEDAKEKDEKTTQDQLEKPQNEEK FLKTVAQNYSSVTHLHSIGKSVKGRNLWVLVVGRFPKEHRIGIP EFKYVANMHGDETVGRELLLHLIDYLVTSDGKDPEITNLINSTR IHIMPSNNPDGFEAVKKPDCYYSIGRENYNQYDLNRNFPDAFEY NNVSRQPETVAVMKWLKTETFVLSANLHGGALVASYPFDNGVQA TGGLYSRSLTPDDDVFQYLAHTYASRNPNMKKGDECKNKMNFPN GVTNGYSWYPLOGGMODYNYLWACCETTLELGGCKN		5516	3	736	~~~~×~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
KMYGPGGKYFSTTEDYDHEITGLRVSVGLLLVKSVQVKLGDSW DVKLGALGGNTQEVTLQPGGYITKVFVAFQAFLRGMVMYTSKDR YFYFGKLDGQISSAYPSQEGQVLVGIYGQYQLLGIKSIGFEWNY PLEEPTTEPPVNLTYSANSPVGR  5517 246 499 SEIYVAMRTDSSKMTDVESGVANFASSARAGRRNALPDIQSSAA TDGTSDLPLKLEALSVKEDAKEKDEKTTQDQLEKPQNEEK DAWADAWVRAWDLNMDFPCLWLGLLLPLVAALDFNYHRQEGMEA FLKTVAQNYSSVTHLHSIGKSVKGRNLWVLVVGRFPKEHRIGIP EFKYVANMHGDETVGRELLLHLIDYLVTSDGKDPEITNLINSTR IHIMPSNNPDGFEAVKKPDCYYSIGRENYNQYDLNRNFPDAFEY NNVSRQPETVAVMKWLKTETFVLSANLHGGALVASYPFDNGVQA TGGLLYSRSLTPDDDVFQYLAHTYASRNPNMKKGDECKNKMNFPN GVTNGYSWYPLOGGMODYNYLWACCETTLELGGENYM	ı	{		,33	MONDE PUNGEGES PRESETASSELED DELACCEURGE STATE
DVKLGALGGNTQEVTLQPGEYITKVFVAFQAFLRGMYMYTSKDR YFYFGKLDGQISSAYPSQEGQVLVGIYGQYQLLGIKSIGFEWNY PLEEPTTEPPVNLTYSANSPVGR SEIYVAMRTDSSKMTDVESGVANFASSARAGRRNALPDIQSSAA TDGTSDLPLKLEALSVKEDAKEKDEKTTQDQLEKPQNEEK DAWADAWVRAWDLNMDFPCLWLGLLLPLVAALDFNYHRQEGMEA FLKTVAQNYSSVTHLHSIGKSVKGRNLWVLVVGRFPKEHRIGIP EFKYVANMHGDETVGRELLLHLIDYLVTSDGKDPEITNLINSTR IHIMPSNNPDGFEAVKKPDCYYSIGRENYNQYDLNRNFPDAFEY NNVSRQPETVAVMKWLKTETFVLSANULGGALVASYPFDNGVQA TGALYSRSLTPDDDVFQYLAHTYASRNPNMKKGDECKNKMNFPN GVTNGYSWYPLOGGMODYNYLWAOCRETTALE GGGWNGMNFPN		ł	Ì	J	TOTAL TOTAL TERMINATION   TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TO
PLEEPTTEPPVNLTYSANSPVGR  5517 246 499 SEIYVAMRTDSSKMTDVESGVANFASSARAGRNALPDIQSSAA TDGTSDLPLKLEALSVKEDAKEKDEKTTQDQLEKPQNEEK DAWADAWVRAWDLNMDFPCLWLGLLLPLVAALDFNYHRQEGMEA FLKTVAQNYSSVTHLHSIGKSVKGRNLWVLVVGRFPKEHRIGIP EFKYVANMHGDETVGRELLLHLIDYLVTSDGKDPEITNLINSTR IHIMPSNNPDGFEAVKKPDCYYSIGRENYNQYDLNRNFPDAFEY NNVSRQPETVAVMKWLKTETFVLSANLHGGALVASYPFDNGVQA TGALYSRSLTPDDDVFQYLAHTYASRNPMKKGDECKNKMNFPN GVTNGYSWYPLOGGMODYNYLWAOCRETTLELGGKUNGNFPN		1			TOTAL GOODLEST LEDYDHK PTCP, DVCVCT T T 1777 CVCTCC
5517  246  499  SEIYVAMRTDSSKMTDVESGVANFASSARAGRNALPDIQSSAA  TDGTSDLPLKLEALSVKEDAKEXDEKTTQDQLEKPQNEEK  DAWADAWVRAWDLNMDFPCLWLGLLLPLVAALDFNYHRQEGMEA FLKTVAQNYSSVTHLHSIGKSVKGRNLWVLVVGRFPKEHRIGIP EFKYVANMHGDETVGRELLLHLIDYLVTSDGKDPEITNLINSTR IHIMPSNNPPDGFEAVKKPDCYYSIGRENYNQYDLNRNFPDAFEY NNVSRQPETVAVMKWLKTETFVLSANLHGGALVASYPFDNGVQA TGALYSRSLTPDDDVFQYLAHTYASRNPPMKKGDECKNKMNFPN GVTNGYSWYPLOGGMODYNYLWAOCRETTALELGGCKNKMNFPN		1		1	YFYFGKLDGOTSSAVBCOEGOW WATSKDR
SEIYVÄMRTDSSKMTDVESGVANFASSARAGRRNALPDIQSSAA TDGTSDLPLKLEALSVKEDAKEKDEKTTQDQLEKPQNEEK  DÄWADAWVRAWDLINMDFPCLWLGLLLPLVAALDFNYHRQEGMEA FLKTVAQNYSSVTHLHSIGKSVKGRNLWVLVVGRFPKEHRIGIP EFKYVANMHGDETVGRELLLHLIDYLVTSDGKDPEITNLINSTR IHIMPSNNPDGFEAVKKPDCYYSIGRENYNQYDLINRNFPDAFBY NNVSRQPETVAVMKWLKTETFVLSANLHGGALVASYPFDNGVQA TGALYSRSLTPDDDVFQYLAHTYASRNPNMKKGDECKNKMNFPN GVTNGYSWYPLOGGMODYNYIWAOCRETTELSCOCKNEMNFPN	┝				PLEEPTTEPPVNI.TVCANCEUCE
DAWADAWVRAWDLNMDFPCLWLGLLLPLVAALDFNYHRQEGMEA FLKTVAQNYSSVTHLHSIGKSVKGRNLWVLVVGRFPKEHRIGIP EFKYVANMHGDETVGRELLLHLIDYLVTSDGKDPEITNLINSTR IHIMPSNNPDGFEAVKKPDCYYSIGRENYNQYDLNRNFPDAFEY NNVSRQPETVAVMKWLKTETFVLSANLHGGALVASYPFDNGVQA TGALYSRSLTPDDDVFQYLAHTYASRNPNMKKGDECKNKMNFPN GVTNGYSWYPLOGGMODYNYIWAOCRETTLELGCGKWMNFPN	1	221/	246	499	SELYVAMRTDSSKMTDVESGVANFASSARAGRRANALDD
FIKTVAQNYSSVTHLHSIGKSVKGRNLWVLVVGRFPKEHRIGIP EFKYVANMHGDETVGRELLLHLIDYLVTSDGKDPEITNLINSTR IHIMPSNNPDGFEAVKKPDCYYSIGRENYNQYDLNRNFPDAFEY NNVSRQPETVAVMKWLKTETFVLSANLHGGALVASYPFDNGVQA TGALYSRSLTPDDDVFQYLAHTYASRNPNMKKGDECKNKMNFPN GVTNGYSWYPLOGGMODYNYIWAOCRETTLEIGGGCWMNNFPN	$\vdash$	5518			
EFKYVANMHGDETVGRELLLHLIDYLVTSDGKDPEITNLINSTR IHIMPSMNPDGFEAVKKPDCYYSIGRENYNQYDLNRNFPDAFEY NNVSRQPETVAVMKWLKTETFVLSANLHGGALVASYPFDNGVQA TGALYSRSLTPDDDVFQYLAHTYASRNPMKKGDECKNKMNFPN GVTNGYSWYPLOGGMODYNYIWAOCRETTLELGGGWMNFPN	l		3	1375	DANADAW V KAWDLINDEPCI, WIGI, T.I. DI, WAAT DENVIROR
IHIMPSMNPDGFEAVKKPDCYYSIGRENYNQYDLNRNFPDAFEY NNVSRQPETVAVMKWLKTETFVLSANLHGGALVASYPFDNGVQA TGALYSRSLTPDDDVFQYLAHTYASRNPNMKKGDECKNKMNFPN GVTNGYSWYPLOGGMODYNYIWAOCEETT BLECCKNKMNFPN	1	1		ĺ	THE VACUE OF THE HEIGKSVKCDM WOTHING DEDUCTION
NIVSRQPETVAVMKWLKTETFVLSANLHGGALVASYPFDNGVQA TGALYSRSLTPDDDVFQYLAHTYASRNPHMKKGDECKNKMNFPN GVTNGYSWYPLOGGMODYNYLWAOGRETTLELGGGCWNMNFPN		i			The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
TGALYSRSLTPDDDVFQYLAHTYASRNPHMKKGDECKNKMNFPN GVTNGYSWYPLOGGMODYNYLWAOCEETT BLOCCHKMNFPN		j			
GVTNGYSWYPLOGGMODYNYTWAOCEETTE BLCGGWADDEN		1		1	THE PARTICULAR TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY
! I VIANO - UNA - UNA PROPERTATION OF THE CONTROL - I		- 1		i i	- CIMIONSDIFUUDVEOYIAHTVASDNDNMKKCDEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
I STANDARD TELL KOVELGARGOVED ON THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS OF THE ANALYSIS					T THE TOTAL DOGGERSON AND AND AND AND AND AND AND AND AND AN
					THE TENDETT KOVALGV KGQVFDQNGNPLPNVIVEVQDRK

SEO	Predicted	Decade	
ID	)	Predicted end	Amino acid segment containing signal peptide
NO:	beginning nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	to first	to first amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid		P=Proline, Q=Glutamine, R=Arginine,
- l	residue of	residue of	S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	1	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence	ļ	\=possible nucleotide insertion)
Î			HICPYRTNKYGEYYLLLLPGSYIINVTVPGHDPHITKVIIPEKS
ł		1	QNFSALKKDILLPFQGQLDSIPVSNPSCPMIPLYRNLPDHSAAT
5519	87		KPSLFLFLVSLLHIFFK
2213	87	477	IKSKLNQQVEVQESEWRLTEAKGPTMGKESGWDSGRAAVAAVVG
	1		GVVAVGTVLVALSAMGFTSVGIAASSIAAKMMSTAAIANGGGVA
5520			AGSLVAILQSVGAAGLSVTSKVIGGFAGTALGAWLGSPPSS
5520	117	943	PTEGROKVLKTFTVPRSALAMTKTSTCIYHFLVLSWYTFLNYYI
	1		SQEGKDEVKPKILANGARWKYMTLLNLLLQTIFYGVTCLDDVLK
i	}	j	RTKGGKDIKFLTAFRDLLFTTLAFPVSTFVFLAFWILFLYNRDL
1		t	IYPKVLDTVIPVWLNHAMHTFIFPITLAEVVLRPHSYPSKKTGL
]	1		TLLAAASIAYISRILWLYFETGTWVYPVFAKLSLLGLAAFFSLS
1			YVFIASIYLLGEKLNHWKWVSVQILQRWRLESVGICFQWPDWKS
EFAI			PAKHQLVKNIR
5521	546	911	KILNMQKSCEENEGKPQNMPKAEEDRPLEDVPQEAEGNPQPSEE
1	1	1	GVSQEAEGNPRGGPNQPGQGFKEDTPVRHLDPEEMIRGVDFLER
5522			LREEIRRVRNKFVMMHWKQRHSRSRPYPVCFRP
5522	1224	637	GSRPLGQRSREKMWVFGYGSLIWKVDFPYQDKLVGYITNYSRRF
	ì	ŀ	WQGSTDHRGVPGKPGRVVTLVEDPAGCVWGVAYRLPVGKEEEVK
[		(	AYLDFREKGGYRTTTVIFYPKDPTTKPFSVLLYIGTCDNPDYLG
.	j		PAPLEDIAEQIFNAAGPSGRNTEYLFELANSIRNLVPEKADEHL
5523	<del></del>		FALEKLVKERLEGKQNLNCI
2273	3	1280	SKGKKRMGSSMSAATARRPVFDDKEDVNFDHFQILRAIGKGSFG
l i	,	·	KVCIVQKRDTEKMYAMKYMNKQQCIERDEVRNVFRELEILQEIE
			HVFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVQFSEDTV
1		l	RLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI
1 1			ATIIKDGERATALSGTKPYMAPEIFHSFVNGGTGYSFEVDWWSV
			GVMAYELLRGWRPYDIHSSNAVESLVQLFSTVSVQYVPTWSKEM
1			VALLRKLLTVNPEHRLSSLQDVQAAPALAGVLWDHLSEKRVEPG
			FVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRD
			SSQSENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPES
5524	85	2318	RDAAEPVEDEAERSALPMCGPICPSAGSG
5524	85	2318	RERERDHRPGESSQGQSGAGGCFPSPTMELRCGGLLFSSRFDSG
1 1			NLAHVEKVESLSSDGEGVGGGASALTSGIASSPDYEFNVWTRPD
1			CAETEFENGNRSWFYFSVRGGMPGKLIKINIMNMNKQSKLYSQG
1 (			MAPFVRTLPTRPRWERIRDRPTFEMTETQFVLSFVHRFVEGRGA
1 1			TTFFAFCYPFSYSDCQELLNQLDQRFPENHPTHSSPLDTIYYHR
1 1			ELLCYSLDGLRVDLLTITSCHGLREDREPRLEQLFPDTSTPRPF
1 1	1		RFAGKRIFFLSSRVHPGETPSSFVFNGFLDFILRPDDPRAQTLR
			RLFVFKLIPMLNPDGVVRGHYRTDSRGVNLNRQYLKPDAVLHPA
1 1	1		IYGAKAVLLYHHVHSRLNSQSSSEHQPSSCLPPDAPVSDLEKAN
1 1	l	,	NLQNEAQCGHSADRHNAEAWKQTEPAEQKLNSVWINPQOSAGLE ESAPDTIPPKESGVAYYVDLHGHASKRGCFMYGNSFSDESTQVE
1			NMLYPKLISLNSAHFDFQGCNFSEKNMYARDRRDGQSKEGSGRV
1 1		'	ATYKASCTTHSYTLECHYMECHOLBISTER ACTIONS
1	ļ		AIYKASGIIHSYTLECNYNTGRSVNSIPAACHDNGRASPPPPPA
] ]		'	FPSRYTVELFBQVGRAMAIAALDMABCNPWPRIVLSEHSSLTNL RAWMLKHVRNSRGLSSTLNVGVNKKRGLRTPPKSHNGLPVSCSE
} {			NTLSRARSFSTGTSAGGSSSSQQNSPQMKNSPSFPFHGSRPAGL
1 1			PGLGSSTQKVTHRVLGPVRGKPVWEPLQHVFGCLGHCWGK
5525	105	834	SNTLDFERHLFIMGQQISDQTQLVINKLPEKVAKHVTLVRESGS
1 1		074	LTYPEFICOUNELNOUTANTA COOPERITY TO THE SECOND STATES OF THE SECOND STATES OF THE SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECON
1	]		LTYEEFLGRVAELNDVTAKVASGQEKHLLFEVQPGSDSSAFWKV
1 1	<b>[</b>	•	VVRVVCTKINKSSGIVEASRIMNLYQFIQLYKDITSQAAGVLAQ
1			SSTSEEPDENSSSVTSCQASLWMGRVKQLTDEEECCICMDGRAD
1 1	1		LILPCAHSFCQKCIDKWSDRHRNCPICRLQMTGANESWVVSDAP
5526	3		TEDDMANYILNMADEAGQPHRP
	,	853	RRPCNPVRAAKRTGAAARAPRGLEVTMLRVAWRTLSLIRTRAVT
]	J		QVLVPGLPGGGSAKFPFNQWGLQPRSLLLQAARGYVVRKPAQSR
	l		LDDDPPPSTLLKDYQNVPGIEKVDDVVKRLLSLEMANKKEMLKI
1	}		KQEQFMKKIVANPEDTRSLEARIIALSVKIRSYEBHLEKHRKDK
			AHKRYLLMSIDQRKKMLKNLRNTNYDVFEKICWGLGIEYTFPPL
<u> </u>	<u>-</u>		YYRRAHRRFVTKKALCIRVFQETQKLKKRRRALKAAAAAQKQAK

SEC	Dwo di		
ID	-	Predicted end	
NO:	7 3	nucleotide	I M-ALGUANC, CECVSEPINE, D-Armanic, a second
I NO:		location	Officiality ACID, Pephenvialanine C-01
j	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ľ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Tryptophan V=Try
- 1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	1 -	Codon, /=possible nucleotide deletion,
			\=possible nucleotide insertion) RRNPDSPAKAIPKTLKDSQ
5527	3225	565	LIBYVIIVONOVA
	-	1	LLRKYLLHQNPLLLRHQPNRTCISFSATMKLKDTKSRPKQSSCG
ĺ	ţ	1	I M VINGIN V GRAKEVKIDPNMFADGCMDDI.VCEEEI TOVOTVO
}	1	1	FARMPSSEFSKEAPKRKAOAVSEEEEEEECKGGGDVVVTVTVT
	1		NIVALEGISTUKEFEVKDPELEAGGDDMVCDDDEAGEMTGENTIT
I	į.	ł	YIAPAKAKNKGKKGLEPSOSTAAKUDKKAVTWI DEUTIDOKS
- 1	}	1	AMEDIC VEREVERALSELGESAPTPTOALTI, ADATED VIDE OF
ŀ		1	THE TOSON LIMITAL PMINAVIOWOKENA A DODONTE A DACTEMBRE
1	1	1	AGAETRSFGRAEAESDALPEDTVIESEAT.DENTAADADAKMOOM
	1		VSDQALLEGUDJAGEGPSSLIREKPVDKONEMEDENT DVDOGGO
ļ			LKQELDDKSATCKAYPKRPLLGLVLTPTRELAVQVKQHIDAVAR
	I	1	FTGIKTAILVGGMSTQKQQRMLNRRPEIVVATPGRLWELIKEKH
j	j	1	YHLRNLRQLRCLVVDEADRMVEKGHFAELSQLLEMLNDSQYNPK
			RQTLVFSATLTLVHQAPARILHKKHTKKMDKTAKLDLLMQKIGM
ł	1	1.	RGKPKVIDLTRNEATHERE TERRETHERE
ł		İ	RGKPKVIDLTRNEATVETLTETKIHCETDEKDFYLYYFLMQYPG
		1	RSLVFANSISCIKRLSGLLKVLDIMPLTLHACMHQKQRLRNLEQ
- 1	1	j	FARLEDCVLLATDVAARGLDIPKVQHVIHYQVPRTSEIYVHRSG
	<b>}</b>		RTARATNEGLSLMLIGPEDVINFKKIYKTLKKDEDIPLFPVQTK
1	1	f	YMDVVKERIRLARQIEKSEYRNFQACLHNSWIEQAAAALEIELE
- 1	1		EDMYKGGKADQQEERRRQKQMKVLKKELRHLLSQPLFTESQKTK
Ĺ			YPTQSGKPPLLVSAPSKSESALSCLSKQKKKKKKKKKKEPQPEQP QPSTSAN
5528	3	895	QF315AN
1	1	633	GPFLSACRMWGACKVKVHDSLATISITLRRYLRLGATMAKSKFE
	Į.		I TANKEAUDICLAHCWVVVRIDGRNEUDENEVINIENVNIDGES
1	i 1	l	1 ATHE TOTAL A MEETING INTO TAKE A SECOND LANGUE AND A CO.
1	1		FRITA MOQUASSIVEY WRDYFEDOPLI.VDDGEDCDIARANDANOM
1		•	DADIESWRQAUCHINNLYNTVFWAI.TOOCGI.TDVOACGDI.Com
1	1		1 TO CARL TOLOGRAN THE ANNE PENAL KICK AND
5529	48		TIEMEGRAMAVIKIKIKPCKPSHI,PRADCI,DWI
3323	48	640	TERLVSAHLKTRKLINPEAAERRWRDWDSBOOWL SULVODING
1	1	i	TOTAL TORVUM COUNTS CONTRACT TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS TO THE COUNTS T
į.	1 1		MENTILE DEVISES CVEVOEINE E EVILVAT TO PROPUDITOR TOTAL
ļ	1	ĺ	TOTOTA ALLORCLER KHKLETY TSECTHOTED TANDARD I
5530	-		AND THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPER
3330	4541	2606	AQIVHAISYCHKLHVGHRDLKPENVVFFEKQGLVKLTDFGFSNK
	1 1	1	FOPGKKLTTSCGSLAYSAPEILLGDEYDAPAVDIWSLGVILFML
1	1		VCGQPPFQEANDSETLTMIMDCKYTVPSHVSKECKDLITRMLQR
ľ	1	i	DPKRRASLEEIENHPWLQGVDPSPATKYNIPLVSYKNLSEEEHN
1	1	l	SIIQRMVLGDIADRDAIVEALETNRYNHITATYFLLAERILREK
1	1	i	QEKEIQTRSASPSNIKAQFRQSWPTKIDVPQDLEDDLTATPLSH
Į.	1	ļ	ATVPOSPARAADSVI NGHPSVCI COOR WOODLEDDLTATPLSH
	1		ATVPQSPARAADSVLNGHRSKGLCDSAKKDDLPELAGPALSTVP PASLKPTASGRKCLFRVEEDEEEDEEDKKPMSLSTQVVLRRKPS
1	1	J	VTNRLTSRKSA PVI.NOTERECEGERATION TO THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRA
1	]		VTNRLTSRKSAPVLNQIFEEGESDDEFDMDENLPPKLSRLKMNI ASPGTVHKRYHDPKSOCPGSSCEGEREDEDHOLPPKLSRLKMNI
1	1	ł	ASPGTVHKRYHRRKSQGRGSSCSSSETSDDDSESRRRLDKDSGF TYSWHRPDSSPGDDGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
1	1		113 HARDSSEGPEGSEGDGGGOSKDSNASGGUNVASDSBARRA
1	j l		OGSESSGEORETHTSGTTRRCAGPSNSMOTAGDCAGETTEGT
	}	,	DASHCE SQUAGSTRY LIDPONGLS FSSVIKIOF FCTWWW.
			GVAGQV PAVGGIRFTSDHMADTTTRI,ERTKGKNI, VARRIT OF TO
5531	24		EXIIS VNI QRNYKEGLLCASSPASCCHVT
1		ſ	GSOPRAPRPRDSMERPEPELIROSWRAVSRSPLEHGTVLFARLF
[	1	1.	ALEPHOLIPH CROFSSPENCI SSPEET DUT DE LA LETTE DE LE
) 1	j i		INVEDUSSIBLY LASIGRKHRAVGVKI. SEEETMODOL LANGE TO A
5532	3395		GGFAE I FAIRAAWSQLYGAVVOAMSRGWDGE
	5555	1402	SDWMVVGKRKMI IEDETEFCGEELLHSVLOCKSVEDVI DOEDME
l		1 '	CARTRAMPTEMIKGVFFLNRAAMKMANMDFVFDPMFTNDDDGVG
1		{ •	NEUVEDREAELLYFADVCAGPGGFSEYVI.WRKKWUDVCECMDZ K
!	J	1 \	PROPERTY SASSELFEPTYGEGGIDGDGDITTPDDDATES FOR
1	1	[ 1	FVLDNTDRKGVHFLMADGGFSVEGQENLQEILSKQLLLCQFLMA
[	1	1	LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFERVCLFKPITS
			RPANSERYVVCKGLKVGIDDVRDYLFAVNIKLNQLRNTDSDVNL
			THE TENT OF THE AVAILABLE RATES OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERT

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1.0.	location		Glutamic Acid, F=Phenylalanine, G≈Glycine,
}	1	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Ston
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
ł	sequence		\=possible nucleotide insertion)
		<del></del>	VVPLEVIKGDHEFTDYMIRSNESHCSLQIKALAKIHAFVQDTTL
		1	SEDBOAFTBRECH BY MCTROOPER DOGGRAMAKIHAFYQDTTL
	}	İ	SEPRQAEIRKECLRLWGIPDQARVAPSSSDPKSKFFELIQGTEI
			DIFSYKPTLLTSKTLEKIRPVFDYRCMVSGSEQKFLIGLGKSQI
1	ł	l	YTWDGRQSDRWIKLDLKTELPRDTLLSVEIVHELKGEGKAQRKI
1	1		SAIHILDVLVLNGTDVREQHFNQRIQLAEKFVKAVSKPSRPDMN
1	1		PIRVKEVYRLEEMEKIFVRLEMKIIKGSSGTPKLSYTGRDDRHF
1	1		VPMGLYIVRTVNEPWTMGFSKSFKKKFFYNKKTKDSTFDLPADS
1	1		IAPFHICYYGRLFWEWGDGIRVHDSQKPQDQDKLSKEDVLSFIQ
		·	MHRA
5533	94	789	MKERRAPQPVVARCKLVLVGDVQCGKTAMLQVLAKDCYPETYVP
1	}		TVFENYTACLETEEQRVELSLWDTSGSPYYDNVRPLCYSDSDAV
			LLCENTEDDETWOON PRODUCT DISCOURTS TO THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF
1	{		LLCFDISRPETVDSALKKWRTEILDYCPSTRVLLIGCKTDLRTD
1	1		LSTLMELSHQKQAPISYEQGCAIAKQLGPEIYLEGSAFTSEKSI
1	1	Ī	HSIFRTASMLCLNKPSPLPQKSPVRSLSKRLLHLPSRSELISPT
-	<u> </u>		FKKEKAKXCSIM
5534	3	605	LVRGRARAANPGRVGAMDGLRQRVEHFLEQRNLVTEVLGALEAK
<b>)</b>	1		TGVEKRYLAAGAVTLLSLYLLFGYGASLLCNLIGFVYPAYASIK
	1		AIESPSKDDDTVWLTYWVVYALFGLAEFFSDLLLSWFPFYYVGK
j .	j j		CAFLLFCMAPRPWNGALMLYQRVVRPLFLRHHGAVDRIMNDLSG
			RALDAAAGITRNVKPSQTPQPKDK
5535	1029	332	KSFMDSEARLCSLVELSDTQDETQKSDSENEDLKIDCLQESQEL.
1	į		NLQKLKNSERILTEAKQKMRELTVNIKMKEDLIKELIKTGNDAK
1 1	i		CACACAMI AMMA BANDA BOS MANDA MANGED T KEPI KAGNDAK
1			SVSKQYTLKVTKLEHDAEQAKVELTETQKQLQELENKDLSDVAM
	i i		KVKLQKEFRKKVDAAKLRVQVLQKKQQDSKKLASLSIQNEKRAN
			ELEQSVDHMKYQKIQLQRKLQEENEKRKQLDAVIKRDQQKIKVI
5536	84.5		LSYIPAKYNMKC
2236	942	282	AAATAASLSPRGCRLRTPSSDVSPSRAPPPSAAPLPTGRAQMSP
	]		SGRLCLLTIVGLILPTRGOTLKDTTSSSSADATIMDTOVPTPAR
			DAVYTELQPTSPTPTWFADETPQPQTQTQOOLEGTDGPLVTDPET
			HKSTKAAHPTDDTTTLSERPSPSTDVQTDPQTLKPSGFHEDDPF
1_ 1	·		FYDEHTLRKRGLLVAAVLFITGIIILTSGKCRQLSRLCRNHCR
5537	3	2391	RARVSSPQLRVFRSGRPRRLRVLRINRTSVALRLAGTGRFVAKT
1 1	i		PGHPGSWEMGLLTFRDVAVEFSLEEWEHLEPAQKNLYQDVMLEN
			YRNLVSLGLVVSKPDLITFLEQRKEPWNVKSEETVAIQPDVFSH
1	ſ		VNVDI LTEUCTER CEOVILI OPPUGGGDA TOTAL TO THE CONTROL OF THE CEOVILI OPPUGGGDA TOTAL TO THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONT
1 1	1	ı	YNKDLLTEHCTBASFQKVISRRHGSCDLENLHLRKRWKREECEG
			HNGCYDEKTFKYDQFDESSVESLFHQQILSSCAKSYNFDQYRKV
1 1	j.	· ·	FTHSSLLNQQEEIDIWGKHHIYDKTSVLFRQVSTLNSYRNVFIG
1	ł		EKNYHCNNSEKTLNQSSSPKNHQENYFLEKQYKCKEFEEVFLQS
1 1	Í		MHGQEKQEQSYKCNKCVEVCTQSLKHIQHQTIHIRENSYSYNKY
	ł		DKDLSQSSNLRKQIIHNEEKPYKCEKCGDSLNHSLHLTOHOIIP
] 1	1	į	TEEKPYKWKECGKVFNLNCSLYLTKOOOIDTGENLYKCKACSKS
]	Ì		FTRSSNLIVHQRIHTGEKPYKCKECGKAFRCSSYLTKHKRIHTG
1	j	ĺ	EKPYKCKECGKAFNRSSCLTQHQTTHTGEKLYKCKVCSKSYARS
]	( )		SNLIMHQRVHTGEKPYKCKECGKVFSRSSCLTQHRKIHTGENLY
1	[	ſ	KCKVCAKPFTCFSNLIVHERIHTGEKPYKCKECGKAFPYSSHLI
1	j		PHUDIUTGE PROVOCA COVERED COCT
1		ĺ	RHHRIHTGEKPYKCKACSKSFSDSSGLTVHRRTHTGEKPYTCKE
1 1	ŀ	}	CGKAFSYSSDVIQHRRIHTGQRPYKCEECGKAFNYRSYLTTHQR
1			SHTGERPYKCEECGKAFNSRSYLTTHRRRHTGERPYKCDECGKA
1	1		FSYRSYLTTHRRSHSGERPYKCEECGKAFNSRSYLIAHQRSHTR
1			EKL
5538	926	161	HSMMMKIPWGSIPVLMLLLLLGLIDISQAQLSCTGPPAIPGIPG
]			IPGTPGPDGQPGTPGIKGEKGLPGLAGDHGEFGEKGDPGIPGNP
1 1	1	1	GKVGPKGPMGPKGGPGAPGAPGPKGESGDYKATQKIAFSATRTI
Į l		ļ	NVPLRRDQTIRFDHVITNMNNYEPRSGKFTCKVPGLYYFTYHA
1		ſ	CCDCMI_CVNI_MDCDEDA OGRAMOON X BEKSGKFTCKVPGLYYFTYHA
1 1		j	SSRGNLCVNLMRGRERAQKVVTFCDYAYNTFQVTTGGMVLKLEQ
5539	38		GENVFLQATDKNSLLGMEGANSIFSGFLLFPDMEA
22.5	30	1258	HRGPSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPG
1 1		İ	IVDGPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREK
[ [	1	ı	DEIYGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCS
L		Į.	SDSFNEDIAAFAKQVRSERPLFSSNPELDNLVIQAIQVLRFHLL

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	I MANAGEMENT CECVSERING DANGERSHEEL WITH HE
ł	location		1 Crucamic Acid, F=Phenylalanino C di
1 '	corresponding	corresponding	**-**********
- 1	to first	to first	Labelicine, Mamethionine Nanagaragine
	amino acid	amino acid	Perfoline, QeGlutamine Peargining
1	residue of	residue of	S=Serine, T=Threonine V-Valine
1	amino acid	amino acid	Walryptophan, Yarvrosine Yaunknow 4 at
ĺ		sequence	( Codon, /=possible nucleotide deleti-
<u> </u>	sequence	<u> </u>	\=possible nucleotide incertion\
			ELEKVHDLCDNFCHRYITCLKGKMPIDLVIEDRDGGCREDFEDY
l			PASCPSLPDQNNMWIRDHEDSGSVHLGTPGPSSGGLASQSGDNS
	ľ	}	SDQGDGLDTSVASPSSGGEDEDLDQERRRNKKRGIFPKVATNIM
]	1	[	RAWLFQHLSHPYPSEEQKKQLAQDTGLTILQVNNWFINARRRIV
	1	1	QPMIDQSNRTGQGAAFSPEGQPIGGYTETQPHVAVRPPGSVGMS
		Í	LNLEGEWHYL
5540	148	1440	
Į	j	-	PPLGAGAGVHARSPHPARRLPLTTAGVGGRAPDLLPTPWRQHRG
			PSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPGIVD
j			TOPANIAGE PETVPAVPGPYGPHRPPODI, DDGI, DCDGI VDDVDDT
			I TORPOT POLIALVEEKCELATCS PROGRAGAGE GERROCONTOGRADO
)	<b>;</b>		I FREDRIAFAKUVRSERPLESSNPELDNI.MTOATOUT DEUT I DE D
			ROWN TO DE LEUR DE GERRE PE DE LE DOMESTIS DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE DE LE RESERVE D
1	1	'	SGS VALG I PGPSSGGLASOSGDNSSDOCUCT.DTetta choocare
	i		1 DODDY DERKINKRY LEDKATIN THE AMERICAN CHENCE TO THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE COLUMN THE C
1			THE TOTAL THE VIEW TO THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK
5541	148	7440	XEIGGILEIEPHVAFKAPASVGDEFGTPKFFWUVT
1	~**	1440	PPLGAGAGVHARSPHPARRLPLTTAGVGGPAPDLL PTPUPGUS
1			1 PSGAGAPGCALLPRGQALEGPRSCRRDODMADDVDET DYWDGTYDD
1	1 1		GENALIASE PETVPAVPGPYGPHRPPODT, DDGT DCDGT VDDVD
			1 IGHPUPPLUALVPEKCELATCSPRDGAGAGI.GTDDGGDVGGGDG
1	1		I THE DIVIAL AND VISERPLESSNEED NI MICATON PRINTS 1
1			I NOMIFICAL INDESCRIPTION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF T
1	1		DGS VALGI PGPSSGGLASOSGDNSSDOGVGI DTCVA CDCCGGDD
	1		DODD QUERRINARGI FPKVATNIMPAWI POUT CUDYDORDOVING
1	1 1	•	HAUDIGHI LUQVNNWE'LNAKRRIVOPMIDOSMPTCOCA A FORDER
5542			WILGOITEISENVARRAPASVGDEFCTDVEFMUVI
3242	148	1440	PPLGAGAGVHARSPHPARRLPLTTAGVCGPARDY I DEBUNGUE
1	1		FEGAMAPGCALPRGOALEGPRSCPRDCDMADDVDDr Diving
!	ſ		GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREKDEI
1	j j		YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCSSDS
1	]	i	FNEDNTAFAKQVRSERPLFSSNPELDNLMIQAIQVLRFHLLELE
ı	1		KGKMPIDLVIEDRDGGCREDFEDYPASCPSLPDQNNIWIRDHED
	1 (		SGSVHLGTPGPSSGGLASQSGDNSSDQGVGLDTSVASPSSGGED
1	1 1		EDLDQEPRRNKKRGIFPKVATNIMRAWLFQHLSHPYPSEEQKKQ
	1	. !	LAQDTGLTILQVNNWFINARRRIVQPMIDQSNRTGQGAAFSPEG
	<b></b>	1	QPIGGYTETEPHVAFRAPASVGDEFGTRKEEWHYL
5543	2405	665	RWVREQPWPLRTSEAVKTPALRPFPGPRGVSPFPKPDWGKSPAP
1		i	KRPFSDSGAFWSPERRPGVLEAPRRRPVPASFRAVPPKPTRVHG
	}	}	SSASRDRVI.ARTMIVADERCRAFI KRIVE PROFESTRAVPPKPTRVHG
1	1 1	1	SSASRDRVLARTMIVADSECRAELKDYLRFAPGGVGDSGPGEEQ
]	!		RESRARRGPRGPSAFIPVEEVLREGAESLEQHLGLEALMSSGRV
]	1	1	DNLAVVMGLHPDYFTSFWRLHYLLLHTDGPLASSWRHYIAIMAA ARHOCSYLYGSUMAERIOTGGPLASSWRHYIAIMAA
]		į.	ARHOCSYLVGSHMAEFLQTGGDPEWLLGLHRAPEKLRKLSEINK
1 1	i (	ť	LLAHRPWLITKEHIQALLKTGEHTWSLAELIQALVLLTHCHSLS
1 1	1	ı	SFVFGCGILPEGDADGSPAPQAPTPPSEQSSPPSRDPLNNSGGF
1 1		i	ESARDVEALMERMQQLQESLLRDEGTSQEEMESRFELEKSESLL
] ]	ŀ	i	VTPSADILEPSPHPDMLCFVEDPTFGYEDFTRRGAQAPPTFRAQ
1	f		DYTWEDHGYSLIQRLYPEGGQLLDEKFQAAYSLTYNTIAMHSGV
1 1		j	DTSVLRRAIWNYIHCVFGIRYDDYDYGEVNQLLERNLKVYIKTV
]	1	1	ACIPARI I RRMINLEWRHERHSEKVII VNLLLLEARMOAATI.VAT.
5544	1895		RATIRIMI
i i		1 3	LGGLLGRQRLLLRMGAGRLGAPMERHGRASATSVSSAGEQAAGD
]	Í	1 .	FEGRRUEP DRRRASSASVPAVGASAFGTDDDDI CCVCCDDGiron
	l	1 3	2KVESLKKKKPLFPWFGLDIGGTI.VKI.VVFFPVDTTAXFFFFFFF
	}	1 '	COURSTRAY DISNVAYGSTGT POURTEL VOI TI CODVOY
]	ì	) 4	F FIRDMPAF I QMGRDKNFSSI.HTVFCATCCCAVVDDOODS mt an
1	1	1 -	DESCRIPTION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF
1	1	1 4	JEFULINE I PULLIVNIGSGVSTI. AVVSKOM VKRIMGMOV GOOMS
' }	1	í <del>-</del>	COLCULISCII FEEALEMASRCDSTKVDKI VDD TVCCDVEDEC
ļ		4	FGWAVASSEGNEMSKEKREAVSKEDI.ADATT.TTTTMITTAGE
- 1	ļ	, .··	CALINENTINGVVFVGNFLRINTIAMPLIAVALDVIGVGOT VATE
			SEHEGYFGAVGALLELLKIP
	-		

SEQ	Predicted	Predicted end	Amino roid company
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
) )	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1 1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1 1	sequence		\=possible nucleotide insertion)
5545	802	131	GAMWSAGRGGAAWPVLLGLLLALLVPGGGAAKTGAELVTCGSVL
)			KLLNTHHRVRLHSHDIKYGSGSGQQSVTGVEASDDANSYWRIRG
1 (			GSEGGCPRGSPVRCGQAVRLTHVLTGKNLHTHHFPSPLSNNQEV
, ,			SAFGEDGEGDDLDLWTVRCSGCHWEREAAVRFQHVGTSVFLSVT
j			GEQYGSPIRGQHEVHGMPSANTHNTWKAMEGIFIKPSVEPSAGH
1 1		1	DEL
5546	1592	146	FVPRGGHSSMGQSGRSRHQKRARAQAQLRNLEAYAANPHSFVFT
1 1			RGCTGRNIRQLSLDVRRVMEPLTASRLQVRKKNSLKDCVAVAGP
1			LGVTHFLILSKTETNVYFKLMRLPGGPTLTFQVKKYSLVRDVVS
1		l	SLRRHRMHEQQFAHPPLLVLNSFGPHGMHVKLMATMFQNLFPSI
1			NVHKVNLNTIKRCLLIDYNPDSQELDFRHYSIKVVPVGASRGMK
1 1		(	KLLQEKFPNMSRLQDISELLATGAGLSESEAEPDGDHNITELPQ
1 1		İ	AVAGRGNMRAQQSAVRLTEIGPRMTLQLIKVQEGVGEGKVMFHS
1			FVSKTEEELQAILEAKEKKLRLKAQRQAQQAQNVQRKQEOREAH
1 1			RKKSLEGMKKARVGGSDEEASGIPSRTASLELGEDDDEQEDDDI
1 1			EYFCQAVGEAPSEDLFPEAKQKRLAKSPGRKRKRWEMDRGRGRL
L			CDQKFPKTKDKSQGAQARRGPRGASRDGGRGRGRGRGRPGKRVA
5547	1592	146	FVPRGGHSSMGQSGRSRHQKRARAQAQLRNLEAYAANPHSFVFT
1 1			RGCTGRNIRQLSLDVRRVMEPLTASRLQVRKKNSLKDCVAVAGP
1 1			LGVTHFLILSKTETNVYFKLMRLPGGPTLTFQVKKYSLVRDVVS
1			SLRRHRMHEQQFAHPPLLVLNSFGPHGMHVKLMATMFQNLFPSI
1 1			NVHKVNLNTIKRCLLIDYNPDSQELDFRHYSIKVVPVGASRGMK
1 1			KLLQEKFPNMSRLQDISELLATGAGLSESEAEPDGDHNITELPQ
			AVAGRGNMRAQQSAVRLTEIGPRMTLQLIKVQEGVGEGKVMFHS
1			FVSKTEEELQAILEAKEKKLRLKAQRQAQQAQNVQRKQEQREAH
į			RKKSLEGMKKARVGGSDEEASGIPSRTASLELGEDDDEQEDDDI
1			EYFCQAVGEAPSEDLFPEAKQKRLAKSPGRKRKRWEMDRGRGRL
5548	1	2153	CDQKFPKTKDKSQGAQARRGPRGASRDGGRGRGRGRGRPGKRVA DQTGPPETIAFTFPRSTMEPLCPLLLVGFSLPLARALRGNETTA
	~	2455	DSNETTTTSGPPDPGASQPLLAWLLLPLLLLLLVLLLAAYFFRF
1 1		:	RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI
			PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN
]			REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK
1 1			FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEEKCHQY
1 1			WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR
1 1			LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC
1 1	ł		SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ
i 1			TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK
} {	ļ		IGLEEEFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR
1			VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW
į l	l		RMIWEWKSHTIVMLTEVQEREQDKCYQYWPTEGSVTHGEITIEI
1	}		KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG
j 1			IPAEGKGMIDLIAAVQKQQQQTGNHPITVHCSAGAGRTGTFIAL
] [		•	SNILERVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ
<del>                                     </del>			DFIDIFSDYANFK
5549	915	256	FEATGGKRLAFKMAGTARHDREMAIQAKKKLTTATDPIERLRLQ
( )			CLARGSAGIKGLGRVFRIMDDDNNRTLDFKEFMKGLNDYAVVME
(			KEEVEELFQRFDKDGNGTIDFNEFLLTLRPPMSRARKEVIMQAF
1			RKLDKTGDGVITIEDLREVYNAKHHPKYQNGEWSEEQVFRKFLD
5550	3364		NFDSPYDKDGLVTPEEFMNYYAGVSASIDTDVYFIIMMRTAWKL
2350	2364	1210	RKRKVFLKMRRLNRKKTLSLVKELDAFPKVPESYVETSASGGTV
j l			SLIAFTTMALLTIMEFSVYQDTWMKYEYEVDKDFSSKLRINIDI
1	İ		TVAMKCQYVGADVLDLAETMVASADGLVYEPTVFDLSPQQKENQ
			RMLQLIQSRLQEEHSLQDVIFKSAFKSTSTALPPREDDSSQSPN
	[	[	ACRIHGHLYVNKVAGNFHITVGKAIPHPRGHAHLAALVNHESYN
i	j	j	FSHRIDHLSFGELVPAIINPLDGTEKIAIDHNQMFQYFITVVPT
		ŀ	KLHTYKISADTHQFSVTERERIINHAAGSHGVSGIFMKYDLSSL
		}	MVTVTEEHMPFWQFFVRLCGIVGGIFSTTGMLHGIGKFIVEIIC
5551	211	1700	KLHTYKISADTHQFSVTERERIINHAAGSHGVSGIFMKYDLSSL MVTVTEEHMPFWQFFVRLCGIVGGIFSTTGMLHGIGKFIVEIIC CRFRLGSYKPVNSVPFEDGHTDNHLPLLENNTH MQRDHTMDYKESCPSVSIPSSDEHREKKKRFTVYKVLVSVGRSE

SEQ Predicted med nucleotide location of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of the programme of	CE			
No.: Incleation corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding		-	Predicted end	Amino acid segment contain
location   location   corresponding		1 ~ 0 3 ~ 1 111 111 111	nucleotide	
Cortesponding	NO:		location	Glutamic Acid & De-Aspartic Acid, E=
corresponding to first amino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid acid acid acid acid acid acid acid	1		corresponding	W-Histiding T Tenenylalanine, G-Glycine,
to first amino acid residue of section of the controlling and cold and cold and cold and cold and cold and cold acid acid sequence colon, "possible number, Valling, which cold device, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Artypeople, "Arty	ĺ	corresponding	to first	/ / " I=ISO/AND/ V-I
amino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid	l			De need : M=Methionine, N=Asparagine,
residue of sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence s		amino acid		I regionally Office the programme to the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the sec
amino acid sequence  Codon, ("Apossible nucleotide deletion,"  FFFFRENZIS DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEOTISTE DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE NUCLEO DE		residue of		Seserine, T=Threonine, V=Valine,
Sequence    Appossible mulles timestion	- 1			Wellyptophan, YaTvrosine Valleles
### STYPERSTREETING WILKERGE PROMINENTAL ISSUEDED FOR GREAT AS A CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE C	i i		seduence	"PUSSIDIE NUCLEOFIGE dalasia.
WYPERACAPEDILINTLIKOS PAMALKITAKRI TEGINEDETIL ORRAGIAET IGAI NYEPELYINDEVAR LOMOS PKOGODES DE DERSOCKLISTSONING SIGNPHARPTOPPILKVIKOKS PKW DERSOCKLISTSONING SIGNPHARPTOPPILKVIKOKS PKW DERSOCKLISTSONING SIGNPHARPTOPPILKVIKOKS PKW DERSOCKLISTSONING SIGNPHARPTOPPILKVIKOKS PKW DERSOCKLISTSONING SIGNPHARPTOPPILKVIKOKS PKW DERSOCKLISTSONING SIGNPHARPTOPPILKVIKOKS PKW DEPLANCIA SIGNPHARPTOPPILKVIKOKS PKW PVARIA SIGNPHARPTOPPILKVIKOKS PKW REGIAIS DEPLANCIA SIGNPHARPTOPPILKVIKOKS PKW REGIAIS PKW PKW PKW PKW PKW PKW PKW PKW PKW PKW	<b>—</b>	1-0400000		\-POSSIDIE NUCLEOFIDE incertion\
DERSONLHSTEON THEOREM SPECKOSDESDES DE DESSONLHSTEON THROUGH SPECKOSDES OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLO		Į.	}	WEVERNAEFDKLYNTILKKOFPAMALKIDAUDITGO
LLAMKKLDOKF VAN KUJOKK LYJAKROSAN HARPTOFPELKVIJKKSFOKM PEPLVOLILY PEPLVOLILY PEPLVOLILY PEPLVOLILY PEPLVOLILY PEPLVOLILY PEPLVOLILY PEPLVOLILY PEPLVOLILY PEPLVOLILY PEPLVOLILY PEPLVOLILY PEPL OF DEPLVOLITY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PEPLVOLICY PE	- 1	}	1	QRRAGINEFIONLURYPELYNHDDURAELONDORING
PFLUGLIN'S ECTIENT UND WIS GENEFIC PRESENTATION OF THE PARLISAS LOUIS AS RELIVED LYPEN ILLES SERVING FYARILAS ALGORITHM FOR THE PARLISAS LOUIS AND THE PARLISAS LOUIS AND THE PARLISAS LOUIS AND THE PARLISAS LOUIS AND THE PARLISAS LOUIS AND THE PARLISAS LOUIS AND THE PARLISAS LOUIS AND THE PARLISAS LOUIS AND THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAND TO THE PARLISAS LAN		l.	1	DERSSOKI USTSONINI CDECARDURANTE CONDENSEDE
PYABELIASALGYLBISKI VYRDILKFRILLDSKAPLOVLIDFOIL KEGLAIDT FYABELIASALGYLBISKI VYRDILKFRILLDSKAPLVLIDFOIL KEGLAIDT FYEDE FOR SYNDRY LIKEPLE STANDLOGKEL PROCEDURAL STANDLOGKEL PROCEDURAL STANDLOGKEL PROCEDURAL STANDLOGKEL PROCEDURAL STANDLOGKEL PROCEDURAL STANDLOGKEL PROCEDURAL STANDLOGKEL PROPERTY SEVENSORY STANDLOGKEL PROPERTY SEVENSORY STANDLOGKEL PROPERTY SEVENSORY SEVENSUAL SANDLOGKEL PROPERTY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSO	1	}	1	LLAKEKI DCKEYAWKII OWKI TO THE TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOTAL OKKI TOK
PYABELIASALGYLBISKI VYRDILKFRILLDSKAPLOVLIDFOIL KEGLAIDT FYABELIASALGYLBISKI VYRDILKFRILLDSKAPLVLIDFOIL KEGLAIDT FYEDE FOR SYNDRY LIKEPLE STANDLOGKEL PROCEDURAL STANDLOGKEL PROCEDURAL STANDLOGKEL PROCEDURAL STANDLOGKEL PROCEDURAL STANDLOGKEL PROCEDURAL STANDLOGKEL PROCEDURAL STANDLOGKEL PROPERTY SEVENSORY STANDLOGKEL PROPERTY SEVENSORY STANDLOGKEL PROPERTY SEVENSORY SEVENSUAL SANDLOGKEL PROPERTY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSORY SEVENSO	- 1		1	PELVOLUVO DOMENTA LINKE OKHIMAERNVLLKNVKH
KEGLAISDTTTTE GENERALE PURING VIDNOTUME CARALLE ENERGY STATES LEELI ENERGY STATES LEELI ENERGY STATES LEELI ENERGY STATES LEELI ENERGY STATES LEELI ENERGY STATES LEELI ENERGY STATES LEELI ENERGY STATES LEELI ENERGY STATES LEELI ENERGY STATES LEELI ENERGY STATES LEELI ENERGY STATES LEELI ENERGY STATES LEELI ENERGY STATES LEELI ENERGY STATES LEELI ENERGY STATES LEELI ENERGY STATES LEELI ENERGY STATES LEELI ENERGY STATES LEELI ENERGY STATES LEELI ENERGY STATES LEELI ENERGY STATES LEELI ENERGY STATES LEELI ENERGY STATES LEELI ENERGY STATES LEELI ENERGY STATES LEELI ENERGY STATES LEELI ENERGY STATES LEELI ENERGY STATES LEELI ENERGY STATES LEELI ENERGY STATES LEELI ENERGY STATES LEELI ENERGY STATES LEELI ENERGY STATES LEELI ENERGY STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN STATES LEELI EN	1	<b>,</b>	1	T = T T T T T T T T T T T T T T T T T T
EMLKOLP PYCKOVAEWONI LHKPELINGSYLTAMS LEELL EKNGUN LGAKED FLE QUNIPFESIS WANDLYQKI PPFNPHY AGPDI LONDTAFTEETVYSVUSSTYSVISVASVLEADDAFVO FSYD PARDE LONDTAFTEETVYSVUSSTYSVISVASVLEADDAFVO FSYD PARDE LONDTAFTEETVYSVUSSTYSVISVASVLEADDAFVO FSYD PARDE LONDTAFTEETVYSVUSSTYSVISVASVLEADDAFVO FSYD PARDE LONDTAFTEETVYSVUSSTYSVISVASVLEADDAFVO FSYD PARDE LONDTAFTEETVYSVUSSTYSVISVASVLEADDAFVO FSYD PARDE LONDTAFTEETVYSVUSSTYSVISVASVLEADDAFVO FSYD PARACRIQAEMOSTYTODASDHERERKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	ſ	1	1	( ACCOMMODITUDITAL ALBERTAL POLYCYMER
EXINGNICARED LE QUILIPPE SLEMADLYOKKT PPEPEPN AGDDIENTAT TEET VPIS VCUSSTYS I VNAS VLEADDAFUS AGDDIENTAT TEET VPIS VCUSSTYS I VNAS VLEADDAFUS FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADPSEDLET FSVADP	ļ	1	1	" COLFIED I I I I CGTPEY LAPEVI DE CONTROL TORON OF THE COLF
AGDDIENTOTAFTEETVSVUGSSTYSIVASVUEADDAPVO PSYADDEEDLIT  STATE  GRAAGAMGKGIKKHKAEWRSSYEDYADKPLEKPLKLUVLKVGG SEVTELGGGGHDSSTYDDRSDHERBERHKEKKKKKKKKKSEKEKHL DEERRARKEKEKKKERECTTEGGADGKUVEWPPDR PVRACRTOPARNSTPIOCULEHPLROLORKOVEWPPDR PVRACRTOPARNSTPIOCULEHPLROLORKOVEWPPDR PVRACRTOPARNSTPIOCULEHPLROLORKOVEWPPDR PVRACRTOPARNSTPIOCULEHPLROLORKOVEWPPDR PVRACRTOPARNSTPIOCULEHPLROLORKOVEWPPDR PVRACRTOPARNSTPIOCULEHPLROLORKOVEWPPDR PVRACRTOPARNSTPIOCULEHPLROLORKOVEWPPDR PVRACRTOPARNSTPIOCULEHPLROLORKOVEWPPDR PVRACRTOPARNSTPIOCULEHPLROLORKOVEWPPDR PVRACRTOPARNSTPIOCULEHPLROLORKOVEWPPDR PVRACRTOPARNSTPIOCULEHPLROLORKOVEWPPDR PVRACRTOPARNSTPIOCULEHPLROLORKOVEWPPDR PVRACRTOPARNSTPIOCULEHPLROLORKOVEWPPDR PVRACRTOPARNSTPIOCULEHPLROLORKOVEWPPDR PVRACRTOPARNSTPIOCULEHPLROLORKOVEWPPDR PVRACRTOPARNSTPIOCULEHPLROLORKOVEWPPDR PVRACRTOPARNSTPIOCULEHPLROLORKOVEWPPDR PVRACRTOPARNSTPIOCULEHPLROLORKOVEWPPDR PVRACRTOPARNSTPIOCULEHPLROLORKOVEWPPDR PVRACRTOPARNSTPIOCULEHPLROLORKOVEWPPDR PVRACRTOPARNSTPIOCULEHPLROLORKOVEWPPDR PVRACRTOPARNSTPIOCULEHPLROLORKOVEWPPDR PVRACRTOPARNSTPIOCULEHPLROLORKOVEWPPDR PVRACRTOPARNSTPIOCULEHPLROLORKOVEWPPDR PVRACRTOPARNSTPIOCULEHPLROLORKOVEWPPDR PVRACRTOPARNSTPIOCULEHPLROLORKOVEWPPDR PVRACRTOPARNSTPIOCULEHPR PVRACRTOPARNSTPIOCULEHPR PVRACRTOPARNSTPIOCULEHPR PVRACRTOPARNSTPIOCULEHPR PVRACRTOPARNSTPIOCULEHPR PVRACRTOPARNSTPIOCULEHPR PVRACRTOPARNSTPIOCULEHPR PVRACRTOPARNSTPIOCULEHPR PVRACRTOPARNSTPIOCULEHPR PVRACRTOPARNSTPIOCULEHPR PVRACRTOPARNSTPIOCULEHPR PVRACRTOPARNSTPIOCULEHPR PVRACRTOPARNSTPIOCULEHPR PVRACRTOPARNSTPIOCULEHPR PVRACRTOPARNSTPIOCULEHPR PVRACRTOPARNSTPIOCULEHPR PVRACRTOPARNSTPIOCULEHPR PVRACRTOPARNSTPIOCULEHPR PVRACRTOPARNSTPIOCULEHPR PVRACRTOPARNSTPIOCULEHPR PVRACRTOPARNSTPIOCULEHPR PVRACRTOPARNSTPIOCULEHPR PVRACRTOPARNSTPIOCULEHPR PVRACRTOPARNSTPIOCULEHPR PVRACRTOPARNSTPIOCULEHPR PVRACRTOPARNSTPIOCULEHPR PVRACRTOPARNSTPIOCULEHPR PVRACRTOPARNSTPIOCULEHPR PVRACRTOPARNSTPIOCULEHPR PVRACRTOPARNSTPIOCULEHPR PVRACRTOPARNSTPIOCULEHPR PVRACRTOPARNSTPIOCULEHPR PVRACRTOPARNSTPIOCULEHPR PVRACRTOPARNSTPIOC		1	1	
FSYAPDSEDLFL  FSYAPDSEDLFL  JOPAGRAMGKRIKKHKARAWRSSYEDYADKYLEKPLKIVLIKVOG SEVTELSGSCHDSSYYDDRSDHERERHEKKKKKKKKSEKEKHIL DDEERRIKKEEKKRREREHCIDTEGGADDFDGKOPHOPPAPPUTDA LAPGYSMI IKHPMDFGTMKDKLVAWYKSVTEFKADFKLMCDNA MYNKEPTVYKLAKKLHAGFGMGALALISMEDTAVEEPVP EVVEVQVETAKKSKKPREVISCHTGADKADFALANDEN ANYNKEPTVYKLAKKLHAGFGMGALALISMEDTAVEEPVP EVVEVQVETAKKSKKPREVISCMFPEGGACSLTDSTAESHVI ALVEHAADBEARGRINRFLEGKMGYLAALISMEDTAVEEPVP EVVEVQVETAKKSKKPREVISCMFPEGGACSLTDSTAESHVI ALVEHAADBEARGRINRFLEGKMGYLAALISMEDTAVEEPVP EVVEVQVETAKKSKKPREVISCMFPEGGACSLTDSTAESHVI ALSVANDADEARGRINRFLEGKMGYLAGGSALVSTVARAP DADGEETHVVDLSSLSSKLLPGTTLGFKDERRAVTFLESAFT ALSSANDAVGGABCARTINGTUNGSLSSVLETMSKSTPDVSDVISSLGKKVKELDPDDS HLMLDETTKLLQDLHEAQAERGGSRPSNLSLSNAESRDCHHL GSPSRISSVLETMSKSYPDVSDVISSLGKVKKELDPDDS HLMLDETTKLLQDLHEAQAERGGSRPSNLSLSNAESRDCHHL GSPSRISSVLETMSKSYPDVSDVISSLGKVKKELDPDDS HLMLDETTKLLQDLHEAQAERGGSRPSNLSLSNAESRDCHHL GSPSRISSVLETMSKSYPDVSDVISGLGKVKELDPDDS HLMLDETTKLLQDLHEAQAERGGSRPSNLSLSLGKVKKELDPDDS HLMLDETTKLLQDLHEAQAERGGSRPSNLSLSLGKVKELDPDDS HLMLDETTKLLQDLHEAQAERGGSRPSNLSLSLGKVKELDPDDS HLMLDETTKLLQDLHEAQAERGGSRPSNLSLSLGKVKELDPDDS HLMLDETTKLLQDLHEAQAERGGSRPSNLSLGKVKELDPDDS HLMLDETTKLLQDLHEAQAERGGSRPSNLSLGKVKELDPDDS HLMLDETTKLLQDLHEAQAERGGSRPSNLSLGKVKELDPDDS HLMLDETTKLLQDLHEAQAERGGSRPSNLSLGKVKELDPDDS HLMLDETTKLLQDLHEAQAERGGSRPSNLSLGKVKELDPDDS HLMLDETTKLLQDLHEAQAERGGSRPSNLSLGKVKELDPDDS HLMLDETTKLLQDLHEAGAERGUNGCHANGERWD DANAPAARKLGIPATIVLPSSTILOVORIOGGARAUGHVKHA HTMLDLTULTDSTAMATAGATATAGATAGATAGATAGATAGATAGATAGATA		ļ	ļ	1 THE TOTAL DESCRIPTION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE
SSSS	- I	ľ	ł	1 DETRIEDIALIEETVPYSVCVSSDVSTIMINGUT DE DE I
LGPANGAMOKKJIKKHKAEWES YEDYADKELEK PJKLVLKVGG SEVTELSGSCHDSS YJDROSHDERSHKKKKKKKKKSEKE KHIL DDEERRKKEEKKRKREHCHOTEGEADDTDPGKKVEVEPPDR PVARCTOPAEMEST PLOLLEH FLRQUQKEDHFFAFFEVTDA LAFGYSHI I KHEMDFGTMKDK I VAREY KSYTEFKADFKAMCDNA MYNRBDTVYYKLAKKI LINGF FRMSK KQALLGHEFFAFFEVTDA LAFGYSHI I KHEMDFGTMKDK I VAREY KSYTEFKADFKAMCDNA MYNRBDTVYYKLAKKI LINGF FRMSK KQALLGHEFAKHONDA HYNRBDTVYYKLAKKI LINGF FRMSK KQALLGHEFAKHONDA HYNRBDTVYYKLAKKI LINGF FRMSK KQALLGHEFAKHONDA ANTENBDTVYYKLAKKI LINGF FRMSK KQALLGHEFAKHONDA BADEETHFVDLSSLSSK KLEPGTTLGF KDERRNKYTHESATT ALSMONNSVFGOLKSDEMELLYS AVGDETEVOCALSI GEFVKAM GSTEKKVYDLLQJI TGGDEFSTTLG LIFFK KOEKRINGTHESATT ALSMONNSVFGOLKSDEMELLYS AVGDETEVOCALSI GEFVKAM GSTEKKVYDLLQJI TGGDEFSTTLG LIFFK KVELDPUDS HALDLETTKLLQDIHLEGAPAGNGGRAPS SYNLSSLSNASERDOHL GSPERLSVOEQDDVTHDPYEFLGSFEDANSAKT LOFENYLVSKNEDPYDHEJESMALSDVAGMF VFLKCENVOPSGSFKLRG IGHFCOEMAKKGCHLUVCSSGGNAGI AANYAARKLG FPATIVLYSSTLGOVYDGGGGAEVOLTGKWM BANKARLG FPATIVLYSSTLGOVYDGGGGAEVOLTGKWM BANKARLG FPATIVLYSSTLGOVYDGGGGAEVOLTGKWM BANKARLG FPATIVLYSSTLGOVYDGGGGAEVOLTGKWM BANKARLG FPATIVLYSSTLGOVYDGGGGAEVOLTGKWM BANKARLG FPATIVLYSSTLGOVYDGGGGAEVOLTGKWM BANKARLG FPATIVLYSSTLGOVYDGGGGAEVOLTGKWM BANKARLG FPATIVLYSSTLGOVYDGGGAEVOLTGKWM BANKARLG FPATIVLYSSTLGOVYDGGGAEVOLTGKWM BANKARLG FPATIVLYSSTLGOVYDGGGAEVOLTGKWM BANKARLG FPATIVLYSSTLGOVYDGGGAEVOLTGKWM BANKARLG FPATIVLYSSTLGOVYDGGGAEVOLTGKWM BANKARLG FPATIVLPPLPARAVQAVEHEEVARDYHTGAGGGAEVOLTGKWM BANKARLG FPATIVLPPLPARAVQAVEHEEVARDYHTGAGGAA WYDGCCRLAHGENSINSVGAVYGLGAUKHGGGUKYDGAUKHESSR QRLEALREAN I KEETEY YMELLAARKHQVEALKMMOHONGLISM BELIEDUKARARDLEEET EEHBAPDDINKVNIFEAUR.WYSEER ANSKONITKREVEDDLGLSMLIDSONOYILTERPSTIPRADH HITKOI IVIIMISLECOKICTTAIGLFFITIGAGTICGVILLGFSGIN SIKSTVOVETLGEFGVFFTTFLUGGEFFFEKLIKVWKISLGGGC YMTLIMIA FRICLIMGILLIK INFYDSVY ISLUSISSTPLVGFITM GSARGDXEGGI IDYSTVLLIGHLVTODOVI.GLERAVPBTURGFTM GSARGDXEGGI IDYSTVLLIGHLVTODOVI.GLERAVPBTURGFTM GSARGDXEGGI IDYSTVLLIGHLVTODOVI.GLERAVPBTURGFTM GSARGDXEGGI IDYSTVLLIGHLVTODOVI.GLERAVPBTURGFTM GSARGDXEGGI INFORMATIKT HERDEN BANKA	5552	2740		- 0 +1 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DDEERKKEEKRRREEHCUTSEADDFDEGKKKEKKKKSEKEKHIL DDEERKKEEKRRREEHCUTSEADDFDEGKKEVEPPPDR PVRACRTOPAENESTPIOCILEHPIRGLORKSPHOFPEAFPUTDA LAPOTSMII IKHPMEDTTWINKULANEKSUTSFKANDFLAMCOMA MYTAREPOTVYYKLAKKILHAGFKMEKQAALLGHEDTAVEEPVP EVEVÇVQETAKKSKKRSEWISTGKANDFLAMCHAA HAVEHAADEARDRINEFLEGGKMEYLKRNEDGSLLYSVATTAEP DDIEEETHPVDLSSISSKLLEGFTIKFDERRKNYYHSLASTATE ALSMQNNSVEGUKSDEMELLYSAYGDETGVOCALSLGEFVKDA GSYSKKVVDLLDGITGGDHSFTIKGDERRNVYHSLASTATE DTLADSSSSULEPMEMKSYPDVSVDISMLSSLGKVKKELDPDDS HUMLDETTKLLQDLHEAQAREGGSSNLSSLENASERDGHHL GSPSRISVGEGPDVTHDPYEFLGSPEDASJANT JOSE LGREAVLVISRINDGVAEHARGESSNLSSLENASERDGHHL GSPSRISVGEGPDVTHDPYEFLGSPEDASJANT VFLKCENVOPSGSFKIRGIGHPCOEMAKKGCRHLVCSSGGNAGI AAAYARAKGIPATIVPESTSLOVVQRLOGGAGVOLTGKVMD EANLRADELAKRDGWENVPPDFUL IMGGHASLVQELKAVLRTP FGALVLAVGGGGLLAGVVAGELLEVGWGIVPI ILMETHGAHCFNA AITAGKLUTLDDITSVAKSLGAKTVARARDLECMVCKHISEVVE DTEAVSAVQOLLDDERRILVEPACGAALAATYSGLLRAVLATEP FGALVLAVGGGGLLAGVVAGELLEVGWGIVPI ILMETHGAHCFNA AITAGKLUTLDDITSVAKSLGAKTVARARDLECMVCKHISEVVE PPSLTSVVVI VOGGNIN INSRELQAKVIKLHERGKVAKLHSEVVE PPSLTSVVVI VOGGNIN INSRELQAKLGYDKDVWIKLSGGCL PPSLTSVVVI VOGGNIN INSRELQAKLGYDKDVWIKESGR WIRDSCRILSGELRGAKNAVLINKLKTAIGAVERGUF LAVARDLE GRSFFWILFPVLEWAQAVEHEEVAGHOFIKLHGGWGISSM. DEILEDWGKAADRLEEPIEHAFDNVGLTFCKLSGAETGGLLCPALRTWIKKU, GRSFFWILFPVLEWAQAVEHEEVAGHOFIKLORGDKIN SIKSIVOVETLGFFGTFFTLEVGLEFSPEKLAGDFTURADH HTKID IVTIGMSLBCGGMICTAIGLPWGTYI COULDEGGIN SIKSIVOVETLGFFGTFFTLEVGLEFSPEKLAKVWIKLGGGIN SIKSIVOVETLGFFGTFFTLEVGLEFSPEKLAKVWIKLGGGIN SIKSIVOVETLGFFGTFTLUNGLEFSPEKLAKVWIKLGGGIN SIKSIVOVETLGFFGTFTLUNGLEFSPEKLAKVWIKLGGGIN SIKSIVOVETLGFFGTFTLUNGLIFFSSOTIKMIVSGLAGV SSCPPVVIERIANTIGGIFFSAAGVATSVWINTEDER GSAGDKEGDIDYSTVLLIGHLAVTFLUNGKLIGGFTYRK LIMMSKKNIK ILLIGISAFIFLULTVFRAIGHTYFTVAVEL VILVELTLSVVMKSLLAALVISLILIPRSSOTIKMIVSGLAGV SSCPPVIERIANTIGGGRAKKONGOL SSSPPVILGFSBARRAGVISREVYLLILIVTTUSLLLARVENDER GSSIVVDLEVTLESVYARGFPENTERLICHTFTFORGTPKTLORGE MRTOLGGGRAFGRAGGRGGRGGRCKCNOCOG MRTOLGGGRAFGRAGGGRGGGRCKCNOCOG MRTOLGGGRAFGRAGGGGGGGGGRAKLUKRGGGL PNEDNNIKKGLIITTEVADFPREAREGIKGLLKOGGVK VYMGLOC	1 -552	2/48	930	LGPAAGAAMGKKHKKHKAEWRSSYEDVADKDVEKEVE
PVRACETOPAENES TPIOCLEHI-RICORKO-PHEPAFPUTDA LAPGYSHI IN-PROPETHINDIVANDE KSUTEFRADEKINCOMA MTYMREDTUTYKLIAKKI ILHAPG KHONKOLVANDE KSUTEFRADEKINCOMA MTYMREDTUTYKLIAKKI ILHAPG KHONKOLVANDE KSUTEFRADEKINCOMA MTYMREDTUTYKLIAKKI ILHAPG KHONKOLVANDE KSUTEFRADEKINCOMA MTYMREDTUTYKLIAKKI ILHAPG KHONKOLVANDEK SUTEFRADEKINCOMA MTYMREDTUTYKLIAKKI ILHAPG KHONKOLVANDEK SUTEFRADEKINCOMA LAVERAADEARDRI INRE FLPGGKMENKENGEGELLI SYVANTABP DADEEETHPUDLSSISSKLLBGFTTIG FKDERRIKVTPLOSATA ALSMONISVEGIL KSUDEMELLI SADETIGVOCALSI SUFWIKA GSYSKKVUDDILLOG TITGGUBISTTI-POLKORRIVOMEP DEBAKUG GTANGENSS SVLEPRIMSKY PUDVE SUMS ISL SLASERDOHL GSPERKISVOED PUTHOPY KEILOS PEPAASAKT LOGEDAVILUS RICKEVOP SUMS SIGNIK KEILOPDOS HINLDETTKLLODLHEADARRIGGSPESSILSSINASERDOHL GSPERKISVOED PUTHOPY KEILOS PEPAASAKT VPLKENVOP SOS FKIRG IGHFCQEMAKIGCRHLVCSSGGNINGI AAAYAARKLGI PATI VIPESTSLOVELOGGGGAGEVOLTIGKWO EANLRAGELARDEWENVP PPOHPLI WIGHALIVOEL KAVLRIT P FOALVILAVGGGGLLAGVVAGLLEVORLOGGGGAGVOLTIGKWO EANLRAGELAR COMBENIUP PROCENCIAGE GEOROVICK HIS EVVE DFRAVSAVOQLLDERINUP PROCENCIAC GEOROVIC LITEKUND EANLRAGELAR COMBENIUP PROCENCIA GEOROVIC LITEKUND GRSFFWULF PULPAWAQAVEHEEVAORVI KHERGEVAAMOSRO WEDSTGRISSIS PROVICTICK LOGAVIKUV ILHARGOVAAMOSRO WEDSTGRISSIS PROVICTICK LOGAVIKUV GIONEMESSA ORIEALIREAAI KEBTEVISILAA EKROVENLIKMHOKNOOLISMI DEILEDUKKAADALEEELI EHAPIDINIS VUKMESSA ORIEALIREAAI KEBTEVISILAA EKROVENLIKMHOKNOOLISMI DEILEDUKKAADALEEELI EHAPIDINIS VISCOS VANDUS GRSCHLOGALOOVIKUMESSA ANSKONTAKHEVEDDILGIMI IDSONOVILIKREDSTI PRADH HTIKI VITIGHLSE LOGAMOT TITOLOGAGA ASSI VOVETULGE GEOROF TITLUS LIESTELLIKERTUM GSARGDIC TATLUKKALIGOT FROM TITULOGAGA ASSI VOVETULGI JUKULGI JUSTAAVELLICU VIKKYLIGOTYKK LHMIS KONKE ILI LIGI SAPI ILILI VITTELLUS FILM USSCOPVUTELTATI LIGI JUSTAA SIGLIHV PTETVATEL TULVILILIS VUMKI LIGILIS RIPOTKALTUVIK VISAGLAQV SSESPIVUS RARRAGVIS REVYLLI LILI VITTELLILAPULWARAAI TRCVPRERRSSI  SISTI VIGENGBARRAGVIS REVYLLILIA VITKASI LARVENNATTEDR GTWAPONLSTFOLLILLI LIGAVI AGRDEYKLLOOPASASI KOI KAYKKLAUQHER ROOR GRONDOR LIPOTKOR GRONDOR LIGOR		1	1	SEVTELSGSGHDSSYVDDBSDUSS
PVRACETOPAENES TPIOCLEHI-RICORKO-PHEPAFPUTDA LAPGYSHI IN-PROPETHINDIVANDE KSUTEFRADEKINCOMA MTYMREDTUTYKLIAKKI ILHAPG KHONKOLVANDE KSUTEFRADEKINCOMA MTYMREDTUTYKLIAKKI ILHAPG KHONKOLVANDE KSUTEFRADEKINCOMA MTYMREDTUTYKLIAKKI ILHAPG KHONKOLVANDE KSUTEFRADEKINCOMA MTYMREDTUTYKLIAKKI ILHAPG KHONKOLVANDEK SUTEFRADEKINCOMA MTYMREDTUTYKLIAKKI ILHAPG KHONKOLVANDEK SUTEFRADEKINCOMA LAVERAADEARDRI INRE FLPGGKMENKENGEGELLI SYVANTABP DADEEETHPUDLSSISSKLLBGFTTIG FKDERRIKVTPLOSATA ALSMONISVEGIL KSUDEMELLI SADETIGVOCALSI SUFWIKA GSYSKKVUDDILLOG TITGGUBISTTI-POLKORRIVOMEP DEBAKUG GTANGENSS SVLEPRIMSKY PUDVE SUMS ISL SLASERDOHL GSPERKISVOED PUTHOPY KEILOS PEPAASAKT LOGEDAVILUS RICKEVOP SUMS SIGNIK KEILOPDOS HINLDETTKLLODLHEADARRIGGSPESSILSSINASERDOHL GSPERKISVOED PUTHOPY KEILOS PEPAASAKT VPLKENVOP SOS FKIRG IGHFCQEMAKIGCRHLVCSSGGNINGI AAAYAARKLGI PATI VIPESTSLOVELOGGGGAGEVOLTIGKWO EANLRAGELARDEWENVP PPOHPLI WIGHALIVOEL KAVLRIT P FOALVILAVGGGGLLAGVVAGLLEVORLOGGGGAGVOLTIGKWO EANLRAGELAR COMBENIUP PROCENCIAGE GEOROVICK HIS EVVE DFRAVSAVOQLLDERINUP PROCENCIAC GEOROVIC LITEKUND EANLRAGELAR COMBENIUP PROCENCIA GEOROVIC LITEKUND GRSFFWULF PULPAWAQAVEHEEVAORVI KHERGEVAAMOSRO WEDSTGRISSIS PROVICTICK LOGAVIKUV ILHARGOVAAMOSRO WEDSTGRISSIS PROVICTICK LOGAVIKUV GIONEMESSA ORIEALIREAAI KEBTEVISILAA EKROVENLIKMHOKNOOLISMI DEILEDUKKAADALEEELI EHAPIDINIS VUKMESSA ORIEALIREAAI KEBTEVISILAA EKROVENLIKMHOKNOOLISMI DEILEDUKKAADALEEELI EHAPIDINIS VISCOS VANDUS GRSCHLOGALOOVIKUMESSA ANSKONTAKHEVEDDILGIMI IDSONOVILIKREDSTI PRADH HTIKI VITIGHLSE LOGAMOT TITOLOGAGA ASSI VOVETULGE GEOROF TITLUS LIESTELLIKERTUM GSARGDIC TATLUKKALIGOT FROM TITULOGAGA ASSI VOVETULGI JUKULGI JUSTAAVELLICU VIKKYLIGOTYKK LHMIS KONKE ILI LIGI SAPI ILILI VITTELLUS FILM USSCOPVUTELTATI LIGI JUSTAA SIGLIHV PTETVATEL TULVILILIS VUMKI LIGILIS RIPOTKALTUVIK VISAGLAQV SSESPIVUS RARRAGVIS REVYLLI LILI VITTELLILAPULWARAAI TRCVPRERRSSI  SISTI VIGENGBARRAGVIS REVYLLILIA VITKASI LARVENNATTEDR GTWAPONLSTFOLLILLI LIGAVI AGRDEYKLLOOPASASI KOI KAYKKLAUQHER ROOR GRONDOR LIPOTKOR GRONDOR LIGOR	1	}	1	DDEERRKRKEEKKRKBEREUGDBERGKKKKKKKKKKKKKKKKKKKLL
IAPGTSMI IKHPMDRGTMKDKUVANDEKSVETERKADEKUMCINA MYYMREDTVYYKLAKKILHAGFKMMSKQAALLGMEDTAVEEPVP EVVVVQVETAKKSKKYSERVI SCHYSKYSTEFKADEKUMCINA MYYMREDTVYYKLAKKILHAGFKMMSKQAALLGMEDTAVEEPVP EVVVVQVETAKKSKKYSERVI SCHYSKOFKORVAKINGDGSLLYSVVMTAEP DADEEETHPVDLSSISSKLLDGFTGFDERRINVYTHASATT ALSMQNNSVYGOLKSDEMELLYSAYGDETGVQCALSIQEFVKDA GYSKKVVDDLLDGI TGGDHSFTT-FOLKORRIVMKPDEAKVG DTLGDSSSSVLEPMSMKSYPDVS VDISMLSSIGKVKEKLDPDGS HINLDETTKLLDDLHAQARRGGSRESSNLSSISMASERDOHHL GSPERISVCEQODVTHDPYBETLGSFEPAASKT  LGREAVYLVSRNDCFVAEHAKGSFPHVVTPLLESWALSOVAGMP VFIKCENVQPSGSFKIRGIGHFCGEMKGCFHLVCSSGGNAGI AAAYAARKLG IPATIVLPSSTSLQVVGKLGGGAGVULTGKWND EANLRADGLAKRDGMENVPPFDHD PIWKGHASLUQGLKAVLGTP FGALVLAVGGGGLAGVAGLLEVGMQHVPI LIMETHCAHCFNA AITAGKLVTLPDITISVAKSLGAKTVAAAALLECMQVCKLHSEVVPE DTEAVSAVQOLLDERRILVEPACGAALAAIYSGLLRRLQASGCL PSELTSVVI VVCGGNINNSRELQALKTHLGOV VHTERIPGKEHINSEENSVEQAVYGLQAALGOVKDVMKMESSR QSFFWVLPPVLPWAVQAVEHEEVAQRVINLHKRGRVAAMGSRQ WVDDSCRKLSGLLRGGMAVLANLKTAGAVEKDVGLISEEKLFQ VHTTFI PQKEHINSEENSVEQAVYGLQAALGOVKDVAWKMESSR QRIEALRRAAIKEETYSMELAAREKRWKVAIGAGGCL VHTTFI PQKEHINSEENSVEQAVYGLQAALGOVKDVAWKMESSR QRIEALRRAAIKEETYSMELAAREKRWKVISLQGGC YMTLLMALAFGLLMGSLLFIK BYDGSVPI STCLSESTEPLAGER ASKONITRIKEVEDDIGJSMILTBOONQYLTKRPEDSTIPADH HTKIDIVTIGMLSLPCGMLCTAIGLPPMFOYI ICQVLIGFSGIN SIKSIVQVETIGEFGYFFTILLVGLARKWWISLQGGC YMTLLMAFGLLMGSLLHIK BYDGSVPI STCLSESTEPLAGET ASSGNITKREVEDDIGJSMILTBOONAYLIKKPWISLGGGG YMTLLMAFGLLMGSLLHIK BYDGSVPI STCLSESTEPLAGET ASSGNITKREVEDDIGJSMILTBOAMPLLQAGAS ASSSIVVEUR ILVIGGIFSLAAMFLLCHUKWINGGLAQV SSGSPVUTEBIATSIE RIPPLAIVTUELLDVSNELIGFTYRAF LLEMESKGNKEI LILGISAFIFICHLTVTELLDVSNELIGFTYRAF LLEMESKGNKEI LILGISAFIFICHLTVTELLDVSNELIGFTYRAF LLEMESKGNKEI LILGISAFIFICHLTVTELLDVSNELIGFTYRAF LLEMESKGNKEI LILGISAFIFICHLTVTELLDVSNELIGFTYRAF LLEMESKGNKEI LILGISAFIFICHTTVTELLDAVRINGGAAG VYTGLGGGFPUTGGERGFNUTGEVAGRGFRKCNCCQG MRTTQLGFGRRAFAGVTREVYLLILSVTINGTTRGAKNINGGGL MRTTQLGFGRRAFAGVGCCCPCNVKRVNRGFRTREVEREGERGNCGNED GNSDINTLEVAGGGGLANDKGGGLCFDRONGT TRPGAKLMKKGGGL PNPDNNNIKGSLIITTPVDFPKBQLTFERGAKLMKKGGGL PNPDNNNIKGSLIITTPV	Ì	ı	1	
MYYNRPDTYYYKLAKILHAGYKNACAALIGMEDTAVERPYP EVVPVQVETAKKSKKPSREVISCHFPBEGNACSLITDTAVERPYP EVVPVQVETAKKSKKPSREVISCHFPBEGNACSLITDTAVERPYP EVVPVQVETAKKSKKPSREVISCHFPBEGNACSLITDTAVERPYP EVVPVQVETAKKSKKPSREVISCHFPBEGNACSLITDTAVERPYP DADEBETHPVDLSSISSKLLBGFTTLGFKDERRNKYTPLSSATT ALSMONISVEGLKSDEMELIYSAKRBGOSLIYSVANTARPP DADEBETHPVDLSSISSKLLBGFTTLGFKDERRNKYTPLSSATT ALSMONISVEGLKSDEMELIYSAKUSGLGFVVDA GSYSKKVVDDLLDQITGGDBISTTI-FOLKORRNVPMKPPDBAKVG DTLGDSSSSVLEFBMKSYPDVSVIMSSLGKVKEDPDDS HLMLDETTKLLDDLHEAQARRGGSRESSHLSSLSNASERDOHHL GSPRISVGCPDVTHDYFFLOSMISSLGKVKADPDDS HLMLDETTKLLDDLHEAQARRGGSPSSNLSSLSNASERDOHHL GSPRISVGCPDVTHDYFFLOSMISSLGKVKADPDDS HLMLDETTKLLDDLHEAQARRGGSPSSNLSSLSNASERDOHHL GSPRISVGCPDVTHDYFFLOSMISSLGVKAMASEROHHUCSSOSMIGI AAAYARKLG IPATIVIPESTSLOVVORLOGGGAGAVOLTGKWD EANLRADELAKRDGWERVPPFDHPIJWKHGHAGHACKAN AITAGKLVTLDDITSVAKSLGAKTVAARADLECHQVCKHISSVVE DFBALVAVQGLDLEGGWAVQLLGGGGGAGVOLTGKWD EALLRADELAKRDGWERVPPFDHPIJWKHGHAGHCAGACA AITAGKLVTLDDITSVAKSLGAKTVAARADLECHQVCKHISSVVE PFSLTSVVVIVCGGNININSREQALKTHLGOV CSGRTGGRSISPRAPRVCUTCKLSGATAVISGLERCHQVCKHISSVVE PFSLTSVVVIVCGGNININSREQALKTHLGOV VINTESITYVIVLOGGNININSREQALKTHLGOV VINTESITYVIVLOGGNININSREQALKTHLGOV VINTESITYVIVLOGGNININSREQALKTHLGOV VINTESITYVIVLOGGNININSREQALKTHLGOV VINTESITYVIVLOGGNININSREQALKTHLGOVYKNVMKELSA QRIEALRRAAIKESTEYMELLABKHQVZALKMHONOGISMI DBILLDUKKAADALEESITEEHAPDURSVGWIFFSAVLRVEEE ANSKONITKHEVEDDINSILDSQNIQVILLKRRDSTIPRADH HTKINITTIGHLSLPCKGHLCTAGLEPMFYTICQLGFSGLM SIKSIVQVVTLGGFGFGYFTLLVQLEFSSPKKRYWKISLOGFC YMTLLMARGLWGALLHIKTOSVFISTCLLSSTFILVSFIM GSARGDREGDIDYSTVLLGMLVTQDVQLGLFRAMPTLLQAGAS ASSIVVVETLGFFMITTUTLLGULFSFEKKRYWKISLOGFC YMTLLMARGLWGARDAAAVELLCUVIKKYLLGFYFK LHMSKONKEILILGISAFIFLMLTVTELLDVSRELGCTLAGAL VSSGGPVVTEEIATSIERIFFLANGVELLGFSTFWATEL TULVPLILSVVMKSLLAALVLSLILPSSOYIKWIVSAGLAQV SSGFFWVTEETATSIERIFFLANGFTENGTICHVPTFVAYEL TULVPLILSVVMKSLLAALVLSLILPSSOYIKWIVSAGLAQV SSGFFWLGGRRARAGVISREVYLLILLSVTTISLLAPVLMARAI TRCVPRPERRSSL SLETTEFTAPPPCECARAGGGRGGMCADAAAEEAVRSWNNRTEDR GTMAPONLSTFCLLLLTENVAGRIPTKVLKURPGRTICHVULDFORNITGER MRTIG		ļ	Í	IAPGVSMITVUDMD BOTTONIC THE LRQLQRKOPHGFFAFPVTDA
EVUPVQVETAKKSK KPSREV 15 GEFFFF SENAS LIDSTABERIU ALVERAADEARDR INAF LPGGKMGYLKRINGGSLLYSVUNTAEP DADEEETHPVDLSSLSSKLLPGFTILG FKDERRIKVTPILSSATT ALSMONNSVYGDLKSDEMELLYSAVGDETGVCALSLGEFVKDA ALSMONNSVYGDLKSDEMELLYSAVGDETGVCALSLGEFVKDA GSYSKKVDDLLOD TIGGDHSTLFOLKORRNUPMKPPDEAKVG DTLGGSSSSVLEFMSMKSYPDVSVDISMLSSLGKVKKELDPDDS HLNLDETTKLLODLHEADAREGOLKSDEMISLSNASRGOHL GSPERLSVGEOPDVTHDPVEFLOSPEPAASAKT  1095	1	İ		MTVNPDDTTVVVV
ALVEHAADEARDRINSTENDERMSZIENTSTAEERUL ALVEHAADEARDRINSTENDERMSZIENTSVINTAEP DADEETHPVDLSSLSSKLLPGFTTIGFEKBERNKYTPIJSSATT ALSMONNSVEGULKSDEMELLYSVAGDETGVGCALSIGEFVKDA GSYSKKVVDDLLDGITGGHSRTLFOLKORRNVPMKPPDEARVG DTLAGESSSVLEFMSKSYPDVSISMLSSLGKVKKELDPDDS HINLDETTKILDDLHEADAERGGSRPSSNLSSLSNASERDOHHL GSPSRILVGEOPDVTHDPYEFLGSFERAAGKT VERSTENDER VOOR OP VERLEGSFERAAGKT VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDER VERSTENDE VERSTENDER VERSTENDER VERSTENDE VERSTENDER VERSTENDER VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERSTENDE VERST	1	j .		1 TANKEDIVIINLAKKILHAGEKMMCVOXXII ONTONO
DADEETHPVDLSSLSKLLEGEMGYLTGFORERSLYSVNYTAEP  DADEETHPVDLSSLSKLLEGEMGYTTLGFORERSKYTPILSSATT ALSMONSVYGDLKSDEMBLLYSAYGDETGGCALSLGFVKDA GSYSKKVVDDLLODITGGHSKTLFOLKORRNVWPHSPDEAKVG DTLGBSSSSVLEFMSMKSYPDVSVDISMLSSLGKVKKELDPDDS HLNLDETTKLLODLHEAQARRGGSPSNISSLSNASREDOHHL GSPSRLSVGEOPDVTDPYEFLGSPEPAASAKT VFLKCENVQPSGSFIRGIGHFORMKKCGRHLVCSSGGNAGI AAAYAARKLGIPATIVLPESTSLQVVQRLQGGAAEVOLTGKVWD EANLRAQELAKRGGENVPPPTDLFUKGGGAEVOLTGKVWD AAAYAARKLGIPATIVLPESTSLQVVQRLQGGAAEVOLTGKVWD EANLRAQELAKRGGENVPPPTDLFUKGGASLVGELGAVLRTP FGALVLAVGGGGLLAGVVAGLLEVGWQHVPIIAMSTHGAHCFNA AITAGKLVTLPDITSVAKSLGAKTVAARALCMQVCKHHSEVVE DTEAVSAVQOLLDDERHLVEFBACGAALAAIYSGLLRFLQABGGL PPSLTSVVIVUCGGNINSRELQALKTHLGOV GRSFFWVLFPVLPWAVQAVGLQALKTHGOV GRSFFWVLFPVLPWAVQAVGHEEVAGRVIKLHRGRGVAAMQSRQ WVMDSCRKLSGLLKGKNAVLMKTALTAGAVEKDVGLOSDEKLFQ VWHTFEIFOKRINESENSVFQAVVGLQRALQGYKUVVNMKESSR QHELAREAAIKESTEYMBLLAARKHQVEALWMCHONGSLGNL DEILEDVRKAADRLEEBIEEHAFDDNKSVKGVNFEAVLRVEEBE ANSKONITKREVEDDLGLSHLIDSONQYIHTKPROSTIPRADH HTKDIVTIGMLSJECGWLCTATGLPTMFGYIIGVLLGPSGLN SIKSIVQVETIGFFGVFFTIFLVGLEFFSPEKLRVWKISLQOPC YNTLLIMIAFGLLWGLILRIKPTQDVQLGLEMAWMPTLQAGAS ASSIVVEVIRILAFULGGILFSAFFILMITVTELLDVSMELGCFLAGAL VSSGGPVTEEIATSIEPIRDFLAAVFFLLCVIKKVLIGGPYRK LHMSSKSNKBILLIGSAFFIRMITVTLLDVSKELGGCLAGAL VSSGGPVTEEIATSIEPIRDFLAVFFASIGHVPFTVAYEL TULVFLTLSVVMKVELLAARLVSLIJPRSOYIKWIVSRGLAGV SSFSFVLGSRARRAGVISREVYLLILLFRSOYIKWIVSRGLAGAV SSFSFVLGSRARRAGVISREVYLLILLFRSOYIKWIVSRGLAGAV SSFSFVLGSRARRAGVISREVYLLILLFRSOYIKWIVSRGLAGAV SSFSFVLGSRARRAGVISREVYLLILLFRSOYIKWIVSRGLAGAV SSFSFVLGSRARRAGVISREVYLLILLFRSOYIKWIVSRGLAGAV SSFSFVLGSRARRAGVISREVYLLILLFRSOYIKWIVSRGLAGAV SSFSFVLGSRARRAGVISREVYLLILLFRSOYIKWIVSRGLAGAV SSFSFVLGSRARRAGVISREVYLLILLFRSOYIKWIVSRGLAGAV SSFSFVLGSRARRAGVISREVYLLILLFRSOYIKWIVSRGLAGAV SSFSFVLGSRARRAGVISREVYLLILLFRSOYIKWIVSRGLAGAV SSFSFVLGSRARRAGVISREVYLLILLFRSOYIKWIVSRGLAGAV SSFSFVLGSRARRAGGVISRGVYCHARAAAEEAVRSVWNRTRDR GTWAPQNLSTFCLLLLVLIGAVIAGROPFKYLDARVSAGAGGKKCNNCRG MRTTOLGGPGPMTQEVCCUCCONVLVWEERTLEEVELEPEVRD GRSILVDLEVTLEEVYAGNFVEVVVRNKLVRAGAGGKKRCNNCRG MRTTOLGGPGPMTQEVCCUCC	i		ĺ	1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -
ALSMONIS V FODLKSDEMELLY SAYOBETS VCALSLOGF WAD A GYSKKVVDDLLDQI TIGGDISR TILFOLKORRIV PMK PDENAKU GYSKKVVDDLLDQI TIGGDISR TILFOLKORRIV PMK PDENAKU DILGDSSS VILEPMSMKS Y PDVS VDI SMLSSI GKVKKELDPDDS HLNLDETTKLLQDLHEAQARROGSR PSSMLSSI GNVKKELDPDDS HLNLDETTKLLQDLHEAQARROGSR PSSMLSSI GNVKKELDPDDS HLNLDETTKLLQDLHEAQARROGSR PSSMLSSI SNASR PDHHL GSPRILS VGROUP VELKCENVQ PSGF KIRGIGH CQEMAKGCHLU VCSSGGNAGI AAAYAAR KUGI PATI VLPBST SLQVVORLOGGAB VOUTKVED EARLRAQELAK RDGWEN VP PFOH PLU TAMETHCAHCPNA AAITAGKLU VLLVETP FGALU LAVOGGGGLLAC VVAGLUE VOWOH VQF GAGAB VALU KURTP FGALU LAVOGGGGLLAC VVAGLUE VOWOH VQF I AMETHCAHCPNA AITAGKLU VLLVETP FGALU LAVOGGGGLLAC VVAGLUE VOWOH VQF I AMETHCAHCPNA AITAGKLU VLLVETP JURG VALU VLLVETP FGALU LAVOGGGLLAC VVAGLUE VOWOH VQF I AMETHCAHCPNA AITAGKLU VLLVETP JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLLVET JURG VALU VLL	J			T TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPE
GSYRKVUDDLLDQITGGDHEVQCALSLGEFVKDA GSYRKVUDDLLDQITGGDHEVQCALSLGEFVKDA DTLGDSSSSVLEPMSMKSYPDVSVDYSMSSIGKVKKELDPDDS HLMLDETTKLLQDLHEAQARGGSRESMLSSLNASERDQHHL GSPRLSVGEQPDVTHDVEFLQSPBPAASAKT  LGREAVYLVSRMCEPVAEHAKQEFFVVFLLESMALSOVAGMP VFLKCENVQPSGSFKIRGIGHECQEMAKKGCHLVCSSGGMGI AAAYARAKGIPATIVLPSSTSLQVVGRLQGEGAEVOLTGKVMD EANLRAQELAKRGGENPIPLJWKGHGLAVQELKAVLRTP FGALVILAVGGGGLLAGVVAGLLEVGMQHVPIIAMETHGAKCFRA AITAGKLVTLIPDITSVAKSLGAKTVAARALECMQVCKHBEVVE DTEAVSAVQOLLDDERMLVEPACGAALAAIVSGLARRICGEGL PESLTSVVVIVCGGNIINSRELQALKTHLGQV GRSFFWVLPVLPWAPAQAVEHEEVAQRVIKHRGRGVAAMQSRQ WVRDSCRKLSGLKRCKNAVKKTAIGAVEKDUGLSEVEKFQ UHTFEIFGKEINESSNSVQAVYGLQRALQGDYKDVVNNKESSR QRIEALREAAIKESTEVMELLAARKQVOLKHMQHGNGSLEML DEILEDVKRAADRLEEEEBHAFDDNKSVKGWFEAVLRVEEEE ANSKONITKREVEDDLGISMILDSONNGVILTKPRDSTIPRADH HEIKDIVTIGMLGSLFCGWLCTAIGLPTMFGYIIGGULGPSGL SIKSIVQVETLGEFGVFFTLFLVGLEFSPEKLRKVWKISLGGGC WYNTLMIAFGLIMGGLIKLRIKDVEVISTCSLLSTSTFUSSFIM GSARGDKEGDIDYSTVLLIGMLVTODVOLGLFRAVWFTLIQAGAS ASSIVVEVELRILVLIGQILFSLAAVFLLCLVIKKYLIGPYTRK GSARGDKEGDIDYSTVLLIGMLVTODVOLGLFRAVWFTLIQAGAS ASSIVVEVELRILVLIGGILFSLAAVFLLCLVIKKYLIGPYTRK USSGGPVVTEEIATSIEPIRDFLAIVFFASIGIHVPFPTVAYEL TULVFLTLSVVWNFLLIAALUTTTSLLLDAWBLGCFLAGAL VSSGGPVVTEEIATSIEPIRDFLAIVFFASIGIHVPFPTVAYEL TULVFLTLSVVWNFLLIAALUTTSLLLDAWBLGCFLAGAL VSSGGPVVTEEIATSIEPIRGFAIVFFRIGHTPFVAYEL TULVFLTLSVVWNFLLIAALUTTSLLLDAWBLGCFLAGAL VSSGGPVVTEEIATSIEPIRGFAIVFFRIGHTPFVAYEL TULVFLTLSVVMNFLIAALUTTSLLLDAWBLGCFLAGAL VSSGGPVUTEEIATSIEPIRGFAIVFFRIGHTPFVAYEL TULVFLTLSVVMNFLIAALUTTSLLLDAWBLGCFLAGAL VSSGGPVUTEEIATSIEPIRGFAIVFFRIGHTPFVAYEL TULVFLTLSVVMNFLIAALUTTSLLLDAWBLGCFLAGAL VSSGGPVUTEEIATSIEPIRGFAIVFVELVMRAFTERDK TRAGAGAAG ASSITUTEVELTEEVYAGNYFVELVMRAVELSDEKKQV DTYGEGGLKNGGGSGRGDTFGFFRGGTFRGODRN IR R GRAFTOLGFGGFGMTQEVGCDECPDNVKLVMERTLEVEIEFGVDD GMEYPFIGEGFPHVGGEFDDLFFRIKVVKHPIFFRRGDDLYTTNV TISLVESLVGFFMDTTHLDGIKVFRDRKTTFROAKLMKKGGGL PNDNNNIKGSLIITFDVDFFREQLTEEAREGIKQLLKOGGVQK	1	- J	•	1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
DTLGDSSSYLEFMSMKSYPDVSVDISMCSIGKVKELIPDDS HLMLDETTKLLQDLHEAQAERGGSRPSSKLSGKVKELIPDDS HLMLDETTKLLQDLHEAQAERGGSRPSSKLSLSNASERDOHHL GSPSRLSVGEDPDVTHDPVELGSPEPAASH, LGREAVYLVSRMCEPVAEHAKQEPFFVVTFLLESWALSOVAGMP VFLKCENVQPSGSFKIRGIGHFCQENKKGCHLVCSSGGNAGI AAAYAARKLGIPATIVLPSTLQVVGRLQGGGAEVOLTGKVMD EANLRAQELAKRDGWENVPFDHPLIMKCHASLVQELKAVLRTP FGALVLAVGGGGGLAGVVAGLLEVGWGHVPILMAETHGAHCFNA AITAGKLVTLPDITSVAKSLGAKTVAARALECMQVCKHBEVVE DTEAVSAVQOLLDDERMLVEPACGAALAAIVSGLLERIQAEGCL PPSLTSVVIVCGGNNINSEREQALKTHLGQV GRSFFFWLFPVLPPWQAQAVELQARAGISHCPALKTHLGQV WVRDSCRKLSGLLRQKNAVLNKLKTAIGAVEKDVGLSDEEKLFQ WVRDSCRKLSGLLRQKNAVLNKLKTAIGAVEKDVGLSDEEKLFQ ONLEALREAAIKEETEVMELLAAEKHQVEALKMMOHNOSLEML DEILEDVKRAADRLEEBIEBEHAFDDNKVKGVMFEAVLRVEEEB ANSKONITKREVEDDLGLSMLIDSQNNOYLITERDSTIPRADH HFIKDIVTIGMLSIPCGWLCTAIGLPTMFGYIICGVLLGPSGLN SIKSIVQVETLGGFFVFFTLFUCGLEFFSPKURKVWKISLQGGPC YMTLLMIAFGLLMGHLLRIKPTDSVFISTCLSLSSTPLVSFFLM GSARGDKEGDIDYSTVLLIGNLDVTQDVGLGIFNAVMFTLQAGAS ASSIVVEVURIULUGQILFTSVFISTCLSLSSTPLVSFFLM GSARGDKEGDIDYSTVLLIGNLDVTQDVGLGIFNAVMFTLQAGAS ASSIVVEVURIULUGQILFTSVFISTCLSLSSTPLVSFFLM GSARGDKEGDIDYSTVLLIGNLDVTGNVGINFRSGALAV LHMESKGNKEILLIGSAFFFLMLTVTELLDVSMELGCFLAGAL VSSCGPVVTEBIATSIEPIRFFLANVFLSLUFFYVARFL LHMESKGNKEILLIGSAFFFLMLTVTELLDVSMELGCFLAGAL VSSCGPVTTEBIATSIEPIRFTSVGIKFTSGALAVVELCALV SEFSFVLGSRARRAGVISREVYLLLISVTTLSLLLAPVLWRAAI TRUVPPRERRSSI SEFSFVLGSRARRAGVISREVYLLLISVTTLSLLAPVLWRAAI TRUVPPRERRSSI SEFSFVLGSRARRAGVISREVYLLLISVTTLSLLAPVLWRAAI TRUVPPRERRSSI SEFSFVLGSRARRAGVISREVYLLLISVTTLSLLAPVLWRAAI TRUVPPRERRSSI GSDIIVDLEVTLEEVYAGNFVEVYRKPVARQAPGKRKCNCRGG MRTTOLGGGRFGMTQEVGCDECPNVKLVNRQAPGKRKCNCRGG MRTTOLGGGRFGMTQEVGCDECPNVKLVNREPTLEVBIEFGVED GMEYPFIGEGEPHVDGEBGDLEFRIKVVKHPIFFRRGDDLYTTNV TISLVESLUGFFRMDTTHLDGKKTRFRKITRFRAKLERGALLMKKGGGL PNDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK	1	1		1 - TONGLING VIGOURSDEMENTASSAVGDETCHOCKT OF COMMISSION
HLMLDETTKLLQDIHEAQAERGGSRPSSNLSSLANASSRQOHHL  SPSRLSVEEQPDVTHDPYEFLGSFPAASAKT  LGEAVYLVSKMDCPVAEHAKQEFPHVYPLLESWALSOVAGMP VFLKCENVQPSGSFKIRGIGHFCQEMAKKGCRHLVCSSGGNAGI AAAYAARKLGIPATIVLPESTSLQVVQRLQGEGGEVQLTGKVWD EANLRAQELAKRDGWENVPFDHPLINKGHASLVQELKAVLRTP PGALVLAVGGGGLLAGVVAGLLEVWGHVPITAMETIGAICFNA AITAGKLVTLPDITSVAKSLGAKTVAARALECMQVCKHISEVVE DTEAVSAVQQLLDDERMLVPPACAALAATYSGLLRRLOAEGGL PPSLTSVVVIVCGGNNINTALECMQVCKHISEVVE DTEAVSAVQQLLDDERMLVPPACAALAATYSGLLRRLOAEGGL PSSLTSVVVIVCGGNNINTALECMQVCKHISEVVE OTEAVSAVQQLLDDERMLVPPACAALAATYSGLLRRLOAEGGL VEHTFEIFQKELMESENSVPQAVYGLORALAGDYKDVNNKESR WRDSCRKLSGLRQKNAVLNKLKTAIGAVEKNOVGSDEEKLFQ WWRDSCRKLSGLRQKNAVLNKLKTAIGAVEKNOVGSDEEKLFQ VHTFEIFQKELMESENSVPQAVYGLORALAGDYKDVVNNKESR QRLEALREAATKETEYMFLLAAEKKQVEALKOMQHQNGSLSML DEILEDVRKAADRLEEBIECHAFDDNKSVKGVNFEAVLRVEEEE ANSKONITKREVEDDLGLSMLTDSQNNQVILTKPRDSTIPRADH HFIKDIVTIGMLSHPCGMLCTAIGLPTMGFYIICGVLLGPSGLN SIKSIVQVETLGEFGVFFTLFLVGLEFSPEKLRKWKKSLQGDC YMTLLMIAFGGLLGGALLGGLUTHGVILGSSLNNLTHAGAS ASSSIVVEVILGELMGLLIKTGLGPTFNEVILGSFSLMVKKISLQGDC VSGCGVVTEEIATSIEPIRDFLAIVTPASIGLHYFPTFVAYEL LHMSKGNKEILILGISAFILMTUTTLUSVSMELGEFLAGAL VSSCGPVVTEEIATSIEPIRDFLAIVTFASIGLHYFPTFVAYEL LHMSKGNKEILILGSAFILMTUTTLUSVSMELGEFLAGAL VSSCGPVVTEEIATSIEPIRDFLAIVTFASIGLHYFPTFVAYEL LYLVPLTLSVVVMFLLAALVILLISVITLSLLAPVLMRAAI TCCYPPPERRSSL  SETSFYLGSRARRAGVISREVYLLILSVTTLSLLLAPVLMRAAI TCCYPPPERRSSL LSLETTETPAPPRCEAASGGRVGWRADAAEEAVRSVMNTREDR GTMAPQNLSTFCLLLLVLIGAVTAGRPYKLLGVPRSASIKDIK KAYNKLALQLHPRNPDDPDGAQEKFQDLGARVEVLDSERKRQT DTYGEGGLKDGHGSSHGDIFSHFFGDFFMFGSTPRQODRNIFR GSDIJVDLEVTLLEVVAGRPVEVVRNKVARAAFEGKKCNCRQE MRTTOLGFGRPQMTQEVGCDECPNVKLVWEERTLEVEIEFGWD GMEYPPIGGEPHVOEGFGDLRFIKVVKHPIFERGDDLYTNV TISLVESLVGFEMDTTHLDGHCKWHISGDKITRGGAKKCNCRQE MRTTOLGFGRPQMTQEVGCDECPNVKLVWEERTLEVEIEFGWD GMEYPPIGGEPHVOEFGDLRFIKVVKHPIFERGDDLYTNV TISLVESLVGFEMDTTHLDGHCKWHISGDKITRGGALLKKKGGCL PNEDNNNINGSSLIITTDVDFPKEQLTEEAREGIKQLLKQGSVQK	- (	f i		1
CSPSRLSVGEOPDVTHDPYEPLQSPEPASAKT	l			T = = = = = = = = = = = = = = = = = = =
1095 IGREAVIUSEMDEPUNELSEMALSOVAGMP VFLKCENVOPSGSFKIRGIGHFCQEMAKKGCRHLVCSSGGNACI AAAYAARKIGIPATIVLESTSLQVVQRLQGGGAEVQLTKKWD EANLRAQELAKRDGWENVPFPDHPLIKKGHASLUQELKAVLRTP PGALVLAVGGGLLAGVVAGLLGVGWOHVPIIAMETHGAHCFNA AITAGKLUTLDDITSVAGLGAKTVAARALECMQVCKHISEVVE DTEAVSAVQQLLDDERMLVEPACGAALAAIYSGLERRLQAEGCL PPSLTSVVVIVCGGNININSELQAKKTHLGQV GRSFFWULPPVLPWAVQAVEHEEVAQRVIKLHRGRGVAAMQSRQ WWADSCRKLSGLLRQCNALVKLKKTAIGAVERVE VHTFSIFQKFLNESENSVFQAVYGLQRALQDYKDVWNKESSR QRLEALREAAIKESTEYMELLAARKHQVEALKAMMOHQNOSLSML DEILEDVRRAADRLEEBIEHAFDDNKSVKGVNFEAVLRVEEBE ANSKONITRREVEDDLGLSMLIDSONNQYILTRRDSTIPRADH HHIKDIVTIGMLSLPCGWLCTAGLPTMFGYIIGGVLLGPSGLN SIKSIVQVETLGEFGYFFTLFLVGLEFSPERLRXWKISLGGPC YMTLLMIAFGLLWGSLLRIKPTQSVFISTCLSLSSTPLVSRFLM GSARGDKEGDIPSTVLLGVLTAFAGIGLHVPFTVAYEL LHMESKGNKEILILGISAFIFLMLITVTLLDVXMELGCFLAGAL VSSCGPVVTEEIATSIEFDFLAAVFLLCLVIKKVILGPYRK LHMESKGNKEILILGISAFIFLMLITVTLLDVXMELGCFLAGAL VSSCGPVVTEEIATSIEFDFLAAVFLLCLVIKKVILGPYRK LHMESKGNKEILLGISAFIFLMLTVTLLSVILLSVTLLSVTLLSVTLGFLAGAV SSSSIVVEVTEEIATSIEFDFLAAVFLLCLVIKKVILGPYRK LHMESKGNKEILLGISAFIFLMLTVTLLSVILLGVARAAI TRCVPRPERRSSL  5555 212 1425 LSLETTETPAPPRCEAASGGRVGWRADAAAEEAVRSVWNRTRDR GTMAPQULSTFLLLLVILLIGAVILAGAHEAVRSVWNRTRDR GTMAPQULSTFLLLLIVILLIGAVILAGAHEAVRSVWNRTRDR GTMAPQULSTFLLLLIVILLIGAVILAGAHEAVRSVWNRTRDR GTMAPQULSTFLLLLIVILLIGAVILAGAHEAVRSVWNRTRDR GSDIIVDLEVVILEEVVARGHPOHVARGAPGKRKCNCRQE MRTTGLGPGSFQMTGEVGCCDECPNVKLVNEETTLEVEIEFGVRD MRTTGLGPGSFQMTGEVGCCDECPNVKLVNEETTLEVEIEFGVRD GMSTPFIEGGEPHVDGEGPGDLFRIKVVKHPIFFERGDDLYTNV TISLVESLVGFEMDITHLDEHKVVIRRPGKRKCRCRCQE MRTTGLGPGFRQMTGEVGCCDECPNVKLVNEETTLEVEIEFGVRD GMSTPFIEGGEPHVDGEGPGDLFRIKVVKHPIFFERGDDLYTNV TISLVESLVGFEMDITHLDEHKVITRDRKKVKGEGL PNFDNNINIKGSLIITFDVDFFKEQLTEEREGIKQLLKQGSVQK	- (	1 1		1 TO DESCRIPTION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPER
VFILCENVOPSGSFRIGHFOGEMAKKGCRHLVCSSGGNAGI AAAYAARKIGIPATIVLPESTSLQVVQRLQGEGAEVOLTGKVWD EANLRAQELAKROUWENVPPEDPLIWKGHASLVQELKAVLRTP PGALVLAVGGGGLLAKVOUGRLQGEGAEVOLTGKWND EANLRAQELAKROUWENVPPEDPLIWKGHASLVQELKAVLRTP PGALVLAVGGGGLLAGVVAGLLEVGWOHVPIIMETHGAHCFNA AITAGKLVTLPDITSVAKSLGAKTVARARALECMQVCKHISEVVE DTEAVSAVQOLLDDERRILVEPACGAALAAIYSGLLRRLQAEGCL PPSLTSVVVIVCGGNININSRELQALKTHLGQV CSGRTGGRGSLRPAENVCLTCKLSGAETRGLCPALRTWIMKVL GSGFFWVLPPVLPWAVQDVEHEEVAQRVIKHRGKGVAAMQSRQ WVRDSCRKLSGLLRQKNAVLNKLKTAIGAVERDVALNGSBEKLFQ VVHTFEIFQRKLINESENSVFQAVYGLQRALQCDYKDVVNNKESSR QRLEALREAAIKESTETVWELLAARKHQVAALMOHQNQSLGML DBILEDVRKAADRLEEBIEEHAFDDNKSVKGVNFEAVLRVEEEE ANSKONITKREVEDDLGLSMLIDSQNNQYLITRPROSTIPRADH HFIKDIVTIGMSSLPGCGMLCTATGLPTWFGYIICGVLLGPSGLN SIKSIVQVETLGGFGVFFTLFLVGLEFSPEKLRKVWKISLGGPC YMTLLMIARGLLWGHLLRIKPTQSVFISTCLSLSSTELVSRFLM GSARGDKEGDIDYSTVLLGMLVTQDVQLGFMAVMPTLOAGAS ASSSIVVEVLRILULIGQILFSLAAVFLLCLVIKKYLIGPYYRK LHMESKGMKELILLGISAFTLFMLTVTELLDVSMELGCFLAGGL VSGCPVVTEEIATSIEPIRDFLAIVFFASIGLHVFFTVAYEL TVLVPLTLSVVVMKSLLAALVLSLILPRSSOYIKWIVSAGLAQV SSCSPVTEEIATSIEPIRDFLAIVFFASIGLHVFFTVAYEL TVLVPLTLSVVVMKSLLAALVLSLILPRSSOYIKWIVSAGLAQV SSSFSVLIGSRARRAGVISREVYLLILSVTTLSLLLAPVLWRAAI TRCVPRPERRSSL LSLRTFFPAPPRCEAASQGRVGWRADAAAEEAVRSVWNRTRDR GTMAPQULSTFCLLLLVLIGAVIAGRBPYKLLQVBRSASIKDIK KAYKKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQY DTYGEBGLKDGHQSSHGDIFFHFFGDFGFMFGGTRQODRNT PR GSDIIVDLEVTLEEVYAGNFVEVVENKPVARAGAFGKKCNCRQE MRTTGLGFGRFQMTOEVGCDECPRVKVLVWERETLEVEIEPGVRD GMSPFITGEGEPHVDGEGPDLDFRIKVVVKNIPERGRDDLTYNNV TISLVESLVGFEMDITHLDCHKVWHISRKITRPGRKLWKRGGL PWRDNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK	5553	- <del> </del>		1 32 3Ktt VGEQEDVTHDPYEFT,OGDFDXXGXvm
AAAYAARKIGIPATIVIPESTSLOVOKIQGEAEVOLTGKUWD EANLRAGELAKRDGWENVPPIDPDIPLIMKGHASLVQELKAVLETP PGALVIAVAGGGLLAGVVAGLLEVGWQHVPIIAMETHGAHCFNA AITAGKLUTLPDITSVAKSLGAKTVARARLEKOVOKIHGEVVE DTEAVSAVQQLLDDERMIVPEPAGAALAAIYSGLLRRLQAEGCL PPSLTSVVIVVGGGNININSRELQALKHLGQV  CSGRTGGGGSLRPAENVCLTCKLSGAETRGLLCPALRTWIMKVL GRSFFWVLPPVLPWAVQAVEHEEVAQRVIKHRGGRVAAMQSRQ WVRDSCRKLSGLLRQKNAVLNKIKTAIGAVEKUVGLSDEEKLFQ VHITFEIFQKELINESENSVFQAVVGLQRALQGDYKDVVNMKESSR QRLEALREAAIKEETEWELLAAEKRQVEALKMWQHONGSLSML DEILEDVRKAADRLEEBIEEHAFDDNKSVKGWFEAVLRVEEE ANSKONITKREVEDDLGLSMLIDSONNQYLITKPRDSTIPRADH HHIKDIVTIGMLSLPGCWLCTAIGLFTMFGYIICGVLLGFGGLN SIKSIVOVETLGEFGVFFTLFLVGLEFSPEKLRKVWKISLQGPC YMTLLMIAFGLLWGHLLRIKPTGSVFISTCLSLSSTPLVSRFIM GSARGDKEEDIDYSTVLLGMLTVTOVOLGLFRAVMPPLIQAGAS ASSSIVVEVLRILVLIGQIFSLAAVFLLCLVIKKYLIGPYYRK LHMSSKGNKEILILGISAFIFLMLTVTELLDVSMELGGFLAGAL VSSCGPVVTEEIATSIEPIRDFLAIVFFASIGLHVPFFVAYSL TVLVFLTLSVVVMKFLLAALVISLILPRSSOYIKWIVSAGLAQV SEFSFYLGSRARRAGISREVYLLILSVTTLSLLLAPVUMRAAI TRCVPRPERRSSL  1425 LSETTETFAPPRCEAASGGRVGWRADAAAEEAVRSVMNTRTRDR GTMAPQULSTFCLLLLYLIGAVTAGRPFYKILGVPRSASIKDIK KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDBEKRRQY DTYGEGGLKDGHQSSHGDIFSHFFGDFFMGGTFRQODRNIPR GSDIIVDLEVTLEEVYAGRFVEVVRNEVARAPGKRKCNCRQE MRTTGLGFGRFOMTGEVGCDECPNVKLVNEERTLEVEIEFGURD GMRYPFIEGEGPHVOGEPGDLFFRIKVVKHPIFERRGDDLYTNV TISLVESLVGFFMOITHLDGHKVHISRDKITRFGAKLMKKGGGL PRIPDINNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK		<b>'</b>	1095	LGREAVYLVSRMDGPVAEHAKOE DEHOLUTERY Y FROM STATES
EANLRAGELARROGNENVPPTBHPLIMGHASLVOELKAVLRTP FGALVLAVGGGGLLAGVVAGLLEVGWQHVPIIAMETHGAHCFNA AITAGKLUTLPDITSVAKSLGAKTVAARALECMQVKHISEVVE DTEAVSAVQQLLDDERMLVEPACGAALAAIVSGLURRLQAEGCL PFSLTSVVVIVCGGNNINSRELQALKTHLGOV  CSGRTGGGGSLRPADVCLTCKLLSGAETRGLLCFALRTWIMKVL GRSFFWVLFPVLPWAVQAVEHEEVAGRVIKHRGRGVAAMGSRQ WVRDSCRKLSGLLRQKNAVLNKIKTAIGAVEKDWGLSDEEKLFQ VITTEIFFORKEINESERSVFQAVYGLORALQGDYKDVVMKESGR QRLEALREAAIKEETEYMELLAARKRQVEALKMWQHONGSLSML DEILEDVRKAADRLEERIEEHAFDDNKSVKGWFFEAVLRVEEEE ANSKONITRREVEDDLGLSMLIDSOMOVILTKPRDSTIPRADH HFIKDIVTIGMLSLPCGWLCTAIGLPTMFGYIICGVLLGESGLN SIKSIVQVETLGEFGVFFTLFVGLEFSPEKLRKWNKISLQGPC YMTLLMIARGLLWGHLLRIKFPGSVFISTCLGLSSTPLVSRFLM GSARGDKEGDIDYSTVLLGMLVTQDVQLGLFMAVMPTLIQAGAS ASSSIVVEVRILVLIGGILFSLAAVFLLCLVIKKVLIGPYYRK LHMESKGNKEILILGISAFIFLMITVTELLDUSMELGGFLAGAL VSSCGPVVTEEIATSIEPIRDFLAIVFFASIGLHVFPTFVAYSL TVLVPLTLSVVMKFLLAALVLSLILPRSSQYIKWIVSAGLAQV SEFSPVLGSRARRAGVISREVYLLILSVTTLSLLLAPVLWRAAI TRCVPRPERRSSL  5555 212 1425 LSLETEFTPAPPRCEAASGGRVGWRADAAAEEAVRSVWNRTRDR GTMAPQNLSTFCLLLLYLIGALVAGRPFYKILGVPRSASIKDIK KAYKKLALQLHPDRNPDDPOAQBKFQDLGAAYEVLSDEKKRQY DTYGEGGLKDCHQSSHGDIFFSHFFGDFFFMGGRTPRQODRNIPR GSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQE MRTTQLGPGRFQMTQEVGCDECPNVKLVNREETLEVEIEPGVRD GMRYPFIGGEGPHVDLGFGDPLAFRIKVVKHPIFERRGDDLTTNV TISLVESLVGFEMDITHLDGHKVHISRDKITRFGRAKNKKGGGL PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK	j	j j		1
PGALVLAVGGGLLAGVVAGILEVGWGHVPI IAMETHGAHCFNA AITAGKLUTLPDITSVAKSLGAKTVAARALECMQVCKIHSEVVE DTRAVSAVQQLLDERMIVEPACGAALAAIYSGLLRRLQAEGCL PPSLTSVVIVCGGNNINSRELQAKKTHGAQV  CSGRTGGGGSLRPAENVCLTCKLSGAETRGLLCPALRTWIMKVL GRSFFWLFPVLPWAVQEHEEVAQRVIKLHRGRGVAAMGSRQ WVRDSCRKLSGLLRQKNAVLNKLKTAIGAVERUVGLSDEEKLFQ VHTFEIFOKRINESENSVEGAVYGLQRALQGDYKDVUNMKESSR QRLEALREAAIKEETEYMELLAARKHQVGALKNMQHONQSLSML DEILEDVRKAADRLEERIEEHAPDDNKSVKGWNFEAVLRVEEEE ANSKONITRREVEDDLGLSMLIDSQNNQYILTKPRDSTIPRADH HEIKDIVTIGMLSIPCGWLCTAIGLPTMFGYIICGVILGFSGLN SIKSIVQVETLGEFGVFFTLFLVGLEFSPEKLRKVWKISLQGPC YMTLLMIARGLLWGALLRIKPTQSVFISTCLSLSSTPLVSRFIM GSARGDKEGDIDYSTVLIGNLVTQDVQLGLFWAVMPTLYQAGAS ASSSIVVEVLRILVLIGGILFSLAAVFLLCLVIKYLIGPYRK LHMESKGNKEILILGISAFIFLMLTVTELLDVSMELGCFLAGAL VSSCGPVVTEEIATSIEIPTSPLAIVFFASIGLHVFFTFVAYEL TVLVFLTLSVVVMKFLLAALVLSLILPRSSQYIKWIVSAGLAQV SSFSFVLGSRARRAGVISREVYLLILSVTTISLLLAPVLWRAAI TRCVPRPERSSL  LSLETTETPAPPRCEAASQGRUGWRADAAAEEAVRSVWNRTRDR GTWAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIK KAYRKLALQHFDRNPDDFQAQEKRQDLGAAYEVLSDSEKRQY DTYGEGGLKDCHQSSIGDIFSHFFGDFGFMFGSTFRQODRNIPR GSDIIVDLEVTLEEVYAGNFVEVVNNKEVARQAFGKRKCNCRQE MRTTQLGPGRFQMTGEVGCDECPDVKLVWEERTLEVBIEPGURD GGMSYPFIGGEGPHVDTGVVGCDECPDVKLVWEERTLEVBIEPGURD TISLVESLVGFEMDITHLDGHKVHISRNKITRPGAKLWKRGEGL PNFDNNNIKGSLIITFDVDFPKEQLITEEAREGIKQLLKKGEGV	- 1	1 1		AAAYAARKLGIPATIVLPESTSLOWOODLOGEGA TUGE
AITAGKLVTLPDITSVAKSLGAKTVARALLECMOVCKIHSEVVE DTEAVSAVQOLLDDERMIVEPACGAALAAIYSCLLRRLQAEGCL PPSLTSVAVIVCGINNINSRELQALKTHLGOV  CSGRTGGRGSLRPAENVCLTCKLSCAETRGLCCPALRTWIMKVL GRSFFWVLFPVLPWAVQAVEHEEVAQRVIKLHRGGVAAMGSRQ WVRDSCRKLSGLLRGKNAVLNKLKTAIGAVEKDVGLSDEEKLFQ VHTFEIFQKELNESENSVPQAVVGLQRAILQGPYKDVONKESSR QRLEALREAAIKEETEYMELLABEKHQVEALKNMQHCNQSLSML DEILEDVRKAADRLSEETEHHAPDDINKSVKGVNFEAVLRVEEEE ANSKQNITKREVEDDLGLSMLIDSQNNQYILITKPRDSTIPRADH HFIKDIVTIGMLSLPCGHLCTATGLPTWFGYIICGVLLGPSGLN SIKSIVQVETLGEFEVFFTLFLVGLEFSPEKLRKVWKISLQGPC YMTLLMIAFGLLWGHLLRIKPTQSVFISTCLSSTPLVSRFLM GSARGDKEGDIDVSTVLLGMLVTQDVQLGLEMAVMPTLIQAGAS ASSSIVVEVLRILVIGQILFSLAAVFLLCLVIKKYLIGPYYRK LHMESKGNKEILILGGILFSLAAVFLLCLVIKVYLIGPYYRK LHMESKGNKEILILGGSAFIFLMLTVTELLDVSMELGCILAGAL VSSGPVVTEEIATSIEPIRDFLAIVFFASIGLHYFPTFVAYEL TVLVFILTSVVVMKFLLAALVLSLILPRSSQYIKWIVSAGLAQV SEPSFVLGSRARRAGVISREVYLLILSVTTLSLLLAPVLWRAAI TRCVPRPERRSSL  5555 212 1425 LSLRTRETPAPPRCEAASQGRVGWRADAAAEEAVRSVWNRTRDR GTMAPQNLSTFCLLLYLIGAVIAGRDFYKILGVPRSASIKDIK KAYKKLALQLHPDRNPDDEQAQEKCQDLGAAYEVLSDSEKRKQY DTYGEGGLKDGHQSSHGDIFSHFFGDFGFMFGSTPRQDRRIPR GSDIIVDLEVTLEEVYAGRFVEVVENKEVAQAPGKRKCNCRQE MRTTQLGGGRRGMTGDEGCDCPRVKLVMEERTLEVEIEPGUND TISLVESLVGFEMDITHLDCHKVHISRNKITRPGAKLMKKGEGL PNFDNNNIKGSLITTFDVDFPKEQLTEEAREGIKQLLKQGSVQK	· I	1		EANLRAQELAKRDGWENVPDEDHDI TWYCUR CLAYOFT
DTEAVSAVQOLLDDERMIJVEPACGAALAAI YSGLLRRLQAEGCL PPSITSVVVIVCGGNIINSRELQALKTHIGGV  CSGRTGGRGSLRPAENVLTCKLSGAETRGLLCPALRTWIMKVL GRSFFWVLFPVLPAVQAVEHEEVAQRVIKLHRGRGVAAMQSRQ WVRDSCRKLSGLLRQKNAVLNKLKTAIGAVEKUVGLSDEEKLFQ VHTFEIFQKELNESENSVFQAVYGLQRALQCDYKDVUNMKESSR QRLEALREAAI KEETEYMELLAAEKHQVEALKNMQHQNGSLSML DEILEDVRKAADRLEEB IEEHAFDDNKSVKGVNFEAVLRVEEBE ANSKONITKREVEDDLGJESMLIDSONNQYILTKPRDSTIPRADH HFIKDIVTIGMLSPCGWLCTAIGLPTMFGYIICGVLLGPSGLN SIKSIVQVETLGEFGVFFTLFLVGGEFSPEKLRVWKISLQGPC YMTLLMIARGLLWGILLERIKPTQSVFISTCLSLSSTPLVSRFLM GSARGDKEGDIDYSTVLLGMLVTQDVQLGLFMAVMPTLIQAGAS ASSSIVVEVLRILVLIGQILFSLAAVFLLCVIKKYLIGPYYRK LHMESKGNKEILILGISAPIFLMITVTELLDVSMELGCFLAGAL VSSCGPVVTEBIATSIEPIRDFLAIVFFASIGLHVFPFTVAYEL TVLVFLTLSVVVMKFLLAALVLSLILPRSSOYIKWIVSAGLAQV SSFSFVLGSRARRAGVISREVYLLILSVTTLSLLAPVLWRRAI TCVPPPERRSSL SESFYLGSRARRAGVISREVYLLILSVTTLSLLAPVLWRRAI TCVPPPERRSSL LSLRTRETPAPPRCEAASQGRVGWRADAAEEAVRSVWNRTRDR GTMAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIK KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQV GSSIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCKQE MRTTQLGGGRTQMTGEVGCDECPNVKLVNEERTLEVEIEPGVRD GREYPFIGGGEPHVGGEPGGDLRFRIKVVKHPIFERRGDLYTNV TISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGGGL PNFDNNNIKGSLIITFDVDFFKEQLTEEAREGIKQLLKQGSVQK	1	1 1		PGALVLAVGGGGLI AGVVACT I FYGUGURA TO THE TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL T
PSSITSVVIVCGGNITNSRELQALKTHLGQV  CGGRTGGGGSLRPAENVCLTCKLSGAETRGLLCPALRTWIMKVL GRSFFWLIPVLPWAVQAVEHEEVAORVIKLHRGGGVAAMQSRQ WWRDSCRKLSGLLRQKNAVLNKLKTAIGAVEKUVGLSDEEKLFQ VHTFEIFQKFLNESENSVFQAVYGLQRALQCDYKDVVMKESSR QRLEALREAAIKEETEYMELLAAEKHQVEALKUMQHQNQSLSML DEILEDVKRAADRLEEBIEEHAFDDNKSVKGVNTFAVLRVEEBE ANSKQNITKREVEDDLGLSMLIDSQNNQYLITKPRDSTIPRADH HFIKDIVTIGMLSEPCGWLCTAIGLPTMFGYIICGVLLGPSGLN SIKSIVQVETLGEFGVFFTLFLVGLEFSPEKLRKVWKLSLQGPC YMTLLMIAFGLLWGHLLRIKPTQSVFISTCLSLSSTPLVSRFLM GSARGDKEGDIDYSTVLLGMLVTQDVQLGLFMAVMPTLIQAGAS ASSSIVVEVLRILULIGGILFSLAAVFLLCLVIKKYLIGPYYRK LHMESKGNKEILILGISAFIFLMITVTELLDVSMELGGFLAGAL VSSQGPVVTEEIATSIEFIRDFLAIVFFASIGLHVFPFTVAYEL TVLVPLTLSSVVMKFLLAALVLSLILPRSSQYIKWIVSAGLAQV SESFSVLGSRARRAGVISREVYLLILSVTTLSLLLAPVLWRAAI TRCVPRPERRSSL  SILTTRETPAPPRCEAASQGRVGWRADAAEEAVRSVWNRTRDR GTMAPQNLSTFCLLLLVLIGAVIAGRDFYKLIGAVPRSASIKDIK KAYRKLALQLHPDRNPDDDPQAQEKFQDLGAAYEVLSDSEKRKQY DTYGEEGLKDGHQSSHGDIFSHFFGDFGFMFGGTPRQODRNIPR GSDIIVDLEVTLEEVYASNFVEVVRNKPVARQAPGKRKCNCRQE MRTTQLGPGRFQMTQEVGCDECPNVKLINGERTLEVEIEPGVRD GMEYPFIGGGEPHVDCEPGDLFFRIKVVKHPIFERRGDDLYTNV TISLVESLVGFFMDITHLDGHKVHISRDKITRPGAKLWKKGGGL PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK		1. 1		AITAGKLUTI.PDITGUAVCI.CAVTUAREN ARTHURANCENA
CSGRTGGRSLRPAENVCLTCKLSGAETRGLLCPALRTWIMKVL GRSFFWULPPVLPWAVQAVEHEEVAQRVIKLHRGRGVAAMOSRQ WVRDSCRKLSGLLRQKNAVLNKLKTAIGAVEKEDVGLSDEEKLFQ VHTFEIFOKENESENSVFQAVYGLQRALQGDYKDVVNMKESSR QRLEALREAAIKEETEYMELLAAEKHQVEALKHWQHQNQSLSML DEILEDVKAADRLEEBIEEHAFDDNKSVKGVNFEAVLRVEEEE ANSKQNITKREVEDDLGLSMLIDSQNNQYILTRPRDSTIPRADH HFIKDIVTIGMLSLPCGWLCTAIGLPTMFGYILCGVLLGPSGLN SIKSIVQVETLGEFGVPFTLFLWGLEFSPEKLRKVWKISLQGPC YMTLLMIAFGLLWGHLLRIKPTQSVFISTCLSLSSTPLVSRFIM GSARGDKEGDIDYSTVLLGMLVTQDVQLGLFRAVMPTLIQAGAS ASSSIVVEVLRILVLIGQILFSLAAVFLLCLVIKKYLIGPYYRK LHMESKGNKEILILGISAFIFLMLTVTELLDVSMELGCFLAGAL VSSCGPVVTEEIATSIEPIRDFLAIVFFASIGLHVFPTFVAYEL TVLVPLTLSVVVMKFLLAALVLSLILPRSSQYIKMIVSAGLAQV SSPSPVLSGRARRAGVISREVYLLILSVTTLSLLAPVLWRAAI TRCVPRPERRSSL  LSLRTRETPAPPRCEAASQGRVGWRADAAEEAVRSVWNRTRDR GTMAPQNLSTFCLLLVLIGAVIAGRDFYKILGVPRSASIKDIK KAYRKLALQHPDRNPDDPQAQEKFQDLGAAYEVLSDSERKKQT OTYGEEGLKDGHQSSHGDIFSHFFGDFGFMFGGTPRQODRNIPR GSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAFGKRKCNCRQE MRTTQLGPGRFQMTQGVCGDECPNVKLVWEERTLEVEIEPGVRD GMEYPFIGGGEPHVDGGFDGLARFIKVVKHPIFFERGDLYTNV TISLVESLVGFEMDITHLDGHKVHISRDKITRDGAKLWKKGEGL PNFDNNINGKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK	ł	1 1		DTEAVSAVOOLI DDERMI VEDA COLLARALECMQVCKIHSEVVE
CSGRTGGGRSLRPAEDVCLTCKLSGAETRGLLCPALRTWIMKVL GRSFFWVLPPVLPWAVQAVEHEEVAQRVIKLHRGRGVAAMQSRQ WVRDSCRKLSGLLRQKNAVLNKLKTAIGAVEKDWGLSDEEKLFQ VHTFEIFQKELLWESENSVFQAVYGLQRALQGDYKDVVMNKESSR QRLEALREAAIKEETEYMELLAABKHQVEALKUMQHQNQSLSML DEILEDVKKAAADRLEEBIEEHAFDDNKSVKGVNFEAVLKVEEEE ANSKQNITKREVEDDLGLSMLIDSQNNQYILTRPRDSTIPRADH HFIKDIVTIGMLSLPCCWLCTAIGLPTMFGYIICGVLLGPSGLN SIKSIVQVETLGEFGVFFTLFLVGLEFSPEKKKVWKISLQGPC YMTLLMIAFGLLWGHLLRIKPTQSVFISTCLSLSSTPLVSRFLM GSARGDKEGDIDYSTVLLGMLVTQDVQLGLFMAVMPTLIQAGAS ASSSIVVEVLILULGQILFSLAAVFLLCLVIKKVLIGPYSRK LHMESKGNKEIILLGISAFIFLMLTVTELLDVSMELGGFLAGAL VSSCGPVVTEEIATSIEPIRDFLAIVFFASIGLHVFFTFVAYEL TVLVFLTSVVVMKSLLAALVLSLILPRSSQYIKWIVSAGLAQV SEFSPVLGSRARAGVISREVYLLILSVTTLSLLAAPVLWRAAI TRCVPRPERRSL  5555 212 1425 LSLETRETFAPPRCEAASQGRVGWRADAAAEEAVRSVWNRTRDR GTMAPQNLSTFCLLLVYLGAVIAGRDFYKILGVRSASIKDIK KAYRKLALQLHPDNPDDPDQAQEKFQDLGAAYEVLSDSEKKQT DTYGEEGLKDGHQSSHGDIFSHFFGDFGFMFGGTFRQODRNIPR GSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQE MRTTQLGFGRFQMTQCVGCDECPNVKLVMEERTLEVEIEPGVRD GMEYPFIGEGEFHVDGEFGDLFRFIKVVKHPIFFBRRGDLYTNV TISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGL PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK				PPSLTSWALLYCCOMMINGER
GRSFFWLIPPVLPWAVQAVEHEEVAQRVIKLHRGRGVAMQSRQ WWRDSCRKLSGLLRQKNAVLNKLKTAIGAVEKDVGLSDEKLFQ WWRDSCRKLSGLLRQKNAVLNKLKTAIGAVEKDVGLSDEKLFQ VHTFEIFQKELBESENSVFQAVYGLQRALQGDYKDVVMKESSR QRLEALREAAIKEETEYMELLAABKHQVEALKNMQHQNQSLSML DEILEDVRKAADRLEEBIEEHAFDDNKSVKGWNFEAVLRVEEEE ANSKQNITKREVEDDLGLSMLIDSQNNQYILTKPRDSTIPRADH HFIKDIVTIGMLSLPCGWLCTAIGLPTMFGYIICGVLLGPSGLN SIKSIVQVETLGEFGVFFTLFLVUGLEFSPEKLRKVWKISLGGPC YMTLLMIAFGLLWGHLLRIKPTQSVFISTCLSLSSTPLVSNFLM GSARGDKEGDIDYSTVLLGMLVTQDVQLGLFMAVMPTLIQAGAS ASSSIVVEVLITLVLIGGILFSLAAVFLLCUIKKYLIGPYYRK LHMESKGNKEILILGISAFIFLMITVTELLDVSMELGGFLAGAL VSSQGPVVTEEIATSIEPIRDFLAIVFFASIGLHVFPTFVAYEL TVLVFLTLSVVVMKFLLAALVLSLILPRSSOYIKNIVSAGLAQV SSEFSPVLGSRARRAGVISREVYLLILSVTTLSLLLAPVLWRAAI TRCVPRPERRSSL  5555 212 1425 LSLRTEFTPAPPRCEAASQGRVGWRADAAAEEAVRSVWNRTRDR GTMAQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIK KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQY DTYGEEGLKDGHQSSHGDIFSHFFGDFGFFFGGDFRNIPR GSDIIVDLEVTLEEVYAGNFVEVVRNRPVARQAFGKRKCNCRQE MRTTOLGFGRFQMTQEVGCDECPNVKLVNEERTLEVELEFGVRD GMEYPFIGEGEPIVDGEPGDLRFRIKVVKHPIFERRGDDLYTNV TISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGRGL PNFDNNNIKGSLIITFDVDFPKEQLTFEAREGIKQLLKQGSVQK	5554	166	2318	CSGRTGGRGSLDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
WYRDSCRKLSGLERQKNAVLNKLKTAIGAVEKDVGLSDEKKLFG WHTFEIFQKFLNESENSVFQAVYGLQRALQGPYKDVYMKESSR QRLEALREAAIKEETEYMELLAAEKHQVEALKNMQHQNQSLSML DEILEDVRKAADRLEEBIEEHAFDDNKSVKGVNFEAVLRVEEBE ANSKQNITKREVEDDLGLSMLIDSQNNQYILTKPRDSTIPRADH HFIKDIVTIGMLSLPCGWLCTAIGLPTMFGYIICGVLLGPSGLN SIKSIVQVETLGEFGVFFTLFLVGLEFSPEKLRKVWKISLQGPC YMTLLMIAFGLLWGHLLRIKPTQSVFISTCLSLSSTPLVSRFLM GSARGDKEEGDIDYSTVLLIGMLVTQDVQLGLFMAVMPTLIQAGAS ASSSIVVEVLRILVLIGQILFSLAAVFLLCLVIKKYLIGPYYRK LHMESKGNKEILLIGISAFIFLMLTVTELLDVSMELGCFLAGAL VSSCGPVVTEEIATSIEPIRDFLAIVFFASIGLHVFPFTVAYEL TVLVFLTLSVVVMKFLLAALVLSJLLPRSSQYIKWIVSAGLAQV SEFSPVLGSRARRAGVISREVYLLILSVTTLSLLLAPVLWRAAI TRCVPRPERRSSL  5555 212 1425 LSETRETPAPPRCEAASQGRVGWRADAAAEEAVRSVWNRTRDR GTMAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIK KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQY DTYGEEGLKDGHQSSHGDIFSHFFGDFGFMFGSTPRQODRNIPR GSDIIVDLEVTLEEVYAGRFVEVVRNKPVARQAFGKRKCNCRQE MRTTQLGFGFFQMTQEVGCDECPNVKLVNEERTLEVEIEPGVRD GMEYPFIGEGEPHVDGEPGDLFFRIKVVKHPIFERRGDDLYTNV TISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGL PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK	1	1		GREEFING ROLL PARTY CLTCKLSGAETRGLLCPALRTWIMKVL
VHTFE IFOKFILNESENSVFQAVYGLQRALQGDYKDVVNMKESRR QRLEALREAA I KEETEYMELLAABKHQVEALKOMOHONGSLSML DEILEDURKAADRIEBEI EEHAFDDNKSVKGVNFEAVLRVEEEE ANSKQNITKREVEDDLGLSMLIDSQNNQYILTKPRDSTIPRADH HFIKDIVTIGMLSLPCGWLCTAIGLPTMFGYI I CGVLLGPSGLN SIKSIVQVETLGEFGVFFTLFLVGLEFSPEKLRKVWKISLQGPC YMTLLMIAFGLLWGHLLRIKPTOSVFISTCLSLSSTPLVSRFLM GSARGNKEGD IDYSTVLLGMLVTQDVQLGLFMAVMPTLIQAGAS ASSSIVVEVLRILVLIGQILFSLAAVFLLCALVIKKYLIGPYYRK LHMESKGNKEILILGISAFIFLMLTVTELLDVSMELGCFLAGAL VSSQGPVVTBEIATSIEPIRDFLAIVFFASIGLHVFPTFVAYEL TVLVPLTLSVVVMKFLLAALVLSLILPRSSQYIKW IVSAGLAQV SEPSFVLGSRARRAGVISREVYLLILSVTTLSLLLAPVLWRAAI TRCVPPPERRSSL  1425  1425  1425  LSLTTETPAPPRCEAASQGRVGWRADAAAEEAVRSVWNRTRDR GTMAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRGASIKDIK KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYVLSDSEKRKQY DTTGEEGLKDGHQSSHGDIFSHFFGDFGFMFGSTPRQODRNIPR GSDIIVDLEVTLEBYVAGNFVEVVRNKPVARQAPGKRKCNCRQE MRTTQLGFGRFQMTOEVGCDECPNVKLVNEERTLEVEIEPGURD GMEYPFIGEGEPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNV TISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGL PNFDNNNIKGSLIITFDVDFFKEQLTEEAREGIKQLLKQGSVQK	Ì	1		THE TAKE VERNAVUAVERENVADDUTVT UDODOUBARA
QRLEALREAN KEETEYMELLAAEKHQVEALKUMQHONQSISMIL DEILEDVRKAADRLEEBIEEHAFDDNKSVKGVMFEAVLRVEEEE ANSKQNITKREVEDDLGISMLIDSQNNQYILTKPROSTIPRADH HFIKDIVTIGMLSLPCGWLCTAIGLPTMFGYIICGVLLGPSGLN SIKSIVQVETLGEFGVFFTLFLVGLEFSPEKLRKVKKISLQGPC YMTLLMIAFGLLWGHLLRIKPTQSVFISTCLSLSSTPLVSRFLM GSARGDKEGDIDYSTVLLGMLVTQDVQLGLFMAVMPTLIQAGAS ASSSIVVEVURILULIGQILFSLAAVFLLCLVIKKYLIGPYYRK LHMESKGNKEILILUGISAFIFLMLTVTELLDVSMELGGFLAGAL VSSCGPVVTBEIATSIEPIRDFLAIVFFASIGLHVFPTFVAYEL TVLVPLTLSVVVMKFLLAALVLSLILPRSSQYIKWIVSAGLAQV SSFSPVLGSRARRAGVISREVYLLILSVTTLSLLLAPVLWRAAI TRCVPRPERSSL  LSLRTRETPAPPRCEAASQGRVGWRADAAAEEAVRSVWNRTRDR GTMAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIK KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQY DTYGEGGLKDGHQSSHGDIFSHFFGDFGFFMFGGTPRQODRNIPR GSBIIVDLEVTLEEVYAGNFVEVVRNKPVARQAFGKRKCNCRQE MRTTQLGFGRFQMTQEVGCDECPNVKLVNEERTLEVEIEPGVRD GMEYPFIGEGEPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNV TISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGL PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK		1	i	CARLOGILKUKNAVINKI.KTATCAMPURITOT OR
DEILEDVRKAADRLEEBIEHAFDDNKSVKGVNFEAVLRVEEEE  ANSKQNITKREVEDDLGLSMLIDSQNNQYILTKPRDSTIPRADH HFIKDIVTIGMLSLPCGWLCTAIGLPTMFGYIICGVLLGFSGLN SIKSIVQVETLGEFGVFFTLFLVGLEFSPEKLRKVWKISLQGPC YMTLMIAFGLLWGHLURIKPTQSVVFISTCLSLSSTPLVSRFLM GSARGBKEGDIDYSTVLLGMLVTQDVQLGLFMAVMPFILQAGAS ASSSIVVEVLRILVLIGQILFSLAAVFLLCLVIKKYLIGPYYRK LHMESKGNKEILILGISAFIFLMLTVTELLDVSMELGGFLAGAL VSSCGPVVTEEIATSIEPIRDFLAIVFFASIGLHVFPTFVAYEL TVLVPFLTLSVVVMKFLLAALVLSLILPRSSOYIKWIVSAGLAQV SSFSFPVLGSRARRAGVISREVYLLILSVTTLSLLLAPVLWRAAI TRCVPRPERRSSL LSLRTRETPAPPRCEAASQGRVGWRADAAEEAVRSVWNRTRDR GTWAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIK KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQY DTYGGEGIKDGHQSSHGDIFSHFFGDFGFMFGGTPRQODRNIPR GSDIIVDLEVTLEEVYAGNFVEVVVRNKPVARQAPGKRKCNCRQE MRTTQLGPGRFQMTQEVGCDECPNVKLVNEERTLEVEIEPGVRD GMEYPFIGEGEPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNV TISLVESLVGFEMDITHLDCHKVHISRDKITRPGAKLWKKGEGL PNFDNNNIGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK		1 !		***** *** VACIDADE SENS VEO DAVVOT OF A TOOR VERNER
ANSKONITREVEDDLGLSMLIDSQNNQYLITKPRDSTIPRADH HFIKDIVTIGMLSLPCGWLCTATGLPTMFGYLICGVLLGPSGLN SIKSIVQVETLGEFGVFFTLFLVGLEFSPEKLRKVWKISLQGPC YMTLLMIAFGLLWGHLLRIKPTQSVFISTCLSLSSTPLVSRFLM GSARGDKEGDIDYSTVLLGMLVTQDVQLGLFMAVMPTLIQAGAS ASSSIVVEVLRILVLIGQILFSLAAVFLLCLVIKKYLIGPYYRK LHMESKGNKEILILGISAFIFLMLTVTELLDVSMELGCFLAGAL VSSCGPVVTEEIATSIEPIRDFLAIVFFASIGLHVFPTFVAYEL TVLVPLTLSVVVMKFLLAALVLSLILPRSSQYIKWIVSAGLAQV SSEFSPVLGSRARRAGVISREVYLLILSVTTLSLLLAPVLWRAAI TRCVPRPERRSSL  SLSLTTRETPAPPRCEAASQGRVGWRADAAAEEAVRSVWNRTRDR GTMAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIK KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQY DTYGEEGLKDGHQSSHGDIFSHFFGDFGFMFGSTPRQODRNIPR GSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQE MRTTQLGPGRFQMTQEVGCDECPNVKLVMEERTLEVEIEPGVRD GMEYPFIGEGEPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNV TISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGL PNFDNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK	1	1 . 1	ł	E
HFIKDIVTIGMLSLPCGWLCTAIGLPTMFGYIICGVILLGPSGLN SIKSIVQVETLGEFGVFFTLFLVGLEFSPEKLRKVWKKISLQGPC YMTLLMIAFGLLWGHLLRIKPTQSVFISTCLSLSSTPLVSRFLM GSARGDKEGDIDYSTVLLGMLVTQDVQLGLFMAVMPTLIQAGAS ASSSIVVEVLRILVLIGQILFSLAAVFLLCLVIKKYLIGPYYRK LHMESKGNKEILILGISAFIFLMLTVTELLDVSMELGCFLAGAL VSSCGPVVTEEIATSIEPIRDFLAIVFFASIGLHVFPTFVAYEL TVLVPLTLSVVVMKFLLAALVLSLILPRSSQYIKWIVSAGLAQV S3FSFVLGSRARRAGVISREVYLLILSVTTLSLLLAPVLWRAAI TRCVPRPERRSSL  LSLRTRETPAPPRCEAASQGRVGWRADAAAEEAVRSVWNRTRDR GTMAPQNLSTFCLLLVILGAVIAGRDFYKILGVPRSASIKDIK KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQY GSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAFGKRKCNCRQE MRTTQLGPGRFQMTQEVGCDECPNVKLVNEERTLEVEIEPGVRD GMEYPFIGEGGFHNDGEPGDLRFRIKVVKHPIFERRGDDLYTNV TISLVSLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGL PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK		j l		
SIKSIVQVETLGEFGVFFTLFLVGLEFSPEKLRKVWKISLQGPC YMTLLMIAFGLLWGHLLRIKPTQSVFISTCLSLSSTPLVSRFLM GSARGDKEGDIDYSTVLLGMLVTQDVQLGLFMAVMPTLIQAGAS ASSSIVVEVLRILVLIGQILFSLAAVFLLCLVIKKYLIGPYYRK LHMESKGNKEILLILGISAFIFLMLTVTELLDVSMELGCFLAGAL VSSCGPVVTEEIATSIEPIRDFLAIVFASIGLHVFFTVAYEL TVLVFLTLSVVMKFLLAALVLSLILPRSSQYIKWIVSAGLAQV SEFSFVLGSRARRAGVISREVYLLILSVTTLSLLLAPVLWRAAI TRCVPRPERRSSL  LSLRTRETPAPPRCEAASQGRVGWRADAAAEEAVRSVWNRTRDR GTMAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIK KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQY DTYGEEGLKDGHQSSHGDIFSHFFGDFGFFFGSTPRQODRNIPR GSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQE MRTTQLGPGRFQMTQEVGCDECPNVKLVNEERTLEVEIEPGVRD GMEYPFIGEGEPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNV TISLVESLVGFEMDITHLDCHKVHISRDKITRPGAKLWKKGEGL PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK	1	[	1	THE TANKE VEDULGESMI, I DECOMMONTATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE
YMTLLMIAFGLLWGHLLRIKPTQSVFISTCLSLSSTPLVSRFLM GSARGDKEGDIDYSTVLLGMLVTQDVQLGLFMAVMPTLIQAGAS ASSSIVVEVLRILVLIGQILFSLAAVFLLCLVIKKYLIGPYYRK LHMESKGNKEILILGISAFIFLMLTVTELLDVSMELGCFLAGAL VSSCGPVVTEEIATSIEPIRDFLAIVFFASIGLHVFPTFVAYEL TVLVPLTLSVVVMKFLLAALVLSLILPRSSQYIKWIVSAGLAQV SEFSPVLGSRARRAGVISREVYLLILSVTTLSLLLAPVLWRAAI TRCVPRPERRSSL  LSLRTRETPAPPRCEAASQGRVGWRADAAAEEAVRSVWNRTRDR GTMAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIK KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQY DTYGEEGLKDGHQSSHGDIFSHFFGDFGFMFGGTPRQODRNIPR GSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQE MRTTQLGPGRFQMTQEVGCDECPNVKLVNEERTLEVEIEPGVRD GMEYPFIGEGEPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNV TISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGL PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK	J	]	į	THE TARGET A TECHNOLOGY COMMENT AND
GSARGDKEGDIDYSTVLLGMLVTQDVQLGLFMAVMPTLIQAGAS ASSSIVVEVLRILVLIGQILFSLAAVFLLCLVIKKYLIGPYYRK LHMESKGNKEILILGISAFIFLMLTVTELLDVSMELGCFLAGAL VSSQGPVVTEEIATSIEPIRDFLAIVFFASIGLHVFPTFVAYEL TVLVPITLSVVVMKFLLAALVLSLILPRSSQYIKWIVSAGLAQV SEFSPVLGSRARRAGVISREVYLLILSVTTLSLLLAPVLWRAAI TRCVPRPERRSSL  LSLRTRETPAPPRCEAASQGRVGWRADAAAEEAVRSVWNRTRDR GTMAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIK KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQY DTYGEEGLKDGHQSSHGDIFSHFFGDFGFMFGGTPRQODRNIPR GSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAFGKRKCNCRQE MRTTQLGPGRFQMTQEVGCDECPNVKLVNEERTLEVEIEPGVRD GMEYPFIGGEGEPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNV TISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGL PNFDNNNIKGSLIITFDVDFFKEQLTEEAREGIKQLLKQGSVQK	1	1 1	1	TOTAL X VELLUCE FULL WILLIAM TO THE TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL
ASSSIVVEVLRILVLIGQILFSLAAVFLLCLVIKKYLIGFYYRK LHMESKGNKEILILGISAFIFLMLTVTELLDVSMELGCFLAGAL VSSQGPVVTBEIATSIEPIRDFLAIVFFASIGLHVFPTFVAYEL TVLVPLTLSVVVMKFLLAALVLSLILPRSSQYIKWIVSAGLAQV SEFSFVLGSRARRAGVISREVYLLILSVTTLSLLLAPVLWRAAI TRCVPRPERRSSL  LSLRTRETPAPPRCEAASQGRVGWRADAAAEEAVRSVWNRTRDR GTMAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIK KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQY DTYGEEGLKDGHQSSHGDIFSHFFGDFGFMFGGTPRQODRNIPR GSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAFGKRKCNCRQE MRTTQLGPGRFQMTQEVGCDECPNVKLVNEERTLEVEIEPGVRD GMEYPFIGGEPPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNV TISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGL PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK	1	1		**************************************
LHMESKGNKEILILGISAFIFLMLTVTELLDVSMELGCFLAGAL  VSSCGPVVTBEIATSIEPIRDFLAIVFFASIGLHVFPTFVAYEL  TVLVFLTLSVVVMKFLLAALVLSLILPRSSQYIKWIVSAGLAQV SSEFSPVLGSRARRAGVISREVYLLILSVTTLSLLLAPVLWRAAI  TRCVPRPERRSSI  LSLRTRETPAPPRCEAASQGRVGWRADAAAEEAVRSVWNRTRDR GTMAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIK KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQY DTYGEEGLKDGHQSSHGDIFSHFFGDFGFMFGGTPRQORNIPR GSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQE MRTTQLGPGRFQMTQEVGCDECPNVKLVNEERTLEVEIEPGVRD GMEYPFIGGEPPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNV TISLVESLVGFEMDITHLDCHKVHISRDKITRPGAKLWKKGEGL PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK	[	1	j	
VSSCGPVTTEIATSIEPIRDFLAIVFFASIGLHVFFTFVAYEL  TVLVPLTLSVVVMKFLLAALVLSLILPRSSQYIKWIVSAGLAQV SEFSFVLGSRARRAGVISREVYLLILSVTTLSLLLAPVLWRAAI TRCVPRPERRSSL  LSLRTRETPAPPRCEAASQGRVGWRADAAAEEAVRSVWNRTRDR GTMAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIK KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQY DTYGEEGLKDGHQSSHGDIFSHFFGDFGFFFGGTPRQODRNIPR GSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQE MRTTQLGPGRFQMTQEVGCDECPNVKLVNEERTLEVEIEPGVRD GMEYPFIGEGEPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNV TISLVESLVGFEMDITHLDCHKVHISRDKITRPGAKLWKKGEGL PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK	1	1		ASSSIVVEVLRILVLIGOTIFCLARUET CONTROL OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PR
TVLVPITLSTVVMKFLLAALVLSLILPRSSQYIKWIVSAGLAQV SEPSPVLGSRARRAGVISREVYLLILSVTTLSLLLAPVLWRAAI TRCVPRPERRSSL  LSLRTRETPAPPRCEAASQGRVGWRADAAAEEAVRSVWNRTRDR GTMAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIK KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQY DTYGEEGLKDGHQSSHGDIFSHFFGDFGFFFGSTPRQODRNIPR GSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQE MRTTQLGPGRFQMTQEVGCDECPNVKLVNEERTLEVEIEPGVRD GMEYPFIGEGEPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNV TISLVESLVGFEMDITHLDCHKVHISRDKITRPGAKLWKKGEGL PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK	1	1	1	LHMESKGNKEILILGIGA PIET WITTER WITTER
TVLVPITLSTVVMKFLLAALVLSLILPRSSQYIKWIVSAGLAQV SEPSPVLGSRARRAGVISREVYLLILSVTTLSLLLAPVLWRAAI TRCVPRPERRSSL  LSLRTRETPAPPRCEAASQGRVGWRADAAAEEAVRSVWNRTRDR GTMAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIK KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQY DTYGEEGLKDGHQSSHGDIFSHFFGDFGFFFGSTPRQODRNIPR GSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQE MRTTQLGPGRFQMTQEVGCDECPNVKLVNEERTLEVEIEPGVRD GMEYPFIGEGEPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNV TISLVESLVGFEMDITHLDCHKVHISRDKITRPGAKLWKKGEGL PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK		1	1	VSSCGPVVTREIATGIRDIDGE
SEFSPUGSRARRAGVISREVYLLILSVTTLSLLLAPVLWRAAI TRCVPRPERRSL  LSLRTRETPAPPRCEAASQGRVGWRADAAEEAVRSVWNRTRDR GTMAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIK KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQY DTYGEEGLKDGHQSSHGDIFSHFFGDFGFMFGSTPRQODRNIPR GSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQE MRTTQLGPGRFQMTQEVGCDECPNVKLVNEERTLEVEIEPGVRD GMEYPFIGEGEPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNV TISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGL PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK	1	]	ĺ	TVLVFLTLSUMMYST TARIS OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STA
TRCVPRPERRSSL  1425  LSLRTRETPAPPRCEAASQGRVGWRADAAEEAVRSVWNRTRDR GTMAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIK KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQY DTYGEEGLKDGHQSSHGDIFSHFFGDFGFMFGGTPRQODRNIPR GSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQE MRTTQLGPGRFQMTQEVGCDECPNVKLVNEERTLEVEIEPGVRD GMEYPFIGEGEPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNV TISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGL PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK	1	į į		- TOTAL DISTRICT TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPER
LSLRTRETPAPPRCEAASQGRVGWRADAAEEAVRSVWNRTRDR GTMAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIK KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQY DTYGEEGLKDGHQSSHGDIFSHFFGDFGFMFGGTPRQODRNIPR GSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAFGKRKCNCRQE MRTTQLGPGRFQMTQEVGCDECPNVKLVNEERTLEVEIEPGVRD GMEYPFIGEGEPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNV TISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGL PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK	L			VII OI VII OI CARRAGVISKE VYI.T.TI.CVTTT CTTT NOVI III
LSLKTRETPAPPRCEAASQGRVGWRADAAEEAVRSVWNRTRDR GTMAPQNLSTFCLLLYLIGAVIAGRDFYKILGVPRSASIKDIK KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQY DTYGEEGLKDGHQSSHGDIFSHFFGDFGFMFGGTPRQODRNIPR GSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQE MRTTQLGPGRFQMTQEVGCDECPNVKLVNEERTLEVEIEPGVRD GMEYPFIGEGEPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNV TISLVESLVGFEMDITHLDCHKVHISRDKITRPGAKLWKKGEGL PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK	5555	212		THE TRANSP
KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQY DTYGEEGLKDGHQSSHGDIFSHFFGDFGFMFGSTPRQODRNIPR GSDIIVDLEVTLEEVYAGNFVEVVRNRPVARQAPGKRKCNCRQE MRTTQLGPGRFQMTQEVGCDECPNVKLVNEERTLEVEIEPGVRD GMEYPFIGEGEPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNV TISLVESLVGFEMDITHLDCHKVHISRDKITRPGAKLWKKGEGL PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK VYNGLQGY	<b>!</b> !		i i	LOLKTRETPAPPRCEAASQGRVGWRADAAAEEAVRSVWNPTPDD
DTYGEEGLKDGHQSSHGDIFSHFFGDFGAAYEVLSDSEKRKQY GSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQE MRTTQLGPGRFQMTQEVGCDECPNVKLVNEERTLEVEIEPGVRD GMEYPFIGEGEPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNV TISLVESLVGFEMDITHLDCHKVHISRDKITRPGAKLWKKGEGL PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK VYNGLQGY	! [	ſ	. 1	VIII VII DO LE CULLUY LI IGAVTACED DEVETT OUDD ON COMP
GSDIIVDLEVYLGEVYAGNFVEVVRNKPVARQAPGKRKCNCRQE MRTTQLGPGRFQMTQEVGCDECPNVKLVNEERTLEVEIEPGVRD GMEYPFIGEGEPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNV TISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGL PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK VYNGLQGY		1		THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY O
MRTTQLGPGRFQMTQEVGCDECPNVKLVNEERTLEVEIEPGVRD GMEYPFIGEGEPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNV TISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGL PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK VYNGLQGY		'	, ,	~ - · · · · · · · · · · · · · · · · · ·
GMEYPFIGEGEPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNV TISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGL PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK VYNGLQGY	į I	i i		ACCULATION AND A LINE A LATINE A EACHADAN AND AND AND AND AND AND AND AND AND
TISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGL PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK VYNGLQGY	· 1	ĺ	1 1	MRTTQLGPGRFOMTOEVGCDFCDNEUVIINTERNEUM
PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK VYNGLQGY		l	10	MEYPFIGEGEPHYDGEPGDI BEDIGARDANEERILEVEIEPGVRD
PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK VYNGLQGY	1	1	J -3	TISLVESI VCEEMD TILL DOWNER I KVVKHPIFERRGDDLYTNV
VYNGLQGY  VYNGLQGY		ļ		TOD TOD TO THE
5556   6035			1.	THE DIRECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SELECT TO SE
TANGER TO THE PEEY LIRM FOR TYLLOKITK DNNAHTVKSR	5556	5835		
				THE FELY DIRMFQGTFYLLQKITKDNNAHTVKSR

SEQ Predicted beginning nucleotide nucleotide nucleotide nucleotide location corresponding to first amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence	FK YE LR SS AR AQ ST SA LII
No: nucleotide location corresponding to first amino acid residue of amino acid sequence Secure (Codon, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide /=possible nucleotide /=possible	FK YE LR SS AR AQ ST SA III FL SS P
Corresponding corresponding to first amino acid residue of amino acid sequence   E-Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serinc, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stophanine, Sequence   E-Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serinc, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stophanine, Sequence   E-Louine, M=Tryptophan, Y=Tyrosine, X=Unknown, *=Stophanine, Sequence   E-Louine, M=Tryptophan, Y=Tyrosine, X=Unknown, *=Stophanine, Sequence   E-Louine, M=Methionine, N=Asparagine, D=Louine, M=Methionine, N=Asparagine, D=Louine, M=Methionine, N=Asparagine, D=Louine, M=Methionine, N=Asparagine, D=Louine, M=Methionine, N=Asparagine, D=Louine, M=Methionine, N=Asparagine, D=Louine, M=Methionine, N=Asparagine, D=Louine, M=Methionine, N=Asparagine, D=Louine, M=Methionine, N=Asparagine, D=Louine, M=Methionine, N=Asparagine, D=Louine, M=Methionine, N=Asparagine, D=Louine, M=Methionine, N=Asparagine, D=Louine, M=Methionine, N=Asparagine, D=Louine, M=Methionine, N=Asparagine, D=Louine, M=Methionine, N=Asparagine, D=Louine, M=Methionine, N=Asparagine, D=Louine, M=Methionine, N=Asparagine, D=Louine, M=Methionine, N=Asparagine, D=Louine, M=Methionine, N=Asparagine, D=Louine, M=Methionine, N=Asparagine, D=Louine, M=Methionine, N=Asparagine, D=Louine, M=Methionine, N=Asparagine, D=Louine, M=Methionine, N=Asparagine, D=Louine, M=Methionine, N=Asparagine, D=Louine, M=Methionine, N=Asparagine, D=Louine, M=Methionine, N=Asparagine, D=Louine, M=Methionine, N=Asparagine, D=Louine, M=Methionine, N=Asparagine, D=Louine, M=Methionine, N=Asparagine, D=Louine, M=Methionine, N=Asparagine, D=Louine, M=Methionine, N=Asparagine, D=Louine, M=Methionine, N=Asparagine, D=Louine, M=Methionine, N=Asparagine, D=Louine, M=Methionine, N=Asparagine, D=Louine, M=Methionine, N=Asparagine, D=Louine, M=Methionine, N=Asparagine, D=Louine, M=Methionine, N=Asparagine, D=Louine, M=Methionine, N=Asparagine, D=Louine, M=Methionine, N=Asparagin	FK VE LR SS AQ ST SA LI CR SC SP
Corresponding to first amino acid residue of amino acid residue of amino acid sequence   P=Proline, Q=Glutamine, N=Arginine,   P=Proline, Q=Glutamine, V=Valine,   P=Proline, Q=Glutamine, N=Arginine,   N=Serine, T=Threonine, V=Valine,   N=Serine, T=Threonine, V=Valine,   N=Serine, T=Threonine, V=Valine,   N=Serine, T=Threonine, V=Valine,   N=Serine, T=Threonine, V=Valine,   N=Serine, T=Threonine, V=Valine,   N=Serine, T=Threonine, V=Valine,   N=Serine, T=Threonine, V=Valine,   N=Serine, T=Threonine, V=Valine,   N=Serine, T=Threonine, V=Valine,   N=Serine, T=Threonine, V=Arginine,   N=Serine, T=Threonine, V=Arginine,   N=Serine, T=Threonine, V=Valine,   N=Serine, T=Threonine, V=Arginine,   N=Serine, T=Threonine, V=Valine,   N=Serine, T=Threonine, V=Valine,   N=Serine, T=Threonine, V=Valine,   N=Serine, T=Threonine, V=Valine,   N=Serine, T=Threonine, V=Valine,   N=Serine, T=Threonine, V=Valine,   N=Serine, T=Threonine, V=Valine,   N=Serine, T=Threonine, V=Valine,   N=Serine, T=Threonine, V=Valine,   N=Serine, T=Threonine, V=Valine,   N=Serine, T=Threonine, V=Valine,   N=Serine, T=Threonine, V=Valine,   N=Serine, T=Threonine, V=Valine,   N=Serine, T=Threonine, V=Valine,   N=Serine, T=Threonine, V=Valine,   N=Serine, T=Threonine, V=Valine,   N=Serine, T=Threonine, V=Valine,   N=Serine, T=Threonine, V=Valine,   N=Serine, T=Threonine, P=Poline,   N=Serine, T=Threonine, V=Valine,   N=Serine, T=Threonine, P=Poline,   N=Serine, T=Threonine, P=Poline,   N=Serine, T=Threonine, P=Poline,   N=Serine, T=Threonine, P=Poline,   N=Serine, T=Threonine, P=Poline,   N=Serine, T=Threonine, P=Poline,   N=Serine, T=Threonine, P=Poline,   N=Serine, T=Threonine, P=Poline,   N=Serine, T=Threonine, P=Poline,   N=Serine, T=Threonine, P=Poline,   N=Serine, T=Threonine, P=Poline,   N=Serine, T=Threonine, P=Poline,   N=Serine, T=Threonine, P=Poline,   N=Serine, T=Threonine, P=Poline,   N=Serine, T=Threonine, P=Poline,   N=Serine, T=Threonine, P=Poline,   N=Serine, N=Serine, N=Serine, N=Serine, N=Serine, N=Serine, N=Serine, N=Serine, N=Serin	FK VE LR SS AQ ST SA LI CR SC SP
to first amino acid residue of residue of amino acid sequence  P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stopension acid sequence  W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stopension acid sequence  LEELDESYIEKFTDFLRLFVSVHLRRIESYSQFPVVEFLTLL; YTFHQPTHEGYFSCLDIWTLFLDYLTSKIKSRLGDKEAVLNE; DALVLLLTEVLNRIQFRYNQAQLEELDDETLDDDQQTEWQRYI QSLEVVAKVMELLPTHAFSTLFPVLQDNLEVYLGLQQFIVTSG GHRLNITAENDCRRLHCSLRDLSSLLQAVGRAEAEYFIGDVFFA FNDALTVVERLVKVTLYGSQIKLYNIETAVPSVLKPDLIDVHM SLAALQAYSHWLAQYCSEVHRQNTQQFVTLISTTMDAITPLIS KVQDKLLLSACHLLVSLATTVRPVFLISIPAVQKVPNRITDAS LRLVDKAQVLVCRALSNILLLPWPNLPENEQQWPVRSINHASI SALSRDYRNLKPSAVAPQRKMPLDDTKLIHQTLSVLEDIVEN SGESTKSRQICYQSLQESVQVSLALFPAFIHQSDVTDEMLSFFI TLFRGLRVQMGVPFTEQIIQTFLNMFTREQLAESILHEGSTGG VVEKFLKILQVVVQEPGQVFKPFLPSIIALCMEQVYPIIAERE PDVKAELFELLFRTLHHNWRYFFKSTVLASVQRGIAEEQMENE	FK VE LR SS AQ ST SA LI CR SC SP
amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)  LEELDESYIEKFTDFLRLFVSVHLRRIESYSQFPVVEFLTLL; YTFHQPTHEGYFSCLDIWTLFLDYLTSKIKSRLGDKEAVLNR; DALVLLLTEVLNRIQFRYNQAQLEELDDETLDDDQQTEWQRYI QSLEVVAKVMELLPTHAFSTLFPVLQDNLEVYLGLQQFIVTSC GHRLNITAENDCRRLHCSLRDLSSLLQAVGRLAEYFIGDVFAY FNDALTVVERLVKVTLYGSQIKLYNIETAVPSVLKPDLIDVHY SLAALQAYSHWLAQYCSEVHRQNTQQFVTLISTTMDAITPLIS KVQDKLLLSACHLLVSLATTVRPVFLISIPAVQKVFNRITDAS LRLVDKAQVLVCRALSNILLLPWPNLPENEQQWPVRSINHASI SALSRDYRNLKPSAVAPQRKMPLDDTKLIHQTLSVLEDIVEN SGESTKSRQICYQSLQESVQVSLALFPAFIHQSDVTDEMLSFI TLFRGLRVQMGVPFTEQIIQTFLNMFTREQLAESILHEGSTGC VVEKFLKILQVVVQEPGQVFKPFLPSIIALCMEQVYPIIAERE PDVKAELFELLFRTLHHNWRYFFKSTVLASVQRGIAEEQMENE	FK VE LR SS AQ ST SA LI CR SC SP
residue of amino acid sequence    W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,	FK VE LR SS AQ ST SA LI CR SC SP
amino acid sequence  Codon, /=possible nucleotide deletion,  LEELDESYIEKFTDFLRIFVSVHLRRIESYSQFPVVEFLTLLI YTFHQPTHEGYFSCLDIWTLFLDYLTSKIKSRLGDKEAVLNR: DALVLLLTEVLNRIQFRYNQAQLEELDDETLDDDQQTEWQRYI QSLEVVAKVMELLPTHAFSTLFPVLQDNLEVYLGLQQFIVTSC GHRLNITAENDCRRLHCSLRDLSSLUQAVGRLAEYFIGDVFAX FNDALTVVERLVKVTLYGSQIKLYNIETAVPSVLKPDLIDVHX SLAALQAYSHWLAQYCSEVHRQNTQQFVTLISTTMDAITPLIS KVQDKLLLSACHLLVSLATTVRPVFLISIPAVQKVFNRITDAS LRLVDKAQVIVCRALSNILLLPWPNLPENEQQWPVRSINHASI SALSRDYRNLKPSAVAPQRKMPLDDTKLIHQTLSVLEDIVEN SGESTKSRQICYQSLQESVQVSLALFPAFIHQSDVTDEMLSFFI TLFRGLRVQMGVPFTEQIIQTFLNMFTREQLAESILHEGSTGC VVEKFLKILQVVVQEPGQVFKPFLPSIIALCMEQVYPIJAERE PDVKAELFELLFRTLHHNWRYFFKSTVLASVQRGIAEEQMENE	FK VE LR SS AQ ST SA LI CR SC SP
Sequence   \=possible nucleotide insertion	E R S R Q T A I I L R S P
LEELDESYIEKFTDFLRLFVSVHLRRIESYSQFPVVEFLTLLI YTFHQPTHEGYFSCLDIWTLFLDYLTSKIKSRLGDKEAVLNR: DALVLLTEVLNRIQFRYNQAQLEELDDETLDDDQQTEWQRYI QSLEVVAKVMELLPTHAFSTLFPVLQDNLEVYLGLQQFIVTSG GHRLNITAENDCRRLHCSLRDLSSLLQAVGRLAEYPIGDVFAY FNDALTVVERLVKVTLYGSQIKLYNIETAVPSVLKPDLIDVHY SLAALQAYSHWLAQYCSEVHRQNTQQFVTLISTTMDAITPLIS KVQDKLLLSACHLLVSLATTVRPVFLISIPAVQKVPNRITDAS LRLVDKAQVLVCRALSNILLLPWPNLPENEQQWPVRSINHASI SALSRDYRNLKPSAVAPQRKMPLDDTKLIIHQTLSVLEDIVEN SGESTKSRQICYQSLQESVQVSLALFPAFIHQSDVTDEMLSFI TLFRGLRVQMGVPFTEQIIQTFLNMFTREQLAESILHEGSTGG VVEKFLKILQVVVQEPGQVFKPFLPSIIALCMEQVYPIIAERE PDVKAELFELLFRTLHHNWRYFFKSTVLASVQRGIAEEQMENE	E R S R Q T A I I L R S P
YTFHQPTHEGYFSCLDIWTLFLDYLTSKIKSRLGDKEAVLNR: DALVLLTEVLNRIQFRYNQAQLEELDDETLDDDQQTEWQRYI QSLEVVAKVMELLPTHAFSTLFPVLQDNLEVYLGLQQFIVTSC GHRLNITAENDCRRLHCSLRQLSSLLQAVGRLAEYPIGDVFAY FNDALTVVERLVKVTLYGSQIKLYNIETAVPSVLKPDLIDVHY SLAALQAYSHWLAQYCSEVHRQNTQQFVTLISTTMDAITPLIS KVQDKLLLSACHLLVSLATTVRPVFLISIPAVQKVFNRITDAS LRLVDKAQVLVCRALSNILLLPWPNLPENEQQWPVRSINHASI SALSRDYRNLKPSAVAPQRKMPLDDTKLIIHQTLSVLEDIVEN SGESTKSRQICYQSLQESVQVSLALFPAFIHQSDVTDEMLSFI TLFRGLRVQMGVPFTEQIIQTFLNMFTREQLAESILHEGSTGC VVEKFLKILQVVVQEPGQVFKPFLPSIIALCMEQVYPIIAERE PDVKAELFELLFRTLHHNWRYFFKSTVLASVQRGIAEEQMENE	E R S R Q T A I I L R S P
DALVLLLTEVLNRIQFRYNQAQLEELDDETLDDDQQTEWQRYI QSLEVVAKVMELLPTHAFSTLFPVLQDNLEVYLGLQQFIVTSG GHRLNITAENDCRRLHCSLRDLSSLLQAVGRLAEYFIGDVFFA FNDALTVVERLVKVTLYGSQIKLYNIETAVPSVLKPDLIDVHY SLAALQAYSHWLAQYCSEVHRQNTQQFVTLISTTMDAITPLIS KVQDKLLLSACHLLVSLATTVRPVFLISIPAVQKVFNRITDAS LRLVDKAQVLVCRALSNILLLPWPNLPENEQQWPVRSINHASI SALSRDYRNLKPSAVAPQRKMPLDDTKLIIHQTLSVLEDIVEN SGESTKSRQICYQSLQESVQVSLALFPAFIHQSDVTDEMLSFF TLFRGLRVQMGVPFTEQIIQTFLNMFTREQLAESILHEGSTGG VVEKFLKILQVVVQEPGQVFKPFLPSIIALCMEQVYPIIAERE PDVKAELFELLFRTLHHNWRYFFKSTVLASVQRGIAEEQMENE	R S R Q T A I I L R S P
QSLEVVAKVMELLPTHAFSTLFPVLQDNLEVYLGLQQFIVTSG GHRLNITAENDCRRLHCSLRDLSSLLQAVGRLAEYPIGDVFAF FNDALTVVERLVKVTLYGSQIKLYNIETAVPSVLKPDLIDVHF SLAALQAYSHWLAQYCSEVHRQNTQQFVTLISTTMDAITPLIS KVQDKLLLSACHLLVSLATTVRPVFLISIPAVQKVFNRITDAS LRLVDKAQVLVCRALSNILLLPWPNLPENEQQWPVRSINHASI SALSRDYRNLKPSAVAPQRKMPLDDTKLIHQTLSVLEDIVED SGESTKSRQICYQSLQESVQVSLALFPAFIHQSDVTDEMLSFF TIFRGLRVQMGVPFTEQIIQTFLNMFTREQLAESILHEGSTGG VVEKFLKILQVVVQEPGQVFKPFLPSIIALCMEQVYPIIAERE PDVKAELFELLFRTLHHNWRYFFKSTVLASVQRGIAEEQMENE	S AR AQ T A A I I I L R S P
GHRLNITAENDCRRLHCSLRDLSSLLQAVGRLAEYFIGDVFAY FNDALTVVERLVKVTLYGSQIKLYNIETAVPSVLKPDLIDVHY SLAALQAYSHWLAQYCSEVHRQNTQQFVTLISTTMDAITPLIS KVQDKLLLSACHLLVSLATTVRPVFLISIPAVQKVFNRITDAS LRLVDKAQVLVCRALSNILLLPWPNLPENEQQWPVRSINHASI SALSRDYRNLKPSAVAPQRKMPLDDTKLIHQTLSVLEDIVEN SGESTKSRQICYQSLQESVQVSLALFPAFIHQSDVTDEMLSFF TIFRGLRVQMGVPFTEQIIQTFLNMFTREQLAESILHEGSTGG VVEKFLKILQVVVQEPGQVFKPFLPSIIALCMEQVYPIIAERE PDVKAELFELLFRTLHHNWRYFFKSTVLASVQRGIAEEQMENE	IR IQ ST SA III III IR SS P
FNDALTVVERLVKVTLYGSQIKLYNIETAVPSVLKPDLIDVHY SLAALQAYSHWLAQYCSEVHRQNTQQFVTLISTTMDAITPLIS KVQDKLLLSACHLLVSLATTVRPVFLISIPAVQKVFNRITDAS LRLVDKAQVLVCRALSNILLLPWPNLPENEQWPVRSINHASI SALSRDYRNLKPSAVAPQRKMPLDDTKLIHQTLSVLEDIVEN SGESTKSRQICYQSLQESVQVSLALFPAFIHQSDVTDEMLSFF TIFRGLRVQMGVPFTEQIIQTFLNMFTREQLAESILHEGSTGG VVEKFLKILQVVVQEPGQVFKPFLPSIIALCMEQVYPIIAERE PDVKAELFELLFRTLHHNWRYFFKSTVLASVQRGJAEEQMENE	Q STALI II II II II II II II II II II II II I
SLAALQAYSHWLAQYCSEVHRQNTQQFVTLISTTMDAITPLIS  KVQDKLLLSACHLLVSLATTVRPVFLISIPAVQKVFNRITDAS  LRLVDKAQVIVCRALSNILLLPWPNLPENEQQWPVRSINHASI  SALSRDYRNLKPSAVAPQRKMPLDDTKLIIHQTLSVLEDIVEN  SGESTKSRQICYQSLQESVQVSLALFPAFIHQSDVTDEMLSFF  TLFRGLRVQMGVPFTEQIIQTFLNMFTREQLAESILHEGSTGG  VVEKFLKILQVVVQEPGQVFKPFLPSIIALCMEQVYPIIAERE  PDVKAELFELLFRTLHHNWRYFFKSTVLASVQRGIAEEQMENE	ST SA SI SI SR SS SP
KVQDKLLLSACHLLVSLATTVRPVFLISIPAVQKVPNRITDAS LRLVDKAQVIVCRALSNILLLPWPNLPENEQQWPVRSINHASI SALSRDYRNLKPSAVAPQRKMPLDDTKLIIHQTLSVLEDIVEN SGESTKSRQICYQSLQESVQVSLALFPAFIHQSDVTDEMLSFI TLFRGLRVQMGVPFTEQIIQTFLNMFTREQLAESILHEGSTGG VVEKFLKILQVVVQEPGQVFKPFLPSIIALCMEQVYPIIAERE PDVKAELFELLFRTLHHNWRYFFKSTVLASVQRGIAEEQMENE	A II II IR IR
LRLVDKAQVLVCRALSNILLLPWPNLPENEQQWPVRSINHASI SALSRDYRNLKPSAVAPQRKMPLDDTKLIIHQTLSVLEDIVEN SGESTKSRQICYQSLQESVQVSLALFPAFIHQSDVTDEMLSFI TLFRGLRVQMGVPFTEQIIQTFLNMFTREQLAESILHEGSTG VVEKFLKILQVVVQEPGQVFKPFLPSIIALCMEQVYPIIAERE PDVKAELFELLFRTLHHNWRYFFKSTVLASVQRGIAEEQMENE	II IL IR IS IP
SALSRDYRNLKPSAVAPQRKMPLDDTKLIIHQTLSVLEDIVEN SGESTKSRQICYQSLQESVQVSLALFPAFIHQSDVTDEMLSFI TLFRGLRVQMGVPFTEQIIQTFLNMFTREQLAESILHEGSTGG VVEKFLKILQVVVQEPGQVFKPFLPSIIALCMEQVYPIIAERE PDVKAELFELLFRTLHHNWRYFFKSTVLASVQRGIAEEQMENE	II R S
SGESTKSRQICYQSLQESVQVSLALFPAFIHQSDVTDEMLSFI TLFRGLRVQMGVPFTEQIIQTFLNMFTREQLAESILHEGSTGC VVEKFLKILQVVVQEPGQVFKPFLPSIIALCMEQVYPIIAERE PDVKAELFELLFRTLHHNWRYFFKSTVLASVQRGIAEEQMENE	L R S
TLFRGLRVQMGVPFTEQIIQTFLNMFTREQLAESILHEGSTGC VVEKFLKILQVVVQEPGQVFKPFLPSIIALCMEQVYPIIAERE PDVKAELFELLFRTLHHNWRYFFKSTVLASVQRGIAEEQMENE	R S
VVEKFLKILQVVVQEPGQVFKPFLPSIIALCMEQVYPIIAERE PDVKAELFELLFRTLHHNWRYFFKSTVLASVQRGIAEEQMENE	s P
PDVKAELFELLFRTLHHNWRYFFKSTVLASVQRGIAEEQMENE	P
OPEN THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPE	₽
	٠,
TIME PORTING I OU THE ROUTE I BETENTROKE THE KET	Α.
TAMLFQFVNVLLQVLVHKSHDLLQEEIGIAIYNMASVDFDGFE AFLPEFLTSCDGVDANQKSVLGRNFKMDRVRRERGRAKRRAEW	A
RKPGTCAARRGHIEASGRGLCPPCSLAAAHEMPADLVL	A
5557 1712 491 VILGAGLRDKDMWIPVVGLPRRLRLSALAGAGRFCILGSEAAT	
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	R
KHLPARNHCGLSDSSPQLWPEPDFRNPPRKASKASLDFKRYVT RRLAETLAQIYLGKPSRPPHLLLECNPGPGILTQALLEAGAKV	D
ALEGO TELEVICIONE DE LE CONTROLLE CONTROLLE AGAK	<u>v</u> ]
ALESDKTFIPHLESLGKNLDGKLRVIHCDFFKLDPRSGGVIKF AMSSRGLFKNLGIEAVPWTADIPLKVVGMFPSRGEKRALWKLA	P
DI VOCTO TVVECO TVVECO TVVI AND TO VVI AND TO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVECO TVVEC	Y
DLYSCTSIYKFGRIEVNMFIGEKEFQKLMADPGNPDLYHVLSV	I
WQLACEIKVLHMEPWSSFDIYTRKGPLENPKRRELLDQLQQKL LIQMIPRQNLFTKNLTPMNYNIFFHLLKHCFGRRSATVIDHLR	Y
LTPLDARDILMQIGKQEDEKVVNMHPQDFKTLFETIERSKDCA	S
KWLYDETLEDR	Υ
5558 1509 96 RAGCTHPQVPADLGAPAEPRRPQKTCVCLLQPQPGGQRGPTTM	
TGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDR	-
LLKLKMVQVVFRHGARSPLKPLPLEEQVEWNPQLLEVPPQTQF	s
YTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQLTKVGMQQMF	- 1
LGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLL	A
GLFQCQKEGPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQT	A
SLQPGISEDLKKVKDRMGIDSSDKVDFFILLDNVAAEQAHNLP	A
CPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFLHILE	<u> </u>
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWP	
FAVDLTMELYQHLESKEWFVQLYYHGKEQVPRGCPDGLCPLDM	۱ ۲
LNAMSVYTLSPEKYHALCSQTQVMEVGNEE	٠
5559 150 1983 PLAATAHFAKMSRVAKYRRQVSEDPDIDSLLETLSPEEMEELE	البير
ELDVVDPDGSVPVGLRQRNQTEKQSTGVYNREAMLNFCEKETK	۱ ځ
LMQREMSMDESKQVETKTDAKNGEERGRDASKKALGPRRDSDL KEPKRGGLKKSFSRDRDEAGGKSGEKPKEEKIIRGIDKGRVRA	5
VDKKEAGKDGRGEERAVATKKEEEKKGSDRNTGLSRDKDKKRE	<u> </u>
WELLA KURDDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WARDEN WA	5
MKEVAKKEDDEKVKGERRNTDTRKEGEKMKRAGGNTDMKKEDE	5
VKRGTGNTDTKKDDEKVKKNEPLHEKEAKDDSKTKTPEKQTPS	<i>i</i>
PTKPSEGPAKVEEEAAPSIFDEPLERVKNNDPEMTEVNVNNSD(	
ITNEILVRFTEALEFNTVVKLFALANTRADDHVAFAIAIMLKAI	1
KTITSLNLDSNHITGKGILAIFRALLQNNTLTELRFHNQRHIC	
GKTEMEIAKLLKENTTLLKLGYHFELAGPRMTVTNLLSRNMDK(	<u> </u>
RQKRLQEQRQAQEAKGEKKDLLEVPKAGAVAKGSPKPSPQPSP	١,
PSPKNSPKKGGAPAAPPPPPPLAPPLIMENLKNSLSPATQRK	1
GDKVLPAQEKNSRDQLLAAIRSSNLKQLKKVEVPKLLQ  5560 9 921 SSWEFSALSVSMACLEDSOLOVBOODGELVLEGES OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT OF THE COLUMN ASSAULT O	
321 SSVEFSALSVSMACLSPSQLQKFQQDGFLVLEGFLSAEECVAN	ıΠ
QQRIGEIVAEMDVPLHCRTEFSTQEEEQLRAQGSTDYFLSSGD	
IRFFFEKGVFDEKGNFLVPPEKSINKIGHALHAHDPVFKSITHS	
FKVQTLARSI.GLQMPVVVQSMYIFKQPHFGGEVSPHQDASFLYT	
EPLGRVLGVWIAVEDATLENGCLWFIPGSHTSGVSRRMVRAPVC	
SAPGTSFLGSEPARDNSLFVPTPVQRGALVLIHGEVVHKSKQNI	
SDRSRQAYTFHLMEASGTTWSPENWLQPTAELPFPQLYT  5561 2175 1775 CYFTFOFFSSPYRGLUPHOTDARY PNRCL YRPRYCHARGONDRO	í
S561 2175 1775 CYFIFQFFSSPYPGLHPHQTPAPLPNPGLYPPPVSMSPGQPPPC	

SEO	Prodict		_
ID	;	Predicted end	
NO:	beginning nucleotide	nucleotide	The state of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of t
	location	location	
1	corresponding	corresponding	1 V Taraballe, 1=1801010100 V Taraballa
,	to first	to first	Dedeucine, Memerhicaine Management
)	amino acid	amino acid	~~++U++iic, U=()(III)amina D_A
ı	residue of	residue of	DESCRIPE, TETRIFORING V-V-1:
	amino acid	amino acid	Welryptophan, Yervrosine Vething
		sequence	
<u> </u>	sequence		("Possible nucleotide incertion)
Į.			VOLAPTYFSAPGVMNFGNPSVPVAPGAL DDDDDDDD VICTOR
ì	1	1	QVYGGVTYYNPAQQQVQPKPSPPRRTPQPVT_KPPPPEVVSRGS
5562			S STREET OF TEACHER VISINGS
3302	342	1385	SSGKNDMAAAGAAGLVRGLKAGVLSQADYLNLVQCETLEDLKLH
- 1	}		LQSTDYGNFLANEASPLTVSVIDDRLKEKMVVEFRHMRNHAYEP
1	j	1	LASFLDFITYSYMIDNVILLITGTLHQRSIAELVPKCHPLGSFE
- 1	į.	l	QMEAVNIAQTPAELYNAILVDTPLAAFFQDCISEQDLDEMNIEI
		1	IRNTLYKAYLESFYKFCTLLGGTTADAMCPILEFEADRRAFIIT
l l		1	INSFGTELSKEDRAKLFPHCGRLYPEGLAQLARADDYEQVKNVA
1	1	İ	DYYPEYKLLFEGAGSNPGDKTLEDRFFEHEVKLNKLAFLNQFHF
			GVFYAFVKLKEQECRNIVWIAECIAQRHRAKIDNYIPIF
5563	342	1385	SSGKNDMAAAGAAGLVRGLKAGVLSQADYLNLVQCETLEDLKLH
)	1		LOSTDYCHRIAMEACHI MYCHITEDER LANGUETLEDLKLH
}	į į	ı	LQSTDYGNFLANEASPLTVSVIDDRLKEKMVVEFRHMRNHAYEP
- 1	1		LASFLDFITYSYMIDNVILLITGTLHQRSIABLVPKCHPLGSFE
i	1		QMEAVNIAQTPAELYNAILVDTPLAAFFQDCISEQDLDEMNIEI
[	1 1		IRNTLYKAYLESFYKFCTLLGGTTADAMCPILEFEADRRAFIIT
	]		INSFGTELSKEDRAKLFPHCGRLYPEGLAQLARADDYEQVKNVA DYYPEYKLLFEGAGSNDCDVIII
			DYYPEYKLLFEGAGSNPGDKTLEDRFFEHEVKLNKLAFLNQFHF GVFYAFVKLKEQECRNIVWIAECIAQRHRAKIDNYIPIF
5564	3	914	RVRRDKRAVWTABCRRDCGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
ł			RVRRDKRAVWTARGRRRCGDSMSGGWMAQVGAWRTGALGLALLL
[	1 1		LLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCRTSGLC
1	] [		VPLTWRCDRDLDCSDGSDEEECRIEPCTQKGQCPPPPGLPCPCT
	1 i		GVSDCSGGTDKKLRNCSRLACLAGELRCTLSDDCIPLTWRCDGH
	1 1		PDCPDSSDELGCGTNEILPEGDATTMGPPVTLESVTSLRNATTM
			GPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAAVLSASLV TATLLLLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP
5565	993	138	RWNSPNPARAGSISRPQRAPGSVSAVAMTAAVFFGCAFIAFGPA
ı	1		LALYVFTIATEDIDITELAGARDAN
1	1		LALYVFTIATEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIID NKDGPTOKYLLIFGAFYSVYJOFMED
İ	1 1		NKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSIN PGETAPSMRLLAYVSGLGFGIMSGVFSFVNTLSDSLGPGTVGIH
	)		GDSPQFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKWGILLIVL
1	1		LTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRS
5566	<u> </u>		LKLCLLCODKNFLLYNORSR
3366	2043	1232	SHIQHHGRGAQAPVKMVSWMISRAVVLVFGMLYPAYYSYKAVKT
1 1		1	KNVKEYVRWMMYWIVFALYTVIETVADQTVAWFPLYYELKIAFV
}			IWLLSPYTKGASLIYRKFLHPLLSSKEREIDDYIVQAKERGYET
		1	THE CASSUMMAN AND TABLE BOTO TO THE TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL
1 1	1	ĵ	DEPVGQRPYQPLPEAKKKSKPAPSESAGYGIPLKDGDEKTDEEA
1 1			EGPYSDNEMLTHKGPRRSQSMKSVKTTKGRKEVRYGSLKYKVKK
5567			RPQVYF
336/	1554	233	EFLGSGVSPDLANEDGLTALHQCCIDDFREMVQQLLEACANINA
1 1	ļ		CDSECWTPLHAAATCGHLHLVELLIASGANLLAVNTDGNMPYDL
1	}	ł	CDDEQTLDCLETAMADRGITQDS I EAARAVPELRMLDDIRSRLQ
1 1	]		AGADLHAPLDHGATLLHVAAANGFSEAAALLLEHRASLSAKDQD
1 1	i	j ·	GWEPLHAAAYWGQVPLVELLVAHGADLNAKSLMDETPLDVCGDE
1 1	}	j	EVRAKLLELKHKHDALLRAQSRQRSLLRRRTSSAGSRGKVVRRV
]	ĺ		SLTQRTDLYRKQHAQEAIVWQQPPPTSPEPPEDNDDRQTGAELR
1	i		PPPPEEDNPEVVRPHNGRVGGSPVRHLYSKRLDRSVSYQLSPLD
1 1	į.		STTPHTLVHDKAHHTLADLKRQRAAAKLQRPPPEGPESPETAEP
		1	GLPGDTVTPOPDCGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFPAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLTAGGDDDLLVGFTAGGDDLTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLLVGFTAGGDDDLTAGGDDDLTAGGDDDLLVGFTAGGDDDLT
5568	1731	587	GLPGDTVTPQPDCGFRAGGDPPLLKLTAPAVEAPVERRPCCLLM AEDRQPASRRGAGTTAAMAASGPGCRSWCLCPEVPSATFFTALL
, !	1	1 8	SLLVSGPRLFLLOOPLAPSCITT KOULD TO THE PARTY TALL
] {		l i	SLLVSGPRLFLLQQPLAPSGLTLKSEALRNWQVYRLVTYIFVYE VPISLLCGAIIIW FACNED WIGHT THE TOTAL
		ا ا	NPISLLCGAIIIWRFAGNFERTVGTVRHCFFTVIFAIFSAIIFL
] [	1	, -	CONSIGNOUS VEDARCINITOVA DAMI CIMBRID CONSIGNOUS I
( )			MVPSVLVPWLLLGASWLIPQTSFLSNVCGLSIGLAYGLTYCYS
l l	ĺ		
		1 -	PTLPPYQPASGLCYVQNHFGPNPTSSSVYPASAGTSLGIQPPTP NSPGTVYSGALGTPGAAGSKESSRVPMP
5569			
	2	835 O	TPCPLAWERGSRSEDISVPGQKPPTCSSFSGMDVGPSSLPHLG

Predicted

beginning

location

nucleotide

Predicted end

corresponding

nucleotide

location

SEQ

ID

NO:

Amino acid segment containing signal peptide

(A=Alanine, C=Cysteine, D=Aspartic Acid, E=

Glutamic Acid, F=Phenylalanine, G=Glycine,

EIILVDDASTEEHLKEKLEQYVKQLQVVRVVRQEERKGLITARL LGASVAQAEVLTFLDAHCECFHGWLEPLLARIAEDKTVVVSPDI VTIDLNTFEFAKPVQRGRVHSRGNFDWSLTFGWETLPPHEKORR KDETYPIKSPTFAGGLFSISKSYFEHIGTYDNQMEIWGGENVEM

SEQ	Predicted	( D	
ID	beginning	Predicted end	
NO:	nucleotide	location	I thentallitie, C=CVSEeine D-Achareta x-:
	location	corresponding	Columnia Acid, Fephenylalanine C-Classica
	corresponding	to first	n=nistidine, I=Isolencine V-Tucine
	to first	amino acid	==Leucine, M=Methionine N-Asparagin-
ı	amino acid	residue of	P=Proline, O=Glutamine, D=Argining
}	residue of	amino acid	S=Serine, T=Threonine, V=V=line
	amino acid	sequence	N=Tryptophan, Y=Tvrosine Y-Unknown + at-
- }	sequence	sequence	Codon, /=possible nucleotide deletion
		<del> </del>	\-possible nucleotide insertion\
İ			SFRVWQCGGQLEIIPCSVVGHVFRTKSPHTFPKGTSVIARNQVR
	ŀ		DAE VMMDSIKKIFYKRNLOAAKMAOEKSEGDISEDI OLDDOVIII
		l	I THE SWILDING I PEME VPDLTPTFYGATKNI GTMOCI DUCENDES
- 1	ļ	)	GREATHISCHGLGGNOYFEYTTORDI. PHNITAKOI CI INTOXOS -
}	ì		LOSCH TOWNSOV PROFEMELACION, TRANSCECTCI TECTERS
5577	3	1285	LINE CHESDSHOPMPLA
	1	1275	RNSDCSCGEISVHCLPWVLFILDLKVESSMFCPLKLILLPVLLD
	1		1 SIGHWILM VSPPELTVHVGDSALMGCVFOSTFDVCTEVTDVm
}	}		JEGERARDEIVLYYSNLSVPIGREONRUMINGDII OXDOGE
	İ		1 VDVQEADQGTY1CE1RLKGESOVFKKAVVILHIT DDEDVDY AGENT
	}		GGDIQMGCVFQSTEVKHVTKVEWIFSGRDAKEETVEDVVVVV
1	1		SVEISQSWGHFQNRVNLVGDIFRNDGSTMI.OGVDESDGCNVMGG
{	į		- ALIGNIA FARTIVOHVSPEEPRTI VTPAAT POLITI COMOLITETT
1			GIVCALILLEPVLILIVKKTCGNKSSVNSTVLAVNTVVTNDDITK
	<b>(</b> :		ERPCHERKLEGEKHIYSPIIVREVIEREEDQEKGERTUMTMUNT
5578	3		WESTKSDRINGLERKSGGGMPKTOOAF
1 22.0	1	783	AVESMASPGACRAPPELPERNCGYREVEVWDORYOGAADGADVA
}			"" ODE SOF KALLEPELRPEDRILVI, GCGNGALGVEL ET GGERNA
	i		13 VDISS V V V AAMOARYAH V POI R WETMIN V P KI DED CA GEDING
			T DATE DATE AGERD PWTVSSEGVHTVCOVI. SEVERYI VDCCDD
1 1			OHISAMEMERIKATAQAYYGWSLRHATYGSGGUGUT VI MIYOOY
5579	3		T HS VAQUALGAQILSPPRPPTSPCFLODSDHFDFT.CA TOT
1 30.3	3	1540	RNSGLARGASALARHGGGLAGGVGWDCGACAGBCGCCARAGG
1 1	i		CRALIFALIATUS ROLLS GYVPCR FHHCA PROPORTITION OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF TH
1 1	ł	•	TREBRADSDUCTCKSORTMLOVCLTABSCBCOMMA * *******
1 1			TOTAL DO TO THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TO
1 1	{		ADDRESS AND ASSESS OF THE EAST AS OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPE
1 1	1		1 VIARTADEPRESEGLERGREFYMKDMVTFDQQDFAAOOMYOTTO
]	1		DATES OF INCLUSIVE VKVOADVGT IGGTVICTURE OF DATE OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE C
1	ľ		1 TOPROSESAMMETEDESOMNCPACOCRITETERICITETE CONTROL OF
]			A ISSIANA CATANACATANA CATANA CATANA CATANA CATANA CATANACATANA CATANACATANA CATANACATANA CATANACATANA CATANACATANA CATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATANACATA
1	1		CVRWPSDDAPIQACDIPPKKGSKEOAASET.TGOT.VDUTTERANDO
) )	1		DIGE VOLDER THE TIGNRE KDANKEGY DEVITE ACK DATE DATE:
5580	1681		1 EVACONIGRAMITIKUGAMDITI. LIDAOLA
1	1001	450	ADAGTRCIPGFVVPSGAGYSAPAOPGPPSSCDMDAAAADG
1 1			I WELLOCCELLEAGELGMAVPAAAMGPSALCOSCDCCMADWGGLIGG
1 1	ł		GFSRIVEGMQELFRGHSKTREFLAHQAKUMQUAWQQQQQQQ
1 1	l		SPECIAS VELLEKORLVKENNYRGHGDSUDOLGWUDGWDDZ TETT
1			ADDRITKIMUVKITKCIATVNTKGENTNICWSDDCOUTAISCHTE [
1 1	į.		I DD V V I C I DAN I DESKAR KORKER INIC I CUMMINISTER THE TRANSPORT
1			INTESTPEDATE VOSINAMPSNCICI KEDDMCKVERTCCA DALUG
1 1	1	l	LUDY DEDVC VRCFSRLDWPVRTLSFSHDGKMI, A GAGEDUET DIE
, 1		ł	EVELODALWEVQCESPTFTVAWHPKRPLLAFACDDKDCKVDCCD
5581	54		EAGTVKLFGLPNDS
	24	947	GGGSGPRAPSATLLDTGESVAAVASGEDKGIAASAAAAAVFACS
j		j	CSPUPUSSIMNPVYSPVOPGAPYGNPKNMAVTGVPTAVDAAADA
1	}	ļ	INFOUTPINOPSTAPEFOFTHSAVATITMKONURONCEGORDO
j i	1		THIS VOICENKTIOASSAAFRYTAGTOVKUDDTOCKUR DDOCK
1 1	1	1	SESENCE QUAMIPIESAYPOONLYAOGAYYTODUVA AODUUTUUT
] }		i	TIVVQPNSIPSALIPAPVAAPRTNGVAMGMVAGTUMAMGAGTUT
5582			TIPUNIALGARPVSMPTYRAOGTPAVGVVPDUW
5362	5775	2739	11TNNNNVIIPLVIAYHLSGSAOARGERSDAERI MEROVEKAR
	}	Į.	PRODUCT LAST TENTACE LEVEL L'ALTAONIT EN ECNIST ED EL STERNISSE
	1	J	ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY
	ļ		EKALEDSEKALGLDSESIRALFRKARALNELGRHKEAYECSSRC
1	1	1	SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELETFSLLSNG
	J	1	TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF
1	-	1	PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL
1	j	]	VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP
		ſ	ASFGLVMDPSKKLAASVLDALDPPGPTLDPLDLLPYSETRLDAL
			- COADD F GF I LDFLDLLPYSETRLDAL

SEO	Predicted	I Decade and and	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	1	\=possible nucleotide insertion)
<b> </b>	<del> </del>	<del> </del>	DSFGSTRGSLDKPDSFMEETNSQDHRPPSGAQKPAPSPEPCMPN
ì			TALLIKNPLAATHEFKQACQLCYPKTGPRAGDYTYREGLEHKCK
1	1		RDILLGRLRSSEDQTWKRIRPRPTKTSFVGSYYLCKDMINKQDC
	,		KYGDNCTFAYHQEEIDVWTEERKGTLNRDLLFDPLGGVKRGSLT
1	(	İ	IAKLLKEHQGIFTFLCEICFDSKPRIISKGTKDSPSVCSNLAAK
J	j		HSFYNNKCLVHIVRSTSLKYSKIRQFQEHFQFDVCRHEVRYGCL
1	Į.	ĺ	REDSCHFAHSFIELKVWLLQQYSGMTHEDIVQESKKYWQQMEAH
1	1	)	AGKASSSMGAPRTHGPSTFDLQMKFVCGQCWRNGQVVEPDKDLK
Ì			YCSAKARHCWTKERRVLLVMSKAKRKWVSVRPLPSIRNFPQQYD
ł	1		LCIHAQNGRKCQYVGNCSFAHSPEERDMWTFMKENKILDMQQTY
i	ļ		DMWLKKHNPGKPGEGTPISSREGEKQIQMPTDYADIMMGYHCWL
1	1		CGKNSNSKKQWQQHIQSEKHKEKVFTSDSDASGWAFRFPMGEFR
1			LCDRLQKGKAC?DGDKCRCAHGQEELNEWLDRREVLKQKLAKAR
	<u></u>		KDMLLCPRDDDFGKYNFLLQEDGDLAGATPEAPAAAATATTGE
5583	3	1265	SSGCRQGRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEE
1			IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD
	1	}	QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV
			HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL
1	ł		CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC
1			SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI
ı			IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
}	J .		LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQFLVIF
			PEKHWLSLEKLPQLEALLP?RQKVRITDDMDQVELKEFCPNEQN
5584			WRQHREAYEEDEDGPQAGVQCQTA
3304	3	1265	SSGCRQGRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEE
1			IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD
	,		QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV
1		,	HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL
1	j		CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC
1	ļ		SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
1			LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQFLVIF
1			PEKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEQN
ł			WRQHREAYEEDEDGPQAGVQCQTA
5585	2619	915	LPAGTPESSLHEALDQCMTALDLFLTNQFSEALSYLKPRTKESM
1			YHSLTYATILEMQAMMTFDPQDILLAGNMMKEAQMLCQRHRRKS
1 .			SVTDSFSSLVNRPTLGQFTEEEIHAEVCYAKCLLQRAALTFLQD
			ENMVSFIKGGIKVRNSYQTYKELDSLVQSSQYCKGENHPHFEGG
			VKLGVGAFNLTLSMLPTRILRLLEFVGFSGNKDYGLLQLEEGAS
j ,		l	GHSPRSVLCVMLLLCYHTFLTFVLGTGNVNIEBAEKLLKPYLNR
[ ]			YPKGAIFLFLAGRIEVIKGNIDAAIRRFEECCEAQQHWKQFHHM
			CYWELMWCFTYKGQWKMSYFYADLLSKENCWSKATYIYMKAAYL
			SMFGKEDHKPFGDDEVELFRAVPGLKLKIAGKSLPTEKFAIRKS
Į l			RRYFSSNPISLPVPALEMMYIWNGYAVIGKOPKLTDGILEIITK
			AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEAEENFRS
1	}		ISANEKKIKYDHYLIPNALLELALLLMEQDRNEEAIKLLESAKQ
F= 5		·····	NYKNYSMESRTHFRIQAATLQAKSSLENSSRSMVSSVSL
5586	2619	915	LPAGTPESSLHEALDQCMTALDLFLTNQFSEALSYLKPRTKESM
] ]			YHSLTYATILEMQAMMTFDPQDILLAGNMMKEAQMLCQRHRRKS
1 1			SVTDSFSSLVNRPTLGQFTEEEIHAEVCYAKCLLQRAALTFLQD
, ,			ENMVSFIKGGIKVRNSYQTYKELDSLVQSSQYCKGENHPHPEGG
			VKLGVGAFNLTLSMLPTRILRLLEFVGFSGNKDYGLLQLEEGAS
<u>, l</u>			GHSFRSVLCVMLLLCYHTFLTFVLGTGNVNIEEAEKLLKPYLNR
1			YPKGAIFLFLAGRIEVIKGNIDAAIRRFEECCEAQQHWKQFHHM
1 1	1		CYWELMWCFTYKGQWKMSYFYADLLSKENCWSKATYIYMKAAYL
1			SMFGKEDHKPFGDDEVELFRAVPGLKLKIAGKSLPTEKFAIRKS
[ ]		1	RRYFSSNPISLPVPALEMMYIWNGYAVIGKQPKLTDGILEIITK
) l			AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEAEENFRS
	İ		ISANEKKIKYDHYLIPNALLELALLLMEQDRNEEAIKLLESAKQ
5587	1768		NYKNYSMESRTHFRIQAATLQAKSSLENSSRSMVSSVSL
	1/08	148	SSAVPDGAVGRPVAVAVGGPPHSCRCRPCCLMAAIGVHLGCTSA

SEQ	Predicted		
ID	beginning	Predicted end	
NO:		nucleotide	(A=Alanine, C=Cvsteine, D=Aspartic Acid B
1	nucleotide	location	Glucamic Acid, F=Phenvialanine G=Glucino
- 1	location	corresponding	n=nistidine, I=Isoleucine K-Ivcine
1	corresponding	to first	b=beucine, M=Methionine N-Asparagine
- 1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ì	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- }	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence	1 -	\=possible nucleotide insertion)
		<del> </del>	CVAVVKDCDRCURATED Insertion)
	1	1	CVAVYKDGRAGVVANDAGDRVTPAVVAYSENEEIVGLAAKQSRI
ĺ		1	RNISNTVMKVKQILGRSSSDPQAQKYIAESKCLVIEKNGKLRYE
	1		IDTGEETKFVNPEDVARLIFSKMKETAHSVLGSDANDVVITVPF
İ	1	1	DFGEKQKNALGEAARAAGFNVLRIJHEDSAAIJAVGTGODGDWG
l	1	ļ	ASMIDVERLEGISLSVMEVNSGIYRVI,STNTDDNIGGAUETD
	i		I LIAVI LASEFORSFRHDVRGNARAMMKI TNSAEVAKUSI STI CO
1	1	<b>{</b>	ANCEDDSDIEGODEDCNVSRARFELLCSPLENKCIEATDGLIDO
1	1		I NGF TADDINKVVLCGGSSRIPKLOOLIKDI FDAVELING TORDO
	( '	1	VIPIGAALEAGILIGKENLLVEDSLMIECSAPDTLUKGUDEGG
1	j		SRFTVLFPSGTPLPARRQHTLQAPGSISSVCLELYESDGKNSAK
	•	<b>[</b>	EETKFAQVVLQDLDKKENGLRDILAVLTMKRDGSLHVTCTDQET
		1	GKCEAISIEIAS
5588	3	589	TPPPPEQAMVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGK
	[	1	LVSLEKYRGSVSLVVNVASECGFTDQHYRALQQLQRDLGPHHFN
)			VLAFPCNOFGOOFDCNKETEGETTDUHYRALQQLQRDLGPHHFN
	[		VLAFPCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG
L	1	j	AHPAFKYLAQTSGKEPTWNFWKYLVAPDGKVVGAWDPTVSVEEV RPQITALVRKLILLKREDL
5589	1884	553	T.DOMMEGO.TOORDARDO
1		333	LRQAWHEGGIGQTDKERGAAALPGEEGDPTRGRSLGRASWESGS
			PREPREPESSED PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER PROJUCT STEER P
	1		1 GUNKSSGLWLGPDRCRPRSRCSCRVMENDSDAAALGVALGALL
}	]		ATLGAAGQPLGGESICSARAPAKYSITFTGKWSOTAFDYOVDIR
1	l i		REPAUWSSILIGAAHSSDYSMWRKNOYVSNGLDDDDDDDDDDDDDDDX
}			LETEAAGEALQSVHAVFSAPAVPSGTGOTSAFLEVOPPUGLVGT
1			VVKI VPSPDWEVGVDSLDLCDGDRWREOAAI,DI VDVDACTDGCT
1 :			TESSPHEATIPODTVTEITSSSPSHPANSEVVPPI.KALDDIADI
			TELRUSPRAFIPPAPVLPSRDNETVDSASVPETPI DOESIGIN
	-		SSWGLCGGHCGRLGTKSRTRYVRVQPANNGSPCPELEEEAECVP
5590			DNCV
5590	72	896	LCSSGALRLLPAMVAWRSAFLVCLAFSLATLVQRGSGDFDDFNL
1 1	1		EDAVKETSSVKQPWDHTTTTTTNRPGTTRAPAKPPGSGLDLADA
1	' I		LDDQDDGRRKPGIGGRERWNHVTTTTKRPVTTRAPANTLGNDFD
{ }	1		LADALDDRNDRDDGRRKPIAGGGGFSDKDLEDIVGGGEYKPDKG
] ]	i	1	KGDGRYGSNDDPGSGMVAEPGTIAGVASALAMALIGAVSSYISY
1	ſ		OOKKECESTOOGINADWIKGDII TAGVASALAMALIGAVSSYISY
}	j	ļ	QQKKFCFS1QQGLNADYVKGENLEAVVCEEPQVKYSTLHTQSAE PPPPPEPARI
5591	68	1494	
i i	{	2.77	AGSSRKAAAERILUSAGCRSLAGRASGVLLLPAELLPGEEEAMA
] [	ľ		LRVTRNSKINAENKAKINMAGAKRVPTAPAATSKPGLRPRTALG
[	1	ł	DIGNKVSEQLQAKMPMKKEAKPSATGKVIDKKLPKPLEKVPMLV
1 1	J		PVPVSEPVPEPEPEPEPEPVKEEKLSPEPII.VDTASPSPMPTCG (
1	(	1	CAPAEEDLCQAFSDVILAVNDVDAEDGADPNICGRYVKDTVAVT
1 1	1	ļ	RQLEEEQAVRPKYLLGREVTGNMRAILIDWI.VOVOMKERI.LORT
	l l	Į	MINI VSI IDKEMQNNCVPKKMLOLVGVTAMETASKVEEMVDDBT
1	!	1	GDFAFVTDNTYTKHQIRQMEMKILRALNFGLGRPLDLUFT.DDAG
1	i	ļ	KIGEVDVEQHTLAKYLMELTMLDYDMVHFPPSOTAAGAECIAI V
f		}	ILDNGEWTPTLQHYLSYTEESLLPVMOHLAKNAAMUNGGLTVUM
EECO			TVKNKYATSKHAKISTLPQLNSALVQDLAKAVAKV
5592	242	924	YGESKDWNQKDLLSALVLTTVNCLPTPIMAKSAEVKLAIFGRAG
1	j	J	VGKSALVVRFLIKRFIWEYDPTLESTYRHQATIDDEVVSMEILD
1		1	TAGQEDTIQREGHMRWGEGFVLVYDITDRGSFEEVLPLKNILDE
- (	· · · · · · · · · · · · · · · · · · ·	1	IKKPKNVTLILIGMKADI DUGBOYOTTI DEGSFEEVLPLKNILDE
• 1	į.	1	IKKPKNVTLILVGNKADLDHSRQVSTEEGEKLATELACAFYECS
			ACTGEGNITEIFYELCREVRRRRMVQGKTRRRSSTTHVKQAINK MLTKISS
5593	3		METRISS
[	-		HASGGRAANMAAERGAGQQQSQEMMEVDRRVESEESGDEEGKKH
j	1		SSGIVADLSEQSLKDGEERGEEDPEEEHELPVDMETINLDBDAR
1			DADPWHIKIGKTEGEEAFKKAKAFFCFBOMPTKCTENTEET OCLD
1	İ	1.	BUULIUNQIKKIENLEALTELEILDISFNIIRNTEGUDYI TOT V
ſ			ALFLVNNKISKIENLSNLHOLOMLELGSNRIRATENTDTLTNI R
- 1		į ·	SUFLIGENEET REQUEDALT NET VISMOS NRITER TO A TOWN R
I	J	1 3	ELILSHNGIEVIEGLENNNKI.TMI.DTACNDTKKIENITGUI TOTA
		1	EFWMNDNLLESWSDLDELKGARSLETVYLERNPLQKDPQYRRKV
	<del></del>		

Seg	650	Dwodf == = 3	Dredista and	I have a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second an
No. location corresponding to first maino acid residue of sizet maino acid residue of amino acid residue of amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequen	1	T .		Amino acid segment containing signal peptide
Cortisponding				(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
LeLeucine, MeMethionine, Na-Asparagine, Perroline, O-Glutamine, Rehginine, Sescrine, T-Threonine, V-Vallame, amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence seque	10:			Grutamic Acid, F=Pnenylalanine, G=Glycine,
to first amino acid residue of amino acid amino acid residue of amino acid sequence  8-Serine, T-Thronine, V-Valine, w-Tryptophan, Y-Tyrosine, K-Unknown, *-stop codon, *-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide insertion)  8-BASGGRANNAABEGGGOGOSGEMMEUDRRVESEEGGBEGKER BASGGRANNAABEGGGOGOSGEMMEUDRRVESEEGGBEGKER BASGGRANNAABEGGGOGOSGEMMEUDRRVESEEGGBEGKER BASGGRANNAABEGGGOGOSGEMMEUDRRVESEEGGBEGKER BASGGRANNAABEGGGOGOSGEMMEUDRRVESEEGGBEGKER BASGGRANNAABEGGGOGOSGEMMEUDRRVESEEGGBEGKER BASGGRANNAABEGGGOGOSGEMMEUDRRVESEEGGBEGKER BASGGRANNAABEGGGOGOSGEMMEUDRRVESEEGGBEGKER BASGGRANNAABEGGGOGOSGEMMEUDRRVESEEGGBEGKER BASGGRANNAABEGGGOGOSGEMMEUDRRVESEEGGBEGKER BASGGRANNAABEGGGOGOSGEMMEUDRRVESEEGGBEGKER BASGGRANNAABEGGGOGOSGEMMEUDRRVESEEGGBEGKER BASGGRANNAABEGGGGAGGGGOGOSGEMEUDRRVESEEGGBEGKER BASGGRANNAABEGGGGGAGGGGGAGGGGAGGGGGAGGGGAGGGGA	1 -			
amino acid residue of amino acid sequence	1		1	
residue of amino acid sequence    Typepophan, X=Typeophae, X=Duknown, *=Stop code, *possible nucleotide delation,    **possible nucleotide insertion)**  **MILEPSWROIDENFUFF**  **SIGUADLSSOLIDGERGEEDPESBREDPUMENTINDRAB DVDLHNYRIGKIEGFEURLENGERGEERER**  **SIGUADLSSOLIDGERGEEDPESBREDPUMENTINDRAB DVDLHNYRIGKIEGFEURLENGERGER**  **ELOLYMOINKIERERLENGELEILDISTENLERITEEURLENGERLENGELEILDISTENLERITEEURLENGERERLENGERER**  **ELOLYMOINKIERERLERITEEUILDISTENLERITEEURLENGERER**  **ELOLYMOINKIERERLERITEEUILDISTENLERITEEURLENGERER**  **ELOLYMOINKIERERLERITEEUILDISTENLERITEEURLENGERER**  **ELOLYMOINKIERERLERITEEUILDISTENLERITEEURLENGER**  **ELOLYMOINKIERERLERITEEUILDISTENLERITEEURLENGER***  **ELOLYMOINKIERERLERITEEURLERITEEURLENGER***  **ELOLYMOINKIERERLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURLERITEEURleiteeurleiteeurleiteurleiteeurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurleiteurl	1	1		
sequence  Sequence  Sequence  Sequence  RLALPSVRGIDATFORP  RLALPSVRGIDATFORP  RLALPSVRGIDATFORP  RLALPSVRGIDATFORP  RLALPSVRGIDATFORP  RLALPSVRGIDATFORP  RLALPSVRGIDATFORP  RLALPSVRGIDATFORP  RLALPSVRGIDATFORP  RLALPSVRGIDATFORP  REAGRANAMARABERGAGGGGGGEMMEVDRRVESSESSGDEGERRM SSCIVADLSSGSLKOGERGEDPESHELPVDMETINLDRGIDATE BUDVINNIKIENLSALITELEIIDISTNILARIEGVDKLTRIK  RLALVANNISISLENUSIALIQUMELGSNIRIRI ENDELIGSLE BLOLTDNIJIKKIENLSALITELEIIDISTNILARIEGVDKLTRILE BLOLTDNIJIKKIENLSALITELEIIDISTNILARIEGVDKLTRILE BLOLTDNIJIKKIENLSALITELEIIDISTNILARIEGVDKLTRILE BLOLTDNIJIKKIENLSALITELEIIDISTNILARIEGVDKLTRILE BLOLTDNIJIKKIENLSALITELEIIDISTNILARIEGVDKLTRILE BLOLTDNIJIKKIENLSALITELEIIDISTNILARIEGVDKLTRILE BLOLTDNIJIKKIENLSALITELEIIDISTNILARIEGVDKLTRILE BLORTDNIJIKKIENLSALITELEINLANDILARIEKSISTOLIERITISTILITELEI BLORTDNIJIKKIENLSALITELEINLANDILARIELISTNILITELEI BLORTDNIJIKKIENLSALITELEINLANDILARIELISTNILITELEI BLORTDNIJIKKIENLSANDILARIENLISTNILITELEIIDISTNILARIELEI BLORTDNIJIKKIENLSANDILARIENLISTNILITELEINLANDILARIELEINLINGHTUSTILITELEINLANDILARIENLISTNILITELEINLANDILARIENLISTNILITELEINLANDILARIENLISTNILITELEINLANDILARIENLISTNILITELEINLANDILARIENLISTNILITELEINLANDILARIENLISTNILITELEINLANDILARIENLISTNILITELEINLANDILARIENLISTNILITELEINLANDILARIENLISTNILITELEINLANDILARIENLISTNILITELEINLANDILARIENLANDILARIENLISTNILITELEINLANDILARIENLISTNILITELEINLANDILARIENLISTNILITELEINLANDILARIENLISTNILITELEINLANDILARIENLISTNILITELEINLANDILARIENLISTNILITELEINLANDILARIENLISTNILITELEINLANDILARIENLISTNILITELEINLANDILARIENLISTNILITELEINLANDILARIENLISTNILITELEINLANDILARIENLISTNILITELEINLANDILARIENLISTNILITELEINLANDILARIENLANDILARIENLISTNILITELEINLANDILARIENLISTNILITELEINLANDILARIENLISTNILITELEINLANDILARIENLISTNILITELEINLANDILARIENLISTNILITELEINLANDILARIENLISTNILITELEINLANDILARIENLISTNILITELEINLANDILARIENLISTNILITELEINLANDILARIENLISTNILITELEINLANDILARIENLISTNILITELEINLANDILARIENLISTNILITELEINLANDILARIENLISTNILITELEINLANDILARIENLISTNILITELEINLANDILARIENLISTNILITELEINLANDILARIENLISTNILITELEINLANDILARIENLISTNILITELEINLANDILARIENLISTNILITELEINLANDILARIEN		i	i .	S=Scrine, T=Threonine, V=Valine,
sequence    Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Namipsy   Nami		1	l e	w=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
S594   3   1113   INSGGRANNANDERGGGGGGGEMEVURRVESEESGDEGGRR   SSGIVADISEGSLNGEERGERDEDEESEIDPUMETINLDROS   SSGIVADISEGSLNGEERGERDEDEESEIDPUMETINLDROS   SSGIVADISEGSLNGEERGERDEDEESEIDPUMETINLDROS   SSGIVADISEGSLNGEERGERDEDEESEIDPUMETINLDROS   SSGIVADISEGSLNGEERGERDEDEESEIDPUMETINLDROS   SSGIVADISEGSLNGEERGERDEDEESEIDPUMETINLDROS   SSGIVADISEGSLNGEERGERDEDEESEIDPUMETINLDROS   SSGIVADISEGSLNGEERGERDEDEESEIDPUMETINLDROS   SSGIVADISEGSLNGEERGERDEDEESEIDPUMETINLDROS   SSGIVADISEGSLNGEERGERDEESEIDPUMETINLDROS   SSGIVADISEGSLNGEERGERDEESEIDPUMETINLBRIS   SSGIVADISEGSLNGEERGERDEESEIDSEIDPUMETINLBRIS   SSGIVADISEGSLNGEERGERDEESEIDSEIDPUMETINLBRIS   SSGIVADISEGSLNGEERGERDEESEIDFUMETINLBRIS   SSGIVADISEGSLNGEERGERDEESEIDFUMETINLBRIS   SSGIVADISEGSLNGEERGERDEESEIDFUMETINLBRIS   SSGIVADISEGSLNGEERGERDEESEIDFUMETINLBRIS   SSGIVADISEGSLNGEERGERDEESEIDFUMETINLBRIS   SSGIVADISEGSLNGEERGERDEESEIDFUMETINLBRIS   SSGIVADISEGSLNGEERGEERGET   SAGIVARGESTEINGERGETINLBRIS   SSGIVADISEGSLNGEERGEERGET   SAGIVARGESTEINGERGETINLBRIS   SSGIVADISEGSLNGEERGERGEERGET   SAGIVARGESTEINGERGEERGET   SAGIVARGESTEINGERGET   SSGIVARGESTEINGERGEERGET   SAGIVARGESTEINGERGERGERGERGERGERGERGERGERGERGERGERGERG			sequence	Codon, /=possible nucleotide deletion,
1113 IRSGGRANMANERGAGOGOSSERMEVDREVESESGDEEGERS SGIVADLS.SOSLANDEEGERSEDEEEHELPVENTINLDROAD DVDLANTRIGKTEGFEVLKKVKTGL.ROLLIKGTENLERLOGE BUDUNDIKKERLERLERLEGE LIDI STRULERIS EGUDKLYTELK KLELVANNISKIENLSALTELE IDI STRULERIS EGUDKLYTELK KLELVANNISKIENLSALTELE IDI STRULERIS EGUDKLYTELK KLELVANNISKIENLSALTELE IDI STRULERIS EGUDKLYTELK KLELVASHNISKIENLSALTELE IDI STRULERIS EGUDKLYTELK KLELVASHNISKIENLSALTELE IDI STRULERIS EGUDKLYNLE ELYLSINGIEVI EGLENNIKLTMID LASNIS IRAI EN IDITLIKU ELYLSINGIEVI EGLENNIKLTMID LASNIS IRAI EN IDITLIKU ELYLSINGIEVI EGLENNIKLTMID LASNIS IRAI EN IDITLIKU ELYLSINGIEVI EGLENNIKLTMID LASNIS IRAI EN IDITLIKU ELYLSINGIEVI EGLENNIKLTMID LASNIS IRAI EN IDITLIKU ELYLSINGIEVI EGLENNIKLTMID LASNIS IRAI EN IDITLIKU ELYLSINGIEVI EGLENNIKLTMID LASNIS IRAI EN IDITLIKU ELYLSINGIEVI EGLENNIKLTMID LASNIS IRAI EN IDITLIKU HALDEVUGI DELEKORATELEV VILOVENTU EVA HALDEVUGI DELEKORATELEV VILOVENTU EVA HALDEVUGI DELEKORATELEV NINGSCTADALLISTALI EN HALDEVUGI EVA EVA HALDEVUGI ELEKTINGI EVA EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN INTERESTE EN		sequence		
SSOIVADLSEGSIKDGERGEDPEESHELPYDMETINLDRAA DVDLNHYRIGKEGFEVLKKYKTLCLSQNIL KEINELGSLIK ELDLYDNOIKKIENGEGFEVLKKYKTLCLSQNIL KEINELDELGSLE ELDLYDNOIKKIENGEALTELEIDISFNILENIEGYDKLYTIK KELVANNIS (SIENJSMINGLOMELGSNILTKIEG)GHUNTIK ELVLSHNOIEVIEGJENNNLTHLDIGASNILTKIEGJGHUNTIK ELVLSHNOIEVIEGJENNNLTHDLOISSNILTKIEGJGHUNTIK ELVLSHNOIEVIEGJENNNLTHDLOISSNILTKIEGJGHUNTIK ELVLSHNOIEVIEGJENNNLTHDLOISSNILTKIEGJGHUNTIK ELVLSHNOIEVIEGJENNNLTHDLOISSNILTKIEGJGHUNTIK ELVLSHNOIEVIEGJENNNLTHDLOISSNILTKIEGJGHUNTIK ELVLSHNOIEVIEGJENSTYLTHENPLOKDOYPRKY MALDSVRIDJAFPIPEPPSWASOPTPITGTHRADLOVIEGSE PIALANSPLILTPEPPLSWASOPTPITGTHRADLOVIEGSE PIALANSPLILTPEPPLSWASORTPITGTHRADLOVIEGSE PIALANSPLILTPEPPLSWASORTPALGHRADLOVIEGSE PIALANSPLILTPEPPLSWASORTPALGHRADLOVIEGSE ARNOGRADIO TUKKVKHRILVENMSSOTADALGISRATILC NDGLYKRIEBLERTAELYKOPTHIKHLILARFOJOHRAPGO VPSVIGVBEPOPAASBAFVKFADAHRSIEKFGIRLLKHTIKRMIT DLNTYLINKAI PPTRILTIKKYLDVKFEYLSYCKEMDDERYSC LAUGBELTRUSTONYEVILLKKORGRARRYSORRIKULLEMBLI LUKKVODIVTOLOKUSTYNSKYVYNOCYAVLEMDDERYSC LAUGBELTRUSTONYEVILLKKORGRARRYSORRIKULLEMBLI LUKKVODIVTOLOKUSTYNSKYVYNOCYAVLEMDDERYSC LAUGBELTRUSTONYEVILLENGEEEEEETAAGGESROTRGAAGPLIKK GSKCDS SSKCDS  219 GRAVLAPSELPRASTRIFTSCSOT GRAVLAPSELPRASTRIFTSCSOT ARICHMENT STANDANSPRINGLOTTYPRAKKYTGSKRODDOMS FORLBHIFSGAVIEGOPTKONGGIHTTPRATVYTGSKKODDOMS FORLBHIFSGAVIEGOPTKONGGIHTTPRATVYTGSKKODDOMS FORLBHIFSGAVIEGOPTKONGGIHTTPRATVYTGSKKODDOMS FORLBHIFSGAVIEGOPTKONGGIHTTPRATVYTGSKKODDOMS FORLBHIFSGAVIEGOPTKONGGIHTTPRATVYTGSKKODDOMS FORLBHIFSGAVIEGOPTKONGGIHTTPRATVYTGSKKODDOMS FORLBHIFSGAVIEGOPTKONGGIHTTPRATVYTGSKKODDOMS FORLBHIFSGAVIEGOPTKONGGIHTTPRATVYTGSKKODDOMS GEHALAFFITANOSKILTALO GIGPTAASFITCROST THE PROTVATAGARAN FENTUTRABANNOSKILGTALO GIGPTAASFITCROST THOROUGH THE PROTVATAGARAN FENTUTRABANNOSKILGTALO GIGPTAASFITCROST GRAVGAPPHYKONGGHENENGAPSNILD GMESTAVELEURUNTUNGANA FENTUTRABANNOSKILGTALO GIGPTAASFITCROSTONOSKALORDOSOR LETLEKSGVYKILTPEGGIFTSBOTGONGHENGOSOROFFSG HILOMEMOGISSPTOSVILLENDOTHONOVYTYCROCOSRIL SARHPYKKONGKILVYSTYTNORKOLLEDOTHONOVYTYCROCOSRIL FENTOR GRAVORYTHENOVALUS FENTO	E 5 0 4			
DVDLINNYRIGKIEDGEPUKKVETILCAGNILI KCIENLERGISCISER BLOLTONGIKKENBLABATELEIDGISFINLERGYOKLITRIK KLETAVINKISKIENLSAITELEIDGISFINLERGYOKLITRIK KLETAVINKISKIENLSAITELEIDGISFINLEGIGALIVINLE SLEHGRNITTULGMOSNILTULASMORSHEGIGALIVINLE ELYLSHIGIEDGIAPFARP ELYLSHIGIEDGIAPFARP  SEPHINDILLESSBULDELKGARSLETYYLERGIGALIVINLE ELYLSHIGIEDGIAPFARP  ARMIGRWÜVDYAPAFÖPGGGTINSGERORQLPRAWRPVGRTIGSE PHALANSPULVLEPIPLESMANSQETTIGTHFADLUTVQFDINTE ALGITYVAGADETTOVINGRSIKGKTKUVAKKALGEVKGEVTITY NKAQADPKQGNSLDIVLKKYKRIKLVENMSSIGHAGGLEKALLC NDGIVKRLEELERTAELYKGYTHEHTKALLRAPYELGYTHRAPGD VFSVIUVERPPAASBAPKYERALBYGLKYKGMENDEEPYSC IALGEPLYKVSTONTEVERLILEKGRORARRFSKULKTIKHVEN DANTYLINKAIPDTRITIKKYLDVKEFELSYCKYKEMDBEFYSC IALGEPLKYKSTONTEVERLILEKGRORARRFSKULKTIKHVEN DANTYLINKAIPDTRITIKKYLDVKEFELSYCKYKEMDBEFYSC IALGEPLKYRSTONTEVERLILEKGRORARRFSKULVELMESL LDCKHVODIVFOLGELUSTHSKYYMGCYAVURDADVFPIEUDLA HTILAYGINGBEPTDGREEEEEEDTAAGESPAKULVELEMBL LDCKHVODIVFOLGELUSTHSKYYMGCYAVURDADVFPIEUDLA HTILAYGINGBEPTDGREEEEEEDTAAGESPAKULVELEMBL LDCKHVODIVFOLGELUSTHSKYYMGCYAVURDADVFPIEUDLA HTILAYGINGBEPTDGREEEEEEDTAAGESPAKULVELEMBL LDCKHVODIVFOLGELUSTHSKRYTSCHVYTYGSKKODUMS FORCHEPSGAVYEGGFKOMMFBLGTTFPRAGAPLIKK KGSGEPTHIQGTRIMVVTPIFTSCSGT  5595  3 731 ISCNWAADGGSISPASWRSTYTHVETPRAGUISGHLAVISLSS VPVIVGVTILIFKEELHTISFIGGLALMEGUNNILKNVIGER PCOGPHTAVOTKYGOPSHINGPROTYSTHENDILIPNUL REPTTARARANGRIKGTILQ GIGHAASFIFTGOVUTELPRITAMVEYSFITLYHMPOTYNAIN RFLDLIMHVLSIGLLAVAFLVSYSRVYLLHHTNSQULYGGIAG GIGHAASFIFTGOVUTELPRIAMVEYSFITLYHMPOTYNAIN FEYTTTRABARNINGRIKGTILQ GIGHAASFIFTGOVUTELPRITAMVEYSFITLYHMPOTYNAIN FEYTTTRABARNINGRIKGTILQ OMEETAVESTIFCHVASLIYIFLSFPPFSVSGVPYSPANSKGCAL VPILASGOPPHPAPSDCCSGGTNILKMLSFKLILLAVALGFFRG GRIPGFLQTTADEFCFYYARKDGGLCFPPPRKQVKGFRSNILD OMEETAVESTIFCKVASLIYIFLERDRUTHLICHVYSTYVSK NPHQVDLATARVTLEVAELHRRHIGGGLLFORGOFCHYSI TRODMEMBUGISPTGSVLALERDRUTHLINGSGIKGGDERGL SARILQIIKKNINGFCGGVSGARRRCLINGRANSHSCAL VPILASGOVPHDAPSCCSGGTNILKMINFFCTIKKLPYSTYNSKECH GRIPGFLORGVSGLARRCLINGRYTHINGKYNTYROSKOCH FERNORGVSGRARRCLINGRANGFORMSGILLGG DAKFGENENGSGARRRCLINGRUFTHINGKYNTYR	3334	3	1113	HASGGRAANMAAERGAGQQQSQEMMEVDRRVESEESGDEEGKKH
BEDLYDNOIKKIENLBALTELEIDISTKLLENISTKLEUDKITKLEK KLELVANNIS (SIENDISMINGLOMBLELSSIN IRE IDIOTLYINLE SLELGRINITKLONLDALTHLITVLSMOSHLEKTERIS, GULDNINE ELVLSHNOIS IVI SOLENNINLHILDLIASNRIKKIENISHLEELO EFMINDINLBSWOLDELKGARSLETVYLERNPLOKDPOYRKV MALPSWOLDAFFVRP  ARMORRWOVPANFOFGGTINASGERORDLFRAMFROGRIGSE PIALANSPEYLIPEPPLYBSWANGOPTELGTHAPADLOYDIEDK GAPTOPOKYTUGKAGANLIGISIGGGAOYCPCLYIVQVPINTA AALDGTVAAGGEITOVANGS IKKKIKVAVAKMIGEVKGEVYIST ARMORRWOVPANFOFGGTINASGERORDLFRAMFROGRIGSE PIALANSPEYLIPEPPLBSKAKKIKVAVAKMIGEVKGEVYIST ARMORRWOVPANFOFGGTINASGERORDLFRAMFROGRIGSE FORDIVARLEELERTAELYKGEVHETHKRULLARYSCOTRADGIGSRALLC NDGIVKREELERTAELYKGEVHETHKRULLARYSCOTRADGIGSRALLC NDGIVKREELERTAELYKGEVHETHKRULLARYSCOTRADGIGSRALLC NDGIVKREELERTAELYKGEVHETHKRULLARYSCOTRADGIGSRALLC NDGIVKREELERTAELYKGEVHETHKRULLARYSCOTRADGIGSRALLC NDGIVKREELERTAELYKGEVHETHKRULLARYSCOTRADGIGSRALLC LDCKHVODIVVOLOQULVSTINSKYYNDCYAVLAUKHDEPEYSE LAIGBELKRYSTONYEVELLECGORARARFSONRKOLVERMIL LDCKHVODIVVOLOQULVSTINSKYYNDCYAVLAUKHDEPEEVJKISFIFF NGCKYNDGLOGEFTDGREEEEEEDTAAGEFSONRKOLVERMIL LDCKHVODIVVOLOQULVSTINSKYYNDCYAVLAUHPETEUVKISFIFF NGCKYDGLOGRIGHOVTHFPRISCOGT  SCOCOS  SCOCOS  498 219 GAVLADSSLPRAELAAGGESGLBELSNISRFTSETEVYKISFIFF NGCKYDGLOGRIGHOVTHFPRISCOGT KGERTAVGTKYGMPSSLSORMWFTSVYSTLAUKHURVIGUSG GERLEHFSGAVYEGOFKONNFRIGGHTTYPROCHYTTSCAG RELEHFSGAVYEGOFKONNFRIGHTTYPROCHYTTSCAG REPLIANSHULLAVILLES PCGEPTAVGTKYGMPSSLSORMWFTSVYSTLELVLRIMICONNA RPLOLLARHVILLAVILLES PCGEPTAVGTKYGMPSSLSORMWFTSVYSTLELVLRIMICONNA RPLOLLARHVILLAVILLES PCGEPTAVGTKYGMPSSLSORMWFTSVYSTLELVLRIMICONNA RPLOLLARHVILLAVILLES PCGEPTAVGTKYGMPSSLSORMWFTSVYSTLEVLRIMICONNA RPLOLLARHVILLAVILLES PCGEPTAVGTKYGMPSSLSORMWFTSVYSTLEVLRIMICONNA RPLOLLARHVILLAVILLES PCGEPTAVGTKYGMPSSLSORMWFTSVYSTLEVLRIMICONNA RPLOLLARHVILLAVILLES PCGEPTAVGTKYGMPSSLSORMWFTSVYSTLAUKHUROCHICANY RPLOLLARHVILLAVILLES PCGEPTAVGTKYGMPSSLSORMWFTSVYSTLAUKHUROCHICANY NEWCONDERNOSHANIA PRICHLARGOVILLAVILLES PCGEPTAVGTKYGMPSSLSORMWFTSVYSTLAUKHUROCHICANY NEWCONDERNOSHANIA PRICHLARGOVILLAVILLES PCGEPTAVGTKYGMPSVILLAVILLAVILLAVILLES PS		ì		SSGIVADLSEQSLKDGEERGEEDPEEEHELPVDMETINLDRDAE
RLFLYNNISKIENLSNIHOLOMELTISKEIGOMLINILE   SLFLGRNINTITULSMOSNIELTKIEGOMLINILE   SLFLGRNINTITULSMOSNIELTKIEGOMLINILE   ELYLSHNGIEVIGOLENNIKLITULSMOSNIELTKIEGOMLINILE   ELYLSHNGIEVIGOLENNIKLITULSNIKKIENISHIELO   EFMINDILLESKUEDLDELKGARSLETYVLERHIGKOPQYRKW   MALDESWOLDAFFORP   MALDESWOLDAFFORP   SANGRWOVD-WAPPGFGGGTNASGERORGLEPAWRPVGRTLGSE   PIALANSPPLYLFYPILESWANGOFTGTTMFADLDYDIEEDK   LGJPTVPGKVTLOKOANLIGISIGGGAQYCTLYOVFONTO   AALDGTVAAGDEITGVNGRSIKKIKVEVAKKNIGEVKGEVTITY   AALDGTVAAGDEITGVNGRSIKKIKVEVAKKNIGEVKGEVTITY   AALDGTVAAGDEITGVNGRSIKKIKVEVAKKNIGEVKGEVTITY   AALDGTVAAGDEITGVNGRSIKKIKVEVAKKNIGEVKGEVTITY   AALDGTVAAGDEITGVNGRSIKKIKVEVAKKNIGEVKGEVTITY   AALDGTVAAGDEITGVNGRSIKKIKVEVAKKNIGEVKGEVTITY   AALDGTVAAGDEITGVNGRSIKKIKVEVAKKNIGEVKGEVTITY   AALDGTVAAGDEITGVNGRSIKKIKVEVAKKNIGEVKGEVTITY   AALDGTVAAGDEITGVNGRSIKKIKVEVAKKNIGEVKGEVTITY   AALDGTVAAGDEITGVNGRSIKKIKVEVAKKNIGEVKGEVTITY   AALDGTVAAGDEITGVNGRSIKKIKVEVAKKNIGEVKGEVTITY   AALDGTVAAGDEITGVNGRSIKKIKVEVAKKNIGEVKGEVTITY   AALDGTVAAGDEITGVNGRSIKVEVAKKNIGEVKGEVTITY   AALDGTVAAGDEITGVNGRSIKSTANTENTENTENTENTENTENTENTENTENTENTENTENTEN	ļ			
SLEIGENKITHLONLOALTHILISMOSNRITKIEGIONLIVILE ELVISHNOIS EVISCLENNIKLTIMILDASKIENISHIELO EFWINDNILESWISLDELKGARSLEITVYLERNPLOKOPOYRRKY MALPEYRGIDATFVIP  ARNOGRWQVPAWGGGCSTARSGERORGLERAWRYCHTIGSE PHALMSPEYLISPILESPENAVSOPPTHICTMENDLOVIDLEDK LGIPTYPGKVYLOKDAONLIGISIGGAQYCPCLIYUVQFDNTA AALDGUVAAGDEITGYNOGSIKKKKTUVENIGEVKGEVYIHY NKLQADPKOGNSLDIVLKKVGHRUVENNSSCTADALGISRAILC NDGLVKRILEGLERTABLKVGTHEHTNILGYKENGVIHY NKLQADPKOGNSLDIVLKKVGHRUVENNSSCTADALGISRAILC NDGLVKRILEGLERTABLKVGTUDVENSICKLKKURUMDEEPSC LAIGBELRTABLKVGTUDVENSICHLEKMENDEEPSC LAIGBELRTAGEVKGTDENTSKYNNCVALDAUPFILEDVILEMSI. LDOKHVODIVOROLUVENNSKYNNCVALDAUPFILEDVILEMSI. LDOKHVODIVOROLUVENNSKYNNCVALDAUPFILEDVILEMSI. LDOKHVODIVOROLUVENNSKYNNCVALDAUPFILEDVILEMSI. LDOKHVODIVORTOSOKSTANKYNNCVALDAUPFILEDVILEMSI. LDOKHVODIVORTOSOKSTANKYNNCVALDAUPFILEDVILEMSI. LDOKHVODIVORTOSOKSTANKYNNCVALDAUPFILEDVILEMSI. LDOKHVODIVORTOSOKSTANKYNNCVALDAUPFILEDVILEMSI. LDOKHVODIVORTOSOKSTANKYNNCVALDAUPFILEDVILEMSI. LDOKHVODIVORTOSOKSTANKYNNCVALDAUPFILEDVILEMSI. LDOKHVODIVORTOSOKSTANKYNNCVALDAUPFILEDVILEMSI. GSCCDS SOKCDS SOKCDS SOKCDS SOKCDS ADALBAGGGSSIDABRISVILIHVEYPAGDLGGHLIAVIGUS GGENETYSOKSTANKYNDIGHTHITUVISTARKOPUNKOM FGELEBFSGAVYSOOPKINMSHGLGYTFPRGAKYTGNFNENV KGEGEYTHLIGOTENDIGHTHITUSGGANTAUTIGENDAUPFINV KGEGEYTHLIGOTENDIGTHTISTIGGLAURAUTIGSUPPINV KGEGEYTHLIGOTENDIGTHTISTIGGLAURAUTIGSUPPINV KGEGEYTHLIAURAUTISTIGLAURAUTISTIGGLAURAUTIGSUPPINV ROKANADGGSSIDABRISVILIHVEYPAGDLGGHLIAVIGEDA POGGPHTAVOTLITERGETITISTIGGLAURAUTISTIGUNGANA REPLDLUMBRUNGSGARRRCLANGNPENVLIKHTNOOLINGGIAG GLAALAWFIFTOSUTTIFFFENDALAURAUTISTICUNGANA REPLDLUMBRUNGSGARRRCLANGNPENVLIKHTNOOLINGGIAG GLAALAWFIFTOSUTTIFFFENDALAURAUTISTICUNGANA REPLDLUMBRUNGSGARRRCLANGNPENVLIKHTNOOLINGGANA BURGANADGGANATAUTISTICUNGANATAUTISTICUNGANA GENOOLINGANA REPLDLUMBRUNGSGARRRCLANGNPUNGANANATAUTISTICUNGANA ARHOUDLATARVELEVABLAURGULEPPINATERGORGANATAUTISTICUNGANATAUTISTICUNGANATAUTISTICUNGANATAUTISTICUNGANATAUTISTICUNGANATAUTISTICUNGANATAUTISTICUNGANATAUTISTICUNGANATAUTISTICUNGANATAUTISTICUNGANATAUTISTICUNGANATAUTISTICUNGANATAUT	j	}		
ELYLSHNOIEVISCLENNNKLTMLDIASNRIKKIENISHLTELG EFFNNNNKLENSSLDELKSARSLETVYLERNPLØKDOVRRKV MLALPSVRQIDATFVPP  5595  3 1476  ARNINGRWOVPAWEGGGCTMASGERORLDFAWRPVGRTLGSE PIALAWSPPLYLPPIPLSWAVSOPTPTLGTMFADLDVDIEDK KANNGRWOVPAWEGGGCTMASGERORLDFAWRPVGRTLGSE PIALAWSPPLYLPPIPLSWAVSOPTPTLGTMFADLDVIEWG ARLDGTVARGDETIGUNGSIKOKTKVEVAKMIQEVKGEVTIHV NKLQADPKGGNSLDVILKVKHRLUENNSTALALGISRAILC NDGIVKRLEBLERTARLYKGYTEHTKILLRFYELSOPHRAFGI VFSVIGVARPDPAASGERVKADAHRSIERILLKKITKMUL DLATYLNKAIDDTRLTIKKYLDVAFSYLSVLLXVKEMDEEYSC IALGEPLVAVSTGMYSTLLILRGRGEARARSGORKDULEKMIL DLATYLNKAIDDTRLTIKKYLDVAFSYLSVLLXVKEMDEEYSC IALGEPLVAVSTGMYSTLLILRGRGEARARSGORKDULEKMIL DLATYLNKAIDTRLTIKKYLDVAFSYLSVLLXVKEMDEEYSC IALGEPLVAVSTGMYSTLLILRGRGEARARSGORKDULEKMIL DLATYLNKAIDTRLTIKKYLDVAFSYLSVLAVKEMDEEYSC IALGEPLVAVSTGMYSTLAVKEMDEEYSC IALGEPLVAVSTGMYSTLAVKEMDEEYSC IALGEPLVAVSTGMYSTLAVKEMDEEYSC IALGEPLVAVSTGMYSTLAVKEMDEEYSC GSKCDS  5596  698  219  GAVLAPSSLPAAELAAGGESQLEDLSNTSTPTSGVYKISFIFD NORKYDGDCTRTSSGIVTRROGGIGHTTPNGAKTTGRFENRV NORGEVTALGGTRMDVVTFHFTSGGIT OKSKODS FORLBERGGAVTSGGFKDMMTHGLGTYFFROGAKTTGRFENRV NORGEVTALGGTRMDVVTFHTSGGGT VFVINGFWITLIFKELSTISFIGGLANGEVAWILIKAVIOPER PCGGPHTAVCTKYGMPSSHSQFMMFSSVYSILLVAHGTMONAA RFLDLLMAMFULSGLLAVAFLVSYSRVLLYHTWSQVLVGGIAG GMAIAMFIFTQSVLTFIFFBRIAAMFVSEFFLLIRDTSLIENVLW FORLDALAMFIFTQSVLTFIFFBRIAAMFVSEFFLLIRDTSLIENVLW FORLDALAMFIFTQSVLTFIFFBRIAAMFVSEFFLLIRDTSLIENVLW FORLDALAMFIFTGSGITTFILSFGGLANGENSSKGCAL VPULGSGVPPHPADSPCCSGOTMLMMSFKLLLLAVALGFFEG DAKFGERNEGSGARRRCLMONPPKRLKRDRRMMSQLELLSGG EMLCGGFFPRLSCCCLRSDSPGLGREENITSVNNTTEGGKLLEE IKCALCSHSGSLFHSPERSPLSRPLVLFILLGDBGNTLTGGBGRGFFFT GHIFFDLYTTADEFCFYYARKDGGLCFPPSGVYGGASRNLD OMESVAVEGISKKKHNCCTCGEVVSGLKODGRGCLL SLAFIHNYKNGKLVVSTTINGERMAIGHLAUFSTSCANGERG TILDDMEMBGLSDFTGSVLRDVDTDMCNYPYSIPRSPHMPMS TNOPPEVFARIGHLEDGGGARRTRCLMONPPKRLKRRDGRAMSGLELLGGG EMLCGGFPPRLGCCRRSDSPGLGRENKITSVNNTTEGGKLLEE IKCALCSHSGLERBERGGARRRCLMONPPKRLKRRDGRAMSQLELLGGG EMLCGGFPREGGGARRRCLMONPPKRLKRRDGRAMSQLELLGGG EMLCGGFFPTGGGARRFTTGGGARGFTFTGGARMT OMESVAFGERNEGGGARRRCLMONPPKRLKRRDGRAMSGLELLGGG EMLCG	i	ĺ		
EFMNONLESWSDLDELKGARSLETVYLENNLOGOGYRKV MALPESVRGIDATFVUP  5595  3 1476  ARNORGWUVDAWGGGCGTMASGERORGLERAMREVCRETIGSE PALAMSPLYLPPIPLESWANSOPTPICTMENDLOVDIEDK LGIPTYPGKVYLLOKDAQMILGISIGGAQYCPCLYIVQYENTIP AALDGTVANAGETIGVUNGSIKKKTVEVUKTURGWENVITIP AALDGTVANAGETIGVUNGSIKKKTVEVUKTURGVENVITIP NKLQADPKQGMSLDJVLKVVHHLVENMSGTADALGLSRAILC MDGLVKRUEBLERTABLYKOVTEHTKNILLARFIELSPHRAFGI VFSVIGVREPOPAASEAFVKGADAHSIEKRGIRLAKTIRMIT DLNTTINKAIPDTRITIKKYLDVYRFISYCLKVKAMDEKYSC IALGEPLRYSGTONYEVLLILGRORGARRYSGMKDVLERMSL LDOKHVQDIVVOLGRUSTMSKYYNDCYAVURDADVFIEVDLA HTTLAYGLNOEEFTGGREEBEEDTAAGEPSRTTRGAAGPLDKG GSMCDS  5596  698  219  GAVLAPSSLPÄAELAAQGESQSLEDLSNTSRFTSEVYKISFIFP NGKYNGGCSTTSSGIYERNGIGHTTTNGIVYTGSWKDDEMMS FGELBERSGAVYSGO/KNOMHHOLGTYTFNGIVYTGSWKDDEMMS FGELBERSGAVYSGO/KNOMHHOLGTYTFNGIVYTGSWKDDEMMS FGELBERSGAVYSGO/KNOMHHOLGTYTFNGIVYTGSWKDDEMMS FGELBERSGAVYSGO/KNOMHHOLGTYTFNGIVYTGSWKDDEMMS FGELBERSGAVYSGO/KNOMHHOLGTYTFNGIVYTGSWKDDEMMS FGELBERSGAVYTGO/KNOMHHOLGTYTFNGIVYTGSWKDDEMMS FGELBERSGAVYTGO/KNOMHHOLGTYTFNGIVYTGSWKDDEMMS FGELBERSGAVYTGO/KNOMHHOLGTYTFNGIVYTGSWKDDEMMS FGEGRHIASSGYVTGO/KNOMHHOLGTYTFNOMINA RFLDLIMHHVLSIGLIAVAFLVSYSRVYLLYHWSOVLYGGIAG GLMAIAMPITOSVVTTELPFPRIAAMVSGVHILTRUTSLIPNVLW FEYTYTRABANNORKLGTKLO GRIPATASFTFCKVASILYTHISPPPSVSGVPYSPANSSKGCL VPLLGSGVPPHPPABSPCCSGOTMIKMLSFKLLLLAVALGFFEG DAKFGERMESGARRRCLAGNDPRKLARGEMSOLCHLESG EMLCGFFPRISGCCLRSDSPDLGRLENKIFSVTINTEGGKLLES LKCALCSPHSQSLPHSPERSVLERDLVIPLLCKDVCKGFFTTCR GHIGFLOTTADEFGFTVARKONGLCFPPPRKQVGGFASNYLD QMEEVDKVEGISRKKRNCCCIGEVVSGLKGFDGGGCGLL SLAFHPYKKNGKLLVSSTTINGSRWAIGPHANITLICGDSMKKNS SARILQIIKGKVYSSEPPLLEFREPSNGPLVGGFYNSGORGFASNYLD QMEEVDKVEGISRKKRNCCCIGRVCTPTGKCGSRCL YGLLGSGOPPHPAPSPFTGSVUTRLUTVIDMCNVPYSIPRSNPHYNS TNOPPEVFARGLHDDGRCANDARPTDININITLICLGDSGCGYPSG HILGGGDELGBVTLSGSSCRARGCLAGOGGFALLAULALALGFFED DAKFGERNEGSGARRRCLAGNGPFRARKGCGSRCL YGLLGSGVPPPPPAPSPFTGGVTTPTHOKGGLFTOTCR GRIPGSDELGRGVTTTGGGGGGGGGGGGGGGGGGGELL SLAFHPYKKGNGLLVSSTTINGERMGIGDGFINTILGGGM ITLDDMEMGGSGFTTTGGRANGHLENGGCFPPFTRGVGRGANTLD QMEEVDKVEGSGARRCLAGGGCFPPFPRGVGRGANTLLD QMEEVDK	ł	ł	l	SEELGROKETKLQNLDALTNLTVLSMQSNRLTKIEGLQNLVNLR
S595   3   1476   ARNINGRWUQVPAWEGGGGTNASGERORGLERAWREVGRTLGSE	1	)	]	
S595   3	1			
PIALAWSPPLYLPPIPLPWARVSQFTFTLGTWRADLYDLTEEN LGIPTYPGKYTJKCRAQNILGISIGGGQYCPELTVQVPBNTP AALDSTVAAGDEITGWURGSIKGKTKVEVAKMIQEVKGEVTIHY NKLQADPKQGMSLDIVLKKVKHRLVERMSSGTADALGISRAILC NGCLVKKLEELERTAELYKKYTTEHKKALLAFYELSGYHRAPGD VFSVIEVREPQPAASEAFVKFADAHRSIEKFGIRLIKTIKPMLT DLMTYLNKRIPTHTIITKKYLDVKRETVEKKOKTEHKKREL LDCKHVOJUVFOLGRUXYEMSYTMATVAGKLUKEWEMDEEYSC IALGSELVRUSTGNYEVRILLGKGCARARAFSOMKDVLEKMSL LDCKHVOJUVFOLGRUXYTMSKYYMGVLKROAVPHEVBULA HTTLAYGLAQEEPTDGEEEEEEDTAAGESSRDTRGAAGPLDKG GSKCDS  5595 698 219 GAVLAFSSLPAAELAAGGESOSLEDLSNTSRPTSEVVKISFIFP MGRKYDGCTTTTSSGT YERNGGIHTPSTVVKISFIFP MGRKYDGCTTTTSSGT YERNGGIHTPSTVVKISFIFF MGRKYDGCTTTTSGT YERNGGIHTPSTVYKISFIFF MGRKYDGCTTTTSGT YERNGGIHTPSTVYKISFIFF MGRKYDGCTTTTSGT YERNGGIHTPSTVYKISFIFF PCGGPTIANTAGTKYGMSPSSLOFMHFGLOTTTPNGAKYTGNFNENRV KGRGETTHIQGTRNDVVTHFPTSCGT  5597 3 731 ISCKMAADGGSSLPASWRSVTLTHVEYPAGDLSGHLLAYLSLSP PCGGPTAASFIFCKVASLYTILSPFPFSVSGVPYSPANSWSCAL PVPLVGFVTLIIFKRELHTISFIGALALEGUMHLIKNVIQGFR PCGGPTAASFIFCKVASLYTFLSPFPFSVSGVPYSPANSSWSCAL GEGAMAIAWSIFTQEVLTTPLFPFRIAAWPSUFLIKFULLWALGFFKG GMAIAWSIFTQEVLTTPLFPFRIAAWPSUFLIKFULLWALGFFKG DAKFGGRRBGSGARRRCLNGNPFKKHKRRDRRMMSQLELLGGG EMLCGGFYPRISCCLESDSPGLGRLENKIFSVTNNTEGGLLLEG GEMCGGFYPRISCCLESDSPGLGRLENKIFSVTNNTEGGLLEG EMLCGGFYPRISCCLESDSPGLGRLENKIFSVTNNTEGGLLEGG EMLCGGFYPRISCCLESDSPGLGRLENKIFSVTNNTEGGLLEGG EMLCGGFYPRISCCLESDSPGLGRLENKIFSVTNNTEGGLLEGG LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGSGR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGSGR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVGSGIKGGSGR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVGSGRAGHLGGGGGR LFILEKGGYNGNNFLTLOGSPTKGCCSSGWEGDFCTNG GRATOGPPTABSFIFCKVASLYYFINGERMGLCCFBGRGGGRGCL SARTOPAGNANSPLTLOGSPTKGCCSSGWEGDFCTNG GRATOGPPTABSFIFCKVASLYYFINGERMGLGCGSGRGGRGCL DAKFGERNEGGGRRRGCLGRAFTGFFTCR GHIPGFLOTTADBFCTYARKDGGLCFPPPRKQVGRASNYLD OMESYDKVEEISRKHKHNCFCIGEVVSGLRQDVGALHSGDGSGR LFILEKEGVVKILTPEGEIFKEPYLDIHKLVGSGIKGEPYTCR GHIPGFLOTTADBFCTYARKDGGLCFPPPRKQVGRASNYLD OMESYDKVEEISRKHKHNCFCIGEVVSGLRQDVGALHSGDGSGR LFILEKEGVVKILTPEGEIFKEPYLDIHKLVGSGIKGDGRGLL SLAPHPNYKROKLVVSYTTNOERMAIGPHHILRVVETTVSK	5595	<del></del>	1220	
LGIPTYPEKVILOKDAQNILGISIGGAQYCPCLITYQVPENTPY AALDGIVAAGDEIIGUNGSIKGKIVGVAKMIQEVKGEVTIIY NKLQADPKQGNSLDIVLKKVKHRLVERMSSGTADALGLSRAILC NDGLVKRLEELERPALYKCYTHEPHALHEPYELSGYHRAPGD VFSVIGVREPQPAASEAFVXFADAHRSIEKFGIRLKTIRPHIL DLNTYLNKAIPTRITIKKYLDVKFETLSYCKKYKEMDBEEYSC IALGBEIVRUSTRINFSYRLILGRCGREARFFSQNKKDVLEKMEL LDOKHYOJVVGLORLVSTMSKYYNDCYAVLRADAVFPIEVDLA HTILAYGINGEFTYGGEBEEEEEDTAAGESDKTGAAGPLDKG GSNCDS  5596 698 219 GAVLAPSSLPAAELAAGGESGSLEDLSNTSRPTSEVVKISFIFP NGOKYDGDCTTTSSGTYERNGIGHTTPNGIVYTGSMKDDKMNG FGRLBEFSGAVYEGGYKDMHENGIGTTPOKAYTGNFNENRV KGSGEYTHLQGTKNDVVTHFTSCSQT FORDAMAN STANDAYTHINEYPAGDLSGHLLAYLSLSP VPVIVGPVTLIIFKERENTISFLGGLALBEGVNWLIKNVIQEPR PCOGPHTAVOTKYMPSSISGOFMFFSVYSELFLYLKMHQTNNA RFLDLLMSHVLSIGLLAVAFLVSYSKYVLLHTMSQOLVGGIG GMALAWSIFTQEVLTPLEPRIAAWVSEFFILROTSLINVLW FEYTVTRABARNORGILGTKLQ GIGPIAASFIFCKVASLYIFLSPPFSVSGVFYSFANSSKSCAL VPLLGSGYPPPPAPSPCCSGOTHLKNLSFKLLLLAVALGFFRG DAKFGERNEGSGARRRCLNGNBPKRLKRDRRMSQLELLSGG EMLCGFFYPRLSCLLSSPGOLGLENKTFSVTNTTCGCKLLEE IKCALCSPHSQSLFHSPEREVLEEDLVLPLLKKYQFRANSKICLL QGEEVLKVEEISKKHHNCFCIGEVVSGLRGPVGAHASGDSGR LFILEKGSVYKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLVSVTTNOGRMADFVSIPRSPHPNS TNOPPEVFANGLIBDFGCSGTHLKNDFVSIPRSPHPNS TNOPPEVFANGLIBDFGCSGTALLAVTVNYSY RNHOVDLRTARVFLEVAELHKHGGLLEGDGSGR LFILEKGSVYKILTPEGEIFKEPYLDIHKLVQSGIKGGSGRCHL VGSTVFGDRNANSHITLQGSPVTKOMGREPLCLGTSGSCROYPSG HLIGGEDELGEVTILSSKSMTQTHRIKIVKIVDPKRPHPNS TNOPPEVFANGLIBDFGCSGTLLAVTVNYSYFPKNSHGCAL VGSTVFGDRNANSHITLQGSPVTKOMGREPLCLGTSGSCROYPSG HLIGGEDELGEVTILSSKSMTQTHRIKIFYKIVTVDFK NPHQVDLRTARVFLEVAELHKKHLGGCLLGTSGSCROYPSG HLIGGEDELGEVTILSSKSKMTQTHRIKIFYKINTCGCKSRL VGSTVFGDRNANSHITLOGSPPHPPAPSPFPRSVGCFTG GRIPSFLOTTABEFCTYARREGGLEGEVTYTOKCCSSGGBGFCCTG GRIPSFLOTTABEFCTYARREGGLEGEVTYTOKGRANSFKLLLAVALGFFEG DAKFGERNESSGARRRCLNGNPFKBLKKRDFRUNGCLELSGGCR GRIPSFLOTTABEFCTYARREGGLEGEVTYTOKCCSGGREGLE IKCAGFTYPLSCCLRSDFGLGERLKFFFFFPRKOVGGPNANDL OMESTOKVERITABFFCTYARREGGLEGGOR LFILEKEGYVKLLTPEGEIFKEPYLDIHKLVVGGIKGGDERGLL SLAPHPMYKNNKLVVSTTNORGRWASFKLLLAVALGFFEG DAKFGERNESSGARRRCLNGNPKSGLRUNGGHCHLLEGGGOR LF	3333	د	74.10	
AALDGTVAAGDEITGVNGRSINGKTYEVAKMIQEVKGEVTIHY MKQADPKQGNSLDIVLKKVKHRUVEMMSSTADLGISRAILC NDGLVKRLEELERTAELYKSMTEPHTKNILERFYELSOTHRAPGD VFSVIGVKREPDPAASERFVYFADAHRSFGGIRLKAYTKRMIT DLMTYLNKAIPDTELTIKYLDVKFEYLSVCLKVVKMDDEBYSC IAIGBELVKRUTEVATGNYSVRILLKERCRARFSGMRKDVLEKMEL LDQXHVODIVPOLORLVSTMSKYTNDCYAVLKDADVFPIEVDLA HTTLAYGLNQEEFTDGEBEBEEDTAAGESSRDTRGAAGPLDKG GSNCDS  5596 698 219 GAVLAPSSIPAAELAAQGESQSLEDLSNTSPTSEVYKISFIFP MOGKYDGDCTTTSSGTYERNGIGHTTPNGIVYTGSWKDDKMNG FGRLEHFSGAVYBGQFKDMMFHGLGTTTFPNGAKYTGNFRENRV KGRGEYTHLGQTKMDVVTHFTSSCGT  5597 3 731 ISCKWAADGGSSLPASWRSVTLTHVEYPAGDLISGHLAYLSLSP PCGGPHTANGTKYGMPSSINSQFMFFSVYSFIFFLYLMHGTNNA RFLDLLWRIVLSIGLLANAFLVSVSTWJLHTWSGVLLYGFRA PCGGPHTANGTKYGMPSSINSQFMFFSVYSFIFFLYLMHGTNNA RFLDLLWRIVLSIGLLANAFLVSVSTWJLHTWSGVLLYGGTAG GLAAIAWFIFTOEVLTPLFPRIAAWPVSEFFLIRDTSLIFNVLM FEYTVTRABARNRQRILGYKLO  5598 326 2440 GIGFIAASFIFCKVASLYTFLSPPPFSVSGVPYSPANSSWSCAL VELLGSGVPPHPBAPSPCCSGGTMLKNLSFKLLLAVALGFFFG DAKFGERREGSGARRRCLNGNPFKLUSPLLAVATLCKLO GHEYDKVEGSSPFSTYGREGGSGR EMCCGFYPRLSCCLRSDSPGLGRLENKTFSVTNTTECGKLLEG EMCCGFYPRLSCCLRSDSPGLGRLENKTFSVTNTTECGKLLEG GEMCCGFYPRLSCCLRSDSPGLGRLENKTFSVTNTTECGKLLEG GEMCCGFYPRLSCCLRSDSPGLGRLENKTFSVTNTTECGKLLEG GEMCCGFYPRLSCCLRSDSPGLGRLENKTFSVTNTTECGKLLEG GEMCCGFYPRLSCCLRSDSPGLGRLENKTFSVTNTTECGKLLEG GEMCGGFYPRLSCCLRSDSPGLGRLENKTFSVTNTTCGKLLEG SLAFFIPNKKNIGKLVYSYTTNOERMAJORGLYSVSRK NPHOVDLRTARVELEVABLHRKHGGGLEPDFPKYTGRGOSRRL YGSYVFGDRAGNFLTLQGSPVTKOMGRENGLELIGGGSGR LFILERGEVYRLITPEGGFTRGCCSSPGMEGFCTTG GTGPTAASFTFCKVASLYTFLSPFPFSVSGVPYSPANSMSCAL YGSYVFGDRAGNFLTLQGSPVTKOMGRENGLLEDGG DAKFGERNEGSGARRRCLINGNPFKLLLAVALSFFEG DAKFGERNEGSGARRRCLINGNPKHLLKFKLLLAVALSFFEG DAKFGERNEGSGARRRCLINGNPKHLKFKLLLAVALSFFEG DAKFGERNEGSGARRRCLINGNPKHLKFKNLLAVALSFFEG DAKFGERNEGSGARRRCLINGNPKHLKFKNLLAVALSFFEG DAKFGERNEGSGARRRCLINGNPKHLKFKNLLAVALSFFEG DAKFGERNEGSGARRRCLINGNPKHLKFKNLLAVALSFFEG DAKFGERNEGSGARRRCLINGNPKHLKFKNLLAVALSFFEG DAKFGERNEGSGARRRCLINGNPKHLKFKNLLAVALSFFEG DAKFGERNEGSGARRRCLINGNPKHLKFKNLLAVALSFFEG DAKFGERNEGSGARRRCLINGNPKHLKFKNLLAVALSFFEG DAKFGERNEGSGARRRCLINGNPKH	]			ICIDENDO CONTROL OF DEPORT AND A STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF TH
NKLQADPKQGMSLDIVLKKVKHLIVENMSSGTADALGLSRALLC NGGLVKRLEELERTAELYKGMTEHLIKAPYELSCITHAPGD VFSVIGWREPQBAAGEAFVKFADAHRSIEKFGIRLLKTIRPMIT DLNTYLINKAI DPITLITIKKLDUVETLYSCIKVKEMDDEKYSC LAIGEBLYRVSTGNYEYRLILRCRQEARAFPSQMRKDVLEKMEL LDQKHVQDIVFQLORLWSTMSKYYNDCYAVLKDADVFPIEVDLA HTTLAYGLNQEEFTIGBEEEEEEDTAAGEFGRDTRGAGGLDKG GSNCDS  5596 698 219 GAVLAPSSLPÄAELAAQGESQSLEDLSNTSRPTSEVYKISFTFP NGGKYDGCTTÄTSGIVERNGIGHTTPMGIVTYGSKKDKMMG FORLEBFSGAVYEGGFKDNMFHGLGTYTFPNGAKYTGNFMENVY KGEGETTHLQGTRMDVVTFHFTSCSGT 97 1 SISKMAADGGSSLDSAMSSVTLTHVSYPAGGLISGHLLAYLSLSP VFVIVGFVTLIFFRELHTISFLGGLALMEGUMULIKNVIQEPR PCSGPHTAVGTKYGMPSSHSSVTLTHVSYPAGULSGHLLAYLSLSP VFVIVGFVTLIFFRELHTISFLGGLALMEGUMULIKNVIQEPR PCSGPHTAVGTKYGMPSSHSSVTLTHVSYPAGULSGHLAYLSLSP VFVIVGFVTLIFFRELHTISFLGGLALMEGUMULIKNVIQEPR PCSGPHTAVGTKYGMPSSHSSVTLTHVSYPANSSWSCAL REDLIMRHVLISLGLLAVAFLUSYSRVVILLHTMSQVIYGGIAG GLMAIAMFIFTGEVLTTELFFRIAMFVSEFFLIRDTSLIFNVIM FEXTVIRABANNGRKLGTKLQ  S598 326 2440 GIGFIAASFIFKVASLYIFLSPPPSVSGVFYSPANSSWSCAL VPLLGSGYPPRISCCIASDSGLGGHKMISFKLLLLAVALGFFEG DAKFGERNEGSGARRRCLNGNPPKRLKRRDRRMSOLELLSGG EMLCGGFYPRISCCIASDSGLGGHKMISFKLLLLAVALGFFEG GRHGFGLOTTADEFECFYVARKOGGLCFPDPPRKQVRGPASNYLD QMEEYDKVEEISRKHKNCFCIQEVVSGLRQPVGALHSGGDSGCL SLAFHFNYKKNGKLYVSYTTNOERMAIPHTDININITLGSDSNGKNRS NPHQVDLRTARVFLEVAELHRRHLGGGLLFGPDGFLYIILGGGM ITUDDMERMOLSDFTSURLLDVINNVYPSI PSRSPHFNS TNOPPEVFAHGLHBOGGCAVURHPTDININITLGSDSNGKNRS SARILGIIKAGMVSEFPSLEFFERPSLEFFERPYSFRANGGCSRC1- YGSYVFGDRNGNFLTLQGSPVKQMCRPLCLGTSGGCRGYPSG HLIGFGEDELGBVYILSSSSKNTGHKKJKYLTDVRTYGCKLEE CRATVOPAOTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCTTG GIFFFAASFIFKVASSLYILSSSKNTGHKKJKYLTOPKSPLHEE CRATVOPAOTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCTTG GIFFFAASFIFKKHNSCFCIQEVVSCLRQPVGANAMSGALL OMEEVDKVEEISRKHKHNCFCIQEVVSCLRQPVGANANGGSRCAL VPLLGSGYPPHPPAPSPCCSGOTMRMSFLYLNITGCKLLEE IKCALCSPHSGSLFHSPFERVLERDTLYNDRYLSSKSAL VPLLGSGYPPHPPAPSPCCSGTPFRKWASGCAL VPLLGSGYPPHPPAPSPCCSGTPFRKWASGCAL VPLLGSGYPPHPAPSPCCSGTPFRKWASGCAL VPLLGSGYPPHPAPSPCGALARMSCALL GREEPTARTSTREENTERSTFTNTTNTTCCKKLLEE IKCALCSPHSGSLFHSPFERVLERDTLYNDRYPSTPRTSWCALL GREEPTARTSTRE				LGIFIVPGKVTLQKDAQNLIGISIGGGAQYCPCLYIVQVFDNTP
NDGLVRRLEELERTAELIYKGWTEHTKINLIRAPYELSQTHRAPGD VFSVIGWRFDPDAADEAPKYRDADHSIEKFGIRLALTIRPMIN DLWTYLINKAI PDTRITITIKKYLDVKFSYLSYCLKVKEMDDESYSC IALGEPLYRVSTGNYEVYRLILRCRQEARARFSGORKDVEKEMEL LDQKHVQDIVFOLORLVSTHSKYYNDCYAVURDADVFPIEVDLA HTTLAYGLINQEEFTDGEEEEEEDTAAGEFSRDTRGAAGPLDKG GSKCDS  5596 698 219 GAVLAPSSIVERNGGIGHTYDRGTVYSKKDKMKM FGRLEHFSGAVYEGGFKDINHFHGLGTYTFPNGAKYTGNFNENRV KGEGEVTHLQGTRHOVTPHFTSCST VFVIVUFVTLII FKRELHTISFIGGLALNECVNNLI KNNIQEPR PCGGPRITAVGTKYGMYSSHSQFWFFSVYSFLFIYLKHGTNNA RFLDLLWRIVUSLGLLAVAFLVSYSRVYLLHTMSQVLYGGIG GEMAIAMFIFTQGULTHIFFRIAMFVSEFFILRDTSLIPNVLW FENTVTRABARNGRKLGTKLO  5598 326 2440 GIGFIAASFIFCKVASSLYFISEPPSVSGVYSPANSSWSCAL VPLLGSGVPPHPPAPSPCCSGOTMLKMLSFKLLLAVALGFFEG DAKFGERNEGSGARRRCLNGNPPRRLKRRDRRMSOLELLSGG EMCLOGFFPRLSCCLRSDSPGLGENNIFSVTNNTECKKLEE IKCALCSPHSGSLFHSEBERVLERDLVLPLLCKDYCKEFFTYTCR GRIPGFLQTTADDEFCFYYRKDGGLPFPPRKVYRGPSNTUD QMEYDKVEEISRKHKINCFCIGEVVSGLRGVYSALHSGDGSGR LFILBREGGYVKLITPGEGIFKBPYTDINKLTLGSDIKKGBERGLL SLAFHENVKNGKLYVSYTTNOERRAIGPHDHILRVVETYVSRK NPROVDLATAPVFLEWAELHRILLGGLLFGPDGFLYI LLGDGM ITLDDMEEMDGLSDFTGSVLRLDVVDTDDCNVPYSI PRSNPHYNS TROPPEVPAHGLHDPGRCAVDRHPTDININLTILGSDSRGKRRS SARILGIIKKGDVSSEPSSLEFKFRSPLVGFCVSGCSSRYSGG HLIGGGEDELGLEVILSSSSKNTGHKYLYTVFLYGGOSRCL YGSYVFGDRNGNFLTTLQGSPVKQGKFPLCLGTSGSCRYPSG HLIGGGEDELGLEVILSSSSKNTGHKYLYTVFLYGGOSRCL YGSYVFGDRNGNFLTTLQGSPVKQGKFPLCLGTSGSCRYPSG HLIGGGEDELGLEVILSSSSKNTGHKYLYTVFLYGGOSRCL YGSYVFGDRNGNFLTTLQGSPVKQQKFPLCLGTSGSCRYPSG HLIGGGEDELGLEVILSSSSKNTGHKYLYTVFLYGGOSRCL YGSYVFGDRNGNFLTTLQGSPVKQQKFPLCLGTSGSCRYPSG HLIGGGEDELGLEVILSSSSKNTGHKYLYTVFLYGGOSRCL VPLLGSGVPPHPPAPSPCCSGGTMLKMLSFKLLLLAVALGFFEG DAKFGERBESGSARRRCLNGMPFRKLKKRDRRWMSQLELLSGG EMCLGGFYPRLSCCLRSDSPGLGRETFSFYNNTNGCKKLLSGG EMCLGGFYPRLSCCLRSDSPGLGRETFSFYNNTNGCKKLLSGG EMCLGGFYPRLSCCLRSDSPGLGRETFSFYNNTNGCKKLLSGG EMCLGGFYPRLSCCLRSDSPGLGRETFSFYNNTNGCKKLLSGG EMCLGGFYPRLSCCLRSDSPGLGRETFSFYNTNTGCKCLEBE IKCALCSPHSGSLFRHSPERRULGGCLLGPQPGGLYTICK GRIPGFFLGTTADBEFCFYNRKDGGCFFFFTFKOWGRPSNYLD OMEYDKYESTSRHKHNGFCIQEVSGLTGPHGFTISCKLLEE IKCALCSPHSGSLFRHGEFTFFTYNTNTGCKALL				
VFSVIGVREPOPAASEAFVKYADAHRSIEKFGIRLLKTIKPMLT DINTYLINKAIPDTRIITIKKYLDWELYSYLKKKVENDDEKYSE IALGEBLYRVSTGNYEYRLLLRCROBARARFSOMRKDVLEKMSL LDOKHVODIVPOLORLVSTMSKYYNDCYAVLRDADVFPIEVDLA HTTLAYGLNQEEFTDGEBEEBEDTAAGEFSRDTRGAAGPLDKG GSKCDS  SOSCDS  698 219 GAVLAPSSLPAABLAAQGESQSLEDLSNTSRPTSEVYKISFTFP NGGKYDGCTTÄTSGGIYERRGIGHTTPRGIYTYRGAKGPLDKG FGRLEBFSGAYYEGGFKDNMFHGLTYPFDKARYTONFHENRY KGEGETTHLQGTRMDVTFHFTSCSGT  1 SCKMAAAGGSSLDSARGSVITHVEYPAGGLISGHLLAYLSLSP VFVIVGFYTLI IFREILHTISFLGGLALMEGWMLI KRWIGPER PCGEPHTAVGTKYGMPSSHSOFWETYSVSPLFLYLRMHOTNNA RFLDLLMRHVLSLGLLAVAFLVSYSRVYLLHTMSQVLYGGTAG GLMALAWFIFTGEVLTTELFFRIAMPVSEFFLIRDTSLIFNVLW FEXTVIRABARNGRKLGTKLQ GIGPIAASFIFCKVASLYIFLSPPFSVSGVFYSPANSSWSCAL VPLLGSGVPPHPAPSFCCGGGTMKMLSFKLLLLAVALGFFEG DAKFGERNEGSGARRRCLNGMPPKRLKRRDRRMMSQLELLSGG EMLCGGFYPRIS.CCLRSDSPGLGHRIFTSVTNITECGKLLEE IKCALCSPHSQSLFHSDERSVLERDLVLJELLCKDYCKEFFYTCR GHIPGFLQTTADEFEFTYARKVGGLFPPPFRKOVROPRANVLD QMEEVDKVEETSRKHKUNCFCIQEVVSGLRQPVGALHSGDGSQR LFILLEKGYVKILTPEGGIFKEPYJDHIKLVGSGIKGGDERGLL SLAFIPNYKRNGKLYVSYTTNOERWAIGPHDHILRVVETTVSKK NPHQVDLRTARVFLEVABLHRRHLGGQLLFGDPGFLYTILLGBGM TITLDMBEMDGLSDFTGSVLRLDUTNOWYPYSIFSNPHFNS SARILQII IKKGDVESEFSLEFKPFSNOPLVGGOSRCL YGSYVFGDRNONFILTLQGSPVTKOMGERPLCLGTSGSCGYPSG HLIGFGEBELGEVTILSSSENSTORKLYKTVTTLGSBSNGKNRS SARILQII IKKGDVESEFSLEFKPFSNOPLVGGOSRCL YGSYVFGDRNONFILTLQSSEVTKOMCKYLVTVDRYRLMPEGGEL SARIFTIKASSERSPLLERRFSNSPLFTSPSPFPSNSPSFRNSBSCAL YGSYVFGDRNONFILTLGSSENSTORKINFSYNNTHCGCKLLEE CRATVOPAOTLTSSCSRLCRMSYCTPTCKCCCSPGWEGDFCTTG GIGPFAASFIFCKVASLYTISSFSHLEFKFTSTNNTHCGCKLLEE IKCALCSPHSGSLFHSPSERSLERRHRINGFGULLBYDLGKLYKGGRSCAL YSLLSSGYPFHPPSPSCSGGTWRKJYKTLLLAVALGFFEG DAKFGERNEGSGARRRCLNGPPFRKVYKFTYFCCKLLEE IKCALCSPHSGSLFHSPSPSPSVERRPSPSPSNSSCAL VOLLSGSVPFHPPSPSVGGTPFRKOKYGCSBRL GRIPGFIGTTADBFCFTYARKDGGLETFSPTRNTCGCKLLEE IKCALCSPHSGSLFHSPSPSPSVERRPSPSPSPSSTRANGL OMEEDBKYETSRKHKHNCFTQEVSCLERGPYGASNYLD OMEEDBKYETSRKHKHNCFTQEGLERGPFGKYTILLGDGM LITLDMBEGGTARTYNTHTGCKLLEE IKCALCSPHSGSLFHSPFFRKVASTGTPHDHILSKVETTVSRK NPHQVDLRTARVFLEVABLHRRHLGGGLLEGGPGGLL SLAFHPYKNGKLYVSYTTNDER				
DINTYINKAIPDTRITIKYLDVKEYILYSCKKVKEMDDEYSC IALGEPLYRWSTONYEYBLIKCROEARARFSOMRKDVIEWSL LDOKHVODIVPOLORLVSTMSKYYNDCYAVLRDADVFPIEVDLA HTTLAYGLNQEFTDGEEEEEEDTAAGEBSRDTRGAAGPLDKG GSNCDS  698 219 GAVLAPSSIPAAELAAQGESÖSLEDLSNTSRPTSEVYKISFIFP NGRKYDGCTTÄTSSGIYRRNGIGHTTTPNGIVYTGSWKDDKMNG FORLEHFSGAVYEGGFKDNMFHGLGTTTFPNGAKYTGNFNENRV KGEGETTHLOGTRMDVYTHFIFFNGAKYTGNFNENRV KGEGETTHLOGTRMDVYTHFIFFNGAKYTGNFNENRV KGEGETTHLOGTRMDVYTHFIFFNGAKYTGNFNENRV TOPIVOFYULI I FRELHTISFLGGLALNEGVWELIKNVIGER PCOGPHTAVGTKYGMPSSHSCPMFFSVYSFLELYLRMHQTRNA RFLDLLWRHVLSIGLLAVAFLVSSKRYVLHYHWSQULYGGTAG GLMAIAWFIFTGEVUTTHFFPRIAAMPVSEFFLLINGTSILPNVLW FEYTVTRABARNRQRKLGTKLQ GIGPIAASFIFCKVASLVIFLSPPPSVSGVPYSPANSSWSCAL VPLLGSGVPPHPPABSPCCSGGTMLKMLSFKLLLLAVALGFFEG DAKFGERNEGSGARRRCLANGRKLATKLQ GIGPIAASFIFCKVASLVIFLSPPPFSVSGVPYSPANSSWSCAL VPLLGSGVPPHPPAPSPCCSGGTMLKMLSFKLLLLAVALGFFEG IKCALCSPHSGRLHASPFEVLERDLIVLPLLCKDYCKEFFYTCR GHPCPLGTTADBFCFYYARKDGLCPPDPPRKQVRGPASNYLD QMEEYDKVESISRKHKHNCFCIQEVVSGLRQPVGALHSCUSGSQR LFILERGGYVKLIPEGEFFFYDHIKLVOGSIKGGBERGLL SLAFHPNYKKNGKLYVSYTTNOERMAIGPHDHLRAVVETTVSRK NPHQVDLRTARVFLEVAELHKHLGGGLL-BGPDGFLYITLOGDGM ITLDDMESMDGLSPFTGSVLRLDVDTDMCNVPYSIPRSNBHFNS TNQPPEVFAHGLHDPGRAVDRHPTDININITLCSDENGKNRS SARILQIIKGKDYBESPBLEFKFENGFLVGGFYYRGCQSERL YGSYVFGDRNGNFITLOQSPVTKQWGERLCLGTSGSCRGYPSG HLIGGEDELGEVYLLSSKSKMTQTTINGKLYKLUPKRPLMPEE CRATVOPAQTITISSCSRLCRNGYCTPTGKCCSPRWEGFFCTTG SARILQIIKGKDYBESPBLEFKFENGRINGKLYRDFRHPEE CRATVOPAQTITISSCSRLCRNGYCTPTGKCCSPRWEGFFCTTG DAKFGERBEGSGARRRCLKNNPPKELKRDRRMMSQLELLSGG EMLCGGFYPRISCCLRSDSDGLGREINKIFSVTNTTECGKLLEE IKCALCSPHSGSGARRRCLKNNPPKELKRDRRMMSQLELLSGG EMLCGGFYPRISCCLRSDSGCAGELEDFPFRKOKGRAPSVLD OMEEDVELSGRYPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG DAKFGERBEGSGARRRCLKNNPPKELKRDRRMMSQLELLSGG EMLCGGFYPRISCCLRSDSGCAGELEDFPFRKOKORGASNYLD OMEEDVELSGRYPHPEGFFTYARKGGCFPPPFRKOKORGANYLD OMEEDVELSGRYPHPEGFFTYARKGGCFPPPRKOKORGALLSGGGGR LILLGEGFYPTLTCCLRSDSGCAGFPPFTCTCLRCPPPFRKOKORGANYLD OMEEDVELSTRIKHKINCCIGEVVSGLRQPVGALHSGDSOR LILLGEGFYPTLTCCLRCPPFFRKOKORGALHSGNSCL LILLERGGYVKLTPPEGFFFTCLRCPPPFRKOKORGLIKGDG				
IAGGEPLYRVSTONYEYRLIKERGGARARFSOMRKDULEKMEL LDOKHVODTVPOLORIAUSTMSKYDOCYAULRADAUPPIEVUL HTTLAYGLNQEEFTDGEEEEEEDTAAGEPSRDTRGAAGPLDKG GSWCDS GSWCDS GAVLAPSSLPAAELAAQGESQSLEDLSNTSRPTSEVYKISFIFP NGDKYDGDCTRTSSGIYERNGIGHTTPNGTVTTGSHKDDKMG FGRLEHFSGAVYEGGFKDNMFGLGTTTFPNGAKYTGNFNENRV KGEGETHLQGTRMDVVTHFTSCSQT  1SCKMAADGGSSLPASWRSVTLTHVEYPAGDLSGHLLAYLSEP PCGSPHTAVGTKYGMPSSHSQFMMFFSYYSFLFLYLRHHGTNNA RFLDLLWRHULSLGLLAVAPLUSKYVLLHHWSQOLYGGIAG GIMAIAWFIFTQGVLTPLFPRIAAWPVSEFFLIRDTSLIPNVLW FESTVYTRABRANGRKLGTKLG)  5598 326 2440 GIGPIAASFIFCKVASLYIFLSPPFSVSGVPYSPANSSWSCAL VPLLGSGVPPHPPAPSPCCSGOTMLINLISKKLLLLAVALGFFEG DAKFGERNEGSGARRRCLNGNPKKLKTKLGKLLESG EMLCGGFYBRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE LIKCALCSPHSQSLFHSPREVLEVMSLGKLVGKDFFYTCR GHIPGFLQTTADEFCFYYARKDGGLCPPDPPRKOVRGPASNYLD QMEEDVALGTHAYEVARKLKHCFCLGUESGLAUFDDFLYTILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPSNPHPNS TNPPEVPAHGHDPGRCAVDRFTDININITLCGSDSKNRS SARILQIIKGKDYSESPBLLEFKDFENGPLVGGFYYRGCGSRL YGSVVFGDRNGNFILLQSPVTKQMGREPLYTILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPSNPHPNS SARILQIIKGKDYSESPBLLEFKDFENGPLVGGFYYRGCGSRL YGSVVFGDRNGNFILLQSPVTKQMGREPLCLGTSGSCRGYFSG HILGFGEDELGEVYILSSSKSMTQTHNGKLYKVDPKRPLEMPE CRATVOPAQITITSCSRLCRNGYCTPTGKCCCSPGWEGDFCRTG VPLLGSGVPPHPPAPSPCCSQTMLKMLSFCLLLAVALGFFEG DAKFGERNEGSGARRRCLLKNRSTLINGKLYKVDPKRPLEMPE CRATVOPAQITITSCSRLCRNGYCTPTGKCCCSPGWEGDFCRTG UNFLAGSFTPRLSCSRLCRNGYCTPTGKCCCSPGWEGDFCRTG GHLPGFLQTTADEFCFYYARKDGLCPPPFRKOVRGPASNYLD QMEEDVELGSGFPRLSCCRRRCLLANDFLLCKDVCKEFFFTCR GHLPGFLQTTADEFCFTYARKDGGLCFPPFPRKOVRGPASNYLD QMEEDVELGSGFPFRKGRARRCLLANDFLLCKDVCKGFFFTCR GHLPGFLQTTADEFCFTYARKDGGLCFPPFPRKOVRGPASNYLD QMEEDVELGSGFFLGTTTARKGGLCFPPFPRKOVRGPASNYLD QMEEDVELGSGFFLGTTTARKGGLCFPPFPRKOVRGPASNYLD QMEEDVELGSGFFLGTTTARKGGLCFPPFPRKOVRGPASNYLD QMEEDVELGSGFFLGTTTARKGGLCFPPFPRKOVRGPASNYLD QMEEDVELGFLGTTTAREFGLGFTTARKGGLCFPPFPRKOVRGPASNYLD QMEEDVELGFLGTTARFTLAKGGLCFPPFPRKOVRGPASNYLD QMEEDVELGFLGTTARGLCFTTYARKGGLCFPPFPRKOVRGPASNYLD QMEEDVELGFLGTTATGRCGLCFTPFFRKORGGLCLLEGGGCGLL SLAFHPNKKNCKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK NPHQVDLTRTARVFLEVALHRRHGGGL	ĺ	ĺ		
LDCKHYODTVFOLGRLVSTMSKYYMDCYAVLRODADVFP1EVOLLA HTTLAYGLNQEFFTDGEEEEEEDTAAGEPSRDTRGAAGPLDKG GSWCDS  5596 698 219 GAVLAFSSLPAAELAAQGESQSLEDLSNTSRPTSEVYKISFIFP NGKKYDGCTTÄTSSGIYERNGIGHTTPNGIVYTGSWKDKMKM FORLEHFSGAVYEGGFKDNMFHGLGTTTFNGAKYTGNFNENRV KGEGETHTLQGTRMDVVTHFHSTSCQT  5597 3 731 ISCKMAADGQSSLPASWRSVTLTHVEYPAGDLSGHLLAYLSLSP VFVIVGPYLLIFKRELHTISFLGGLLANGSWWLIKNVIQEPR PCGGPHTAVGTKYGMPSSHSQFMMFFSVYSFLELYLRMHQTNNA RFLDLLWRHVLSIGLLAVAFLVSYSRVYLLYHRWSQVLYGGTAG GLMALAWFIFTGEVLTPLFPFRLAMPVSFFFLIRDTSLIPNVLW FEXTVYRARARNRQRKLGTKLO  5598 326 2440 GIGFIAASFIFCKVASLYFLSPPFPSVSGVPYSPANSSWSCAL VPLLGSGVPPHPPASPCCSGGTMLKMLSFKLLLLAVALGFFEG DAKFGERNEGSGARRRCLNGNPPKRIKKRDRRMMSQLELLSGG EMLCGGFYPRLSCCLRSDSPGLGLELENLFSVTNTNTECCKLLEE IKCALCSPHSQSLPHSPBREVLEBDLVLPLLCKDYCKEFFYTCR GHIPGFLQTTADEFCFYYARKDGGLCFPDPPRKQVRGFASNYLD QMEEYDKVEEISRKHKINCFCIQEVVSGLRQPVGALHSGDGSQR LFILEREGYVKLITTEGEIFKEPYLDIHKLVQSGIKGGBERGLL SLAFHFNYKKNGKLVYSYTTNGERMAIGPHDHLRAVVETTVSRK NPHOVDLRTRARVFLEVABLHRKHLGGGLLEPGDFPLYILLGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS TNOPPEVPAHGHLDPGRCAVDRHFTDININLTLLCSDSNGKNRS SARILQIIKGKDYSESEPSLLEFKFFSNGFLVGGFTYRGCGSGRC YSSLYFGGRNGNFTLLQSPSVTKGMGKRLCLGTSGSCRGFFSG HILGGGEDBLGBVTILGSSSKSMTQTTINGKLYKLVDPKRPLMPEE CRATVOPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG DAKFGERNEGSGARRRCLANNFKSGLELLSGG EMLCGGFFPRLSCCLRSDSPGLGRLENKIFSVINNTECCKLLEE IKCALCSPHSPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG DAKFGERNEGSGARRRRCLANNFKSGLELLSGG EMLCGGFFPRLSCCLRSDSPDLGRLENKIFSVINNTECCKLLEE IKCALCSPHSPRLSCCLRSDSPDLGRLENKIFSVINNTECCKLLEE IKCALCSPHSPRLSCCLRSDSPDLGRLENKIFSVINNTECCKLLEE IKCALCSPHSPRLSCCLRSDSPOLGRLENKIFSVINNTECCKLLEE IKCALCSPHSPRLSCCLRSDSPOLGRLENKIFSVINNTECCKLLEE IKCALCSPHSPRLSCCLRSDSPOLGRLENKIFSVINNTECCKLLEE IKCALCSPHSPRLSCCLRSDSPOLGRLENKIFSVINNTECCKLLEE IKCALCSPHSPRLSCCLRSDSPOLGRLENKIFSVINNTECCKLLEE IKCALCSPHSPRLSCCLRSDSPOLGRLENKIFSVINNTECCKLLEE IKCALCSPHSPRLSCCLRSDSPOLGRLENKIFSVINNTECCKLLEE IKCALCSPHSPRLSCCLRSDSPOLGRLENKIFSVINNTECCKLLEE IKCALCSPHSPRLSCCLRSDSPOLGRLENKIFSVINNTECCKLLEE IKCALCSPHSPRLS	1			
######################################	i	·		
GSNCDS  GAVLAPSSLØAAELAAQGESQSLØDLSNTSRPTSEVYKISFIFP NGDKYDGDCTRTSSGIYENNGIGIHTTENGIVYTGSWKDDKING FGRLEHFSGAVYEGGYKDMFHGLGTYTFPNGAKYTGNFNENRV KGEGEYTHLQGTRMDVVTFHFTSCSCT  5597  3 731 ISCKMAADGGSSLØASWRSVTLTHVEYPAGDLSGHLLAVLSLSP PCGGPHTAVGTKYGMPSSHSQFMWFFSVYSFLFLVLRHMQTRNA RFLDLLWRIVLSLGLLAVAFLVSYSRVYLLYHTWSQVLYGGTAG GLMALAWFIFTCEVLTPLEFPAAMPUSEFFLIRDTSLIPNVLW FEYTVYRABARNRQRKLGTKLQ GIGPIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL VPLLGSGVPPHPPAPSPCCSGTMLKMLSFKLLLLAVALGFFEG DAKFGERNEGSGARRRCLNGNPPKRLKRRDRRMMSQLELLSGG EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVINNTEGGKLLEE IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR GHIPGFLQTTADEFCFYYARKGLVSTYTNOERWAIGHDHILRVVEYTVSRK NPHQVDLRTARVFLEVBELHRKHLGGOLLFGPDGFLYIILGDGM LFILEKEGVKLILTPEGEIFKEPYLDIVDTDMCMVPYSIPRSNPHFNS TNQPPEVFAHGLHDPGCRAVDRHPTDININTLILCSDSNGKNR SARILQIIKGKDYSEDFSLLEFKEPFSORPLVGGFYPGCGSERL YGSYVYGDRNGRFLTLQGSPYKKQMGERPLCLGTGSGCGCFFSG HILGGGEBELGEVYILSSKSMTOTHNGKLKKIVDPKRPLMPEE CRATVOPAGTLTSECSRLCRNSTPFKLLLAVALGFFEG DAKFGERNESGARRRCLNGCYPTGCCSPGWEGFFGTG GIPGPAASFIFCKVASLYIFLSSPEPPSVSGVYSPANSSWSCAL VPLLGSGVPPHPPAPSPCCSGGTMLKMLSFKLLLLAVALGFFEG GRIPGPELGTSTATGSCRLCRNGPFKRLKRRDRRMSQDELLSGG EMLCGGFYPRLSCCLRSDSPGLGRENNIFSVTNTEGGKLLEE IKCALCSPHSGSARRRCLNGCYTPTGKCCSPGWEGFFGTG GIPGPAASFIFCKVASLYIFLSSPPPSVSGVYSPANSSWSCAL VPLLGSGVPPHPPAPSPCCSGGTMLKMLSFKLLLLAVALGFFEG GRICGGFYPRLSCCLRSDSPGLGREENLIFSVTNNTEGGKLLEE IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR GRIPGFLGTTADEFCFYYARROGGLCFPDFFRKOVGGPSNYLD QMEEYDKVEEISRKHKHNCFCIQEVVSGLRGPVGALHSGDGSQR LFILLEKEGFVKLITTEGEIFKFFYTANGGLCFFPRKOVGGRSNYLD QMEEYDKVEEISRKHKHNCFCIQEVCSGLRGPGLLFGDGSGR LFILLEKEGFTYTARROGGLCFFPRFKOVGGRSANYLD QMEEYDKVEEISRKHKNCFCIQEVCSGLRGPGLILGEGGL SLAPHPNYKKNGKLYVSTTNQERWAIGGHLDFGFLYILICDGM ITLDDMEEMDGLSDFTGSVLKLDUDTDMCNVYSIPPSNEHFNS	(			
S596   S19	1			
NGRKYDGDCTRTSSG/TERNGIGHTTENGIVYTGSMKNDRKNNG FGRLEHFSGAVYEGOFRDNMFHGLGTYTFFPNGAKYTGNFNENRV KGEGEYTHLQGTRMDVVTFHFTSCSQT  1 SCKMAADGGSSLPASMRSVTLTHVEYPAGDLSGHLLAYLSLSP VFVIVGFVTLI FRERLHTISFLGGLALNEGUMBLI KNVIOEPR PCGSPHTAVGTKYGMPSSHSQFMMFFSVYSELFLYLRMHQTINNA RFLDLLWRHULSLGLLAVAFLVSYSRVYLLVHTWSQVLYYGGIAG GLMAIAWFIFTQEVLTPLFPRIAAWPVSEFFLIRDTSLIPNVLW FEXTVTRABARNRQRKLGTKLQ  GIGPIAASFJFCKVASIYFLSPPPFSVSGVPYSPANSWSCAL VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG DAKFGERNEGSGARRRCLNGNPPKRLKRRDRRMMSQLELLSGG EMLCGFYPRLSCCLRSDSPOLGRLENKIFSVTNNTEGKKLLEE IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFFTCR GHIPGFLQTTADSFCFYYARKDGGLCFPDPFRKQVRGFASNYLD QMESYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGL SLAFHENYKKNGKLYVSYTINQERWAIGPHDHLLRVVEYTVSRK NPHQVDLRTARVELEVAELHRKHLGGGLLFGPDGFLVIILGDGM ITLDDMEEMBGLSDFTGSVLDVDTDMCNVPYSIPRSNPHFNS TROPPEVFARGLHDDGRCAVDRHFDININLTLLCSDSNGKNRS SARILQIIKGKDYSSEPSLLEFKPFSNGPLVGGFVYRGCOSERL YGSYVFGDRNGMFLTLQGSPVTKQWGKEPLCLGTSGSCRGYFSG HLLGGGDELGEVYLISSSKSMTQTHRGKLYKLYDPKRPLMPBEE CRATVQPAOTLTSCCSRLCKRNGVCTPTGKCCSGWMSGDFCRTG GRIPGFDELGSVYTLSSSKSMTQTHRKKLYKLVDPKRPLMPBEE CRATVQPAOTLTSCCSRLCKRNGVCTPTGKCCSGWFSGDFCRTG GRIPGSDFLGSULTSCSCRAFTSG HLLGGGDELGEVYLISSSKSMTQTHRKKLYKLVDPKRPLMPBEE CRATVQPAOTLTSCCSRLCKNGVTPTGKCCSGWFSGDFCRTG GRIPGSVFFRSGCFLFRGCLRSGSFSLGLELKKIFSVTNNTEGGKLLEE IKCALCSPHSGSGARRRCLNGNPPKELKRRDRNMSGLELLSGG BMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTEGGKLLEE IKCALCSPHSGSGFFRELCHNOPPFRELVKGPASNYLD QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGAAHSGDGSQR LFILEKEGYVKUTLTPEGEIFPYDLOIKKLVQSGIKGGDRGLL GLEFFPTYCK	5596	698	219	
FGRLEHFSGAVYEGGETNNHHGLGTYTFPNGAKYTGNFNENRV KEGEYTHLGGTRMDVVTHFTSCSQT  1SCKMAADGQSSLPASWRSVTLTHVEYPAGDLSGHLLAYLSLSP VFVIVGPVTLIIFKRELHTISFLEGLALNEGUNNLIKAVIGEPR PCCGPHTAVGTKYGMPSSLYSSLFLYLKHHGYNNA RFLDLLWRHULSLGLLAVAFLVSYSRVYLLYHTMSQVLYGGIAG GLMAIAWFIFTQEVLTPLFPFRIAAWPVSEFFLIRDTSLIPNVLW FEYTVTRABARNRQRKLGTKLQ  5598 326 2440 GIGPIAASFIFCKVASLYIFLSPPPFSVSGVPYSPANSSWSCAL VPLLGSGVPPHPPAPSPSCOTMLKMLSFKLLLLAVALGFFEG DAKFGERNEGSGARRRCLNGNPPKRLKRRDRRMMSQLELLSG EMLCGGFYBRLSCCLRSDSPGLGRLENKIFSVTTNTEGGKLLEE IKCALCSPHSQSLFHFSPERVLERDLVLJPLLCKDYCKEFFTTCR GHIPGFLQTTADEFCFYYARKDGGLCFPDPPRKQVRGPASNYLD QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR LFTLEKEGYVKILTPEGEIFKEPVLDIHKLVQSGIKGGDERGLL SLAFHFNYKKNGKLYVSYTTNGERWAIGPHDHILRVVEYTVSRK NPHQVDLRTARVFLEVABLHRKHLGGGLEPDDFFVIILLGDGN TROPPEVFAHGLHDPGRCAVDRHFTDININLTILGSDSNGKNRS SARILQIIKGNYESSPSLFEFFSFSNGFUGGFVRGCOSBRL YGSYVFGDRNGNFLTLQGSPVTKQWGRKPLCLGTSGSCRGFFSG HILGGFGEDELGEVYILSSKSMTQTHNGKLYKIVDPKRPLMPEE CRATVQPAQTLTSECSRLCRNGYCTPTGKCCCSPGWBGDFCRTG GGPTAASFIFCKVASLYTFLSPPPFSVGGVYSPANSSWSCAL VPLLGSGVPPHPAPSPSCGYMLKMLSFKLLLAVALGFFEG DAKFGERNEGSGARRRCLNGNPFKRLKRRDRRMMSQLELLSG EMLCGGFYPRLSCCLRSDSPGLGRLKHIFSVTNNTECGKLLEE IKCALCSPHSGSFHFNSEFRVLERDLVLPLLCKDYCKEFFYTCR GHIPGFLQTTADEFCYYARKDGGLCFPDPFRKQVRGPASNYLD QMEEYDKVEEISRKHKHNCFCIQEVVGLKQFVGALHSGGDSGQR LEILLKGGTVRULTPBGESTFYLSCLUKLYGSGIKGGDERGL GHPGFLQTTADEFCYYARKDGGLCFPDFFRKQKRGPASNYLD QMEEYDKVEEISRKHKHNCFCIQEVVGGLKPQGAHHSGGOSGQR LEILEKEGYVKLTPBGESTFKSPFVLDIKKLVQSGIKGGDRGLL SLAFHPNYKKNGKLYVSYTTNDERWAIGPHDHILRVVSTYNSRK NPHQVDLRTARVFLLVBALHRKHLGGGLFFPDGFFTIIGDGM ITLDDMEEMDGLSDFTGSVURLLDVGTDCMCVPYSIPRSNPHFFSS	i l	-		NGDKYDGDCTR'TSSGIVERNGTGIHTTPNGTVYTGGWYDDYMMG
S597   3   TSCKMAADGQSLPASWRSVTLTHVEYPAGDLSGHLLAYLSLSP		(	İ	FGRLEHFSGAVYEGOFKDNMFHGLGTYTFPNGAKYTGNFNENDV
SSS97   S	1			
VFVIVGFVTLIIFKRELHTISFLGGLAIMEGVMWLIKNVIOEPR PCGGPHTAVGTKYGMPSSHSQFMWFFSVYSFLFLYLRMHQTINNA RFLDLLWRHVLSLGLLAVAFLVSYSRVYLLYHTWSQVLYGGIAG GLMAIAMFIFTQEVLTPLFFRIAMPVSEFFLIRDTSLIPNVLW FEYTVTRAEARNQRKLGTKLQ  5598 326 2440 GIGPIAASFIPCKVASLYIFLSPPFPSVSGVPYSPANSSWSCAL VPLLGSGVPPHPPAPSPCCSGQTMIKMLSFKLLLLAVALGFFEG DAKFGERNEGSGARRCLIMGNPPKRLKRRDRRMSQLELLSGG EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTINNTECGKLLEE IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR GHIPGFLQTTADEFCFYYARKDGGLCFPDFPRKQWGPPASNYLD QMEEYDKVEEISRKKHNCFCIQEVVSGLRQFVGALHSGDGSQR LFILEKEGYVKILTTEGEIFKEPYLDHKLVQSGIKGGDERGLL SLAFHFNYKKNGKLYVSYTTNOERWALGPHDHILRVVEYTYSRK NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIFRSNPHFNS TRQPPEVFAHGLHDPGRCAVDRHFTDININITLCSDSNGKNRS SARILQIIKGKOYESEPSLLEPKPFSNSPLVGGFVRGCQSERL YGSYVFGDRNGNFLTLQQSPVKKQWGPFVRGCQSERL YGSYVFGDRNGNFLTLQQSPVKKWWGPLGGTSGCGYFSG HILGFGEDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEE CRATVQPAQTLITSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG CRATVQPAQTLITSECSRLCRNGYCTPTGKCCSPGWEGDFCRTG GGIPIAASFIFCKVASLYIFLSPFPPSVSGVPYSPANSSWSCAL VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKILLLAVALGFFEC DAKFGERNEGSGARRRCLNGNPFKRLKRRDRRMMSQLELLSGG EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR GHIPGFLQTTADBFCFYYARKDGGLCFPDFPRKQVRGPASNYLD QMEEYDKVEEISRKHKHNCPCIQEVVSGLRQPVGALHSGDGSQR LFILEKEGYVKLUTPGGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNOERWATGPHOHILRVVETVSKK NPHQVDLRTARVFLEVAELHRKHLGGQLLFGDFGLFYIILGDGM ITLDDMEMDGLSDFTGSVLRLDVDTDMCNVPYSIFRSNPHFNS	5597	3	731	
PCGPHTAVGTKYGMPSSHSQFMFFFSVYSFLFLYLRMHQTNNA RFLDLLWRHVLSIGLLAVAFLVSYSRVYLLHTWSQVLYGGIAG GGMAIAWFIFTQEVLTPLFFRIAAWPVSEFFLIRDTSLIPNVLW FEYTVTRAEARNRQRKLGTKLQ  5598 326 2440 GIGPIAASFIFCKVASLYIFLSPPFPSVSGVPYSPANSSWSCAL VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG DAKFGERNEGSGARRRCLNGNPPKRLKRRDRRMMSQLELLSGG EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR GHLPGFLQTTADEFCFYYARKDGGLCFPDFPRKQVRGPASNYLD QMEEYDKVEEISRKHKHNCFCIGEVVSGLRGPVGALHAGGOSQR LFILEKEGYVKILTTEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK NPHQVDLRTARVFLEVALEHRKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPSNSHFNS TNQPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS SARILQIIKGKDYBSEPSLLEFKFFSNSPLVGGFYYRGCQSBRL YGSYVFGDRNGNFITLQQSPVTKQWQRKPLCLGFGSCRGYFSG HLLGFGEDELGBVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEE CRATVQPAQTITISECSRLCRNGVCTPTGKCCCSPGWEGFCRTG GGPTAASFIFCKVASLYYFLSSPPPSVSGVPSPSDASSMSCAL VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG DAKFGERNEGSGARRRCLNGPFKRLKRRDRRMMSQLELLSGG EMLCGGFYPRLSCCLNGPFKRLKRRDRRMMSQLELLSGG EMLCGGFYPRLSCCLNGPFKRLKRRDRRMMSQLELLSGG EMLCGGFYPRLSCCLNGPFKRLKRRDRRMMSQLELLSGG EMLCGGFYPRLSCCLNGPFKRLKRRDRRMMSQLELLSGG EMLCGGFYPRLSCCLNGPFKRLKRRDRRMMSQLELLSGG GHIPFFLQTTADBFCFYYARKDGGLCFPDFPRKQVRGPASNYLD QMEYDKVEEISRKHKNCFCIQEVVSGLRQDVGALHSGGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHBNYKKNGKLYVSYTTNQERWAIGPHDHILRVVETTVSRK NPHQVDLRTARVFILEVAELHRKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIFRSNPHFNS	1			
GGMAIAWFIFTQEVLTPLFPRTAAWPVSEFFLIRDTSLIPNVLW FEYTVTRAEARNRQRKLGTKLQ GTGFIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG DAKFGERNEGSGARRRCLNGNPPKRLKRDRRMSQLELLSGG EMLGGFYPRLSCCLRSDSPGLGRLENKIFSVTTNTECCKLLEE IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR GHIPGFLQTTADEFCFYYARKDGGLCFPPPFRKOVRGPASNYLD QMEEYDKVEEISRKHKHNCFCIQEVVSGLRGPVGALHSGGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHLIRVVEYTVSRK NPHOVDLRTARVFLEVAELHKKHLGGQLLEGPDGFLYILLGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS TNQPPEVFAHGLHDDGRCAUDRHPTDININLTILCSDSNGKNRS SARILGIIKGKDYSESPSLLEFKPFSNGPLVGGFVYRGCQSERL YGSYVFGDRNGNFLTLQQSPVTKQMQEKPLCLGTSGSCRGYFSG HILGFGEDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEE CRATVOPAQTLTSCSRLCRNGYCTPTGKCCCSPGWEGDFCRTG S599 326 2440 GIGPIAASFIFCKVASLYIPLSPPPFSVSGVPYSPANSSWSCAL VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEC DAKFGERNEGSGARRRCLNGNPPKRLKRRDRRMMSQLELLSGG EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR GHIPGFLQTTADEFCFYYARKDGGLCFPFPFRKQVRGPASNYLD QMEEYNKVEEISRKHKHNCFCIQEVVSGLRQVGALHSGDGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHENYKKNGKLYVSYTTNQERWAIGHDHTLRVVEYTVSRK NPHQVDLRTARVFLEVAELHKKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLBUDDTDMCNVPYSIPRSNPHFNS	1			
GGMAIAWFIFTQEVLTPLFPRTAAWPVSEFFLIRDTSLIPNVLW FEYTVTRAEARNRQRKLGTKLQ GTGFIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG DAKFGERNEGSGARRRCLNGNPPKRLKRDRRMSQLELLSGG EMLGGFYPRLSCCLRSDSPGLGRLENKIFSVTTNTECCKLLEE IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR GHIPGFLQTTADEFCFYYARKDGGLCFPPPFRKOVRGPASNYLD QMEEYDKVEEISRKHKHNCFCIQEVVSGLRGPVGALHSGGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHLIRVVEYTVSRK NPHOVDLRTARVFLEVAELHKKHLGGQLLEGPDGFLYILLGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS TNQPPEVFAHGLHDDGRCAUDRHPTDININLTILCSDSNGKNRS SARILGIIKGKDYSESPSLLEFKPFSNGPLVGGFVYRGCQSERL YGSYVFGDRNGNFLTLQQSPVTKQMQEKPLCLGTSGSCRGYFSG HILGFGEDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEE CRATVOPAQTLTSCSRLCRNGYCTPTGKCCCSPGWEGDFCRTG S599 326 2440 GIGPIAASFIFCKVASLYIPLSPPPFSVSGVPYSPANSSWSCAL VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEC DAKFGERNEGSGARRRCLNGNPPKRLKRRDRRMMSQLELLSGG EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR GHIPGFLQTTADEFCFYYARKDGGLCFPFPFRKQVRGPASNYLD QMEEYNKVEEISRKHKHNCFCIQEVVSGLRQVGALHSGDGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHENYKKNGKLYVSYTTNQERWAIGHDHTLRVVEYTVSRK NPHQVDLRTARVFLEVAELHKKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLBUDDTDMCNVPYSIPRSNPHFNS				RFLDLLWRHVLSLGLLAVAFLVSYSRVYLLYHTWSQVLYGGIAG
GIGPIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL VPILLGSGVPPHPPAPSPCCSGQTMIKMLSFKLLLLAVALGFFEG DAKFGERNEGSGARRCCLNGNPPKRLKRRDRRMMSQLELLSGG EMLCGGFYPRLSCCLRSDSPGLGRLENXIFSVTNNTECGKLLEE IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR GHIPGFLQTTADEFCFYYARKDGGLCFPDPPRKQVRGFASNYLD OMESYDKVEEISRKHKINCFCIQEVVSGLRQPVGALHSGDGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPMYKKNGKLYVSYTTNQERWAIGPHDHLIRVVEXTVSRK NPHQVDLRTARVFLEVAELHRKHLGGGLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFMS TNQPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS SARILQIIKGKDYESEPSLLEFKPFSNOPLVGGFVYRGCQSBRL YGSYVFGDRNGNFLTLQQSPVTKQWQBKPLCLGTSGSCRGYFSG HILGFGEDELGEVYILSSKSMTQTHNGKLYKIVDPKRPLMPEE CRATVQPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG S599 326 2440 GIGPIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG DAKFGERNEGSGARRRCLNGMPFKRLKRRDRRMMSQLELLSGG EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR GHIPGFLQTTADEFCFYYARKDGGLCFPDFPKQVRGPASNYLD QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGAHHSGDGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHLRVVEYTVSRK NPHQVDLRTARVFILEVAELHRRHLGGGLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS				GLMAIAWFIFTQEVLTPLFPRIAAWPVSEFFLIRDTSLIPNVLW
VPLLGSGYPPHPPAPSPCCSGQTMLKMLSFKLLLAVALGFFEG DAKFGERNEGSGARRRCLMGNPPKRLKRRDRMMSQLELLSGG EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTEGKLLEE IKCALCSPHSQSLFHSPEREVLERDLVJPLLCKDYCKEFFYTCR GHIPGFLQTTADEFCFYYARKDGGLCFPDPPRKQVRGPASNYLD QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNQERWAIGPHCHILRVVEYTVSRK NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLVIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS TNQPPEVFAHGLHDPGRCAVDRHPTDININITILCSDSNGKNRS SARILQIIKGKDYESEPSLLEFKPFSNGPLVGGFVYRGCQSERL YGSYVFGDRNGNFLTLQQSPVTKQMQEKPLCLGTSGSCRGYFFGG HILGFGEDELGHVTLQQSPVTKQMQEKPLCLGTSGSCRGYFFGG HILGFGEDELGFVTLQQSPVTKQMQEKPLCLGTSGSCRGYFFGG CRATVQPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG GGPJAASFIFCKVASLYTFLSPPPFSVSGGPYSPANSSWSCAL VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG DAKFGERNEGSGARRRCLNGNPPKRLKRRDRRMMSQLELLSGG EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR GHIPGFLQTTADEFCFYYARKDGGLCFPDFPRKQVRGPASNYLD QMEEYNKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR LFILEKEGYVKLLTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVGYTTNQERWAIGPHDHILRVVEYTVSRK NPHQVDLRTARVFLEVABLHRKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS				FEYTVTRAEARNRQRKLGTKLQ
DAKFGERNEGSGARRRCLNGNPPKRLKRRDRRMMSQLELLSGG EMLCGGFYPRLSCCLRSDSPGLGRLENXIFSVINNTECGKLLEE IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR GRIPGFLQTTADEFCFYYARKDGGLCFPDPPRKQVRGPASNYLD QMESYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNOERWAIGPHDHILRVVEYTVSRK NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS TNQPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS SARILQIIKGKDYESEPSLLEFKPFSNGPLVGGFTYRGCQSBRL YGSYVFGDRNGNFLTLQQSPVTKQWQEKPLCLGTSGSCRGYFSG HILGFGEDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEE CRATVQPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG STARTQPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG GIGPIAASFIFCKVASLYIFLSPPPSVSGVPYSPANSSWSCAL VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG DAKFGERNEGSGARRRCLNGNPPKRLKRDRRMMSQLELLSGG EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR GHIPGFLQTTADBFCFYYARKDGGLCFPDFPRKQVRGPASNYLD QMEEYDKVEEISRKHKHNCPCIQEVVSGLRQPVGALHSGDGSQR LFILEKRGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILKVVYSTVSRK NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS	5598	326	2440	GIGPIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL
EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR GHIPGFLQTTADEFCFYYARKDGGLCFPDFPRKQVRGPASNYLD QMEEYDKVEEISRKHKINCFCIQEVVSGLRQPVGALHSGDGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS TNQPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGRNRS SARILQIIKGKDYESEPSLLEFKPFSNGPLVGGFYPRGCQSBRL YGSYVFGDRNGNFLTLQQSPVTKQWQBKPLCLGTSGSCRGYFSG HILGFGEDELGEVYILSSKSMTQTHNGKLYKIVDPKRPLMPEE CRATVQPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG GIPJASFIFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL VPLLGSGYPPHPPAPSPCCSQCTMLKMLSFKLLLLAVALGFFEG DAKFGERNEGSGARRRCLNGNPPKRLKRRDRRMMSQLELLSGG EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR GHIPGFLQTTADEFCFYYARKDGGLCFPDFPRKQVRGPASNYLD QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK NPPLQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS		j		VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG
IKCALCS PHSQSLFHS PEREVLERDLVLPLLCKDYCKEFFYTCR GHIPGFLQTTADEFCFYYARKDGGLCFPDFPRRQVRGPASNYLD QMEEYDKVEELSRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR LFILEKEGYVKILTPEGEI FKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS TNQPPEVFAHGLHDPGRCAVDRHPTDININLTLLCSDSNGKNRS SARILQIIKGKDYESEPSLLEFKPFSNGPLVGGFVYRGCQSBRL YGSYVFGDRNGNFLTLQQSPVTKQWQBKPLCLGTSGSCRGYFSG HILGFGEDELGEVYILSSSKSMTQTHNGKLYKLVDPKRPLMPEE CRATVQPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG CRATVQPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG GIGPIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG DAKFGERNEGSGARRRCLNGNPPKRLKRDDRRMMSQLELLSGG EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR GHIPGFLQTTADEFCFYYARKDGGLCFPDFPRKQVRGPASNYLD QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK NPPQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS	1			
GHIPGFLQTTADEFCFYYARKDGGLCFPDFPRKQVRGPASNYLD QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS TNQPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS SARILQIIKGKDYESEPSLLEFKPFSNGPLVGGFVYRGCQSERL YGSYVFGDRNGNFLTLQQSPVTKQWQEKPLCLGTSGSCRGYFSG HILGFGEDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEE CRATVQPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG GIGPIAASFTFCKVASLYIFLSPPPPSVSGVPYSPANSWSCAL VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG DAKFGERNEGSGARRRCLNGNPPKRLKRRDRRMMSQLELLSGG EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR GHIPGFLQTTADEFCFYYARKDGGLCFPDFPRKQVRGPASNYLD QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK NPHQVDLRTARVFLEVAELHRKHLGGCLLFGPDGFTYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS	1			EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE
QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS TNQPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS SARILQIIKGKDYESEPSLLEFKPFSNGPLVGGFYYRGCQSERL YGSYVFGDRNGNFLTLQQSPVTKQWQEKPLCLGTSGSCRGYFSG HILGFGEDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEE CRATVQPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG  S599 326 2440 GIGPIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSWSCAL VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG DAKFGERNEGSGARRRCLNGNPPKRLKRDRRMSQLELLEGG EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEGG EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEGG EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEGG GHPGFLQTTADEFCFYYARKDGGLCFPDFPRKQVRGPASNYLD QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR LFILEKEGYVKLITPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS		1		IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR
LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS TNQPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS SARILQIIKGKDYESEPSLLEFKPFSNGPLVGGFVYRGCQSERL YGSYVFGDRNGNFLTLQQSPVTKQWQEKPLCLGTSGSCRGYFSG HILGFGEDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEE CRATVQPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG GIGPIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSWSCAL VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG DAKFGERNEGSGARRRCLNGNPPKRLKRRDRRMMSQLELLSGG EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR GHIPGFLQTTADEFCFYYARKDGGLCFPDFFRKQVRGPASNYLD QMEEYDKVEEISRKHKHNCFCIQEVVSGLKQDVGALHSGDGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS				GHIPGFLQTTADEFCFYYARKDGGLCFPDFPRKQVRGPASNYLD
SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS TNQPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS SARILQIIKGKDYESEPSLLEFKPFSNGPLVGGFVYRGCQSERL YGSYVFGDRNGNFLTLQQSPVTKQWQEKPLCLGTSGSCRGYFSG HILGFGEDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEE CRATVOPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG  S599 326 Q1440 G1GPIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG DAKFGERNEGSGARRRCLLNGNPPKRLKRRDRRMMSQLELLSGG EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR GHIPGFLQTTADEFCFYYARRDGGLCFPDFPRKQVRGPASNYLD QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS	[			QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR
NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS TNQPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS SARILQIIKGKDYESEPSLLEFKPFSNGPLVGGFVYRGCQSERL YGSYVFGDRNGNFLTLQQSPVTKQWQBKPLCLGTSGSCRGYFSG HILGFGEDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEE CRATVQPAQTLTSECSRLCRNGYCTPTGKCCCSPGMEGDFCRTG CRATVQPAQTLTSECSRLCRNGYCTPTGKCCCSPGMEGDFCRTG VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG DAKFGERNEGSGARRRCLNGNPPKRLKRRDRMMSQLELLSGG EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR GHIPGFLQTTADBFCFYYARLGGGLCFPDFPRKQVRGPASNYLD QMEEYDKVEEISRKHKHNCPCIQEVVSGLRQPVGALHSGDGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS	1 1			
ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS TNQPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS SARILQIIKGKDYSESPSLLEFKFFSNGPLVGGFVYRGCQSERL YGSYVFGDRNGNFLTLQQSPVTKQWQBKPLCLGTSGSCRGYFSG HILGFGEDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEE CRATVOPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG CRATVOPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG DAKFGERNEGSGARRRCLNGNPPKRLKRRDRRMMSQLELLSGG EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR GHIPGFLQTTADEFCFYYARVDGGLCFPDFPRKQVRGPASNYLD QMEEYDKVEEISRKHKHNCPCIQEVVSGLRQPVGALHSGDGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS	] ]			
TNOPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS SARILQIIKGKDYESEPSLLEFKPFSNGPLVGGFVYRGCQSERL YGSYVFGDRNGNFLTLQQSPVTKQWQBKPLCLGTSGSCRGYFSG HILGFGEDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEE CRATVQPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG CRATVQPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG GIGPIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG DAKFGERNEGSGARRRCLNGNPPKRLKRRDRMMSQLELLSGG EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR GHIPGFLQTTADEFCFYYARKDGGLCFPDFPRKQVRGPASNYLD QMEEYDKVEEISRKHKHNCPCIQEVVSGLRQPVGALHSGDGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS	{ !			NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM
SARILQIIKGKDYESEPSLLEFKPFSNGPLVGGFVYRGCQSERL YGSYVFGDRNGNFLTLQQSPVTKQMQEKPLCLGTSGSCRGYFSG HILGFGEDELGEVYLLSSSKSMTQTHNGKLYKIVDPKRPLMPEE CRATVQPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG GIGPIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG DAKFGERNEGSGARRRCLNGNPPKRLKRRDRMMSQLELLSGG EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLBE IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR GHIPGFLQTTADBFCFYYARKDGGLCFPDFPRKQVRGPASNYLD QMEEYDKVEEISRKHKHNCPCIQEVVSGLRQPVGALHSGDGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK NPHQVDLRTARVFLEVABLHRKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS	1 1			TTLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS
YGSYVFGDRNGNFLTLQQSPVTKQWQEKPLCLGTSGSCRGYFSG HILGFGEDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEE CRATVQPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG CRATVQPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG UPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG DAKFGERNEGSGARRRCLINGNPPKRLKRDRRMMSQLELLSGG EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR GHIPGFLQTTADEFCFYYARRDGGLCFPDFPRKQVRGPASNYLD QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS	}	)		
HILGFGEDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEE CRATVQPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG  S599 326 2440 GIGPIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG DAKFGERNEGSGARRRCLNGNPPKLKRRDRRMMSQLELLSGG EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR GHIPGFLQTTADEFCFYYARKDGGLCFPDFPKKQVRGPASNYLD QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS	]			
CRATVQPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG  5599  326  2440  GIGPIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL  VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG  DAKFGERNEGSGARRRCLNGNPPKRLKRRDRRMMSQLELLSGG  EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE  IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR  GHIPGFLQTTADEFCFYYARKDGGLCFPDFPRKQVRGPASNYLD  QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR  LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL  SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK  NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM  ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS	1 1			
GIGPIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG DAKFGERNEGSGARRRCLNGNPPKRLKRRDRRMMSQLELLSGG EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE IKCALCSPHSQSLFHSPERBVLERDLVLPLLCKDYCKEFFYTCR GHIPGFLQTTADEFCFYYARKDGGLCFPDFPRKQVRGPASNYLD QMEEYDKVEEISRKHKHNCFCIQEVVSGLRGPVGALHSGDGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS	1			
VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG DAKFGERNEGSGARRRCLNGNPPKRLKRRDRRMMSQLELLSGG EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR GHIPGFLQTTADEFCFYYARKDGGLCFPDFPKKQVRGPASNYLD QMEEYDKVEEISRKHKHNCPCIQEVVSGLRQPVGALHSGDGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS	5500	336		
DAKFGERNEGSGARRRCLNGNPPKRLKRRDRRMMSQLELLSGG EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR GHIPGFLQTTADEFCFYYARVLDGGLCFPDFPKKQVRGPASNYLD QMEEYDKVEEISRKHKHNCPCIQEVVSGLRQPVGALHSGDGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS	3399	240	<b>244</b> 0	
EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR GHIPGFLQTTADEFCFYYARKDGGLCFPDFPRKQVRGPASNYLD QMEEYDKVEEISRKHKHNCPCIQEVVSGLRQPVGALHSGDGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS	1 1	1		
IKCALCSPHSQSLFHSPERBVLERDLVLPLLCKDYCKEFFYTCR GHIPGFLQTTADEFCFYYARKDGGLCFPDFPRKQVRGPASNYLD QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS	Į J	]		
GHIPGFLQTTADEFCFYYARKDGGLCFPDFPRKQVRGPASNYLD QMEEYDKVEEISRKHKHNCPCIQEVVSGLRQPVGALHSGDGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS	}	Į		
QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS	1 1			
LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS	1 1			
SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS	] [	ļ		
NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS	j !	İ		
ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS	1	ł		
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1	1		
TNQPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS	<u> </u>	1	ļ	
		ľ		TNOPPEVFAHGLHDPGRCAVDRHPTDININI.TILCSDSNGKNPS

SEO	1 Day 2 3 2 2 2 3		
ID	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid F-
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine
	location	corresponding	H=Histidine, I=Isoleucine, K=Lvsine
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine.
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
İ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	-	\=possible nucleotide insertion)
			SARILQIIKGKDYESEPSLLEFKPFSNGPLVGGFVYRGCQSERL
1	1	1	YGSYVFGDRNGNFLTLQQSPVTKQWQEKPLCLGTSGSCRGYFSG
1	1	1	HILGEGEDRI GERRITI DOGRAMMOMINIANI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINCERNI SINC
1		1	HILGFGEDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEE
5600	1977	1244	CRATVQPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG
""	1	1244	SLRVLSGHLMQTRDLVQPDKPASPKFIVTLDGVPSPPGYMSDQE
		į.	EDMCFEGMKPVNQTAASNKGLRGLLHPQQLHLLSRQLEDPNGSF
		ì	SNAEMSELSVAQKPEKLLERCKYWPACKNGDECAYHHPISPCKA
-			FPNCKFAEKCLFVHPNCKYDAKCTKPDCPFTHVSRRIPVLSPKP
İ	1	1	AVAPPAPPSSSQLCRYFPACKKMECPFYHPKHCPFNTOCTPPDC
		<u> </u>	TFYHPTINVPPRHALKWIRPQTSE
5601	1977	1244	SLRVLSGHLMQTRDLVQPDKPASPKFIVTLDGVPSPPGYMSDQE
			EDMCFEGMKPVNQTAASNKGLRGLLHPQQLHLLSRQLEDPNGSF
			SNAEMSELSVAQKPEKLLERCKYWPACKNGDECAYHHPISPCKA
1	1		FPNCKFAEKCLFVHPNCKYDAKCTKPDCPFTHVSRRIPVLSPKP
			AVAPPAPPSSSQLCRYFPACKKMECPFYHPKHCRFNTQCTRPDC
		į	TFYHPTINVPPRHALKWIRPQTSE
5602	246	766	VUTCOTVIDTA VEAL TANTA VOLUME
Į.		1.00	YHTSCTVWRTAKEALENTEVPVGCLMVYNNEVVGKGRNEVNQTK
	1	1	NATRHAEMVAIDQVLDWCRQSGKSPSEVFEHTVLYVTVEPCIMC
l	ļ		AAALRIMKIPLVVYGCQNERFGGCGSVLNIASADLPNTGRPFQC
5603	1	5.55	IPGYRAEEAVEMLKTFYKQENPNAPKSKVRKKECQQILNMF
5005	1 +	565	FRGRTPISGGERGCAQYPIPATPARSGENRTMPGAGDGGKAPAR
1			WLGTGLLGLFLLPVTLSLEVSVGKATDIYAVNGTEILLPCTFSS
			CFGFEDLHFRWTYNSSDAFKILIEGTVKNEKSDPKVTLKDDDRI
			TLVGSTKEKRNNISIVLRDLEFSDTGKYTCHVKNPKENNLQHHA
			TIFLQVVDRRMQ
5604	1	1506	EDIFPAQLLKLQRHERVWQQEPPVRDHRSWGGSGAGGVAGREWT
ļ			DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGGDFG
1			GGDFGGGDFGGGGSFGGHCLDYCESPTAHCNVLNWEQVQ
1			RLDGILSETIPIHGRGNFPTLELQPSLIVKVVRRRLAEKRIGVR
			DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV
			VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI
1 1	i i		SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE
			NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG
			LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL
			FSVI ONUFVCI PODVVEVI MIL VOLDENCESKFFIDFSDIGEQQRKL
			ESYLONHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL
1			ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV
5605	35	1821	QPVFTCQQQTYSTWLPCN
-303	ادد	70₹7	SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL
			MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ
1 1			KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG
1			GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAOPKAGGSGSYWP
1 1			ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP
1 1			GSARPWPALRSLLHRNLVLRTHOPARYSLTPEGLELAOKLAESE
1			GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVOOOPLELRP
			GEYRVLLCVDIGETRGGGHRPELLRELORLHVTHTVRKLHVGDF
			VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ
į i		i	KFRLKRCGLERRVYLVEEHGSVHNLSLPESTLLQAVTNTQVIDG
[			FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE
1			SGANTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG
1 1	ł	1	VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL
] !		1	QRNLGPALSRTLSQLYCSYGPLT
5606	3	1099	CDCDCDCADCCOMICDDCCC
	-	1033	GRSRCPGPGARGGTMSPRSCLRSLRLLVFAVFSAAASNWLYLAK
] }	İ		LSSVGSISEEETCEKLKGLIQRQVQMCKRNLEVMDSVRRGAQLA
1			IEECQYQFRNRRWNCSTLDSLPVFGKVVTQGTREAAFVYAISSA
1			GVAFAVTRACSSGELEKCGCDRTVHGVSPOGFOWSGCSDNIAYG
	ĺ	1	VAFSQSFVDVRERSKGASSSRALMNLHNNEAGRKAILTHMRVEC
			KCHGVSGSCEVKTCWRAVPPFRQVGHALKEKFDGATEVEPRRVG
		ļ	SSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGR
		1	TCNKTSKAIDGCELLCCGRGFHTAQVELAERCSCKFHWCCFVKC
, ,			
		İ	RQCQRLVELHTCR

[ SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
ļ	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion,
5607	521	141	\=possible nucleotide insertion)
3007	321	141	PPVCNPAEAMPSPGTVCSLLLLGMIWLDLAMAGSSFLSPEHQRV
j	i		QQRKESKKPPAKLQPRALAGWLRPEDGGQAEGAEDELEVRFNAP
5608	2		FDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK
3000	1 **	983	WFQSPLRQADPGPPRHTLFMDFVAGAIGGVCGDAVGYPLDTVKV
1	1		RIQTEPKYTGIWHCVRDTYHRERVWGFYRGLLLPVCTVSLVSSE
1	1	•	VFGTYRHCLAHICRLRFGNPDAKPTKADITLSGCASGLVRVFLT
1	l	1	SPTEVAKVRLQTQTQAQKQQRRLSASGPLAVPPMCPVPPACPEP
1		1	KYRGPLHCLATVAREEGLCGLYKGSSALVLRDGHSFATYFLSYA
	1	ĺ	VLCEWLSPAGHSRPDVPGVLVAGGCAGVLAWAVATPMDVIKSRL
	ĺ		QADGQGQRRYRGLLHCMVTIVREEGPRVLFKGLVLNCCRAFPVN
5609	1628		MVVFVAYEAVLRLARGLLT
3609	1628	304	AKGVWVLPSPPPRPGRGALVSGSGLRRGRSGTSWRPRRMNHKSK
1		[	KRIREAKRSARPELKDSLDWTRHNYYESFSLSPAAVADNVERAD
			ALQLSVEEFVERYERPYKPVVLLNAOEGWSAOEKWTI,FRI,KPKV
			RNQKFKCGEDNDGYSVKMKMKYYIEYMESTRDDSPLYIFDSSYG
			EHPKRRKLLEDYKVPKFFTDDLFQYAGEKRRPPYRWFVMGPPRS
İ			GTGIHIDPLGTSAWNALVQGHKRWCLFPTSTPRELIKVTRDEGG
			NQQDEAITWFNVIYPRTQLPTWPPEFKPLEILQKPGETVFVPGG
			WWHVVLNLDTTIAITONFASSTNFPVVWHKTVRGRPKLSPKWVP
			ILKQEHPELAVLADSVDLQESTGIASDSSSDSSSSSSSSSSSSSS
			SECESGSEGDGTVHRRKKRRTCSMVGNGDTTSQDDCVSKERSSS
5610	54		R
3010	<b>34</b>	1196	LERTPASADMANTKYQLFLAGLMLVTGSINTLSAKWADNFMAEG
			CGGSKEHSFQHPFLQAVGMFLGEFSCLAAFYLLRCRAAGOSDSS
1 1	i j		VDPQQPFNPLLFLPPALCDMTGTSLMYVALNMTSASSFQMLRGA
	ļ		VIIFTGLFSVAFLGRRLVLSQWLGILATIAGLVVVGLADLLSKH
	ĺ		DSQHKLSEVITGDLLIIMAQIIVAIQMVLEEKFVYKHNVHPLRA
i			VGTEGLFGFVILSLLLVPMYYIPAGSFSGNPRGTLEDALDAECO
1 1			VGQQPLIAVALLGNISSIAFFNFAGISVTKELSATTRMVLDSLR
l i			TVVIWALSLALGWEAFHALQILGFLILLIGTALYNGLHRPLLGR
5611	2		LSRGRPLAEESEQERLLGGTRTPINDAS
3011	2	577	FVLPNRLGIPGSTFRGPGACASSSSLAASAKPGAGGSPALAMSG
			ELSNRFQGGKAFGLLKARQERRLABINREFLCDQKYSDEENLPE
1. 1	J		KLTAFKEKYMBFDLNNEGEIDLMSLKRMMEKLGVPKTHLEMKKM
1 1	j		ISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVMMFEGKANESSP
5612	1	~~~	KPVGPPPERDIASLP
	*	721	ASRDGYMDATIAPHRIPPEMPQYGEENHIFELMQAMWLCKHLNS
	i		SLLTLENLILNEFSYTATEARRLYLQRKTVPSALLVQLIQERLA
1			EEDCIKQGWILDGIPETREOALRIOTLGITPRHVIVI.Sapprvi.
1		İ	IERNLGKRIDPQTGEIYHTTFDWPPBSEIONRLMVPEDISELET
	1		AQKLLEYHRNIVRVIPSYPKILKVISADQPCVDVFYQALTYVQS
5613	115	1000	NHRINAPFIPRVLLLGPVGS
-013	772	1279	RGVDPALRRAEKMLPLSIKDDEYKPPKFNLFGKISGWFRSILSD
1 . 1			KTSRNLFFFLCLNLSFAFVELLYGIWSNCLGLISDSFHMFFDST
1		Ì	AILAGLAASVISKWRDNDAFSYGYVRAEVLAGFVNGI.FI.TPTAF
1 1		1	FIFSEGVERALAPPDVHHERLLLVSILGFVVNLIGIFVFKHGGH
			GHSHGSGHGHSHSLFNGALDQAHGHVDHCHSHEVKHGAAHSHDH
		•	AHGHGHFHSHDGPSLKETTGPSRQILOGVFLHILADTLGSIGVI
1 1	<u> </u>		ASAIMMONFGLMIADPICSILIAILIVVSVIPLLRESVGTLMOR
	,		TPPLLENSLPQCYQRVQQLQGVYSLQEQHFWTLCSDVYVGTLKI.
<del> </del>			IVAPDADARWILSQTHNIFTQAGVROLYVOIDFAAM
5614	3	1268	LLSRNEHACPLQAGLGLTQRKPKAIRGREGRATNOGOGETONEP
	1	1	APWGARQRLGVMAELQQLQEFEIPTGREALRGNHSALLRVADYC
			EDNYVQATDKRKALEETMAFTTQALASVAYQVGNLAGHTLRMLD
	}	i	LQGAALRQVEARVSTLGQMVNMHMEKVARREIGTLATVQRLPPG
]			QKVIAPENLPPLTPYCRRPLNFGCLDDIGHGIKDLSTQLSRTGT
] ]	1	l	LSRKSIKAPATPASATLGRPPRIPEPVHLPVVPDGRLSAASSAS
	•	İ	SLASAGSAEGVGGAPTPKGQAAPPAPPLPSSLDPPPPPAAVEVF
ļ <b>1</b>			QRPPTLEELSPPPPDEELPLPLDLPPPPPLDGDELGLPPPPPGF
			GPDEPSWVPASYLEKVVTLYPYTSQKDNELSFSEGTVICVTRRY

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E
]	location	corresponding	
	corresponding	to final	
ļ	to first	to first	I DEDUCATE, MEMORNION NO NO NO.
1	amino acid	amino acid	
1	residue of	residue of	1 0 0 0 0 Land, land proposition to the transfer
1		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Sto
ł	amino acid	sequence	Codon, /=nossible ==== X=Unknown, *=Sto
<u> </u>	sequence	1	Codon, /=possible nucleotide deletion,
ļ			\=possible nucleotide insertion)
5615	9	1558	SDGWCEGVSSEGTGFFPGNYVEPSC
ļ	1	1	ALGRRRPGDPREMEAAATPAAAGAARREELDMDVMRPLINEQI DGTSDEEHEDELLBYDKHYOLDDAGA
1	l	ł	
	Ī		
	•		LRIYMLCFLPFIILLVETPELVALETT COLORS
			LRIYMLCFLPFIILLVFIRELKNLFVLSFLANVSMAVSLVIIY
l			
}			
ŀ			
	İ		) ====================================
5616			
- }	-	719	DDFVRCGPQSAAMGASARLIRAVIMGABCSCRCMING
}			LKHLSSGDLLRDNMLRGTEIGVLAKAFIDQGKLIPDDVMTRLA
ì			HELKNLTOYSWIJDGEPPTI DOZENI BONENI POD WARAFIDGKLIPDDVMTRLA
- 1	1		HELKNLTQYSWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFE
ļ	į		
5617	176	765	1*-**** ZK3OKASV1D
1	1	,03	PWRGRGSRPRGAGAMAEEQVNRSAGLAPDCEASATAETTVSSVC
1			
	i		
ı	,		
5618	3		
1	3	1692	YLNYINLKSENKLSGKEDLWEKLQYLWKSTLNLPEDLLRVPDES
- 1	ł	J	LFLNSGGDSLKSIDIJGELDERKLQILWKSTLNLPEDLLRVPDES
į	1		LFLNSGGDSLKSIRLLSEIEKLVGTSVPGLLEIILSSSILEIYN
1	1		HILQTVVPDEDVTFRKSCATKRKLSNINQERASGTSLHQKAIMT
	ļ	j	
. 1	1	-1	
1	i	!	
1	į	i	
J		ļ	
1		l	
- 1	ļ	Į.	
j	ł	1	
ı	i		
5619	2160		
	2160	1477	DSPVLPTSGNVISTAOPAOPMONIO I CLDDLLGGNQK
ļ	1	J	DSPVLPTSGNVISTAQPAQPWSAVEAALRSLGSPPGAGRGCPCP AOSLHSHOLAAWDDLWGLPCVCP
ì	l		
1	1		
l	ľ	, i	
{	í		
620	930		
- 1	1	, ,	PLPPPTLAMFLTRSEYDRGVNTFSPEGRLFQVEYAIEAIKLGST
1	j		
l	Ì	1 "	
1	1	I	EEDADPGAMSRPFGVALLFGGVDEKGPQLFHMDPSGTFVQCDAR
ļ		1 2	AIGSASEGAOSSLOFIVUVOMTI
<del></del>		_	
621	3		
ı		, ,	VEFVEYTATDANVKNESLSSVQQLGIKMTVRYGKFLSLLKDGA
1		1	THE SAME DISTRICT OF A CONTRACTOR OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE SAME OF THE S
1	1	1	
1		1 -	THE VIEW COLDAND AND DESCRIPTION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPER
1		ÍQ	CFWNYLDWIEICHYIATCVFLGPDYQVYICIAVFKHLQQDILQ
!		H	TOTODLOVET KERAL HOPPHODY TOTOLOVE ICHAVFKHLQQDILQ
		1	TQTQDLQVFLKEEALHGFRVSDYFEYMEILEQNYRTVLLRDMR
622	1122		20+
		1 42	ASTKDAVSRKRSHSASEKSGTGTSISKRLNMNPQIRNPMKAMY
		1 100	TETEDEKNI WEAMDDNERWI COM TO THE TOTAL THE TETE
	1		TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERT
		Q	GTFYFQFKNLWEANDRNETWLCFTVEGIKRRSVVSWKTGVFRN VDSETHCHAERCFLSWFCDDILSPNTKYQVTWYTSWSPCPDCA EVAEFLARHSNVNLTIFTARLYYFQYPCYQEGLRSLSQEGVAV

SEO	Predicted	Predicted end	Amino acid
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ļ.	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- {	amino acid	sequence	Codon, /=possible nucleotide deletion,
i	sequence		\=possible nucleotide insertion)
	† <b>-</b>	<del> </del>	EIMDYEDFKYCWENFVYNDNEPFKPWKGLKTNFRLLKRRLRESL
l			Q C
5623	3	954	FLPFFIRAPKISRNGQWLFTFTTPFPFANKALPGWEGIVPACFW
1			RKKILTPSTGTMELLQVTILFLLPSICSSNSTGVLEAANNSLVV
		1	TTTKPSITTPNTESLQKNVVTPTTGTTPKGTITNELLKMSLMST
		<u> </u>	ATFLTSKDEGLKATTTDVRKNDSIISNVTVTSVTLPNAVSTLOS
	1	ļ	SKPKTETQSSIKTTEIPGSVLQPDASPSKTGTLTSIPVTIPENT
	i		SQSQVIGTEGGKNASTSATSRSYSSILLPVVIALIVITLSVFVL
	ļ		VGLYRMCWKADPGTPENGNDQPQSDKESVKLLTVKTISHESGEH
ŀ	-	į	SAQGKTKN
5624	159	898	PGVAAAAGALPQYHGPAPALVSCRRELSLSAGSLQLERKRRDFT
1			SCCOPKLYPDTUALUCK F EDVICENTION DETERMINED
İ	ļ		SSGSRKLYFDTHALVCLLEDNGFATQQAEIIVSALVKILEANMD
[	İ		IVYKDMVTKMQQEITFQQVMSQIANVKKDMIILEKSEFSALRAE
			NEKIKLELHQLKQQVMDEVIKVRTDTKLDFNLEKSRVKELYSLN
	1		EKKLLELRTEIVALHAQQDRALTQTDRKIETEVAGLKTMLESHK LDNIKYLAGSIFTCLTVALGFYRLWI
5625	1	1180	TIPSCANACRACRACATION TO THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCARACTER OF THE COCCA
		2200	TIPSSAAAQRAGPPAGALEALSPGGARAHAERRGEMRATPLAAP AGSLSRKKRLELDDNLDTERPVQKRARSGPQPRLPPCLLPLSPP
			TAPDRATAVATASRLGPYVLLEPEEGGRAYQALHCPTGTEYTCR
}			VYPVQEALAVLEPYARLPPHKHVARPTEVLAGTQLLYAFFTRTH
			GDMHSLVRSRHRIPEPEAAVLFRQMATALAHCHQHGLVLRDLKL
			CRFVFADRERKKLVLENLEDSCVLTGPDDSLWDKHACPAYVGPE
			ILSSRASYSGKAADVWSLGVALFTMLAGHYPFQDSEPVLLFGKI
1			RRGAYALPAGLSAPARCLVRCLLRREPAERLTATGILLHPWLRQ
			DPMPLAPTRSHLWEAAQVVPDGLGLDEAREEEGDREVVLYG
5626	3123	2011	PPRALGSVAMENQVLTPHVYWAQRHRELYLRVELSDVQNPAISI
			TENVLHFKAQGHGAKGDNVYEFHLEFLDLVKPEPVYKLTQRQVN
1			ITVQKKVSQWWBRLTKQEKRPLFLAPDFDRWLDESDAEMELRAK
1 1			EEERLNKLRLESEGSPETLTNLRKGYLFMYNLVQFLGFSWIFVN
1			LTVRFCILGKESFYDTFHTVADMMYFCQMLAVVETINAAIGVTT
	i		SPVLPSLIQLLGRNFILFIIFGTMEEMQNKAVVFFVFYLWSAIE
			IFRYSFYMLTCIDMDWKVLTWLRYTLWIPLYPLGCLAEAVSVIQ
	!		SIPIFNETGRESETLPYPVKIKVRESEFLQIYLIMIFLGLYINF
		• .	RHLYKQRRRRYGQKKKKIH
5627	3123	2011	PPRALGSVAMENQVLTPHVYWAQRHRELYLRVELSDVQNPAISI
1 1			TENVLHFKAQGHGAKGDNVYEFHLEFLDLVKPEPVYKLTQRQVN
1	ĺ		ITVQKKVSQWWERLTKQEKRPLFLAPDFDRWLDESDAEMELRAK
1 1	i		EEERLNKLRLESEGSPETLTNLRKGYLFMYNLVQPLGFSWIFVN
1	Į.		LTVRFCILGKESFYDTFHTVADMMYFCQMLAVVETINAAIGVTT
			SPVLPSLIQLLGRNFILFIIFGTMEEMONKAVVFFVFVLWCDIF
1 1	1		IFRYSFYMLTCIDMDWKVLTWLRYTLWIPLYPLGCLAEAUSVIO
)			SIPIFNETGRESETLPYPVKIKVRESEFLQIYLIMIFLGLYINE
H-6232-1			RHLYKQRRRRYGQKKKKIH
5628	75	1455	VAGAMASKCLKAGFSSGSLKSPGGASGGSTRVSAMYSSSPCKLP
1			SLSPVARSFSACSVGLGRSSYRATSCLPALCLPAGGFATSYSGG
[	j		GGWFGEGILTGNEKETMQSLNDRLAGYLEKVROLEOENASLESB
]		İ	IREWCEQQVPYMCPDYQSYFRTIEELOKKTLCSKAENARIJAJET
1 1			DNAKLAADDFRTKYETEVSLRQLVESDINGLRRILDDLTLCKSD
1		,	LEAQVESLKEELLCLKKNHEEEVNSLRCOLGDRLNVEVDAADDV
1 1	Ĭ	·	DLNRVLEEMRCQYETLVENNRRDAEDWLDTOSEELNOOVVSSSR
1	1		QLQSCQAEIIELRRTVNALEIELQAQHSMRDALESTLAETEARV
1 1	1		SSQLAQMQCMITNVEAQLAEIRADLERONOEYOVLLDVRARIEC
			EINTYRGLLESEDSKLPCNPCAPDYSPSKSCLPCLPAASCGPSA
<del> </del>			ARTNCSARPICVPCPGGRF
5629	2287	938	GRPRSSSDNRNFLRERAGLSSAAVQTRIGNSAASRRSPAARPPV
j		ļ	PAPPALPRGRPGTEGSTSLSAPAVLVVAVAVVVVVVSAVAWAMA
]	j		NYIHVPPGSPEVPKLNVTVODQEEHRCREGALSLLQHLRPHWDP
1		ľ	QEVTLQLFTDGITNKLIGCYVGNTMEDVVLVRIYGNKTELLVDR
	ĺ		DEEVKSFRVLQAHGCAPQLYCTFNNGLCYEFIQGEALDPKHVCN
L			PAIFRLIARQLAKIHAIHAHNGWIPKSNLWLKMGKYFSLIPTGF

SEO	Predicted	T =	
ID	beginning	Predicted end	
NO:	nucleotide	nucleotide	\n-nralling, C=CVSCelne, D=Acpartic Acid p
NO.	location	location	Gutamic Acid, F=Phenylalanine G-Clusina
		corresponding	n=nlstldine, I=Isoleucine, K=Lvcine
1	corresponding	to first	D=Leucine, M=Methionine, N=Asparagine
1	to first	amino acid	P=Proline, O=Glutamine R=Arginine
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
		<del></del>	ADEDIANCE CRITECOLIDE Insertion)
1			ADEDINKRFLSDIPSSQILQEEMTWMKEILSNLGSPVVLCHNDL
ĺ			DC ANTITIME KQGDVQFIDYEYSGYNYLAYDIGNHENE FACUSON
		1	DISLYPDRELQSQWLRAYLEAYKEFKGFGTEVTEKEVETTETOV
	i	ł	NOPALASHPFWGLWALIQAKYSTIEFDFLGYATURENOVEVMVD
5630	1304		BATAPKABR
3030	1194	278	GFWAIAQTCAHHLPPGSPWLVPASPWRLPEMSSFGYRTLTVALF
	1		TLICCPGSDEKVFEVHVRPKKLAVEPKGSLEVNCSTTCNQPEVG
l l	}		GLETSLDKILLDEQAQWKHYLVSNISHDTVLQCHFTCSGKQESM
	1		KSNVSVYQPPRQVILTLQPTLVAVGKSFTIECRVPTVEPLDSLT
ł	ł		LELEPCHET HYETECKY > DARGEST TECKVPTVEPLDSLT
	1		LFLFRGNETLHYETFGKAAPAPQEATATFNSTADREDGHRNFSC
	1		LAVLDLMSRGGNIFHKHSAPKMLEIYEPVSDSQMVIIVTVVSVL
5631	1053	290	LSLFVTSVLLCFIFGQHLRQQRMGTYGVRAAWRRLPQAFRP
1		490	SRVDDFVRPEPSRAEPSRSGRRRPARRAATMSVEGKLECACCOV
ı	]		AGRIGGPTPQEAIQRLRDTEEMLSKKOEFLEKKTEOFT.TAAVVIG
	1		I KNIKRAALQALKRKKRYEKOLAOIDGTLSTIEFODED LENDAMM
	i		1EVLKNMGYAAKAMKAAHDNMDIDKVDELMODJADOOFTARRIG
1			TAISKPVGFGEEFDEDELMAELEELEQEELDKNLLEISGPETVP
5632			LPNVPSIALPSKPAKKKEEEDDDMKELENWAGSM
5632	3	952	VVLGWSPPRRLWWGSLGAAQRPAVPVSGLARSLHVETRRPHRRA
			SVRVARGRLGVWAQPQPLLPRPVGSRREMQPPGPPPAYAPTNGD
			FTFVSSADAEDLSGSIASPDVKLNLGGDFIKESTATTFLRQRGY
			CWLLEVEDDDDEDNIKDLEDDVKLNLGGDFIKESTATTFLRQRGY
1 1	[		GWLLEVEDDDPEDNKPLLEELDIDLKDIYYKIRCVLMPMPSLGF
	•		NRQVVRDNPDFWGPLAVVLFFSMISLYGQFRVVSWIITIWIFGS
1 1			LTIFLLARVLGGEVAYGQVLGVIGYSLLPLIVIAPVLLVVGSFE
1 1	1		VVSTLIKLEGVEWAAYSAASLLVGEEFKTKKPLLIYPTFII.VTV
5633	771		FLSLYTGV
	''*	460	QGCSKTMSVGRPFYRSSEFMEQLLSSHLHQVPFFCCFTVVCLCN
1 1	į		CLFENSVSKLYMLCFNFFMSIFFYSLSITKLNLIYLWGLSVOGL
5634			DEF:DESCHRPWGSSMV
3634	1446	855	PRATGRIRSRAMASRPRAGAGASGAEPRSGRERSRLSGRRAPAM
1			ARNTLSSRFRRVDIDEFDENKFVDEQEEAAAAAAEPGPDPSEVD
1	j		GLLRQGDMLRAFHAALRNSPVNTKNQAVKERAQGVVLKVLTNFK
1 1	i		SSEIEQAVQSLDRNGVDLLMKYIYKGFEKPTENSSAVLLQWHEK
1			ALAVGGLGSIIRVLTARKTV
5635	3	. 943	DECDUCTATIONS
1 1	f	713	DRGPRSTATDTGRARVSFWRFPLDPGVKNSNVQISGEKRRFRTL
1 1	1		RSLFHPFPVTRSGAPRAVLVGSSWPAKMVAPAVKVARGWSGLAL
1 1	i		GVRRAVLQLPGLTQVRWSRYSPEFKDPI.TDKEVVPKPUPET TREE
1 1			EXIVEERKTQLIKAAPAGKTSSVFEDPVISKETNMMMICONEN
1 1	ļ		LARSEMIQTLEAVERKOFEKYHAASAEROATTERNEVTTEROAT
1 1		i	ANCEPMIGLVPILKGGRFYOVPVPLPDRRRRRIAMKWMITECOD
1 1	,		KKHQRTLMPEKLSHKLLEAFHNQGPVIKRKHDLHKMAEANRALA
1-600-			TITKWW
5636	2253	1143	LEDTICQHPPAEKKLYLYHRKLREVERNGIPRLPKDVFMDTHQG
	ŀ		LTDVRAKVTGFSEGVVDSVKGGFSSFSQATHSAAGAVVSKPREI
1			ASLIENKEGGADNIENI KOCI TEGOLOGI SAFSQATHSAAGAVVSKPREI
1 1	- 1	1	ASLIRNKFGSADNIPNLKDSLEEGQVDDAGKALGVISNFQSSPK
	Į.		YGSEEDCSSATSGSVGANSTTGGIAVGASSSKTNTLDMQSSGFD
1	1	1	ALLHEIQEIRETQARLEESFETLKEHYORDYSLIMOTLOFERVE
1	į	Į	CERLEEQLIDLTELHQUEILNLKOELASMEEKIAVOGVEDADDI
[ ]	ļ	1	QEALEACQTRISKMELQQQQQQOVVQLEGLENATAPNIT.GVLTNT
1 1	ļ	İ	LLAVMAVLLVFVSTVANCVVPLMKTRNRTFSTI.FI.WVFT N FI WV
F-53-1			HWDALFSIVERFFSSPR
5637	948	2532	MSFCGARANAKMMAAYNGGTSAAAAGHHHHHHHHLPHLPPPHLH
	1		НИННРОННЫНРСКАЛАУИРУОСИТСОВЪВВЕНЕН
]	i		HHHHPQHHLHPGSAAAVHPVQQHTSSAAAAAAAAAAAAAAAMLNPG
[	1		QQQPYFPSPAPGQAPGPAAAAPAQVQAAAAATVKAHHHQHSHHP
	į		QQUDIEPDRPIGYGAFGVVWSVTDPRDGKRVAI.KKMDNIFONT
	į.		VSCKRVFRELKMLCFFKHDNVLSALDII.OPPHTDVFFFTVIAMP
	1	1	LMQSDLHKIIVSPQPLSSDHVKVFLYOII.RGI.KVI.HSAGII UDD
	ļ	1	I KPGNLLVNSNCVLKICDFGLARVEELDESRHMTOEVATOVVDA
			PELLINGSRHYSNAIDIWSVGCTFAELLGRRILFOAGGRIOOT DE
			ITDLLGTPSLEAMRTACEGAKAHILRGPHKQPSLPVLYTLSSQA
	<del></del>		AOSSOTTUVITUSSON

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
- [	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ì	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
,	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			THEAVHLLCRMLVFDPYKRISAKDALAHPYLDEGRLRYHTCMCK
	}		CCFSTSTGRVYTSDFEPVTNPKFDDTFEKNLSSVROVKEIIHOP
L			ILEQQKGNRVPLCINPQSAAFKSFISSTVAOPSEMPPSPLVWE
5638	125	1155	DRKMSELDQLRQEAEQLKNQIRDARKACADATLSOITNNIDPVG
]		·	RIQMRTRRTLRGHLAKIYAMHWGTDSRLLVSASODGKLIIWDSV
ŀ			TTNKVHAIPLRSSWVMTCAYAPSGNYVACGGLDNICSIYNLKTR
1	1		EGNVRVSRELAGHTGYLSCCRFLDDNQIVTSSGDTTCALWDIET
			GQQTTTFTGHTGDVMSLSLAPDTRLFVSGACDASAKLWDVREGM
1			CRQTFTGHESDINAICFFPNGNAFATGSDDATCRLFDLRADQEL
	1	ĺ	MTYSHDNIICGITSVSFSKSGRLLLAGYDDFNCNVWDALKADRA
5639	135		GVLAGHDNRVSCLGVTDDGMAVATGSWDSFLKIWN
3039	125.	1155	DRKMSELDQLRQEAEQLKNQIRDARKACADATLSQITNNIDPVG
1	1	1	RIQMRTRRTLRGHLAKIYAMHWGTDSRLLVSASQDGKLIIWDSY
İ		]	TTNKVHAIPLRSSWVMTCAYAPSGNYVACGGLDNICSIYNLKTR
			EGNVRVSRELAGHTGYLSCCRFLDDNQIVTSSGDTTCALWDIET
	1		GQQTTTFTGHTGDVMSLSLAPDTRLFVSGACDASAKLWDVREGM CRQTFTGHESDINAICFFPNGNAFATGSDDATCRLFDLRADQEL
			MTYSHDNIICGITSVSFSKSGRLLLAGYDDFNCNVWDALKADRA
İ			GVLAGHDNRVSCLGVTDDGMAVATGSWDSFLKIWN
5640	280	1092	QQGNKKTMLSHNTMMKQRKQQATAIMKEVHGNDVDGMDLGKKVS
	1		IPRDIMLEELSHLSNRGARLFKMRQRRSDKYTFENFQYQSRAQI
ļ			NHSIAMQNGKVDGSNLEGGSQQAPLTPPNTPDPRSPPNPDNTAP
1			GYSGPLKEIPPEKFNTTAVPKYYQSPWEOAISNDPELLBALYPK
			LFKPEGKAELPDYRSFNRVATPFGGFEKASRMVKFKVPDFELLI.
!			LTDPRFMSFVNPLSGRRSFNRTPKGWISENIPIVITTEPTDDTT
5641	27		VPESEDL
2041	2'	332	CRHNCNGDVKLLSNQMDKLFAFHLFTFHGLLHFLDGSIQKLIQA
			EIILSDNSSILVLENNFLFKVKSKQFIHLIAKKFYISITIVSAS
5642	199	1247	ITPCRMDFLVLFLFYLASVLMGLVLICVCSKTHSLKGLARGGAQ
			IFSCIIPECLQRAMHGLLHYLFHTRNHTFIVLHLVLQGMVYTEY
1			TWEVFGYCOELELSLHYLLLPYLLLGVNLFFFTLTCGTNPGIIT
	ļ		KANELLFLHVYEFDEVMFPKNVRCSTCDLRKPARSKHCSVCNWC
1			VHRFDHHCVWVNNCIGAWNIRYFLIYVLTLTASAATVAIVSTTF
			LVHLVVMSDLYQETYIDDLGHLHVMDTVFLIOYLFLTFPRIVFM
1	i		LGFVVVLSFLLGGYLLFVLYLAATNOTTNEWYRGDWAWCORCPI
F 5 4 3			VAWPPSAEPQVHRNIHSHGLRSNLQEIFLPAFPCHERKKOR
5643	1	847	PSGGVRDVETRGPGSRAARGPRVVMERRGVGAGAIAKKKLAEAK
1			YKERGTVLAEDQLAQMSKQLDMFKTNLEEFASKHKQEIRKNPEF
l i			RVQFQDMCATIGVDPLASGKGFWSEMLGVGDFYYELGVQIIEVC
1			LALKHRNGGLITLEELHQQVLKGRGKFAQDVSQDDLIRAIKKLK
i			ALGTGFGIIPVGGTYLIQSVPAELNMDHTVVLQLAEKNGYVTVS
			EIKASLKWETERARQVLEHLLKEGLAWLDLQAPGEAHYWLPALF TDLYSQEITAEEAREALP
5644	83	1138	PRRMGSWVQLITSVGVQQNHPGWTVAGQFQEKKRFTEEVIEYFQ
			KKVSPVHLKILLTSDEAWKRFVRVAELPREEADALYEALKNLTP
1 1			YVAIEDKDMQQKEQQFREWFLKEFPQIRWKIQESIERLRVIANE
]			IEKVHRGCVIANVVSGSTGILSVIGVMLAPFTAGLSLSITAAGV
			GLGIASATAGIASSIVENTYTRSAELTASRLTATSTDQLEALRD
1			ILHDITPNVLSFALDFDEATKMIANDVHTLRRSKATVGRPLIAW
			RYVPINVVETLRTRGAPTRIVRKVARNLGKATSGVLVVLDVVNI.
<u> </u>			VQDSLDLHKGEKSESAELLRQWAQELEENLNELTHIHOSLKAG
5645	537	799	VQSVRDLKRLSPTDPPGDSGNRDVTREDPVTGPLNSASSOVPTL
<u></u>			YLCLQNSLLGHSSVEDARATMELYQISQRIRARRGLPRLAVSD
5646	3745	3328	AEQYGTSPHLLPTMLLSSCLPPANVTTKAATPPPLVLSLTTADP
	İ		AGKPAPCRVTLTLLRASIPATKRASFLSSFIKMFFEELEYILGF
			LSLLKFHVHVSVYSAICHFQKEGTGNSRSFTCTPELFPRLQTHL
5647	288	800	RAEGGAQ
	200	800	GVIMATSELSCEVSEENCERREAFWAEWKDLTLSTRPEEGCSLH
			EEDTQRHETYHQQGQCQVLVQRSPWLMMRMGILGRGLQEYQLPY

SEQ	Predicted	Predicted end	Amino acid cogmont
ID	beginning	nucleotide	Amino acid segment containing signal pepti
NO:	nucleotide	location	
	location	corresponding	
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, N=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Sto
	sequence	1 -	"""""
			\=possible nucleotide insertion)
			QRVLPLPIFTPAKMGATKEEREDTPIQLQELLALETALGGQC
5648	7	1518	1 TREET VERSKEGALIREST, SPSMCODA ONG
	1		V DO S D C GRHEALRE V GAEWPPPT CS PN T C CCT CO D CV
	1	ı	A SOUL DOKEMPLONILLGILLMAACETECI CHONT VDD
	ĺ	1	1 TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPE
	ĺ		The state of the control of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the
	ļ		T THE ACCUSAGE OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY
			1 VOLOV VINGUNSTEPTIVKEVANETT CANDOCTER-
			1 DECEMBER 1 THAT BOPL TAKKEVI, PATOCIT DITERITACE
			I
i	1		1
.	ļ		METHOR MITTERDRING POLICIPAL ACT OF ACT
5649	1172		1 = = = 1 APPTIG2 AM2TPKF 1 15
	11/2	3006	MLQEQLDAINEEIRMIOEEKESTELDAFEIDEDIVEGE
i	i		ASSESSMENT TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF
i			TO THE OUDINATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPE
J	1		
- 1		!	
i	i	i	VPAKLGTQAEKDRRLKKKHQLLEDARRKGMPFAQWDGPTVVSW
f			ELWVGMPAWYVAACRANVKSGAIMSALSDTEIQREIGISNALH
j			LKLRLAIQEMVSLTSPSAPPTSRTSSGNVWVTHEEMETLETST
1	1	j	TDSEEGSWAQTLAYGDMNHEWIGNEWLPSLGLPQYRSYFMECL
		ŀ	DARMLDHLTKKDLRVHLKMVDSFHRTSLQYGIMCLKRLNYDRKI
1	1	J	LEKRREESQHEIKDVLVWTNDQVVHWVQSIGLRDYAGNLHESGI
ŀ	}	1	HGALLALDENFOHNTLALILQIPTONTQARQVMEREFNNLLAL(
i	1	1	TDRKLDDGDDKVFRRAPSWRKRFRPREHHGRGGMLSASAETLP
5650			GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSAFRD
0000	1172	3006	MLOEOLDAINEFIRMIOERVEORES
1			MLQEQLDAINEEIRMIQEEKESTELRAEEIETRVTSGSMEALNI KOLRKRGSIPTSLTDLSLAGAGAGAE
	1	i	KQLRKRGSIPTSLTDLSLASASPPLSGRSTPKLTSRSAAQDLDR MGVMTLPSDLDKHDPRIISDLSCASSPPLSGRSTPKLTSRSAAQDLDR
	I		MGVMTLPSDLRKHRRKLLSPVSREENREDKATIKCETSPPSSPR TLRLEKIGHPALSOFFGVSAL
	1	l l	TLRLEKLGHPALSQEEGKSALEDQGSNPSSSNSSQDSLHKGAKR KGIKSSIGPLEGKKEVGRY
	}	<b>}</b> .	KGIKSSIGRLFGKKEKGRLIQLSRDGATGHVLLTDSEFSMQEPM VPAKIGTOAFKDERI KKWIOLI
	İ	ļ.	VPAKLGTQAEKDRRLKKKHQLLEDARRKGMPFAQWDGPTVVSWL
1	J	1 3	ELWVGMPAWYVAACRANVKSGAIMSALSDTEIQREIGISNALHR LKLRLAIOFMYSITS DAN DOMONIA
1			
1		ľ	COCCOMACI LIMI GUMNHEW ) CATEMIT DOT OF DOMESTIC
l		j -	PLANTER VELKWOIDS PUDTET OVERMOT TENEVISION
1	1	, -	
551	646		O TO TO TO PERFER PER KIMPE ANGUVI. VCUMI CARRE
1			MOOORUPWG*EARAKGPASESDPU*ECCCWcop*cp
1			······································
1		1 **	"" " MAY TAGKAPAPRSRAAPPADAT CUCMANANA CO-
		{ -·	D. 0110000PPRG*KWGRSRQADADADADADATA
	1	*	OIL OSCUDAOGWOAEPIGAPGAFDG\ DUDDODODODO
	ľ	1 -	TO MICHAGIO AGAPGIO ATA DE A ACOMPTA A A DALGRESS OF THE
1	j	"	
- 1	1	1 -	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
- 1	İ	-	ov i vegorighorkkighen belle som by breaking and a second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the sec
52	735		
	, 23	343 H	HKKYQHIHQKSFSCPEPACGKSFNEKKHI KEUMKI HOD
1	1	1	- CWOLKISSNUVIHKKIHACEKDI OCETCCEMODOWS
53			ORKHAETVAALRFPCEFCGKRFEKPDSVAAHRSKSHPALLLA
	66	1401 RC	GRLQSRGRLTLGLWILLIBIT CAROTTO
}	1	l Ci	FROPCOPETER CREEK THAT THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF
ļ	}	1 ~	* YE CYPGI KKGKKKSLKEATEDOLAMA EFFERM POPULATION
1	}		DWEQLGLEQGDTFWDTALDNCQDLFLLDPPRPNLTSHPDGSED CPLAGGSPEATSPDVTALTKNSPLMEDFFEEGFSQEI/SRDVIQ
	ſ	) ~~~	" MOOGSEATOPDVIETKNSPIMEDPERECECORY JORSSES
		1.00	LLELQFRRSLYRGHLVR+FARRSRKSSEV+YCHQRGKSHGMQ

SEO	Predicted	Predicted end	Dring poid
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
	amino acid	residue of	S=Serine, T=Threonine, V=Valine
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *-Ston
	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
			ES*IKERTQSCVHRFHGRRFHG\DNVSEKTLTPAKSKEYRGEFF
	,		SYSDHSQQDSVQEGEKPYQCSECGKSFSGSYRLTQHWITHTREK
			PTVHQECEQGFDRKASHSGYPKTHTGYKFYVCNEYGTPFSQSTY
1			LWHQKTHAGEKPCKSQDSDHPPSHDTQSGEHQKTHTDSKSYNCN ECGKAFTRIFHLTRHQKIHTRKRYECSKCQATFNLRKHLIQHQK
1			THAANV
5654	3	598	TLPLFPGRRFRGWRRCGAVAARKNSTGGNVSINQRRDSVRMSAL
			NWKPFVYGGLASITAECGTFPIDLTKTRFQIQGQTNDAKFKEII
ļ		}	YRGMLHALVRIGREEGLKALYSG*VGLHAFLCHCSLFHMGIDFR
			PRLHRSQVKSLRCV*KEQIA**/MFSLLISTLISKYIYYAADVL
			EKLFYYIQVQTDNNKKICLFKNI
5655	2	867	RPPGIRAPROLHPAAGRRPDASARPRFRPTVLLHDPFOLSEPPP
I		<b>j</b>	PLSYPSVFPAVARVLPQRSGDYRAAGMPOLSGGGGGGGGGCDPELC
	1		ATDEMIPFKDEGDPQ\REKIFAEIVNPEEEGDLADIKSSLVNES
1	1		EIIPASNGHEVARQAQTSQEPYHDKAREHPDDGKHPDGGLYNKG
1	!		PSYSSYSGYIMMPNMNNDPYMSNGSLSPPIPRTSNKVPVVQPSH
1	1		AVHPLTPLITYSDEHFSPGSHPSHIPSDVNSKQGMSRHPPAPDI PTFYPLSPGGGGQITPPLGWQGQP
5656	228	1066	PRRVPPLPEFASGPGAAFFHSGRLQRSLTKDSAGCFSQCRSRAM
1	}		LVLRSGLTKALASRTLAPQVCSSFATGPRQYDGTFYEFRTYYLK
1	<u> </u>		PSNMNAFMENLKKNIHLRTSYSELVGFWSVEFGGRTNKVFHIWK
ļ	j		YDNFPHRAEVRKALANCKEWQEQSIIPNLARIDKOETEITYLIP
	]		WSKLQKPPKEGVYELAVFQMKPGGPALWGDAFERATNAHVNI.GV
1			TKVVGVFHTEYGELNRVHVLWWNESADSRAAVRHKSHEDDTSWG
5657	105	1052	GVRESVNYL\VSQQNM
3037	105	1052	GQRLQSPRVQMPVQPPSKDTEEMEAEGDSAABMNGEEEESEEER
			SGSQTESEESSEMDDEDYERRRSECVSEMLDLEKQFSELKEKL
ł l			FRERLSQLRLRLEEVGAERAPEYTEPLGGLQRSLKIRIQVAGIY KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLQGELQERIQR
			LEEDRQSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKKAPLVSG
			PYIVYMLQEIDILEDWTAIKKARAAVSPQKRKSD\DLDPAVHSQ
			GDPQSSWHCTQDSRLPPADRRTHRPLRVCPARLLWCCWALPLHL
			ALVWTPPL
5658	2346	3541	TERRVYNPWPEPDPD\CIQEDPWNLPNSIKTLVDNIQRYVEDGK
1			NQLLLALLKCTDTELQLRRDAIFCQALVAAVCTFSEOLLAALGY
1 1			RYNNNGEYEESSRDASRKWLEQVAATGVLLHCQSLLSPATVKEE
			RTMLEDIWVTLSELDNVTFSFKQLDENYVANTNVFYHIEGSRQA
			LKVIFYLDSYHFSKLPSRLEGGASLRLHTALFTKVLENVEGLPS PGSOAFFDLOODINAOSI RYVOOVYRKI RAFRI HERVINGELPS
] ]			PGSQAAEDLQQDINAQSLEKVQQYYRKLRAFYLERSNLPTDAST TAVKIDQLIRPINALDELCRLMKSFVHPKPGAAGSVGAGLIPIS
1 1			SELCYRLGACQMVMCGTGMQRSTLSVSLEQAAILARSHGLLPKC
[ ]	I		IMQATDIMRKQGPRVEILAKNLRVKDQMPQGAPRLYRLCQPKMN
			GDL
5659	2	696	WKRSGEVSPKGELGAWRGNSGRPKIIGRAAEAENEDRTLGRLLP
	j		GNERSQPRSPLRLLAPQLKAEAAADKGLAPVPPPPFSSGHSGPC\
1			EREGEGORGRGRSRRGAHLELKPSPGLRAGAPTDRGRGGPARVA
1	į		AAGGRRMVQKESQATLEERESELSSNPAASAGASLEPPAAPAPG
1 1			EDNPAGAGG\AAVAGAAGGARRFLCGVVEGFYGRPWVMEQRKEL
5660	229	853	FRRLQKWELNTYL
			PVTMWAFSELPMPLLINLIVSLLGFVATVTLIPAFRGHFIAARL
		·	CGQDLNKTSRQQIPESQGVISGAVFLIILFCFIPFPFLNCFVKE QRKAFPHHEFVALIGALLAICCMIFLGFADDVLNLRWRHKLLLP
		į	TAASLPLLMVYFINFGNTTIVVPKPFRPILGLHLDLGR*SYHCC
1	}		PYGTYFREPFLVLHILLQVFLFCLCVFPDPFW
5661	2	473	LNLYPSPCGGIPKLPGLPREAAAALGAS FLAEAPLPVTVRGSGL
l l			AGMAVTCDPKAFLSICFVTLVFLQLPLASICQN*GTDSCASRGK
] ]			ADFDVTGPHAPILAMAGGHVELQCQLFPNISAEDMELRWYRCQP
ا ـــِــِـا			SLAVHMHERGMDMDGEQKWQYRGRT
5662	2	1318	LRKEGRCRRGSNRGVWAAPAEGLGGRGMLGVRCLLRSVRFCSSA
			PFPKHKPSAKLSVRDALGAQNASGERIKIQGWIRSVRSQKEVLF

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
[	corresponding	to first	L=Leucine, M=Methionine N=Asparagine
[	to first	amino acid	P=Proline, Q=Glutamine R=Arginine
}	amino acid	residue of	S=Serine, T=Threonine V=V=line
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +-Show
	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion\
1 1			LHVNDGSSLESLQVVADSGLDSRELTEGSSVEVOGOLTKSDEVE
			QNVELKAEKIKVIGNCDAKDFPIKYKERHDI.EVI.DOVDUEDCD#
1 1			NVLGSILRIRSEATAAIHSFFKDSGFVHTHTDTTTCNDGEGAGE
1 1			LFQLEPSGKLKVPEENFFNVPAFLTVSGOLHLFUMSGAFTOURT
1 1		1	FGPTFRAENSQSRRHLAEFYMIEAEISFVDSLQDLMQVIEELFK
			ATTMMVLSKCPEDVELCHKFIAPGQKDRL*HMLKNNFLIISYTE
			AVEILKQASQNFTFTPEWGADLRTEHEKYLVKHCGNIPVFVINY
5663	119	698	PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGESTANTEGREE OF THE PADIGE
1		050	PADIGRSTAKTPGPPRSLEMDDPRYGMCPLKGASGCPGAERSLL
			VQSYFEKGPLTFRDVAIEFSLEEWQCLDSAQQGLYRKVMLENYR NLVFLGIALTKPDLITCLEQGKEPWNIKRHEMVAKPFVICSIIFP
1			QDLWAEQDIKDSFQEAILKKYGKYGHANFQLQKGCKSVDECKVH
			KEHDNKLNQCLIPKKKK
5664	118	572	SLSMESNHKSGDGLSGTOKEAALRALVORTGYSLVORNGORVAG
			GPPPGWDAAPPERGCEIFIGKLPRDLFEDELIPLCEKIGKIYEM
		ļ	RMMMDFNGNNRGYAFVTFSNKVEAKNAIKQLNNYEIRNGRLLGV
FEE			CASVDNCRLFVGGIPKTKK
5665	347	702	VVQHLIILLHCERTSPAMITSELPVLQDSTNETTAHSDAGSELE
1			ETEVKGKRKRGRPGRPPSTNKKPRKSPGEKSRIEAGIDGAGDGD
5666			ANGHPQQNGEGEPVTLFEVVKLGKSAMORC
] 2000	213	540	VSCLPTSCKMITLNNQDOPVPFNSSHPDEVKIAALVEVSCIETI
1			GLFVN1TALWVFSCTTKKRTTVTIYMMNVALVDLTFTMTLDEDM
5667	1	695	FYYAKDEWPFGEYFCQILGA
	*	269	HPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLPKRRRARVGSP
1			SGDAASSTPPSTRFPGVAIYLVEPRMGRSRRAFLTGLARSKGFR
			VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPALLD
			ISWLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAWMPAYACQR PTPLTHHNTGLSEALEILAEAAGFEGSEGRLLTFCRAASVLKAL
L			PSPVTTLSQLQ
5668	691	894	CSFLFCIPDLFLQFLLGRKEEEAVLVGGEWSPSLDGLDFQADPQ
			VLVRTAIRCAQAQTGIDLSGCTKW
5669	407	1	DSGAPEGLSPLMSTOEGLSMHAHPOAYTPFIVLHAPKPRGETCD
1	İ		ADSRENDRYAHKSAOLYFLYFVCWIFODVYVPTIKEVNUPPEDV
1	1		ARGAPTKYSGSPIGSPTTTPPTRPPSFNLHPAPHLLASMQLQKL
5670	3	•	NSQ
30,70	,	373	SSECLTMAWIPLLLPLLILCTVSVASYELAQPSSVSVSPGQTAK
	ŀ		TTCSGDVLAKKYARWFOOKPGOAPVI,VTYKDTEPDSGTDEPEGG
5671	280	524	SISGITVILIISGAOVEDEADYFCVSATDNELLWE
		<b>5</b> 24	KFPPKKTPPHLGMESAITLWQFLLQLLLDQKHEHLICWTSNDGE
5672	2	557	FKLLKAKKVAKLWGLRKNKTNMNYDKLSRALRIJFMT
	=	J.,	FVPATPDPGVWLPPSRDPAMAKRSSLYIRIVEGKNLPAKDITGS
ļ j			SDPYCIVKVDNBPIIRTATVWKTLCPFWGEEYQVHLPPTFHAVA
[			FYVMDEDALSRDDVIGKVCLTRDTIASHPKGKFSLPSHTGLPSP WPPSHSETSPLGSVWSPACKNET LORRAGETSLPSHTGLPSP
		j	WPPSHSETSPLGSVWSPAQGKPFLLSPEAGATFCTPGLCSAACS QAWLLLPLP
5673	327	696	ITVADQISHWSAGRIKNRTRIPECIHSSAATTLAGPHTMEGESV
	i	}	KLSSQTLIQAGDDEKNQRTITVNPAHMGKAFKVMNELRSKQLLC
			DVMIVAEDVEIEAHRVVLAACSPYFCAMFTGDMS
5674	17	984	GGGSMEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLLGEVKGE
			AKNSITDSQMDDVEVVYTIDIOKYIPCYOLFSFYNSSGEVNEOA
		}	LKKILSNVKKNVVGWYKFRRHSDQIMTFRERLLHKNLQEHFSNQ
I		ļ	DLVFLLTPSIITESCSTHRLEHSLYKPOKGLFHRVPI.VVANI.C
ŀ			MSEQLGYKTVSGSCMSTGFSRAVQTHSSKFFEEDGSLKEVHKTN
			EMYASLQEELKSICKKVEDSEQAVDKLVKDVNRLKREIEKRRGA
j			QIQAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKID
5675	- PO		MFLKVAVTTTISM
	80	753	EGSRRGPTRLARLSARAGRLHFPPGFSSRLIHFRGVSECRRPPG
I		l l	KSGVPVSAPGSDGKWWEERPGMFSLMASCCGWFKRWREDVRKUT
ľ		1	LLMVGLDNAGKTATAKGIQGEYPEDVAPTVGFSKINLRQGKFEV TIFDLGGGIRIRGIWKNYYAESYGVIFVVDSSDEERMEETKEAM





SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, T=Isoleucine, K=Lysine,
1	corresponding	to first	Lalencine Mamorhiania av a mine
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	Seserine, Ternreonine, Vevaline,
1	amino acid	I control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the cont	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\=possible nucleotide insertion)
1			SEMLRHPRISGKPILVLANKQDKEGALGEADVIECLSLEKLVNE
5676			HKCL
36/6	2	930	FVSSPPPRPVQPARPGGFGLSGRRSLLCQVASTPAHVGVMRSPV
ŀ			RDLARNDGEESTDRTPLLPGAPRAEAAPVCCSARYNLAILAFFG
ĺ	ł		FFIVYALRVNLSVALVDMVDSNTTLEDNRTSKACPEHSAPIKVH
1			HNQTGKKYQWDAETQGWILGSFFYGYIITQIPGGYVASKIGCKM
			LLGFGILGTAVLTLFTPIAADLGVGPLIVLRALEGLGEGVTFPA
1	i		MHAMWSSWAPPLERSKLLSISYAGAQLGTVISLPLSGIICYYMN
		i	WTYVFYFFGTIGIFWFLLWIWLVSDTPQKHKRISHYEKEYILSS
			L
5677	1	1028	PPRDGFLELRRLSVPLCSGPCPLTSLSRQGERSGGHLVAAARAA
1			VTAETHPLPLLAPLAVCQSVKSPAACOVRPRPRAVALPAALGGP
1			GRSLPGLTAATMSSFSESALEKKLSELSNSOOSVOTLSLWLTHH
1			RKHAGPIVSVWHRELRKAKSNRKLTFLYLANDVIONSKRKGPEF
1			TREFESVLVDAFSHVAREADEGCKKPLERLLNIWOERSVYGGEF
1		1	IQQLKLSMEDSKSFPPKATEEKKSLKRTFOOIOEEEDDDYPGSY.
1		ĺ	SPQDPSAGPLLTEELIKALQDLENAASGDATVROKIASLPOEVO
			DVSLLEKITDKEAAERLSKTVDEACLRNRGPGTS
5678	3	593	SSSPPSSTPSLPLPFYLLLGQLRLQLLWGTAHLSGAGEAAPCPG
1			GSGRTAAPRTRADPAAQSLMIMNKMKNFKRRFSLSVPRTETIEE
		į	SLAEFTEQFNQLHNRRNENLQLGPLGRDPPQECSTFSPTDSGEE
			PGQLSPGVQFQRRQNQRRFSMEVRASGALPRQVAGCTHKGVHRR
			AAALQPDFDVSKRLSLPMDI
5679	2	623	LNSRVDDFVAVPGAIMDEDYYGSAAEWGDEADGGQQEDDSGEGE
] :			DDAEVQQECLHKFSTRDYIMEPSIFNTLKRYFOAGGSPENVIOL
			LSENYTAVAQTVNLLAEWLIQTGVEPVQVQETVENHLKSLLIKH
	,		FDPRKADSIFTEEGETPAWLEQMIAHTTWRDLFYKLAEAHPDCL
			MLNFTVKVGRVLELRRKVFMNVYFWLLVCFL
5680	258	592	RRLTSTSEKLQNRNSHTPLESLIHPQPSYKGFGIMFGKKKKKIE
.			ISGPSNFEHRVHTGFDPQEQKFTGLPQQWHSLLADTANRPKPMV
<u> </u>			DPSCITPIQLAPMKTIVRGNKPC
5681	45	869	LLCAKTLGVRTKESQAEGYNRSGINNHQAEDPRFCPSFCWMRSA
ļ			RQTRPQRLRKEAARPPTPGSCPGGTGMDGKKCSVWMFLPI,VFTI.
j			FTSAGLWIVYFIAVEDDKILPLNSAERKPGVKHAPYISIAGDDP
1			PASCVFSQVMNMAAFLALVVAVLRFIQLKPKVLNPWLNISGLVA
	'		LCLASFGMTLLGNFQLTNDEEIHNVGTSLTFGFGTLTCWIQAAL
1			TLKVNIKNEGRRVGIPRVILSASITLCVGPLLHPHGPKHPHVCS
6600			QGPVGPGHVL
5682	39	622	PSRSCLGTMRKWRHREVNLPEVTQQDAVCPAPIPSPGLSAQTGL
1	·		QKIWGTIHCQVCPGAPAWPGSPWHEEMGLLLLVPLLLLPGSYGL
1			PFYNGFYYSNSANDONLGNGHGKDLLNGVKLVVETPEETLFTYQ
			GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIG
<u> </u>			LRHRSFGDYQGRVHLRQD
5683	89	778	GSCGATALITRCLAWSVLISRLAMATYTCITCRVAFRDADMQRA
1			HYKTOWHRYNLRRKVASMAPVTAEGFQERVRAORAVAEEESKGS
	ļ		ATYCTVCSKKFASFNAYENHLKSRRHVELEKKAVQAVNRKVEMM
1			NEKNLEKGLGVDSVDKDAMNAAIQQAIKAQPSMSPKKAPPAPAK
	ļ		EARNVVAVGTGGRGTHDRDPSEKPPRLQWFEQQAKKLAKHSEDD
			SEDEEHDLC
5684	195	677	TWCFRGYLGPRVIMKALDEPPYLTVGTDVSAKYRGAFCEAKIKT
1 1			AKRLVKVKVTFRHDSSTVEVQDDHIKGPLKVGAIVEVKNLDGAY
) ]	ļ	,	QEAVINKLTDASWYTVVFDDGDEKTLRR9SLCLKGERHFAESET
L			LDQLPLTNPEHFGTPVIGKKTNRGRRYE
5685	779	1262	LLLQQPVVHCFLLFPPFRFSHHMIPGPPGPHTTGIPHPAIVTPQ
1			VKQEHPHTDSDLMHVKPQHEQRKEQEPKRPHIKKPLNAFMLYMK
ļ	1		EMRANUVAECTLKESAAINQILGRRWHALSREEQAKYYELARKE
1 1			RQLHMQLYPGWSARDNYVSPSSIPVALHS
5686	128	1181	CTWWQVNITLLDINDNHPTWKDAPYYINLVEMTPPDSDVTTVVA
]	i		VDPDLGENGTLVYSIQPPNKFYSLNSTTGKIRTTHAMLDRENPD
1			PHEAELMRKIVVSVTDCGRPPLKATSSATVFVNLLDLNDNDPTF
·	<del></del>		



SEQ	Predicted	T5	
ID	beginning	Predicted end	
NO:	nucleotide	nucleotide	I IMPORTABLE CELVSTRIDE DEDONARIO DELLA
	location	location	Graduic Acid, Faphenvialaning Carres
i		corresponding	n=nistidine, l=isoleucine K-lyeino
ı	corresponding	to first	"= Leucine, M=Methionine N-Asparagine
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
1			ONLEGATIVE CLEACUE Insertion)
1			QNLPFVAEVLEGIPAGVSIYQVVAIDLDEGLNGLVSYRMPVGMP
ļ			RMDFLINSSSGVVVTTTELDRERIAEYQLRVVASDAGTPTKSST
	Į.		STLTIHVLDVNDETPTFFPAVYNVSVSEDVPR\GSGWSG*AARN
- 1	1		IND VGLINABLIS YFT TGGNVDGKFSVGVRDAIAIDTIAICT DDEEmms 2
5687	17	917	I INDIDEATONG PVGKRHTGTATVFVTVT DVNDVDDT TI OCCIO
i	1 -	317	AAPPAPPDG/PPP/PPPAPPT/PGPAA/ADACCCODDICACTOR
	ĺ	1	OGDGGAAAVGHVLVVPAVGPVRVNDGI,OTDVDDDDT I DODV CCC
ľ		1	LHSDSSYPPDAGLSDDEEPPDAGLPDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
		1	SCRIPSISASE/AAGGOGACTHAKGSETPPPDAGDOTCEDADOD
į.	1		DEPHILIGGEGMYSSEAKLPNSFSCIGLAGTGAGT + CTA CALCING
ļ	İ	}	PPVDPHVCTPSLANPOP\AVGPEASSI.DI.GVSGTGMSA /CARTS
		}	SSPFVAIGSCWLRGIPPPGSGFLCPGRAPGPVPITTHGQEGQGP
			VLDI
5688	1	420	LTKWDLFGNCYRLLKTGIEHGAMPEQVGVYWYS/CLYDSRKLFF
1			*SHMIIRSLL*KVIDDSLGQLPLLRELLL**LNVIDRCIILAYV
ĺ	1		LRVEKTFAITYLKNFTVKVDFSLLGEIPLISMAAILKLWIMKID
			DGYIPAVF
5689	1504	3	
Í			HELSGKHISMVSGNTCNWHPGGHSPGGGGGGEITSKDRGEIPAL
			IWA/RKPIGTWTATKPTHRAG*GGAEEYQPPFQPCEGPRSTSRG
	]		GEG*GHAVGPGREIGKEGSLPFLGPKALGF*SASCQRAFEGGAH
	1		GSTARKPAPATPGTRHPRTMETREVAQGWPAGPRSQFWDQHPHS
1	[		PGEHRPSG\SPLPACPPRAWPKAGAVASATGTG\PQLPGSRGKQ
ł			KLPRTREPPLLQAGWAVRKPPWSEAKEGLGQAGRPSGMDSSAS\
1	1		LATIORKOSPEMCTETALGBHHUAK*BGDDIC*BD*CCCCCCCC
			GAPSIPGPGGEAW*LPOOTSRPKPGPOAV*GE\ GEDGT OGDGGT
1	1		LD-KAPPGSLGPSTOCMYEPTDKHS\GGADAOLEVCTAGERORE
1	ł I		GVELAGPLDAGRLWPGAPSASSSHP*CG*EPAPACACHECGE*
ŀ	]		STATEQUERPRICETSDALADVEGGAES /GOHDWOLDGTT DND /D
5690	1424		GSPPPA*ASAGRRGTVSTLGGGLT.
	1424	58	PSPPAGVCAAPAPLPLLALARRDRRPCSPGAEAAPWQTGGPAID
			GAWRISVSALRRGATG/APCSPGAEAADWOTGGDAIDGA DGD
1 1	1	i	*VKSEBAPKGCGAEGGPGSGPVPPPGAGPGAUACGGPGAPA
		ł	DODARA VIGAASIA KARI, ORI, RDCHUONOUTODO DOS DOGOS -
1		ĺ	GRAMALPEKIKGVAEPPAWAHAGSDAWDAGD*SODM*DDARDRY
}			TITE CONTROL OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY O
]	1		MATERIAL PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPE
	. [	i	SUSTINGE / POARING TAPODR * HCD*CDVDCADCUACEDDDDD .
1			ONE VE DELINE GVA* RHGTS DELGENGGOUDGOUT DOWN
1 !	1		NO BREAFTEST SMEAEKSYWNHOUD DOGGOGGOT INCT. DISCO.
	Į.	í	SEMWGPYSAPRPGTVFLSSFLSPASEEH\PEGSSSFNTPFPPAG
<u> </u>			PEGDPGLNSPGLLP
5691	107	550	ISNDPSPGYNIEQMAKRGKKLVELPYTVKGMDVSFSG_LSFIED
1 1		1	VAHRMLATGECTPEDLCFSLQVMQ*KTGTESWG*RFYIVEQN*S
			GDAPLIFSPYLSLTGNCGFAMLVEITERAMAH\CGSPGGPSLWG
			GVGVYVLLESVPLSYS
5692	1193	548	TQAWTRAEKDRKGSYRALRLHLERGPPT*RGSHPL\QSVPCIQK
		1	PSIESSYPI /CI POCCOPPORIGER COPPT RGSHPL\QSVPCIQK
'	İ	į	PSIFSSYPI/GLPQSGGEPGPVGEQQPVRRPEQPSCGPASRMPL
į		ļ	TSRSVPPGRGALPPDSLSTRKGLPRPSTAGHRVRESGHKVPVSQ
	į.	į	RLNLPVMGATRSNLQPPRKVAVPGPTR*RDQDSKQDFSSKPLQS
5693	1258		VFGLASTQQTLTPADSGPGTGGRDATDAGTDGGGTMGMGMGMG
	1		ALTVVPVRKGTTWWAQPHGCSNLVSRARLDLSSRPSQNTEPQAP
ļ	Į		"VAGPPSSLRPP\SRRR*APEWPKPATGGPCDGLGAPPUDGA-
1	ĺ	1 .	RGE/PGSAPSHAP/PNS2RPSGTRHD/DGDGCDVI.vchcv.ppvc [
5694	3		FEAL VMKSSKEPLWEPLRCCFWVSGFKDDNDVI.D ##
	3	T338 (	GSKEPARSLHRRGSGHKSSAGKWGSVTLSTAGAL C+VOLVO+VIII
1			QRCL\NNLSSEEFNASSSLNSLPSTPTASPPNSTTIT PTDSEIT
!		1 5	SUALSGLSWISESEEKAPKKI.EVDSGGI.KMPDGTGVWDDDDDDDD
1		1 '	CDDSSKGGELKKPISLGHPGSLKKGKTPPVAVTCPTTTTTA OCR.
i		1 4	NAGREBUKATUKGKLAVKNTGLOPSSSDAGDDDI SDAVKDDSS
		:	LARPSTSGSFGYKKPPPATGTATVMQTGGSATLSKIQKSSGIPV
			- THE CONTINUE TO A STATE OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF TH

SEQ	Predicted	Predicted end	Amino agid
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
1.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
j	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	Walter Value, Value,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	boquence	Codon, /=possible nucleotide deletion,
	<del></del>		\=possible nucleotide insertion)
	1		KPVNGRKTSLDVSNSAEPGFLAPGARSNIQYRSLPRPAKSSSMS
1	[	1	VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLKEPTKVASGRTT
			PAPVNQTDREKEKAKAKAVALDSDNISLKSIGSPESTPKNQASH
1	Ì		PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNSNSLDLPSSS
5695	<del>  3</del>	1338	DTTQCI
		1330	GSKEPARSLHRRGSGHKSSAGKWGSVTLSTAGALG*KQLHQ*WT
1			QRCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTIVLRTDSEKR
į	1		SLAESGLSWFSESEEKAPKKLEYDSGSLKMEPGTSKWRRERPES
	1	i ·	CDDSSKGGELKKPISLGHPGSLKKGKTPPVAVTSPITHTAQSAL
-	1		KVAGKPEGKATDKGKLAVKNTGLORSSSDAGRDRISDAKKBBSG
	1		IARPSTSGSFGYKKPPPATGTATVMOTGGSATLSKIOKSSGIDV
]			KPVNGRKTSLDVSNSAEPGFLAPGARSNIOYRSLPRPAKESCMS
	ì		VIGGRGGPRPVSSSIDPSLLSTKOGGLTPSRLKEPTKVASCPTT
	ŀ		PAPVNQTDREKEKAKAKAVALDSDNISLKSIGSPESTPKNOASU
	1		PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNSNSLDLPSSS
5696			DTTQCI
3036	3	1338	GSKEPARSLHRRGSGHKSSAGKWGSVTLSTAGALG*KQLHQ*WT
[ [	ĺ		QRCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTTVI.RTDSFKP
i l	J		SLAESGLSWFSESEEKAPKKLEYDSGSLKMRPGTSKWPPFPDEC
i i	1		CDDSSKGGBLKKPISLGHPGSLKKGKTPPVAVTSPITHTAGSAL
			KVAGKPEGKATDKGKLAVKNTGLORSSSDAGRDRISDAKKDRG
J j			LARPSTSGSFGYKKPPPATGTATVMOTGGSATLSKIOKSSGIDV
1 !			KPVNGRKTSLDVSNSAEPGFLAPGARSNIOYRSLPRPAKSSSMS
1 1			VTGGRGGPRPVSSSIDPSLLSTKOGGLTPSRLKEPTKVASCPTT
}	·		PAPVNQTDREKEKAKAKAVALDSDNISLKSIGSPESTPKNOASU
1 1			PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNSNSLDLPSSS
5697	1110		DTTQCI
309/	1147	47	PSEALSPPACPSAPAPRRSIISRLFGTSPATEAAPPPPEPVPAA
1 1	·		QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKVGAKAAOODS
			DSDGEALGGNPMVAGFQDDVDLEDOPRGSPPLPAGPVPSODITE
1	1		SSEEEAEVAAPTKGPAPAPQQCSEPETKWSSIPASKPRRGTADT
f í	j	•	RTAAPPWPGGVSVRTGPEKRSSTRPPAEMEPGKGEOASSSESDB
1	i		EGPIAAQMLSFVMDDPDFESEGSDTORRADDFPVRDDPSDVTDF
	i		DEGPAEPPPPPKLPLPAFRLKNDSDLFGLGLEEAGPKESSEEGK
1 1	Í		EGKTPSKENKKKKKKGKEEEEKAAKKKSKHKKSKDKEEGKEERR
F600			RRQQRPPRSRERTAA
5698	2	666	GAEAAEPQEDLPPLSQSSRFFQEQQKMNKSLGPVSFKDVAVDFT
1			QEEWQQLDPEQKITYRDVMLENYSNLVSVGYHIIKPDVTSKT.FO
1	j		GEEPWIVEGEFLLQSYPDEVWOTDDLIERIOEEENKPSPOTVET
] ]			ETLI*R/ERGNVPGNTFDVETNPVPSRKTAVTHSLCNSCEP\CE
į į		i	NASSEYISSDGRYARMKADECSGCGKSLLHIKLEKTHPGDQAYE
<u> </u>			ŁuŐ
5699	2	1448	RVRQPPGLWVRRTVPAMQCPAGLSRVPGVAG/DPSLPSFRGPRD
1			EAAHRGTIQTARHTRKLYVQGPASGPPLPRVSTQVAI*DEKPLA
		. 1	RPS/GRTNAPFPQGQKPAGKAAPGPAAAGRVAMR\PGHPGLLAS
			DSQRSSSKGSGWETPVPWS*AQPGWVSGLLLLGDPSGPGSL*RS
1	1		TWLVGGARGPEGSGVRGSGWPSGCSDIGWALAGWNHS*HLDPNT
1 1	ì		WTQKWTGE/SPAPGEEG\VAPAPRGPTAEHGHCELTTESQYSNN
f L	į	I	VPILFQNPSGALRSRRTEPAGWVPPTRHE*DDG*TAAPASGGAP
1 1			VSTPTWAGTP/LNASLGPTDPQGKPGCRPPCALPKPAGPERSA*
1			GGSLGCR/SMLPASSGPPPAPGPRRLAAGAHTSASARCPPAAAA
			GNOPRRPGFAGRAALPGPPHPPSS*RELGGLPGPGW*TLDPLPA
1 !	ſ	!	HPAHPPGSAPPWGALGGWAAARASLPWSPSLCLSFPAVTPVAGL
1 1			FPPGRG
, 1	923	597	
5700			NGHKGVWEINIY*RRSNIHKNSKSESHLNQDHSFPPPTPNSARS
5700	1		
5700			KLHSTGTAKNTGLPLSGAPRQRAVFSGRTICQEFSSCLQCAYLD
5700	59	410	E*CSIASSLIKAILRVSVLSE
	59	410	E*CSIASSLIKAILRVSVLSE IFEKICSDTQEFISPEINPQICSWLIFDKGAK/NHATGKDSLEN
	59		E*CSIASSLIKAILRVSVLSE



SEQ	Predicted	Predicted end	1 mine and
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
ł	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
[	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
5702	. 3	1517	ETFVDPSQCGGIPSDSPHPVITPSRASESSASSDGPHPVITPSR
1	1		ASESSASSDGPHPVITPSRASESSASSDGLHPVITPSRASESSA
ľ	1	1	SSDGPHPVITPSRASESSASSDGPHPVITPSRASESSASSDGLH
	Í	1	PVITPSRASESSASSDGPHPVITPSWSPGSDVTLLAEALVTVTN
ı	1	1	IEVINCSITEIETTTSSIPGASDTDLIPTEGVKASSTSDPPALP
Í			DSTEAKPHITEVTASAETLSTAGTTESAAPHATVGTPLPTNSAT
	i		EREVTAPGATTLSGALVTVSRNPLEETSALSVETPSVVKVSGAA
i	1	•	PVSIEAGSAVGKTTSFAGSSASSYSPSEAALKNETDGETT TMDI
			TTKGPFPTSRDPLPSVPPTTTNSSRGTNSTLAKTTTSAKTTMVD
J			PIATPITARTRETT\A*VOVKNEVSSSCG*VWI.DDVTCI.TDDWO
			KG*CSSSTGNSTPTRLTSRSPYCVSGEANG/PSAAADHUDVAVD
1			GCCP*PGPPPTDCSCVTVLRGTOKVPMKGSMSKDI.TDDVATCDG
5703	14	1115	LTSTGVYVWGGASPVPRGVLGLTLAHVLCFSKEKT
	1 -3	1117	HHKDSRSQGLPRTQECARPELRPLLCPRALWPVTRLSYRCPWQA
	!	,	PRAGIGTKAKPSESHLKLHPGWPSLDROGEPATIGTGTGTCC
	1		RILRWHP*HTAAR*PRWRRLPSSHRWTRHLGVLRVQDKS**VSL
l	[ ]		DPSCRPRFLRTC**YGMRSVASSSNPPPGWSGPGASVFPARPVS
İ	ļ (		ALPTGPRCW*APRGRTRQPCGWPRLSSPHATADWGPGCPLSPSR
}			GSWETAPGS*WCPWL*AARWTGWRTASGASAGLGRAADRPSAWA
			RRVAGLLPGQGLTVRR*H*TAGAPASVRSSQGATRSPAPGGDQC ACGRGPGSC*HPPFWPVSPSSPVPCPSGR*HLRGPLLSAARPRA
			AGWPRHSPHDTQTPEP
5704	23	562	GDYEFDSPYWDDISQAAKDLVTRLMEVEQDQRITAEEAISHEWI
			SGNAASDKNIKDGVCAQIEKNFARAKWKKAVRVTTLMKRLRAPE
1			QSSTAAAQSASATDTATPGAAGGATAAAASGATSAPEGDAARAA
1 1	!		KSDNVAPRRP*LPPQPQMEVPPQPLMAVSPQPPMEASLQPLMGE
5705			SPQP
3703	23	562	GDYEFDSPYWDDISQAAKDLVTRLMEVEQDQRITAEEAISHEWI
1 1	ı ı		SGNAASDKNIKDGVCAQIEKNFARAKWKKAVRVTTT.MKDIDADE
	l l		QSSTAAAQSASATDTATPGAAGGATAAAASGATSAPEGDAARAA
i i	ł	İ	KSDNVAPRRP*LPPQPQMEVPPQPLMAVSPQPPMEASLOPLMGE
5706	1161	610	SPQP
		910	QLGRFXAQDTVAIRKVKEVFGTGAMRHVVILFTHKED*GGQALD
1 1	ŀ		DYVANTDNCSLKDLVRECERRYCAFNNWGSVBEQRQQQAELLAV
1 1	I		IERLGREREGSFHSNDLFLDAQLLQRTGAGACQEDYRQYQAKVE
L 1		ļ	WQVEKHKQELRENESNWAYKALLRVKHLMLLHYEIFVFLLLCSI LFFIIFLF
5707	28	609	
1 1	1		GSPAPTPGFRRRPGRGTPSPGTRHHQGRAEPEPDAPERAPLRR* MFAIQPGLAEGGQFLGDPPPGLCQPELQPDSNSNFMASAKDANE
	1	,	NWHGMPGRVEPILRRSSSESPSDNQAFQAPGSPEEGVRSPPEGA
			EIPGAEPEKMGGAGTVCSPLEDNGYASSSLSIDSRSSSPBPACG
			TPRGPGPPDPLLPSVAQA
5708	44	1925	SFSWEETISPCFPKMPAEPWWLSPVSLGAAGWPGQPRPYLDLPA
1 1	-	İ	QASVSRPHDRA*GEAVSLSLSSGDVCGHTDGGGAGGDDQAVDVD
1	1		PROPETAMPSPRTKQKVRNKVCLLIAIRYSDIPSDVSKAD\GDA
1			GNPHDRSSTAA*LHRRAGAGSLCLSASLLPPSFSLGAPGAPGPI
1 1			RVSPASGGPRKEGROGSGG*AGGGGP\ARTHADI.PCUGEUCCED
			LLK*SDSPVKQLPA\SGQGSGAGMPPVGSSDTLRPRPTGVGGTG
1 1		i	RAAG*CSWQPAACCTPRSO*WAVARSPSRCSRW*PAGGD*PAGE
1 1		l l	SKRRRGP*AAGRSTPAVP*PCS*GGAGRRAYACRTGWGVADED+
1			LEPSGPTSGSAL*TWASHSTGA**SRLCGTAGTGPLCSGSPC*
			AG*RCCCTAASPCGGSGPSHPGSPSAHCLSWSGGRTQPRAPSAH
		1	GRGRAMGSRCVCTCTGLPCPGIPLSGASPGGSGETGAGRSHTLK
] [		1	AARSRLSPRPGSGSRGSY*SHNDNWGTWPAPPSAGHLLVGG*NS
i !	1		QRTSSDH*YTGTRRPWAGPGTRCSTAPSRAAPPVSRCRPPPPPPP
	1		PPRPPRLPAAAS/SGGASGSPAASCSCSCRAPAKPASS/GEAPA PPPRPEPPPPPARRP
5709	2	2031	TTI-CPI-POTEKCIANDERA A DRI COMPANIO
	1	***	ITLCPLPQTEKCLNVVTEAATPLGIYLKARVEAGGLKELEISWG LHQIVVRWGAVVMRAGMGGCRCWGVMAPFAPK/NALSFLVNDCS
			LIHNNVCMAAVFVDRAGEWKLGGLDYMYSAQGNGGGPPRKGIPE
		***	THE TENEDRAL PROPERTY OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE P

Mo: beginning not cotted to location corresponding to first amino acid amino acid residue of saino acid amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid	SEO	Predicted	Predicted end	I Project and the second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second secon
Solitation   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding   Cortesponding				Amino acid segment containing signal peptide
Cortesponding   Coffist   amino acid   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffist   coffi			1	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
corresponding to first amino acid residue of amino acid residue of amino acid sequence  sequence    Province	NO:			Glutamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of amino acid residue of servine, TeThrenine, V-Valine, amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequenc	i	B.		H=H1stidine, I=Isoleucine, K=Lysine,
to first amino acid residue of amino acid residue of servine, TeThrenine, V-Valine, amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequenc	1			L=Leucine, M=Methionine, N=Asparagine,
amino acid sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  seque	ł		Į.	P=Proline, Q=Glutamine, R=Arginine,
### ### ### ### ### ### ### ### ### ##	İ		residue of	S=Serine, T=Threonine, V=Valine.
sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence seq		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Apossible nucleotide insertion		amino acid	sequence	Codon, /=possible nucleotide deletion
LEQUIDPELLADSSERVIVEERSADWINGLEGLINEUPENSPEIDER ALREPOKT PERLUPHICELUGAN KEV REPRAFILONCARGEGEM SIRRIVETINLESIGIKEPAEKQKFYOGLISKSLDAFEDDEGKING SIRRIVETINLESIGIKEPAEKQKFYOGLISKSLDAFEDDEGKING SIRRIVETINLESIGIKEPAEKQKFYOGLISKSLDAFEDDEGKING WESSTDRAMRIRLLQOMEGPICYLDEFTUNTOIPPHUVHIGHTUN NEALBERGYTVEMILLAEKAINEANINMELMKHERADKAGEQPT RONTTUCLGKIGSYLSASTRHEVLTSAFSRATEDPFABSRUNG LEFAATHALISMNOLGAKLIPULGAN EVENDORFAARS. FISSICLESVSEDPTOLESVEROVHAASSPORGAAASSAGKARAINE STERSTLESVSEDPTOLESVEROVHAASSPORGAAASSAGKARAINE STERSTLESVSEDPTOLESVEROVHAASSPORGAAASSAGKARAINE STERSTLESVSEDPTOLESVEROVHAASSPORGAAASSAGKARAINE STERSTLESVSEDPTOLESVEROVHAASSPORGAAASSAGKARAINE STERSTLESVSEDPTOLESVEROVHAASSPORGAAASSAGKARAINE STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV LOUDGYRKUTEEPHERADERVSESTEDVILVISGLASSESSELD STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESVSELDAFTATOORV STERSTLESSTLESVSELDAFTATOORV STERSTLESSTLESVSELDAFTATOORV STERSTLESSTLESSTLESVSTATOORV STERSTLESSTLESVSTATOORV STERSTLESSTAT		sequence	] -	\=possible nucleotide insertion\
ALREPGKIPKTLVEHYCELVGANPEVLPENEARFLUNCRAPGGFM SIRRYTETINLPLEEGIG KERPAGKYFFGLELSADPEPDFCHH VLPGLLTAREFGNAGAVVLTPLEKVGKFLGAERYGOKI 1PVVVK MESSTDRAMT RILLQOMRG FJQLDEPTVTDTOT PHVVHGFLDT REATREQTVKSMLILAPKLMSANLAVELMHIRAKLOAKDEGGPI RCHTTVLCJKGSYLASATERKULTSAFSANGAMATO LGFAATHALYSMNDCAQKILPVLCGLTVDEKSVRDQAFKAIRS. FLSKLESVSEDPTOLEEVEKVHAASSPGHAGGARSAGKGAVTG USSLITSKLI RSHPTTAPTETINIPQRPTEVVAPAPPTPVPATPT TSGMRTGERKUTTABDSTADRINDDEMMSLEASAGKAVTG USSLITSKLI RSHPTTAPTETINIPQRPTEVVAPAPPTPVPATPT TSGMRTGERKUTTABDSTADRINDDEMMSLEASAGKAVATG USSLITSKLI RSHPTTAPTETINIPQRPTEVLAVAGKI RGLLGTGLA MALKGATSI **ATTAGGRY  1 562 ITGGSTLSCEVELMARRAKTI DSFTQNGTRLVVI TIGGLACEGOK MALKGATSI **ATTAGGRY USSLITSKLI RSHPTTAPTEN TOLOGRIFLAV LGANGATAGKA **ATTAGGRY USSLITSKLI RSHPTALGRY USSLITSKLI RSKDPTAPTEVLAVI TALAINOMASVPSGFK MALKGATSI **ATTAGGRY USSLITSKLI RSKDPTAPTEN TALAINOMASVPSGFK MALKGATSI **ATTAGGRY USSLITSKLI RSKDPTAPTEN TALAINOMASVPSGFK MALKGATSI **ATTAGGRY USSLITSKLI RSKDPTAPTEN TALAINOMASVPSGFK MALKGATSI **ATTAGGRY USSLITSKLI RSKDPTAPTEN TALAINOMASVPSGFK MALKGATSI **ATTAGGRY USSLITSKLI RSKDPTAPTRAPHT **ATTAGGRY USSLITSKLI RSKDPTAPTRAPH **ATTAGGRY USSLITSKLI RSKDPTAPTLFFF**S **LQRHILDQUTF**LAN LSEERGHLFESS*/WITTPHALK*/FEIHEHLGSHEGHWTLFF*LL QIL USERGHLFESS*/WITTPHALK*/FEIHEHLGSHEGHWTLFF*LL QIL USERGHLFESS*/WITTPHALK*/FEIHEHLGSHEGHWTLFF*LL QIL SERGHLFESS*/WITTPHALK*/FEIHEHLGSHEGHWTLFF*LL QIL SERGHLFESS*/WITTPHALK*/FEIHEHLGSHEGHWTLFF*LL SLESSALRCADLTLPEDISQLCKDINNYLAERSIEEVYYLWGL AGGDLKELUNNERLIVETHESS*/WITTPHKAPK SLESSARATADLTLPEDISQLCKDINNYLAERSIEEVYYLWGL AGGDLKELUNNERLIVETHESS*/WITTPHKAPK SLESSARADLTLPEDISQLCKDINNYLAERSIEEVYYLWGL AGGDLKELUNNERLIVETHESS*/WITTPHKAPK SLESSARADLTLPEDISQLCKDINNYLAERSIEEVYYLWGL AGGDLKELUNNERLIVETHESS*/WITTPHKAPK SLESSARADLTLPEDISQLCKDINN ILFERENTETIOLITYPHKAPK SLESSARADLTLPEDISQLCKDINN ILFERENTETIOLITYPHKAPK SLESSARADLTHENTETIOLITYPHTYPHKAPK SLESSARADLTREATH SLESSARATHATARAKTAATURGT SLESSARADLTREATH SLESSARADLTREATH SLESSARATHATARAKTAATURGT SLESSARADLTREATH SLESSARADLTREATH SLESSARATHATARAKTAATURGT SLESSARAD		<del>                                     </del>	<u> </u>	LECYDDEL ADSCEDIADER DE DIMERICAL TURISMONT DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA DE LA COLONIA
SNR.FVETNI.FLEETGI KEPAEKOKEF POELS KSLDAPFEDFECHK VLPOLLTARE PERONAGAVILTI-ENVOKELSAEROKET POEVAL I PUVVA MESSTDRAMRIRLIA.PULMERALIAVE MIMITERATIOAKOEGGET REATREUTVESMALLAP PLINERALIAVE MIMITERATIOAKOEGGET REATREUTVESMASTERIAVI.STA-STRATED FFAPSRVAGV LGFAATHALI YSAMOLOGAILI-PULVOGLITUDE ENDAPFEVPATPY TEGRIMETORE PERONAGANA SAGAMATO VSSLTIKKLI REMPTTAPPETIN TOO PETPEV PASTAVAGV USSLTIKKLI RASOON TOO PETVAGOTE ON THE STRATEGE PETVAGOTE ON THE STRATEGE PETVAGOTE ON THE STRATEGE PETVAGOTE ON THE STRATEGE PETVAGOTE ON THE STRATEGE PETVAGOTE ON THE STRATEGE PETVAGOTE ON THE STRATEGE PETVAGOTE ON THE STRATEGE PETVAGOTE ON THE STRATEGE PETVAGOTE ON THE STRATEGE PETVAGOTE ON THE STRATEGE PETVAGOTE ON THE STRATEGE PETVAGOTE ON THE STRATEGE PETVAGOTE ON THE STRATEGE PETVAGOTE ON THE STRATEGE PETVAGOTE ON THE STRATEGE PETVAGOTE ON THE STRATEGE PETVAGOTE ON THE STRATEGE PETVAGOTE ON THE STRATEGE PETVAGOTE ON THE STRATEGE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PETVAGOTE PET			1	AL DADOCKI DETERMINATION OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE
VLPQLLTAREFGNAGAVVLTPLEKVGKFLSAERYQGKIT IPVVVK   MPSSTDRAMRILLQQMBGTQTOLPETVVTVGTPLOT    NPAIRSQTVKSMLLLAPKLMSADALNVELMHIFARLQANDGQGFI     RCNTTVCLGKIGSYLSASTHRUTUSASPSATGAPFAPSRVAGV     LGFAATHALYSMNDCAQKILPVLCGLTVDPEKSVRDQAFKAIRS     FLSKLESVSEDPTQLEPVEKQVHAASSPGMATCH     VSSLTSKLIRSHPTTAPTETNITQRPTTEWVAPAPTPVPATPT     TSGMHETQEBEKDYTABGSSTARRHDDEMGSASASAGWATUTC     VSSLTSKLIRSHPTTAPTETNITQRPTTEWVAPAPTPVPATPT     TSGMHETQEBEKDYTABGSSTARRHDDEMGSASAGWATUTC     VSSLTSKLIRSHPTTAPTETNITQRPTTEWVAPAPTPVPATPT     TSGMHETQEBEKDYTAGGSTARRHDDEMGSHASSAGWATUTC     SGLTAKAVLSQQNSTSTTTNPPNPQSTTAAGK\RGLLGTGLA     GAKLPGATS **HYTAGGRV     VLQNLDTVALVFLKSGPF1ATFASDPHII IKAINONLSSVFSGFK     LNGHDYMENTVALEVFLNSRGL/RQ/LGENDS*     COLLOGYRKLJTSKSPF1ATTPHLK* /*PEIHBLISCHEGHTPLFLM     SGLTAKAVLSQQRPSLPHECAPHFS**SLQRHTINLDQGIP*LLM     LSEERGHLFSSJ/INTTPHLK* /*PEIHBLISCHEGHWTLFFLL     GIL	ŀ	1	İ	ADRIVERTED TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF
MESSTDRAMERILLADRIADIANIAN DE MENTAL NA PRATECTIVA MILADRIADIAN DE MENTAL NA PRATECTIVA MILADRIADIA NA PROPERTIA DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE MENTAL DE				SNRFVEINLFLEEIQIKEPAEKQKFFQELSKSLDAFPEDFCRHK
NPATROTYCKSMLLLAPKLMENATLAVELMHIPARLOAKDOGOFT   RCNTTVCLGKGSYLSASTHRUNISASSPARSPASSRAWGMATOR   LGFAATHALYSMNDCAQKILPVLCGLTVDPEKSVRDQAFKAIRS.   FLSKLESVSDPTQLEPVEKOVHAASSPGMATOR   VSSLTSKLIRSHPTTAPTETNITQRPTTEWVPAPAPTPVPAPATPT   TSGMHETQEEDKTTABDSSTADRHODEMOSEASSAGWGMATOR   VSSLTSKLIRSHPTTAPTETNITQRPTTEWVPAPAPTPVPAPATPT   TSGMHETQEEDKTTABDSSTADRHODEMOSEASSAGWGMATOR   VSSLTSKLIRSHPTTAPTETNITQRPTTEWVPAPAPTPVPAPATPT   TSGMHETQEEDKTTABDSSTADRHODEMOSEASSLAGKAGKAGUATOR   VSSLTSKLIRSHPTTAPTETNITQRPTTEWVPAPAPTPVPATPT   TSGMHETQEEDKTTABGSSTADRHODEMOSEASSLAGKAGKAGLIGTGLA   GAKLPGATS-SYTTAGGRV   VLQNLDTWALPFAKSGPT1AFTASDPH1 I I KAINONLASVYSGFK   LINGHDYMENTVALPVFLNSRGL/RO/LOENFS-LOQOMETPHA   OLLGGYRK/LAFSKAPTAFTAGRV   OLLGGYRK/LAFSKAPTAFTAFTAFTAGRV   CLAOPTNIKDDAT   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE				VLPQLLTAFEFGNAGAVVLTPLFKVGKFLSAEEYQQKIIPVVVK
RONTTVCLOKIGSVLGASTRIRRUTASFRATROPPASPRAGUA  LGFAATHINLYSMIDCAGAK LEPVLGGITVDEEKSYRODAR KAIRS. FLSKLESVSEDPTOLEEVSKOVHAASS PGMGGAASSAGWAVTG  VSSLTIKLI TSHPTTAFTTNI POPTIP SEPAPTPY TSGMBETGEERDKTAERSTALORDOEDMGSLEGEASSVLAQOD  DMSTGGGYSRAGGVS TPTTYDPWINGSPTCAGKK RGLLGTGLA  GAKLPGATS*RYTAGGRV  1 562 IFGSTIGSVELMARMAKTIDSFTONTRLWII DGLDACEDOK  VLONLDTVRVLFSKOPFLAIFASDPHI ITKAINONLASVEGERK  \LINGHDYMRIVHLPPVILANSKCL/RG/LGGACKOR  LINGHDYMRIVHLPPVILANSKCL/RG/LGGACKOR  LINGHDYMRIVHLPPVILANSKCL/RG/LGGACHOR  STALAVLSQORPELHIECHEPTS*SLOPPS*LOQMGTPHA  GILGGYRKCHTEFEHRTALGR*QNUARQPSIDG*DAIGFELYV  CITAIONTIKHODAT  5711 1526 1130 RRHPFGWTTVTGRAFSHHDVAPTSTPVLEYPDSAGPFTVKSESS  SOLKAKUSQORPELHIECHEPTS*SLOPPTS*LOQMGTPHA  GILGGYRKCHTEFEHRTALGR*QNUARQPSIDG*DAIGFELYV  LGERGHLESS/IWTTPHNIK*/FEIHBHLGSHEGHWTLFFLL  GIL  5712 3 1391 GRKLPGSLDISERLKFLLTLDCVUDTLIVLAEBHGCLDII INELD  LGERGHLESS/IWTTPHNIK*/FEIHBHLGSHEGHWTLFFLL  GIL  SETVIDLI INKCLTPHPEKRFTPDELMKOKUSVPLIVLADEDLII INELD  AGGDLKELVAVKEI IESKPH TCHLPRFLESSPLJYLYTPFKAP  SLFSSSLRCADLTLPEDISGLCKDINNDVLAERS IEBVYLLWG-  AGGDLKELVAVKEI IESKPH TCHLPRFLESSPLJYLYNFFKAP  SLFSSSLRCADLTLPEDISGLCKDINNDVLAERS IEBVYLLWG-  AGGDLKELVAVKEI IESKPH TCHLPRFLESSPLJYLTMFFKAP  SLFSSSLRCADLTLPEDISGLCKDINNDVLAERS IEBVYLLWG-  AGGDLKELVAVENI ISKPH TCHLPRFLANDSHIPTINGOL  SLCAPPLINNFMSELUTYCOMEN IEDPTORMEN PLOTYMOLD  EARVOLP PLUTAFOLM TOLAR TENERGEN PLOTYMOLD PLOTYMOLD  EARVOLP PLUTAFOLM TOLAR TENERGEN PLOTYMOLD PLOTYMOLD  EARVOLP PLUTAFOLM TOLAR TENERGEN PLOTYMOLD PLOTYMOLD  SCHLENBEG SCHLARADAN STALLTUR SCHLENDEN PLOTYMOLD  TACCGRRGAQVOHLBPREDITANE*DPHLREVWPOLPTSATSP  *RAVLTSSCHSCOGG,*A-ACHARAVENSHIPLOTYMPIC  LTVFSGMLARADAN ADDITEDERS*HLLCOVSTR  *TACCGRRGAQVOHLBPREDITANE*DPHLREVWPOLPTSATSP  *TACCGRRGAQVOHLBPREDITANE*DPHLREVWPOLPTSATSP  *TACCGRRGAQVOHLBPREDITANE*DPHLREVWPOLPTSATSP  *TACCGRRGAQVOHLBPREDITANE*DPHLREVWPOLPTSATSP  *TACCGRRGAQVOHLBPREDITANE*DPHLREVWPOLPTSATSP  *TACCGRRGAQVOHLBPREDITANE*DPHLREVWPOLPTSATSP  *TACCGRRGAQVOHLBPREDITANE*DPHRLREVMPOLPTSATSP  *TACCGRRGAQVOHLBPREDITANE*DPHRLREVMPOLPTSATSP	j		f	MFSSTDRAMRIRLLQQMEQFIQYLDEPTVNTQIFPHVVHGFLDT
IGFAATHNLYSMNDCAQKLLPULGGITVUPERSVRDQAFKAIRS   FISALESVSEDPTOLESVSKOVHAASS GRAANSWAWATG   VSSLTSKLIRSHPTTAFTETNIPGRFTPEGVPAAPETPYPATPT   TSGMWETGGEPKDTAEDSSTADRIDDEBUGSLEGEASSVLAQQD   DMSTGGCVSRASQVS\TPTTYPPPPBYPAPPTPYPATPT   TSGMWETGGEPKDTAEDSSTADRIDDEBUGSLEGEASSVLAQQD   DMSTGGCVSRASQVS\TPTTYPPPPPPGVPPAAPETPYPATPT   TSGMWETGGEPKDTAEDSSTADRIDDEBUGSLEGEASSVLAQQD   DMSTGGCVSRASQVS\TPTTYPPPPPPGSPTGAAGK\RGLLGTGLA   GAKLPGATS** SYTTAGGWS   VLONLDTVSVLFSKOPP1AIRAFSDPHILTAKAINONLASVPSGEK   VLONLDTVSVLFSKOPP1AIRAFSDPHILTAKAINONLASVPSGEK   VLONLDTVSVLFSKOPP1AIRAFSDPHILTAKAINONLASVPSGEK   VLONLDTVSVLFSKOPP1AIRAFSDPHILTAKAINONLASVPSGEK   VLONLDTVSKLFSKOPP1AIRAFSDPHILTAKAINONLASVPSGEK   VLONLDTVSKLFSKOPP1AIRAFSDPHILTAKAINONLASVPSGEK   VLONLDTVSKLFSKOPP1AIRAFSDPHILTAKAINONLASVPSGEK   VLONLDTVSKLFSKOPP1AIRAFSDPHILTAKAINONLASVPSGEK   VLONLDTVSKLFSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPSKOPP1AIRAFSDPHILTAKAINONLASVPS				NPAIREQTVKSMLLLAPKLNEANLNVELMKHFARLQAKDEQGPI
LGFAATHNLYSMNDCAQKLLPVLCGUTVUPEKSYRQAFKAIRS   FLSKLESVEDPTOLEEVEKOVHAASS FEMGGAAASWAGWATT   VSSLTSKLIRSHPTTAFTETNIPGPTPEGVPAAPTPT   TSGMWETGEBEKDTAGEDESTADRRUDEDWGSLEGEAESVLAQQD   DMSTGGCVSRASQVS\TPTTAPPTBVPAPTPT   TSGMWETGEBEKDKTAGEDSTADRRUDEDWGSLEGEAESVLAQQD   DMSTGGCVSRASQVS\TPTTAPPTPPPPGSPTGAAGK\RGLLGTGLA   GAKLPGATS *RYTAGGWS	ŀ		ł	RCNTTVCLGKIGSYLSASTRHRVLTSAFSRATRDPFAPSRVAGV
FLSKLESVSEDPTOLEEVSKOVHAASSEGMGGAAASMAGMAVTG VSSLTKALTSHPTTAPTETNIPOPETPENPAPPTPT TSGMWETQEEDKDTAEDSSTADRADDEDMGSLEGEAESVLAQQD DWSTGGGVSRASQVS\TPTTYPPPNPGSPTGARGK\RGLLGTGLA GAKLPGATS*RYTAOQRV  1 562 IFGSTISCSVELMARNAKTIDSFTONGTRLWVIJDGLDACEDDK VLQNLDTVRVLFSKGPFIAIFASDPHIIKANIONINNSVSGFK \LUNGHDTVRNVLFSKGPFIAIFASDPHIIKANIONINNSVSGFK \LUNGHDTVRNVLFSKGPFIAIFASDPHIIKANIONINNSVSGFK \LUNGHDTVRNVLFSKGPFIAIFASDPHIIKANIONINNSVSGFK \LUNGHDTVRNVLFSKGPFIAIFASDPHIIKANIONINNSVSGFK \LUNGHDTVRNSKGL/RG/LGRFS+LOQMGFFHA OILOGYRKVLTEFFHRTAIGR*QNIUARQPSIDG*DALGFELYV CITAIPNTKNDAT  5711 1526 1130 RRHPFGWTTVTQEAFSHHUVAFTSTFVLEYPDSAQPFTVKSESS SGJAKAVLSQGRPSLFHEGAFHFFS*SLGGGFTVKSESS SGJAKAVLSQGRPSLFHEGAFHFFS*SLGGFHFFFS*LDGDTFLKFL JSSLRCALTLT,PEDISQLCKDINNDVLAERSIGHTLFLLD  5712 3 1391 GRKLFGSBISERLKFLLTLDCVDDTLIVLAEERGCLDIIKELP STUDIINKCLTPHPSKRFTPDELMKDKVSSPJLYTPPFKPA SLFSSSIRCADLTLPEDISQLCKDINNDVLAERSIGEDVYLJKGL AGGDLKELVVKEITISKPDFDELMKDKVSSPJLYTPFKPA SLFSSSIRCADLTLPEDISQLCKDINNDVLAERSIGEVYLJKGL AGGDLKELVVKEITISKPDFDELMKDKVSSPJLYTPFKPA SLFSSSIRCADLTLPEDISQLCKDINNDVLAERSIGEPVYLJKGL AGGDLKELVVKEITISKPDFDELMKDKVSSPJLYTPFKPA SLFSSSIRCADLTLPEDISQLCKDINNDVLAERSIGEPVYLJKGL AGGDLKELVVKEITISKPDFDELMKDKVATADLIDVFIKNOJINK EARVDIPPLINKENITETDIOCHTOLINENITETTICHTSLILLPYSINSI NELSAAATHPLIIREKDTFDLARTICHTVYLJKFFLKNISHVIJQEV LTVFSGMLAHPDPLISNHNINGIGFIDPLVAIFWFLTMFTHVFPL HKIFHLW\DTLLIGEELPPLLYME  5713 634 284 PVCAVPOVBMPVLDREDGGGGG-AARLBAVVSHIPDLVYRNGLD SLCAPFLVILNFNNEALVYACHSRFTLEXPPLKTMFTHVFPL HKIFHLW\DTLLIGEELPPLLYME TACKCSRGGADVGHLPREDIRAB-PPHLREVMPDLPTSSATSP *RAVITSSCSSILLGADARASHILLCGVSFT *RAVITSSCSSILLGADGOT-SSSSSTNGSGGGSSGFRAGAAD *RAVITSSCSSSSTNGGSGGSGFRAGAAD *RAVADAAAAAASVALADTPPFRRNKSGIISGGGSSGFRAGAAD *RAVADAAAAAASVALADTPPFRRNKSGIISGGGGSGFRAGAAD *RAVADAAAAAASVALADTPPFRRNKSGIISGGGGSGFRAGAAD *RAVADAAAAAASVALADTPPFRRNKSGIISGGGGSGFRAGAAD *RAVADAAAAAA*CVACAABPG *URRATLFT*RATTAGAWNYGNSIFVYSGSPLTUDLBSAGG *TOAPSGROGAGAKFTEGHALDFASSVILTMPCSLAGGG-PPGC *VRNTPLE**LGLGSGFTTTOAGAGSGFTGAAAACVACAABAC *GLBUT-SGFTTIVGGYSCCMPLKT *PLIKEGSGRGFTGAAACAVACAABACCAC		ľ	!	LGFAATHNLYSMNDCAQKILPVLCGLTVDPEKSVRDOAFKAIRS
VSSLTSKLIRSHPTTAPTETNIPGRPTPBUYPAPTPT   TSGMWETGEBENDTAREDESTADRINGDEMOSIEGEAESVLAQQD   DMSTGGGVSRASGVSTPTTAPPTPPPBYPSTPTAPT   TSGMWETGEBENDTAREDESTADRINGDEMOSIEGEAESVLAQQD   DMSTGGGVSRASGVSTPTTAPPPPPPSPTGAAGK\RGLLGTGLA   GAKLPGATS **SYTAGGWS			1	FLSKLESVSEDPTOLEEVEKDVHAASSPGMGGAAASWAGWAVTG
TSGMETQEEDKDTAEDSSTADWDDEDMGSLEQBAESVLAQQD DMSTGGGVSRAGVGY-TRYTNPOPROTAGKK_RGLIGTGLA GAKLPGATS*RYTAGQRY GAKLPGATS*RYTAGQRY			Ì	VSSLTSKLIRSHPTTAPTETNIPOPPTPECUPAPAPAPTPUPATPT
DMSTGGVSRASQVS/TPTTNPPNPGSPTGAACK/RGLLGTGLA GAKLPGATS*RYTAGQRV  1 562 IFGSTISCEVELMARMAKTIDSFTONQTRLVVIIDGLDACEOOK VLONLDIVRVLFSKOPFIAT FASDPHILIKA INONLMSVPGSFK VLONLDIVRVLFSKOPFIAT FASDPHILIKA INONLMSVPGSFK VLONLDIVRVLFSKOPFIAT FASDPHILIKA INONLMSVPGSFK VLONLDIVRVLFSKOPFIAT FASDPHILIKA INONLMSVPGSFK VLONLDIVRVLFSKOPFIAT FASDPHILIKA INONLMSVPGSFK VLONLDIVRVLFSKOPFIAT FASDPHILIKA INONLMSVPGSFK VLONLDIVRVLFSKOPFIAT FASDPHILIKA INONLMSVPGSFK VLONCOMETFIA OLIGGTKKYLTEPFIRTHAGR*ONLVARQES IGFALTIVLOCOMETFIA OLIGGTKKYLTEPFIRTHAGR*ONLVARQES IGFALTIVLOCOMETFIA OLIGGTKKYLTEPFIAT FASDPHILIKA INONLMSVPGSFK VLONCOMETFIA CILIOPATNIKODAT  STATE  5711 1526 1130 RRHPFQNTTVTQFASSHHDVAFTSTPVLFYPDSAQPFIVKSESS SQLAKAVLSQQRPSLFHECAPHFTS*SLQRITINLDQGIP*LLM LSEBROHLFESS/WTTPTNIKA*/FETHELGSHEGHTLFFLLM  5712 3 1391 GRKLFGSLDISERLKFLLTLDCVDDTLIVLAEEHGCLDITKELD FUVDINGNIKCLTFHPSSKYPTDELMKOKVPSEVSPLYTPPTKRA SLFSSSLRCADLTLPEDISQLCKDINNDYLAERS TEEVYTLWCL AGGGLEKELVANET IRSKPPITCHEN FEDGESFGQGRDSS/ TFR*YHWDLVVMPAKK*IBRCGRSILD*ITAKTSLLLPSMSM NELSAAATHPLITERSKRFPTFOLMRITILDFULKAPYYKKONJIK EARVDIPPLMRGLTWARLLGVEGRSILD*ITAKTSLLLPSMSMSM NELSAAATHPLITERSKRFPTGVLMRITILDFULKAPYYKKONJIK EARVDIPPLMRGLTWARLLGVEGRSILD*ITAKTSLLLPSMSMONIK EARVDIPPLMRGLTWARLLGVEGRSTLD*ITAKTSLLLPSMSMONIK EARVDIPPLMRGLTWARLLGVEGRSTLD*ITAKTSLLTPTTVFPL  5713 634 284 PVCAVVVDRWPULPREDGGGGGL*AKLPRFTMTFTMYPL  5714 212 613 WGLGLGPTWSLGGSDDAGGSSSSTNGSGGSGSGFKAGAAD KSAVUARAAPASSHAUDTPPPRRRNNSGI ISEPLANSLRRSRPLS  WGLGLGPTWSSLGGGSDDAGGSSSSTNGSGGSGSGGFKAGAAD KSAVUARAAPASSHAUDTPPPRRNNSGI ISEPLANSLRRSRPLS  4 RAVLTSPCSHLEBGDAAGSSHALCUSFH WGLGLGPTWSSLGGGSDDAGGSSSSTNGSGGSGSGGFKAGAAD MA  5715 131 1979 ESASOGKRSKCLILTLKLELGGSAPKKTSARPSSLLHLPHSVENN  DSTCHEHHEGILAARVTPVP\SGKPCRPPHPAAN  FRPFGS/SDLLOGRPGUADKAPVTAASPLPRWCLEPPHPAAN  PRPPGS/SDLLOGRPGUADKAPVTAASPLPRWCLEPPHPANS PRPPGS/SDLLOGRPGHCANAVANGESADATHPHCEEKTTMS  OTRHETKEP-RKTPRAG/NNYCMST EVGSPOLTVULLBSAGG TOAPSGRGGBAGGHTGAGHAPVTVASPSPLOGRACHAPVORPH VWRNIPLE*LGLERGFGDAGASGRGGPGAGACPER/GG*OPT GLI/GUPGTDPKRGGRKPGGSGCPTQATTWSGPSSPLOPWIP  PKNTACHS	1	i		TSCHWETOFFDKDTAFDSSTADDWDDEDWCGI FORARGULA COD
5710 1 562 IPGSTISCEVELMARMAKTIDSFTQNQTRLWVITDGLDACEQOX VLQNLDTVRVLPSKSPFIAIFASDPHILIKAINQNINSVPSGFK VLQNLDTVRVLPSKSPFIAIFASDPHILIKAINQNINSVPSGFK VLQNLDTVRVLPSKSPFIAIFASDPHILIKAINQNINSVPSGFK VLQNLDTVRVNINTHURDVITSKGL, PGLOEPFS + LQQNGFFHA CHANGHYMNIVHLDVFLNSRGL, PGLOEPFS + LQQNGFFHA CHANGHYMNIVHLDVFLNSRGL, PGLOEPFS + LQRNTFREDE CHAPFEFT VLFYDDSAQFFVVKSESS SQIAXAVLAQQRPSLFHECHESHSGHTTINLDQGIF + LLW QILL  5711 1526 1130 REHFFQNTTVTOGASSHIDVAFFSTPVLFYDDSAQFFVVKSESS SQIAXAVLAQQRPSLFHENLCSHEDHTINLDQGIF + LLW LGEBRQHLFESS/LWTPRNLK*/PEHBLESHSGHTUFFLL GILL  5712 3 1391 GRKLFQSLDISERLKFLLTLDCVDDTLIVLAEEHGCLDIIKELP ETVIDIIANKCLTFHPSKRFTPDDEIMKOKVPSEVSPLYTPFTKPA SLYSSIRCADITLPEDISQLCKNINDVLAERSIEEVYLWCL AGGDLEKELVNKEI IRSKPPICTLDRVFLFEDGSEGQGRDRSS/ TFR*YHINDTVNPAKK* IRSCWGRSID ITLMTSLLLPYSNSN NELSAAATLPLIIREKDTEYQLNRIILFDRLLKAAVYKKNQIIKK EARVOLIPPHRQGIWAALLOVEGAIHAKVDAIDKDTEIPTDRQI EVVIPRCHQYDELLSSSEGHAKFRRVLKAMVVSHPDLYYNGGLD SLCAPPLVLINFNNSALVYACMSAFIT PKYLVNFFLKONSHVIQEY LTVYSQMIAFHDPEISSHLUSSGSHAKAALLOVEGAIHAKVDAIDKDTEIPTDRQI EVVIPRCHQYDELLSSSEGHAKFRRVLKAMVVSHPDLYYNGGLD SLCAPPLVLINFNNSALVYACMSAFIT PSULVATPLORTSPLOYDELLSSEGHAKAAVALADASHLOVESH WEGILGFFILWS TACRCSRRGAQVOILIPPSILVSSH VACHAGE PSULVAN VALVASAADASHALCOVSPH "RAVUTSPCSHLOSGADASHALCOVSPH "RAVUTSPCSHLOSGADASHALCOVSPH "RAVUTSPCSHLOSGADASHALCOVSPH "RAVUTSPCSHLOSGADASHALCOVSPH "RAVUTSPCSHLOSGADASHALCOVSPH "RAVUTSPCSHLOSGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG				DWSTGGOVSBACOVC \ TRETTY DRIVE OF DWG A ROW ROLL OF THE
5710  1 562   IPGSTISCEVELMARMAKTIDSFTONQTELLVIIDGLDACEODX   VLONLDTVRVLFSKOPPIATFASDPHIIIKANIONLNSVPSGFK   VLONLDTVRVLFSKOPPIATFASDPHIIIKANIONLNSVPSGFK   VLONDTVRVLFSKOPPIATFASDPHIIIKANIONLNSVPSGFK   VLONDTVRVLFSKOPPIATFASDPHIIIKANIONLNSVPSGFK   VLONDTVRVLFSKOPPIATFASDPHIIIKANIONLNSVPSGFK   VLONDTVRVLFSKOPPIATFASDPHIIIKANIONLNSVPSGFK   VLONDTVRVLFSKOPPIATFASDPHIIIKANIONLNSVPSGFK   VLONDTVRVLFSKOPPIATFASDPHIIIKANIONLNSVPSGFK   VLONDTVRVLFSKOPPIATFASDPHIKKESES   SCAIKANIOLOGPESLFEICAPHFFE'S SLQRHTINLDQGIF*LLM   LSEBROHLFES; / WTTPHNLK* / FEHRHIGSHEGHTLFFLL   USBERCHLFES; / WTTPHNLK* / FEHRHIGSHEGHTLFFLL   USBERCHLFES; / WTTPHNLK* / FEHRHIGSHEGHTLFFLL   USBERCHLFES; / WTTPHNLK* / FEHRHIGSHEGHTLFFLL   USBERCHLFES; / WTTPHNLK* / FEHRHIGSHEGHTLFFL   USBERCHLFES; / WTTPHKASDE   USBERCHLFES; / WTTPHKASDE   USBERCHLFES; / WTTPHKASDE   USBERCHLFES; / WTTPHKASDE   USBERCHLFES; / WTTPHKASDE   USBERCHLFES; / WTTPHKASDE   USBERCHLFES; / WTTPHKASDE   USBERCHLFES; / WTTPHKASDE   USBERCHLFES; / WTTPHKASDE   USBERCHLFES; / WTTPHKASDE   USBERCHLFES; / WTTPHKASDE   USBERCHLFES; / WTTPHKASDE   USBERCHLFES; / WTTPHKASDE   USBERCHLFES; / WTTPHKASDE   USBERCHLFES; / WTTPHKASDE   USBERCHLFES; / WTTPHKASDE   USBERCHLFES; / WTTPHKASDE   USBERCHLFES; / WTTPHKASDE   USBERCHLFFT   WTTPHKASDE   USBERCHLFFT   WTTPHKASDE   USBERCHLFFT   WTTPHKASDE   USBERCHLFFT   WTTPHKASDE   USBERCHLFFT   WTTPHKASDE   USBERCHLFFT   WTTPHKASDE   USBERCHLFFT   WTTPHKASDE   USBERCHLFFT   WTTPHKASDE   USBERCHLFFT   WTTPHKASDE   USBERCHLFFT   WTTPHKASDE   USBERCHLFFT   WTTPHKASDE   USBERCHLFFT   WTTPHKASDE   USBERCHLFFT   WTTPHKASDE   USBERCHLFFT   WTTPHKASDE   USBERCHLFFT   WTTPHKASDE   USBERCHLFFT   WTTPHKASDE   USBERCHLFFT   WTTPHKASDE   USBERCHT   USBERCHLFFT   WTTPHKASDE   USBERCHLFFT   WTTPHKASDE   USBERCHLFFT   WTTPHKASDE   USBERCHLFFT   WTTPHKASDE   USBERCHLFFT   WTTPHKASDE   USBERCHT   USBERCHT   USBERCH   USBERCHT   USBERCH   USBERCH   USBERCH   USBERCH   USBERCH   USBERCHT   USBERCH   USBERCH   USBERCH   USBERCH   USBERCH   USBERCH   USBERCH   USBERCHT	1	1		CAN DEATH CORE + DATE OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE P
VIQUIDITARVIES KOPF TAI FAS DINT INGLINE COMBET HA VIQUIDITARVIES KOPF TAI FAS DENT SI LOCAMETTHA OLIGINE THA OLIGINE THA OLIGINE THA OLIGINE THA OLIGINE THA OLIGINE THA OLIGINE THA OLIGINE THA OLIGINE THA OLIGINE THA OLIGINE THA OLIGINE THA OLIGINE THA OLIGINE THA OLIGINE THA OLIGINE THA OLIGINE THA OLIGINE THA OLIGINE THA OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIGINE THAN OLIG	5710	<del>                                     </del>	EC 2	
VINGHDYMRNITUREPRITAIGR*QNIVAGOSIDG*DAIGFELYV	1 3,10	1	562	IPGSTISCEVELMARMAKTIDSFTQNQTRLVVIIDGLDACEQDK
OILGGYRK/LITEFFHRTALGR*QNLVARQPSIDG*DAIGFELYV CIAIQPMTNKDDAT SIAKAVLSQQRPSICHEDAPHFS*\$LQRPHTINLDQGIP*LLM LSEERQHLFESS/IWTTPHNLK*/FEIHEHLESHEGHWTLFFLLM LSEERQHLFESS/IWTTPHNLK*/FEIHEHLESHEGHWTLFFLLM LSEERQHLFESS/IWTTPHNLK*/FEIHEHLESHEGHWTLFFLLM LSEERQHLFESS/IWTTPHNLK*/FEIHEHLESHEGHWTLFFLLM LSEERQHLFESS/IWTTPHNLK*/FEIHEHLESHEGHWTLFFLLM LSEERQHLFESS/IWTTPHNLK*/FEIHEHLESHEGHWTLFFLLM LSEERSLICADLILEDEISQLCKUNDVIAERSTEEVYLWCL AGGDLEKELVNKEIIRSKPFPDELMKOKVPSSVSPLYTPFTKPA SLYSSSIRCADLILEDEISQLCKUNDVIAERSTEEVYLWCL AGGDLEKELVNKEIIRSKPFPICTLPNFLFEDGESFGGGRDRSS/ TFR*YHMDIVVNPAKK**1ERWGREJLPTSLHFEDGESFGGGRDRSS/ TFR*YHMDIVVNPAKK**1ERWGREJLPTSLHFENDENSS/ EARVDIPPLMRGITHAALLGUEGHLEPTLPTWGDL EARVDIPPLMRGITHAALLGUEGHLEPTLAKWAUVSHPDLVYMCGLD EVDIPRCHOYDELLSSPEGHAKFRRVLKAWVVSHPDLVYMCGLD SLCAPPLYLNFRINEALVYACMSAFIPKYLYNFFLKDMSHVIGEY LTVFSCMIAFHDPELSHILMEIGFIPPLLYME EARVDIPPLWRGHTHAALLGUEGHLEPTLYNFTLWFDL HKIFHLW\DTILLGEFLEPTLYWE  **TAULTSPCSHLGSGAAACHWACHASHEDGEGGGC-**PAKLPRDFRR**FOILGPMEGH TACRCGRRGAQVQHLPREDIRAAE**DPHLREWWGLPTSSATSP **RAVLTSPCSHLGSGAAACHASHADASHMLCKSPFN **SAVLTSPCSHLGSGAAACHASHADASHMLCKLRSRPRDS-** **HYLTSPCSHLGSGAAACHASHADASHALLKRRSRPLS-** **HYLTSPCSHLGSGAAACHASHADASHALLKRRSRPLS-** **HYLTSPCSHLGSGAAACHAAAAASLLANGHDLAAA-** **NAAAAAAAAAAAAAAASLLANGHDLAAA-** **NAAAAAAAAAAAAAAAAAASLLANGHDLAAA-** **NAAAAAAAAAAAAAAAAAAASLLANGHDLAAA-** **NAAAAAAAAAAAAAAAAAAASLLANGHDLAAA-** **NAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	i	1	İ	VLQMLDTVRVLFSKGPFIAIFASDPHIIIKAINQNLNSVPSGFK
S711   1526	1			\LNGHDYMRNIVHLPVFLNSRGL/RQ/LQENFS*LQQQMETFHA
S711   1526			i	QILQGYRKMLTEEFHRTALGR*QNLVARQPSIDG*DAIGFELYV
SQIAKAVISQQRPSLPHECAPHFFS*SLQRITINLDQGIF*LLM LSEBRQHLFESS/IWTTPINLK*/FEHEHLGSHEGHWTLFFLL QIL  5712 3 1391 GRKLFQSLDISERLKFLLTLDCVDDTLIVLAEEHGGLDIJKELP ETVIDIJINKCLTHPSKRPTPDELMKDKVPSEVSPLYTPPTKPA SLFSSSLRCADLTLPEDISQLCKDINNDYLAERSIEEVYYLWGL AGGDLEKELVNKEI IRSKPICTLDFT-LFBGESFFGGBRSS/ TFR*YHNDIVVNBPAKK*IERGKGRSILDFILKKYPYKKNQINK EARVDIPPLMRGLTWAALGUGGATHAKYDAIDKDTPIPDRQI EVDIPRCHQYDELLSSPECHAKYRUKAWVSHPDLVYWQGLD SLCAPFLYLNFNNEALVYACMSAFIPKYLYNFFLKNOSHVIQEY LTVPSQMIAPHDPEISNHLNEIGFIPDLYAPPHFIMFTHTWPPL HKIFHLW\DTLLLGEFLPFILYWE  5713 634 284 PVCAVPVRRPVLPREDGEGGU-*AKLDFDFRR*FGILGPMECH TACRCSRRGQVOHLPREDIRAD*DPHLRSVWFGLPTSSATSP *RAVLTSPCSHLGSADAASSHWLCGVSFH  5714 212 613 WGLGLGPTHSSLGGSSDAGGSSSSSTNGSGGSGSSGPKAGAAD KSAVVAAAAPASVADDTPPPRRNKSGIISPLLRSVRFGLAAA  5715 131 1979 ESASQOKRSKCLILTLKLELGSAFKKTSARPGSLWLPPHSQE QTPPASKLQGGGGGMMGGSADKATAAAAAASLLANGHDLAAA MA  5715 654 SASQOKRSKCLILTLKLELGSAFKKTSARPGSLWLPPHSQE QTPPASKLQGGGGGLTGWGHPVPVTAASPLPRWCENPHPAAS PRPPGS/SDLOGPROMHLRAPPAHGGPUNTPHGGERKTPMS QIRKETKPL*FKTPAG\NNYOGKPULVPPGGCCRCPPPPAAS PRPPGS/SDLOGPROMHLRAPPAHGGPUNTPHGGERKTPMS QIRKETKPL*FKTPAG\NNYOGKPULVPFGCTLGGAVSK\ GLEGP*LCPSGAA/GGLQRGFGLSPLGAAGKVSCLHPPSWVENN DSTCHSHHBGILAAAVTVPU\SGKPULVPFGCCRCPPPPAAS PRPPGS/SDLOGPROMHLRAPPAHGGPUNTPHGGERKTPMS QIRKETKPL*FKTPAG\NNYOGKPULVPFGCTLGGAUSLCSPT PKNTACHSSGHVALQAGHDSARDVGSCHVLPGCAGGSPFG WKNTILE*LGLSRTGATRRGUNTSPGAAAAVAQALE EGGLRLPGOGRGAQPCSHCPGRAGGAGGSPTCPTVDLLPSAGR VKNTILE*LGLSRTGATRRGUNTSPGRAGAACVACAQALE EGGLRLPGOGRGAQPCSHCPGRAGGAGGSPTCPTVNSPFSSPLDPKO*E TDLTEAQTSQH  5716 1711 1370 RVPSLLCEGFGFGCYGGAVCRSCAAASPGLDSAAPPHRLCEHTD *LPK*GPGYIQHFHCDSNILCILYNISFNLFSYSF*QVARXC- RCPLVL*SGFFTIVGGYSCCMPLKT  5717 44 1489 LPPEALRESEWVSEYGKCGFGGLYPESSVDTEDSLD				
SQIAKAVLSQQRPSLFHECAPHFFS*SLQRHTINLDQGIF*LLM LSERRQHLFESS/WTTPHNLK*/FEIHEHLGSHEGHWTLFFLL QIL  5712  3 1391 GRKUFGSLDISERLKFLLTLDCVDDTLIVLAEEHGCLDIIKELP ETVIDI.INKCLTFHPSKRPTPDELMKDKVYSEVSPLYTPFTKPA SLFSSLRCADLTLPEDISQLCKDINNDYLAERSIEEVYYLWCL AGGLEKELVNKEIIRSKPPICTLPHFLFEDGESFGQGRGS/S TFR*YHMDIVVNPAKK*IERCWGRSILPITLKMTSLILPYSNSN NELSAAATLPILITEKDTEFORNIILLKAYPYKKNQINK EARVDIPPLWRGILWAALLGVEGAIHAKYDAIDKDYPIPTDRQI EVDIPRCHQVDEDLLSSPEGHEKRFRVLKAWVVSHPDLVYWGGLD SLCAPFLYLNFNNEALVYACMSAFIPKYLVNFFLKNSHVIQEY LTVFSQMIAPHDPELSSHLINEIGFIPDLYAIPWFTHWFPL KIFHLW\DTLLLGEFLFPILYWE  5713  634  284 PVCAVPVDRWPVLPREDQEGQQL*AKLPRDFRR*FOILGFMEGH TACRGSRGRGQVGILPREDITAME*DPHLREWYBQLPTSSATSP *RAVLTSPCSHLGSADAASSHWLCGVSPH WGLGLGFTMSSLGGGSODAGGSSSSSTNGSGGSGSGPKAGAAD KSAVVAAAAPASVADDTPPPERNNKSGIISEDLNKSLRRSRPLS HYSSFGSSGGGGGSGMMGGESADKATAAAAASSLLANGHDLAAA MA  5715  131  1979 ESASQQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE OTPPASKLOGGGGGLOTGNGLHPVYTAASPLPFRWCLFGAVAK\ GLPGP*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVENN DSTCHEHHEGILAARVTPVP\SGKPGRVUKPPGRVCPPHPAAS PRPPGS/SDLDGPRPMHLRAPPAAHGGPVNTPHGGEEKKTMSS QIRRKETKRL*RKTPAG\NNYQSNSTPVSQSPQLTVDLLPSAGR TQAPSGRGDAGKPTPGHG\LPKASVLTPNTCCSLAGGG*PPGL YPKTPKQRRWRRPL/LLGISQ-GSRQSTC*EV\GALGEPVTPG L*PDLSCILISNGSKHRREGLSPFSLGPGRRPAGALGSCPT PKNTACHSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP VWRWHPLE*LGLSRFTGOATRRGLWWSPFGRAAACVACAQALE EGPLRLPGQDRGAQPCSHCFGRAAGQPBSGAACPCR/GG*PDT GLT/GVPGTDPKRGGRKPGQSQETQGTVWSGPESPLQPKP*E GLT/GVPGTDPKRGGRKPGQSQETQGTVWSGPSPLQPKP*E GLT/GVPGTDPKRGGRKPGQSQETQGTVWSGPSPLQPKP*E GLT/GVPGTDPKRGGRKPGQSQETQGTVWSGPSPLQPKP*E GLT/GVPGTDPKRGGRKPGQSQETQGTVWSGPSPLQPKP*E FST1CGGGGHCYGGAVCREACAASSPGLDSAAEPHRLCEHTD *LPK*GPGYIQHFCDSNILCILYNISNNLFSYSF*GVARYAC* RCPLUL*SGFFTIIVGGYSCCMPLKT  5717  44  1489 LPFEALRESEWWSEGKCGGREGUTGSTSTSPLPSSVDTEDSLD	5711	1526	1130	RRHPFQWTTVTQEAFSHHDVAFTSTPVLFYPDSAOPFIVKSESS
LSERROHLFESS/IWTTPHNLK*/FEIHEHLGSHEGHWTLFFLL   OIL	1	Ì	i	SQIAKAVLSQQRPSLFHECAFHFFS*SLORHTINLDOGTP*LLM
5712 3 1391 GRKFOGLDISERLKFLLTLDCVDDTLIVLAEEHGCLDIIKELP ETVIDLINKCLTFHPSKRPTPDELMKDKVPSEVSPLYTPFTKPA SLYSSSLRCADLTLPEDISQLCKDINDYLAEESIEEVYYLWCL AGGLEKELVNKEIIRSKPPICTLPFFLFEDGESFGQGRESS/ TFR*YHMDIVVNPAKK*IERCWGRSILPITLKHTSLLPYSNSN NELSAAATLPILITEKDTETSURITIEKDTETSURILKAYPYKKNQIWK EARVDIPPLWRGLTWAALLGVEGAIHAKYDAIDKDTPIPTDRQI EVDIPRCHQVDELLSSPEGHAKFRRVLKAWVSHPDLVXWGGLD SLCAPFLYLNFNNEALVYAGMSAFIPKYLVNFPLKNNSVIQEY LTVPSQMIAPHDPELSNHLNEIGFIPDLYAIPWFLTMFTHVFPL KIFHLW\DTLLLGEFLFPILYFFLKNNSVIQEY LTVPSQMIAPHDPELSNHLNEIGFIPDLYAIPWFLTMFTHVFPL KIFHLW\DTLLLGEFLFPILLGGERGALAEVFDFRR*FQILGFMEGH TACRCSRRGAQVGHLPREDIRAAE*DPHLREWPGLPTSSATSP *RAVLTSPCSHLGGSGDDAGGSSSSTNGSGGGSSGPKAGAAD KSAVVAAAAPASVADDTPPPERRNSGIISEPLNKSLRSRPLS HYSSFGSSGGGGSMMGGESADKATAAAAASLLANGHDLAAA MA  5715 131 1979 ESASQQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSOE QTPPASKLQGGGGGLOTGMGLHPVPVTAASPLPRWCLFGAVAK\GLPGP*LCPGAVAK\GLPGP*LCPGAVAK\GLPGP*LCPGAVAK\GLPGP*LCPGAVAK\GLPGP*LCPGAVAK\GLPGP*LCPGAVAK\GLPGP*LCPGAVAK\GLPGP*LCPGAVAK\GLPGP*LCPGAVAK\GLPGP*LCPGAVAK\GLPGP*LCPGAVAK\GLPGP*LCPGAVAK\GLPGP*LCPGAVAK\GLPGP*LCPGAVAK\GLPGP*LCPGAVAK\GLPGP*LCPGAVAK\GLPGP*LCPGAVAK\GLPGP*LCPGAVAK\GLPGP*LCPGAVAK\GLPGP*LCPGAVAK\GLPGP*LCPGAVAK\GLPGP*LCPGAVAK\GLPGP*LCPGAVAK\GLPGP*LCPGAVAK\GLPGP*LCPGAVAK\GLPGP*LCPGAVAK\GLPGP*LCPGAVAK\GLPGP*LCPGAVAK\GLPGP*LCPGAVAK\GLPGP*LCPGAVAK\GLPGP*LCPGAVAK\GLPGP*LCPGAVAK\GLPGP*LCPGAVAK\GLPGP*CCPPHPAAS PRPFGS\SULDGPRCMHLRAFPAAHGGPVNTPHGGEKTFMSS QIRKETKEL*RETAGANTYQSNSTPVSGPOLTVDLLPSAGR TQAPSGRGDAGKPTPGHG\LPKASVLLTPNCPGSLAGGO*PPGL YPKTPKQRRRRRPRL/LLGPSPFTGGVGAGOPTC*BCVGAGGO*PPGL YPKTPKQRRRRRPRL/LLGPSPFTGGPAAGCVBGGGTAGGO*PPGL YPKTPKQRRRRRPRC/LLGPSPFTGGPAAACVACAQALE EGPLRLPGGDRGAQPCSHCCPGRAAGGPBGAAPACVACAQALE EGPLRLPGGDRGAQPCSHCCPGRAAGGPBGAAPCVACAQALE EGPLRLPGGGHCYGGAVCREACAAASPGLDSAAPPHRLCBHTD *LPK*GGFTIUWGYSCCMPLKT *LPK*GGFTIUWGYSCCMPLKT *LPK*GGFTIUWGYSCCMPLKT *LPK*GGFTIUWGYSCCMPLKT *LPK*GGFTIUWGYSCCMPLKT				LSEBROHLFESS/IWTTPHNLK*/FETHEHLGSHEGHWTLFELT
S712   S		1	ļ	OIL
ETVIDLINKCLTFHPSKRPTDDELMKDKUFSEVSPLYTPFTKPA SLFSSSLRCADLTLPEDISQLCKDINNDYLARRSIEEVYYLWCL AGGDLEKELVAKEI IRSKPPICTLPNFLFEDGESFGGGDRSS/ TFR*YHWDIVVNPAKK*IERCWGRSILPTTLKMTISLILDYSNSN NELSAARTLPLIIREKDTEYQLNRILDFDKLKAYPYKKNQIWK EARVDIPPLMRGLTWAALLGVEGAIHAKYDAIDKDTPIFTDRQI EVDIPRCHQYDELLSSPEGHAKFRAVLKAWVSHPDLVYWGGLD SLCAPFLYLMFNNSALVYACKSAFIPKYLYNFFLKDNSHVIQEY LTVFSQMIAPHDPELSNHLNEIGFTPDLYAIPWFLTMFTHVFPL HKIFHLW\DTHLLGEFLEPTLYWE  5713 634 284 PVCAVPVDRWPVLPREDGEGQQL*AKLPRDFRR*FQILGFMEGH TACRCSRRGAQVOGHLPREDIRAD&*DHILREWWDLPTSSATSP *RAWLTSPCSHLGSDADASSHWLCGVSPH  5714 212 613 WGLGLGFTMSSLGGGSQDAGGSSSSSTMGGSSGSGFKAGAAD KSAVVAAAAPANADADTPPRRNKSGIISPPLNKSLRRSPPLS HYSSFGSSGGSGGSMMGGESADKATAAAAASLLANGHDLAAA MA  5715 131 1979 ESASQOKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSOE OTPPASKLQGGGGGLOTGWGLHPVPVTAASPLPRRCLFGAVAK\ GLPGP*LCPSCAA/GGLQRGPGLSPLGAAGKVSCLHPPSWVENN DSTCHEHHEGILAARVTTVVP\SGKPGRVLKPPGRVCRPPHPAAS PRPPGS/SDLDGPRPQMHLRAFPAAHGGPVNTPHGGEEKTFMSS QIRKETKQPL*RKTPAG\NYGNSIFVYGSPGILVDLPSAGR TOAPSGRGDAGKPPGHG\LPKASVULTPNCPCSLAGGQ*PPGL YPXTPKORRWRPL/LLGPSQ*GSRQSCTC*EV\GALGEPVRIPG L*PDLSCILSNGSKHRREGJSFPRSLGPGRRGPAGLQSLGCSPT PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP VWRWIPLE**LGLSRETGOARGLWYSTGFRAAACVACQALE EGGPLRLPGQDRGAQPCSHCPGRAAGGPBPGAGAAPCRS/GG*DPT GLT/GVPGTDPKRGGRKPCGSQGTC*EV\GALGEPVRPE GLT/GVPGTDPKRGGRKPCGSQGTCTQPTVWSGPSPPLQKY*E RQE/VCAGASSGVGLSRGRRGQDSSAWEVAAMLLLLRHGSHSEL TDLTEAQTSGH  5716 1711 1370 RVPSLLCEGGFGHCYQGAVCREACAAASPGLDSAAPPHRLCEHTD *LDFRAGGGYTQHFHCDSNILCILYNISPNLFSYSF*QVARYAC* RCPLVL*SGFFTIIVGGYSCCMPLKT TLPEALRESEWVSEYCKCGPGELVPESETSPLPSSVDTEDSLD	5712	3	1391	
SLFSSSLRCADLTLPEDISQLCKDINNDYLARESIENEVYYLMCL AGGDLEKELVMKEIIRSKPICTAPNFLFEDGESFGQGRDRSS/ TFR*YHWDIVVMPAKK*IERCWGRSILPITLKMTSLILPYSMSN NELSAAATLPLIIREKDTEYQLNRILFPILKMTSLILPYSMSN NELSAAATLPLIIREKDTEYQLNRILFPILKMTSLILPYSMSN NELSAAATLPLIIREKDTEYQLNRILFPILKAYDYKKNQIWK EARVDIPPLWRGLTWAALLGVGGATHAKYADATUKDTPJEDRQI EVDIPRCHQYDELLSSPEGHAKFRRVLKAWVVSHPDLVYWQGLD SLCAPFLYLNFNNEALVYACMASAFIPKYLYWFFLKDNSHVIQEY LTVFSQMIAFHDPELSNHLMEIGFIPDLYWAIEWFLTMFTHVFPL HKIFHLM\DTLLLGEFLFPILYWE  5713 634 284 PVCAVPVDTRBWPUPPERDGOQL*AKLPRDFRR*FOILGFMEGH TACRCSRRGAQVQHLPREDIRAAE*DPHLREWWPGLPTSSATSP *RAVLTSPCSHLGSADAASSHWLGGVSFH TACRCSRRGAQVQHLPREDIRAAE*DPHLREWWPGLPTSSATSP *RAVLTSPCSHLGSADAASSHWLGGVSFH KSAVVAAAAPASVADDTPPPERRNKSGIISEPLNKSLRRSRPLS HYSSFGSSGGGGSMMGGESSSSTMGSGGSGSSGPKAGAAD KSAVVAAAAPASVADDTPPPERRNKSGIISEPLNKSLRRSRPLS HYSSFGSGGGGGMMGGESADKATAAAAAASLLANGHDLAAA MA  5715 131 1979 ESASQOKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE OTPPASKLQGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\ GLPGP+LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVENN DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS PRPPGS/SDLDGFPPQMHLAPPAHGGPWTPHGGEKTTMSS OIRRKETKPL*RXTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR TOAPSGRGDAGKPTPGHG\LPKASVLLTPHCPCSLAGGQ*PPGL YPXTPKQGRRWRRFL/LLGSGS*GRSGTSC*SC*SC*SVC*SC*SC*SC*SC*SVC*SVC*SVC*SVC	1		1 1331	FTVIDI I NVCI TEUDOVODEN MICOVODITATIVA E ENGCLOS I KELD
AGGDLEKELVNKEIIRSKPIETLENFLFEDGESFGQGRDRSS/ TFFFYHNDIVUMPAKK* IERCWGRS ILP ITLKMTSLILPYSNSN NELSAAATLPLIIRKOTEYQLMR ILFDRLLKAYPYKKNQIWK EARVDIPPLMRGLTWAALLGVEGAIHAKYDAIDKDTPIPTDRQI EVDIPRCHQYDELLSSPGHAKFRRVLKAWVUSHPDLVYWQGLD SLCAPFLYLNFNNEALVYACMSAFIPKYLYNFFLKDNSHVIQEY LTVFSQMIAFHDPELSNHLNEIGFIPDLYAIPWFLTMFTHVFPL HKIFHLMV,DTLLLGEFPILTWE  5713 634 284 PVCAVPVDRWPVLPREDQEGQQL*AKLPRDFRR*FQILGFMEGH TACRCSRRGAQVQHLPREDIRAB*DPHLEFWFGLPTSSATSP *RAVLTSPCSHLGSADAASSHULCGVSFH  5714 212 613 WGLGIGPTMSSLGGGSODAGGSSSSSTNGSGGGSGSGKAGAAD KSAVVAAAAPASVADDTPPPERRNKSGIISEPLNKSLRRSPLS HYSSFGSSGGSGGGGGGGGADKATAAAAAAALLANGHDLAAA MA  5715 131 1979 ESASQQKRSKCLILTKKLELSGSAPKKTSARPGSSLWLPPHSQE QTPPASKLQGGGGGLQTGWGLHPVFVTAASPLPRWCLFGAVAK\ GLPGP*LCPSGAA/GGLQRGGLSPLGAAAGKVSCLHPPSWWBNN DSTCHEHHEGILAARVTPA/SGKPGRVCKPPGRVCKPPHPAAS PRPPGS/SDLDGPRPQMHLRAFPAAHGGPVNTPHGGEEKTFMSS QIRRKETKPL*RKTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR TQAPSGRGDAGKPTPGHG\LPKASVLITPNCPCSLAGGQ*PPGL YPKTPKQRRWRPL/LLGPSQ*GSRQSTC*EV\GALGEPVRIPG L*PDLSCILSNGSKHRREGLSFPRSLGPGRRGPGGLQSLGCSPT PKNTACHSSCHVALQAGHDSARDVGSGFVALQAGHDSTQDVGRP VWWNIPLE*LGLSKETGQATRRGLVWISPGRAAAACVACAQALE EGPLLPGQDRGAQPCSHCPGRAAGGPBFGAGACCRE/GG*DFT GLT/GVPGTDPKRGGRKPGQSQQETQGPTWNSGPESIQPKP*E RQE/VCAGASSGVCLSRGRAGGPSSAWEVAAMLLLLRHGSHSEL TDLTEAQTSQH  5716 1711 1370 RVFSLCEGFGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD *LPK*GGFGYIOHHCDSNILCILYNISPNLFSYSF*GVARYAC* RCPLVL*SGFFTIIVGGYSCCMPLKT  5717 44 1489 LPTEALRESEWVSEYGKCGPRGLVPSGSTSDLPSSVDTEDSLD				CLESCAL BOLDI MI DED TOOL CHE DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL DE TOOL CHE CONTROL CHE CONTROL DE TOOL CHE CONTROL CHE CONTROL CHE CONTROL CHE CONTROL CHE CONT
TFR*YHWDIVVMPAKK*IRKWGRSILPITIKMTSLILPYSMSN NELSAAATLPLIIREKDTEYQLMRIIJEDRILKAYPYKKNQIWK EARVDIPPLMRGLTWAALLGVEGAIHAKYDAIDKDTEIPTDRQI EVDIPRCHQYDELLSSPECHAKFRRVLKAWVVSHPDLYYWGGLD SLCAPFILVINFNNEALVYACMSAFIPKYLVMFKKLKDSHVIQEY LTVFSQMIAFHDPELSNHLNEIGFIPDLYAIPWFLTMFTHVFPL HKIFHLW\DTLLLGEFIFPILYWE  5713 634 284 PVCAVPVDRWPVLPREDQEGQQL*AKLPRDFRR*FQILGFMEGH TACRCSRRGAQVGHLPREDIRAB*DPHLREVWPGLPTSSATSP *RAVLTSPCSHLGSADAASSHWLCGVSFH ARVLTSPCSHLGSADAASSHWLCGVSFH SSAVVAAAAPASVADDTPPPERRNKSGIISEPLMKSLRRSRPLS HYSSFGSGGGGMMGGESSDSSTNGSGGSGSGSGFKAGAAD KSAVVAAAAPASVADDTPPPERRNKSGIISEPLMKSLRRSRPLS HYSSFGSGGGGMMGGESADKATAAAAALLANGHDLAAA MA  5715 131 1979 ESASQQKRSKCLILTLKLELSGSAFKKTSARPGSSLWLPPHSQE OTPPASKLQGGGGGLOTWGLHPVPVTAASPLPRWCLFGAVAK\ GLPGP*LCPSCAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVENN DSTCHEHHEGILAARVTTVPVSGKPGRVLKPPGKVCRPPHPAAS PRPPGS/SDLDGPRPQMHLRAPPAAHGGPVNTPHGGEKTFMSS QIRKETKPL*RKTPAG\NNYQSNSIPVSGSPQLTVDLLPSAGR TQAPSGRGDAGKPTFGHG\LLPKASVILTPNCPCSLAGGQ+PPGL YPKTPKQRRWRRPL/LLGPSQ*GSGTC*EVGALGECSPT PKNTACHSSGHVALQAGHDSTQDVGRP VWRWIPLE*LGLSRETGQATRRGLVWISPGRAAACVACAQALE EGFLRPGQDRGAQPCSHCPGRAAGQPEBGAGAPCRE/GG*DPT GLIT/GVPGTDPKRGGRKPGGSGGTC*GTTWSGGPSLQPKGP*E GEPLYGTDPKRGGRKPGGSGGTC*GTTWSGGPSLQPKD*E RQE/VCAGASSGVGLSRGRAGGPSSAWEVAAMLLLLRHGSHSEL TDLTEAQTSQH  5716 1711 1370 RVPSLLCEGGFGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD *LPK*GFGYIOHHCDSNILCILYMISPNLFSYSF*GVARYAC* RCPLVL*SGFFTIIVGGYSCCMPLKT	1	1		SUPSSERCADLTLPEDISQLCKDINNDYLAERSIEEVYYLWCL
NELSAAATLPLITREKDTEYGLNRITLFDRLLKAYPYKKNOIWK EARVDI PPLMRGLTWAALLGVEGAIHAKYDAIDKDTPIPTDRQI EVDIPRCHQYDELLSSPEGHAKFRRVLKAWVSHPDLVYWGGLD SLCAPFLYLINFNNEALVYACMSAFIPKYLYNFFLKDMSHVIQEY LTVPSQMLAFHDPELSHNLMEIGFIPDLYAIPWFLTMFTHVFPL HKIFHLW\DTLLLGEFLFPILYWE  5713 634 284 PVCAVPVDRWPVLPREDQEGQL*AKLPRDFRR*FQILGFMEGH TACRCSRRGAQVOHLPAEDQEGQL*AKLPRDFRR*FQILGFMEGH TACRCSRRGAQVOHLPAEDQEGGLASSSSTMSGGSSGSGSGPKAGAAD TACRCSRRGAQVOHLPAEDQEGGSSSSSTMSGGSSGSGSGPKAGAAD KSAVVAAAAPASVADDTPPPERRNKSGIISEPLMKSLRRSRPLS HYSSFGSSGGSGGSMMGGESADKATAAAAAASLLANGHDLAAA MA  5715 131 1979 ESASQQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE OTPPASKLQGGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\ GLPGP*LCPSGAA/GGLQRRPGLSPLGAAGKVSCLHPPSWVENN DSTCHEHHEGILAARVTPVP\SGKPGVLKPPFSWCCPPHPAAS PRPPGS/SDLDGPRPQMHLRAPPAAHGGPVNTPHGGEEKTFMSS QIRKETKPL*RKTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR TQAPSGRGDACKPTPGHG\LPKASVILTPNCPCSLAGGQ*PPGL YPKTPKQRRWRPL/LLGPS9*GSRQSTC*EV\GAIGEPVRIPG L*PDLSCILSNGSKHRREGLSFPRSLGPGRRGPAGLQSIGCSPT PKNTACHSSGHVALQAGHBSTQDVGRP VMRWIPLE*LGLSRETGOATRRGLVWISPGRAPAQCVACAQALE EGPLRLPGQDRGAQPCSHCPGRAAGQPBPBAGAPCRP/GG*DDT GLT/GVPGTDPKRGGRKPGGSGGETQGPTVWSGPESPLQPKP*E RQE/VGAGASSGVGLSRGRAGGPSSAWEVAAMLLLLRHGSHSEL TDLTEAQTSQH  5716 1711 1370 RVFSLCEGFGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD *LPK*GFGYIGHFHCDSNILCILYNISPNIFSYSF*GVARYAC* RCPLVIX*SGFFTIIVGGYSCCMPLKT  FS717 44 1489 LPTEALRESEWVSEYGKCCBPRGLVPBEGSSTDPLDSSLD		1		AGGDLEKELVNKEIIRSKPPICTLPNFLFEDGESFGQGRDRSS/
EARVDIPPEMRGLTWAALLGVEGATHAKVDAIDKDTPIPTDRQI EVDIPRCHQYDELLSSPEGHAKFRRVLKAWVSHPDLVYWGGLD SLCAPFLYLNFRNEALVYACMSAFIPKYLYNFFLKDNSHVIQEY LTVFSQMTAFHDPELSHHLWEIGFIPDLYAIPWFTLKDNSHVIQEY LTVFSQMTAFHDPELSHHLWEIGFIPDLYAIPWFTLKDNSHVIQEY HKIFHLW\DTLLLGEFLFPILYWE  5713 634 284 PVCAVPVDRWFVLPREDQEGQQL*AKLPRDFRR*FQILGFMEGH TACRCSRRGAQVQHLPREDTRAAE*DPHLREVWPGLPTSSATSP *RAVLTSPCSHLGSADAASSHWLCGVSPH  5714 212 613 WGLGLGFTMSSLGGGSQDAGGSSSSSTNGSGGGSGSGPKAGAAD KSAVVAAAAPASVADDTPPERRNKSGIISEPLNKSLRRSPLS HYSSFGSSGGSGSMMGGESADKATAAAAASLLANGHDLAAA MA  5715 131 1979 ESASQQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE QTPPASKLQGGGGLQTGMGHLPVPVTAASPLPRWCLFGAVAK\ GLEGP*LCPSGAA\GGLQRGPGLSPLGARKVSCLHPPSWYENN DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS PRPPGS/SDLLDGPRPQMHLKAFPAAHGGPVNTPHGGEEKTFMSS QIRRKETKPL*RKTPAG\NNYQSNSIPVSGSPDLTVDLLPSAGR TQAPSGRGDAGKPTPGHG\LPKASVILTPNCPCSLAGGQ*PPGL YPKTPKQRRWRRPL/LLGRSQ*GSRGSTC*EV\GALGEPVRIPG L*PDLSGILSMSSKHREGLSFPRSLGFGRRGPGLQSLGCSPT PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP VWRWIPLE*LGLSRESTEGASTRRGLVWISPGRAAAACVACAQALE EGGPLRLPGODRGAQPCSHCPGRAAGQPBGAGAPCRE/GG*DPT GLT/GVPGTDPKRGGRKPGQSQQETQGPTVWSGPSPLQPKP*E RQE/VGAGASSGVGLSRGRAGGPSSAWEVAAMLLLRHGSHSEL TDLTEAGTTOH  5716 1711 1370 RVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD *LDK*AGFGYIQHFHCDSNILCILYNISPINFSYSF*GVARYAC* RCPLVIX*SGFFTIIVGGYSCCMPLKT  *EPK*GFGYIQHFHCDSNILCILYNISPINFSYSF*GVARYAC* RCPLVIX*SGFFTIIVGGYSCCMPLKT	ŀ			TFR*YHWDIVVMPAKK*IERCWGRSILPITLKMTSLILPYSNSN
EVDIPRCHGYDELLSSPEGHAKFRRULKAWVVSHPDLVYWGGLD SLCAPFLYLNFNNEALVYACMSAFIPKYLYNFFLKDNSHVIQGY LTVFSQMIAFHDPELSHHLNEIGFIPDLYATPWFTLKDRSHVIQGY HKIFHLW\DTLLLGEFLFPILYWE  5713 634 284 PYCAVYDRWPVLPREDQEGQQL*AKLPRDFRR*FQLGPMEGH TACRCSRRGAQVQHLPREDIRAAE*DPHLREWWPGLPTSSATSP *RAVLTSPCSHLGSADAASSHWLCGVSFH  5714 212 613 WGLGLGPTMSSLGGGSQDSGSSSSTMGSGGSGSGFKAGAAD KSAVVAAAAPASVADDTPPPERRNKSGI ISEPLNKSLRSRPLS HYSSFGSSGGSGGSMMGGESADKATAAAAASLLANGHDLAAA MA  5715 131 1979 ESASQQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE QTPPASKLQGGGGGLQTGWGHPVPVTAASPLPRMCLFGAVAK\ GLPGP*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVENN DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS PRPPGS/SDLCGPRPCMHLRAFPAAHGGPVNTPHGGEEKTFMSS QIRRKETKPL*RRTPAG\NNVQSNSIPVSQSPQLTVDLLPSAGR TQAPSGRGDAGKPTPGHG\DFKASV1LTPNCPCSLAGGG*PPGL YPKTPKQRRWRPL/LLGPSQ*GSRGSTC*EV\GALGEEPVRIPG L*PDLSCILSNGSKHREGLSFPRSLGPGRRGPAGLQSLGCSPT PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP VWRWIPLE*LGLSRETGOATRRGLWHSPGRAAAACVACAQALE EGFBLRLPGQDRGAQPCSHCPGRAAGQPEPGAGAPCRE/GG*DPT GLT/GVPGTDPKRGGRKPGQSGQETQGPTWNGGPESPLQPKX*E RQE/VGAGASSGVGLSRGRAGGPSSAWEVAAMLLLLRHGSHSEL TDLTEAQTSQH  5716 1711 1370 RVFSLLCEGFFGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD *LPK*GGFYIQHFHCDSNILCILYMISFNLFSYSF*GVARYAC* RCPLVIX*SGFFTIIVGGYSCCMPLKT  5717 44 1489 LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD		Į.		NELSAAATLPLIIREKDTEYQLNRIILFDRLLKAYPYKKNQIWK
EVDIPRCHGYDELLSSPEGHAKFRRULKAWVVSHPDLVYWGGLD SLCAPFLYLNFNNEALVYACMSAFIPKYLYNFFLKDNSHVIQGY LTVFSQMIAFHDPELSHHLNEIGFIPDLYATPWFTLKDRSHVIQGY HKIFHLW\DTLLLGEFLFPILYWE  5713 634 284 PYCAVYDRWPVLPREDQEGQQL*AKLPRDFRR*FQLGPMEGH TACRCSRRGAQVQHLPREDIRAAE*DPHLREWWPGLPTSSATSP *RAVLTSPCSHLGSADAASSHWLCGVSFH  5714 212 613 WGLGLGPTMSSLGGGSQDSGSSSSTMGSGGSGSGFKAGAAD KSAVVAAAAPASVADDTPPPERRNKSGI ISEPLNKSLRSRPLS HYSSFGSSGGSGGSMMGGESADKATAAAAASLLANGHDLAAA MA  5715 131 1979 ESASQQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE QTPPASKLQGGGGGLQTGWGHPVPVTAASPLPRMCLFGAVAK\ GLPGP*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVENN DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS PRPPGS/SDLCGPRPCMHLRAFPAAHGGPVNTPHGGEEKTFMSS QIRRKETKPL*RRTPAG\NNVQSNSIPVSQSPQLTVDLLPSAGR TQAPSGRGDAGKPTPGHG\DFKASV1LTPNCPCSLAGGG*PPGL YPKTPKQRRWRPL/LLGPSQ*GSRGSTC*EV\GALGEEPVRIPG L*PDLSCILSNGSKHREGLSFPRSLGPGRRGPAGLQSLGCSPT PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP VWRWIPLE*LGLSRETGOATRRGLWHSPGRAAAACVACAQALE EGFBLRLPGQDRGAQPCSHCPGRAAGQPEPGAGAPCRE/GG*DPT GLT/GVPGTDPKRGGRKPGQSGQETQGPTWNGGPESPLQPKX*E RQE/VGAGASSGVGLSRGRAGGPSSAWEVAAMLLLLRHGSHSEL TDLTEAQTSQH  5716 1711 1370 RVFSLLCEGFFGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD *LPK*GGFYIQHFHCDSNILCILYMISFNLFSYSF*GVARYAC* RCPLVIX*SGFFTIIVGGYSCCMPLKT  5717 44 1489 LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD				EARVDIPPLMRGLTWAALLGVEGAIHAKYDAIDKDTPIPTDROI
SLCAPFLYLINFNNEALVYACMSAFIPKYLYNFFLKDNSHVIQEY LTVFSQMIAPHDPELSNHLNEIGFIPDLYAIPWFLTMFTHVFPL HKIFHLW\DTLLIGEFLFPILYWE  5713 634 284 PVCAVPVDRWPVLPREDGEGQL*AKLPRDFRR*FQILGPMEGH TACRCSRRGAVQHLPREDIRABE*DPHLREEWPGLPTSSATSP *RAVLTSPCSHLGSADAASSHHLCGVSFH  5714 212 613 WGLGLGPTMSSLGGGSQDAGGSSSSSTNGSGGSGSGSGKAGAAD KSAVVAAAAPASVADDTPPERRNKSGI ISEPLNKSLRRSRPLS HYSSFGSSGGSGGGGMMGGESADKATAAAAASLLANGHDLAAA MA  5715 131 1979 ESASQQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE OTPPASKLQGGGGLOTGWGLHPVPVTAASPLPRWCLFGAVAK\ GLPGP*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVENN DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS PRPPGS/SDLDGPRPQMHLRAFPAAHGGPVNTPHGGEEKTFMSS QIRRKETKPL*KTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR TQAPSGRGDAGKPTPGHG\LPKASVILIPNCPCSLAGGQ*PPGL YPKTPKQRRWRRPL/LLGPSQ*CSCTC*EV\GALGEPVRIPG L*PDLSCILSNGSKHREGGLSFPRSLGPGRRGPAGLQSLGCSPT PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP VWRWIPLE*LGLSRETGQATRRGLWWISPGRAAAACVACAQALE EGPLRLPGQDRGAQPCSHCPGRAAGGPBPGAGAPCR*CGG*DPT GLT/CVPGTDPKRGGRKPGQSGQETQGPTVWSGPESPLQPKP*E RQE/VGAGASSGVGLSRGRAGGPSSAWBVAAMLLLLRHGSHSEL TDLTEAGTSQH  5716 1711 1370 RVFSLLCEGFFGHYQGAVCREACAAASPGLDSAAEPHRLCEHTD *LDK*GGFGY1QHFHCDSNIICLILYMISFNIFSYSF*GVARYAC* RCPLVI*SGFFTIIVGGYSCCMPLKT  5717 44 1489 LPTEALRESEWWSEYGKCGFRGLVPEGSETSPLPSSVDTEDSLD	1	ļ		EVDIPRCHQYDELLSSPEGHAKFRRVLKAWVVSHPDLVYWOGLD
LTVFSQMIAFHDPELSNHLNEIGFIPDLYAIPWFLTMFTHVFPL	l i			SLCAPFLYLNFNNEALVYACMSAFIPKYLYNFFLKDNSHVIOEY
HKIFHLW\DTLLLGEFLFP1LYWE  5713 634 284 PVCAVPVDRWPVLPREDQEGQQL*AKLPRDFRR*FQILGPMEGH TACRCSRRGAQVQHLPREDIRAD&*DPHLREWPGLPTSATSP *RAVLTSPCSHLGSADAASSHWLCGVSFH  5714 212 613 WGLGLGPTMSSLGGGSQDAGGSSSSSTMGSGGSGSGSKAGAAD KSAVVAAAAPASVADDTPPPPRRNKSGISEPLNKSLRRSRPLS HYSSFGSSGGSGGSMMGGSADKATAAAAASLLANGHDLAAA MA  5715 131 1979 ESASQQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE QTPPASKLQGGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\ GLPGP*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVENN DSTCHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS PRPPGS/SDLDGPRPQMHLRAFPAAHGGPVNTPHGGEKKTFMS QIRKETKPL*RKTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR TQAPSGRGDAGKPTPGHG\LPKASVLLTPNCPCSLAGGQ*PPGL YPKXTPKQRRWRPL/LLGPSQ*GSQSTC*EV\GALGEPVRIPG L*PDLSCILSNGSKHRREGLSFPRSLGPGRRGPAGLQSLGGSPT PKNTACHSSGHVALQAGHDSTQDVGRP VWRWIPLE*LGLSRETGQATRRGLVWISPGRAAACVACQALE EGFLRFCQDRGAQPCSHCTGRAAGQPEPGAGAPCRE/Gg*DPT GLT/GVPGTDPKRGGRKPGQSQCETQGPTVWSGPESPLQPKP*E RQE/VGGASSGVLSRGRAGGPSSAWEVAMLLLRHGSHSEL TDLTEAQTSQH  5716 1711 1370 RVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD *UPK*GPGYIQHFHCDSNILCILYNISFNLFSYSF*GVARYAC* RCPLVL*SGFFTIIVGGYSCCMPLKT  5717 44 1489 LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD				LTVFSQMIAFHDPELSNHLNEIGFIPDLYAIPWFLTMFTHVFDI.
5713   634   284   PVCAVPVDRMPVLPREDQEGQQL*AKLPRDFRR*FQILGPMEGH   TACRCSRRGAQVQHIDPREDIRABE*DPHILREWMPGILPTSSATSP   *RAVITSPCSHIGSADAASSINLCGVSFH     5714   212   613   WGLGLGPTMSSLGGGSQDAGGSSSSSTMGSGGSGSGFKAGAAD   KSAVVAAAAPASVADDTPPPERRNKSGIISEPLNKSLRRSRPLS   HYSSFGSSGGSGGGGMMGGESADKATAAAAASLLANGHDLAAA   MA				HKIFHLW\DTLLIGEFI.FPTI.YWE
TACRCSRRGAQVQHLPREDIRAAS*DPHLREVWPGLPTSSATSP  *RAVLTSPCSHLGSADAASSHWLCGVSFH  5714  212  613  WGLGLGPTMSSLGGGSQDAGGSSSSSTNGSGGSGSGSKAGAAD  KSAVVAAAAPASVADDTPPPERRNKSGI ISEPLNKSLRRSRPLS  HYSSFGSSGGSGGGSMMGGESADKATAAAAAASLLANGHDLAAA  MA  5715  131  1979  ESASQQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE  QTPPASKLQGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\ GLPGP*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVENN  DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS  PRPPGS/SDLDGPRPOMHLRAFPAAHGGPVNTPHGGEEKTFMSS QIRKETKPL*RKTPAG\NNYQSMSIPVSQSPQLTVDLLPSAGR TQAPSGRGDAGKPTPGHG\LPKASVILTPNCPCSLAGGQ*PPGL YPKTPKQRRWRRPL/LLGPSQ*GSRQSTC*EV\GALGEPVRIPG L*PDLSCILSNGSKHRREGLSFPRSLGPGRRGPAGLQSLGCSPT PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP VWRWIPLE*LGLSRETGQATRRGLVWISPGRAAAACVACAQALE EGFLRLPGQDRGAQPCSHCPGRAAGQPBEGAGAPCRE/GG*DPT GLT/GVPGTDPKRGGRKPGQSGQETQGPTVWSGPPESPLQPKV*E RQE/VGAGASSGVGLSRGRAGGPSSAWEVAAMLLLLRHGSHSEL TDLTEAQTSQH  5716  1711  1370  RVPSLLCEGFGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD *LPK*GGFYICHCDSNILCILYNISPNLFSYSF*GVARYAC* RCPLVL*SGFFTIIVGGYSCCMPLKT  5717  44  1489  LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD	5713	634	284	PVCAVPVDRWPVI.PPEDOECOOL*AKI.PPDEDD*EOTI CDMDCII
*RAVLTSPCSHLGSADAASSHWLCGVSFH  5714 212 613 WGLGLGPTMSSLGGGSQDAGGSSSSTMGSGGSGSGFKAGAAD KSAVVAAAAPASVADDTPPPERRNKSGIISEPLNKSLRRSRPLS HYSSFGSSGGGGSMMGGESADKATAAAAAASLLANGHDLAAA MA  5715 131 1979 ESASQQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE OTPPASKLQGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\ GLPGP+LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVENN DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS PRPPGS/SDLDAPRYDPHLRAFPAAHGGPVNTPHGGEEKTFMSS QIRRKETKPL*RKTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR TQAPSGRGDAGKPTPGHG\LPKASVILTPNCPCSLAGGQ*PPGL YPKTPKQRRWRRPL/LLGPSQ*GSRQSTC*EV\GALGEPVRIPG L*PDLSCILSNGSKHRREGLSFPRSLGPGRRGPAGLQSLGCSPT PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP VWRWIPLE*LGLSRETGQATRRGLVWISPGRAAACVACQALE EGPLRLPGQDRGAQPCSHCPGRAAGQPEPGAGAPCRE/GG*DPT GLT/QVPGTDPKRGGRKPCQSGQETQGPTVWSGPESPLQPKP*E RQE/VGGAASSGVGLSRGRAGGPSSAWEVAAMLLLLRHGSHSEL TDLTEAQTSQH  5716 1711 1370 RVFSLLCEGFGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD *LPK*GPGYIGHFHCDSNILCILYNISFNLFSYSF*GVARYAC* RCPLVL*SGFFTIIVGGYSCCMPLKT  5717 44 1489 LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD				TACECCEPCAOVOHI DEEDIDANE + DRIII DESENDO DECORREGIO
5714 212 613 WGLGLGPTMSSLGGGSQDAGGSSSSTNGSGGSGSGPKAGAAD KSAVVAAAAPASVADDTPPPERRNKSGI ISEPLMKSLRRSRPLS HYSSFGSSGGGGMMGGESADKATAAAAAASLLANGHDLAAA MA  5715 131 1979 ESASQQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE OTPPASKLQGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\ GLPGP+LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVENN DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS PRPPGS/SDLDGPRPQMHLRAFPAAHGGPVNTPHGGEEKTTMSS QIRKETKPL*RKTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR TQAPSGRGDAGRTPGHG\LPKASVILTPNCPCSLAGGQ*PPGL YPKTPKQRRWRRPL/LLGPSQ*GSRQSTC*EV\GALGEPVRIPG L*PDLSCILSNGSKHRREGLSFPRSLGPGRRGPAGLQSLGCSPT PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP VMRWIPLE*LGLSRETGQATRRGLVWISPGRAAAACVACAQALE EGPLRLPGQDRGAQPCSHCPGRAAGQPBPGAGAPCRE/GG*DPT GLT/GVPGTDPKRGGRKPGQSQCETQGPTVWSGPESPLQPKP*E RQE/VGAGASSGVGLSRGRAGGPSSAWEVAAMLLLRHGSHSEL TDLTEAQTSQH  5716 1711 1370 RVFSLLCEGFCHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD *LPK*GPGYIQHFHCDSNILCILYNISPNLFSYSF*GVARYAC* RCPLVIL*SGFFTIIVGGYSCCMPLKT  5717 44 1489 LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD	1			*PAVITEDCENT.GEADARCOUNT CONTRACTOR
KSAVVAAAAPASVADDTPPPERRNKSGI ISEPLNKSLRRSRPLS HYSSFGSSGGSGGSMMGGESADKATAAAAAASLLANGHDLAAA MA  5715 131 1979 ESASQQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE QTPPASKLQGGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\ GLPGF*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVENN DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS PRPPGS/SDLDGPRPQMHLRAFPAAHGGPVNTPHGGEEKTFMSS QIRRKETKPL*RKTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR TQAPSGRGDAGKPTPGHG\LPKASVILTPNCPCSLAGGQ*PPGL YPKTPKQRRWRRPL/LLGPSQ*GSRQSTC*EV\GALGEPVRIPG L*PDLSCILSNGSKHRREGLSFPRSLGPGRRGPAGLQSLGCSPT PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP VWRWIPLE*LGLSRETGQATRRGLVWISPGRAAAACVACAQALE EGPLRLPGQDRGAQPCSHCPGRAAGQPEPGAGAPCRE/GG*DPT GLT/GVPGTDPKRGGRKPGQSQETQGPTVWSGPESPLQPKD*E RQE/VGAGASSGVGLSRGRAGGPSSAWEVAAMLLLRHGSHSEL TDLTEAQTSQH  5716 1711 1370 RVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD *LPK*GPGYIQHFHCDSNILCILYNISFNLFSYSF*GVARYAC* RCPLVL*SGFFTIIVGGYSCCMPLKT  5717 44 1489 LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD	5714	212	613	WCLCLCDTMCCLCCCCODAGGGCCCC
HYSSFGSSGGGGSMMGGESADKATAAAAAASLLANGHDLAAA MA  5715  131  1979  ESASQQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE OTPPASKLQGGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\ GLPGP*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVENN DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS PRPPGS/SDLDGPRPQMHLKAFPAAHGGPVNTPHGGEEKTFMSS QIRKKETKPL*RKTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR TQAPSGRGDAGKPTPGHG\LPKASVILTPNCPCSLAGGQ*PPGL YPKTPKQRRWRRPL/LLGPSQ*GSRQSTC*EV\GALGEFVRIPG L*PDLSCILSNGSKHRREGLSFPRSLGPGRRGPAGLQSLGCSPT PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP VWRWIPLE*LGLSRETGQATRRGLVWISPGRAAAACVACAQALE EGGPLKJPGQDRGAQPCSHCPGRAAGQPEPGAGAPCRE/GG*DPT GLT/GVPGTDPKRGGRKPGQSGQETQGPTVWSGPESPLQPKP*E RQE/VGAGASSGVGLSRGRAGGPSSAWEVAAMLLLLRHGSHSEL TDLTEAQTSQH  5716  1711  1370  RVFSLLCEGFGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD *LPK*GPGYIQHFHCDSNILCILYNISFNLFSYSF*GVARYAC* RCPLVVL*SGFFTIIVGGYSCCMPLKT  5717  44  1489  LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD			013	
5715 131 1979 ESASQQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE QTPPASKLQGGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\ GLPGP+LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSWVENN DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS PRPPGS/SDLDGPRPQMHLKAFPAAHGGPVNTPHGGEKTFMSS QIRKETKPL*RKTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR TQAPSGRGDAGKPTPGHG\LPKASVILTPNCPCSLAGGQ*PPGL YPKTPKQRRWRRPL/LLGPSQ*GSRQSTC*EV\GALGEPVRIPG L*PDLSCILSNGSKHRREGLSFPRSLGPGRGPAGLQSLGCSPT PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP VWRWIPLE*LGLSRETGOATRRGLVWISPGRAAAACVACAQALE EGPLRLPGQDRGAQPCSHCPGRAAGQPEPGAGAPCRE/GG*DPT GLT/GVPGTDPKRGGRKPCQSGQETQGPTVWSGPESPLQPKP*E RQE/VGAGASSGVGLSRGRAGGPSSAWEVAAMLLLLRHGSHSEL TDLTEAQTSQH  5716 1711 1370 RVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD *LPK*GPGYIQHFHCDSNILCILYNISFNLFSYSF*GVARYAC* RCPLVL*SGFFTIIVGGYSCCMPLKT  5717 44 1489 LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD	1			
5715  131  1979  ESASQQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE QTPPASKLQGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\ GLPGP*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVENN DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS PRPPGS/SDLDGPRPQMHLRAFPAAHGGPVNTPHGGEEKTFMSS QIRRKETKPL*RKTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR TQAPSGRGDAGKPTPGHG\LPKASVILTPNCPCSLAGGQ*PPGL YPKTPKQRRWRRPL/LLGPSQ*GSRQSTC*EV\GALGEPVRIPG L*PDLSCILSNGSKHRREGLSFPRSLGPGRRGPAGLQSLGCSPT PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP VWRWIPLE*LGLSRETGQATRRGLVWISPGRAAAACVACAQALE EGPLRLPGQDRGAQPCSHCPGRAAGQPEPGAGAPCRE/GG*DPT GLT/GVPGTDPKRGGRKPGQSGQETQGPTVWSGPESPLQPKP*E RQE/VGAGASSGVGLSRGRAGGPSSAWEVAAMLLLLRHGSHSEL TDLTEAQTSQH  1370  RVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD *LPK*GPGYIQHFHCDSNILCILYNISFNLFSYSF*GVARYAC* RCPLVL*SGFFTIIVGGYSCCMPLKT  5717  44  1489  LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD	1 1			
OTPPASKLQGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\ GLPGP*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSWVENN DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS PRPPGS/SDLDGPRPQMHLRAFPAAHGGPVNTPHGGEEKTFMSS QIRRKETKPL*RKTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR TQAPSGRGDAGKPTPGHG\LPKASVILTPNCPCSLAGGQ*PPGL YPKTPKQRRWRRPL/LLGPSQ*GSRQSTC*EV\GALGEPVRIPG L*PDLSCILSNGSKHRREGLSFPRSLGPGRRGPAGLQSLGCSPT PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP VWRWIPLE*LGLSRETGQATRRGLVWISPGRAAAACVACAQALE EGPLRLPGQDRGAQPCSHCPGRAAGQPBPGAGAPCRE/GG*DPT GLT/GVPGTDPKRGGRKPGQSGQETQGPTVWSGPESPLQPKP*E RQE/VGAGASSGVGLSRGRAGGPSSAWEVAAMLLLRHGSHSEL TDLTEAQTSQH  1370 RVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD *LPK*GPGYIQHFHCDSNILCILYNISFNLFSYSF*GVARYAC* RCPLVL*SGFFTIIVGGYSCCMPLKT  5717 44 1489 LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD	<u>                                     </u>		·	
OTPPASKLQGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\ GLPGP*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVENN DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS PRPPGS/SDLDGPRPQMHLRAFPAAHGGPVNTTPHGGEEKTFMSS QIRRKETKPL*RKTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR TQAPSGRGDAGKPTPGHG\LPKASVILTPNCPCSLAGGQ*PPGL YPKTPKQRRWRRPL/LLGPSQ*GSRQSTC*EV\GALGEPVRIPG L*PDLSCILSNGSKHRREGLSFPRSLGPGRRPPAGLQSLGCSPT PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP VWRWIPLE*LGLSRETGQATRRGLVWISPGRAAAACVACAQALE EGPLRLPGQDRGAQPCSHCPGRAAGQPEPGAGAPCRE/GG*DPT GLT/GVPGTDPKRGGRKPGQSGQETQGPTVWSGPESPLQPKP*E RQE/VGAGASSGVGLSRGRAGGPSSAWEVAAMLLLLRHGSHSEL TDLTEAQTSQH  1711 1370 RVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD *LPK*GPGYIQHFHCDSNILCILYNISFNLFSYSF*GVARYAC* RCPLVL*SGFFTIIVGGYSCCMPLKT  5717 44 1489 LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD	5715	131	1979	ESASQQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSOE
GLPGP*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVENN DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS PRPPGS/SDLDGPRPQMHLRAFPAAHGGPVNTPHGGEKKFMSS QIRRKETKPL*RKTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR TQAPSGRGDAGKPTPGHG\LPKASVILTPNCPCSLAGGQ*PPGL YPKTPKQRRWRRPL/LLGPSQ*GSRQSTC*EV\GALGEPVRIPG L*PDLSCILSNGSKHRREGLSFPRSLGPGRRCPAGLQSLGCSPT PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP VWRWIPLE*LGLSRETGQATRRGLVWISPGRAAAACVACAQALE EGPLRLPGQDRGAQPCSHCPGRAAGQPEPGAGAPCRE/GG*DPT GLT/GVPGTDPKRGGRKPGQSGQETQGPTVWSGPESPLQPKP*E RQE/VGAGASSGVGLSRGRAGGPSSAWKVAAMLLLLRHGSHSEL TDLTEAQTSQH  5716 1711 1370 RVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD *LPK*GPGYIQHFHCDSNILCILYNISFNLFSYSF*GVARYAC* RCPLVL*SGFFTIIVGGYSCCMPLKT  5717 44 1489 LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD				QTPPASKLQGGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\
DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS PRPFGS/SDLDGPRPQMHLRAFPAAHGGPVNTPHGGEEKTFMSS QIRRKETKPL*RKTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR TQAPSGRGDAGKPTPGHG\LPKASVILTPNCPCSLAGGQ*PPGL YPKTPKQRRWRRPL/LLGPSQ*GSRQSTC*EV\GALGEPVRIPG L*PDLSCILSNGSKHRREGLSFPRSLGPGRRGPAGLQSLGCSPT PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP VWRWIPLE*LGLSRETGQATRRGLVWISPGRAAAACVACAQALE EGPLRLPGQDRGAQPCSHCPGRAAGQPEPGAGAPCRE/GG*DPT GLT/GVPGTDPKRGGRKPGQSGQETQGPTVWSGPESPLQPKP*E RQE/VGAGASSGVGLSRGRAGGPSSAWEVAAMLLLLRHGSHSEL TDLTEAQTSQH  1711 1370 RVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD *LPK*GPGYIQHFHCDSNILCILYNISFNLFSYSF*GVARYAC* RCPLVL*SGFFTIIVGGYSCCMPLKT  5717 44 1489 LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD		]		GLPGP*LCPSGAA/GGLORGPGLSPLGAAGKVSCLHPPSMVPMM
PRPPGS/SDLDGPRPQMHLRAFPAAHGGPVNTPHGGEEKTFMSS QIRRKETKPL*RKTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR TQAPSGRGDAGKPTPGHG\LPKASVILTPNCPCSLAGGQ*PPGL YPKTPKQRRWRRPL/LLGPSQ*GSRQSTC*EV\GALGEPVRIPG L*PDLSCILSNGSKHRREGLSFPRSLGPGRRGPAGLQSLGCSPT PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP VWRWIPLE*LGLSRETGQATRRGLVWISPGRAAAACVACAQALE EGPLRLPGQDRGAQPCSHCPGRAAGQPEPGAGAPCRE/GG*DPT GLT/GVPGTDPKRGGRKPGQSGQETQGPTVWSGPESPLQPKP*E RQE/VGAGASSGVGLSRGRAGGPSSAWEVAAMLLLIRHGSHSEL TDLTEAQTSQH  1370 RVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD *LPK*GPGYIQHFHCDSNILCILYNISFNLFSYSF*GVARYAC* RCPLVL*SGFFTIIVGGYSCCMPLKT  5717 44 1489 LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD				DSTCHEHHEGILAARVTPVP\SGKPGPVI.KDDGDVCDDDDDAAG
QIRRKETKPL*RKTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR TQAPSGRGDAGKPTPGHG\LPKASVILTPNCPCSLAGGQ*PPGL YPKTPKQRRWRRPL/LLGPSQ*GSRQSTC*EV\GALGEPVRIPG L*PDLSCILSNGSKHRREGLSFPRSLGPGRRGPAGLQSLGCSPT PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP VWRWIPLE*LGLSRETGQATRRGLVWISPGRAAAACVACAQALE EGPLRLPGQDRGAQPCSHCPGRAAGQPBPGAGAPCRE/GG*DPT GLT/GVPGTDPKRGGRKPGQSGQETQGPTVWSGPESPLQPKP*E RQE/VGAGASSGVGLSRGRAGGPSSAWEVAAMLLLRHGSHSEL TDLTEAQTSQH  1370 RVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD *LPK*GPGYIQHFHCDSNILCILYNISFNLFSYSF*GVARYAC* RCPLVL*SGFFTIIVGGYSCCMPLKT  5717 44 1489 LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD	, 1	' I		PRPPGS/SDLDGPRPOMHT.PAFPAAUGGDIAMPDUGGPRWWW.
TQAPSGRGDAGKPTPGHG\LPKASVILTPNCPCSLAGGQ*PPGL YPKTPKQRRWRRPL/LLGPSQ*GSRQSTC*EV\GALGEPVRIPG L*PDLSCILSNGSKHRREGLSFPRSLGPGRREPAGLQSLGCSPT PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP VWRWIPLE*LGLSRETGQATRRGLVWISPGRAAAACVACAQALE EGPLRLPGQDRGAQPCSHCPGRAAGQPEPGAGAPCRE/GG*DPT GLT/GVPGTDPKRGGRKPGQSGQETQGPTVWSGPESPLQPKP*E RQE/VGAGASSGVGLSRGRAGGPSSAWEVAAMLLLLRHGSHSEL TDLTEAQTSQH  1370 RVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD *LPK*GPGYIQHFHCDSNILCILYNISFNLFSYSF*GVARYAC* RCPLVL*SGFFTIIVGGYSCCMPLKT  5717 44 1489 LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD	] !			OTRPKETKDL*DKTDAG\ MIVOCNGT DUGGGGGGT MITTER
YPKTPKQRRWRRPL/LLGPSQ*GSRQSTC*EV\GALGEPVRIPG L*PDLSCILSNGSKHRREGLSFPRSLGPGRRGPAGLQSLGCSPT PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP VWRWIPLE*LGLSRETGQATRRGLVWISPGRAAAACVACAQALE EGPLRLPGQDRGAQPCSHCPGRAAGQPBPGAGAPCRE/GG*DPT GLT/GVPGTDPKRGGRKPGQSGQETQGPTVWSGPESPLQPKP*E RQE/VGAGASSGVGLSRGRAGGPSSAWEVAAMLLLLRHGSHSEL TDLTEAQTSQH  5716 1711 1370 RVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD *LPK*GPGYIQHFHCDSNILCILYNISFNLFSYSF*GVARYAC* RCPLVL*SGFFTIIVGGYSCCMPLKT  5717 44 1489 LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD				TOADCCDCDACVDTDCUC TOWN CUTT MOTORCOT
L*PDLSCILSNGSKHRREGLSFPRSLGPGRRGPAGLQSLGCSPT PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP VWRWIPLE*LGLSRETGQATRRGLVWISPGRAAAACVACAQALE EGPLRLPGQDRGAQPCSHCPGRAAGQPBPGAGAPCRE/GG*DPT GLT/GVPGTDPKRGGRKPGQSGQETQGPTVWSGPESPLQPKP*E RQE/VGAGASSGVGLSRGRAGGPSSAWEVAAMLLLLRHGSHSEL TDLTEAQTSQH  5716 1711 1370 RVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD *LPK*GPGYIQHFHCDSNILCILYNISFNLFSYSF*GVARYAC* RCPLVL*SGFFTIIVGGYSCCMPLKT  5717 44 1489 LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD	1		1	ADAMPAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA
PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP VMRWIPLE*LGLSRETGQATRRGLVWISPGRAAAACVACAQALE EGPLRLPGQDRGAQPCSHCPGRAAAGQPEPGAGAPCRE/GG*DPT GLT/GVPGTDPKRGGRKPGQSGQETQGPTVWSGPESPLQPKP*E RQE/VGAGASSGVGLSRGRAGGPSSAWEVAAMLLLLRHGSHSEL TDLTEAQTSQH 5716 1711 1370 RVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD *LPK*GPGYIQHFHCDSNILCILYNISFNLFSYSF*GVARYAC* RCPLVL*SGFFTIIVGGYSCCMPLKT 5717 44 1489 LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD	1			IFAIFAQKKWKKPL/DLGPSQ*GSRQSTC*EV\GALGEPVRIPG
VWRWIPLE*LGLSRETGQATRRGLVWISPGRAAAACVACAQALE EGPLRLPGQDRGAQPCSHCPGRAAGQPEPGAGAPCRE/GG*DPT GLT/GVPGTDPKRGGRKPGQSGQETQGPTVWSGPESPLQPKP*E RQE/VGAGASSGVGLSRGRAGGPSSAWBVAAMLLLLRHGSHSEL TDLTEAQTSQH  5716 1711 1370 RVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD *LPK*GPGYIQHFHCDSNILCILYNISFNLFSYSF*GVARYAC* RCPLVL*SGFFTIIVGGYSCCMPLKT  5717 44 1489 LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD	1			L*PDLSCILSNGSKHRREGLSFPRSLGPGRRGPAGLQSLGCSPT
EGPLRLPGQDRGAQPCSHCPGRAAGQPBPGAGAPCRE/GG*DPT GLT/GVPGTDPKRGGRKPGQSGQETQGPTVWSGPESPLQPKP*E RQE/VGAASSGVGLSRGRAGGPSSAWEVAAMLLLLRHGSHSEL TDLTEAQTSQH  5716 1711 1370 RVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD *LPK*GPGYIQHFHCDSNILCILYNISFNLFSYSF*GVARYAC* RCPLVL*SGFFTIIVGGYSCCMPLKT  5717 44 1489 LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD	1			PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP
EGPLRLPGQDRGAQPCSHCPGRAAGQPBPGAGAPCRE/GG*DPT GLT/GVPGTDPKRGGRKPGQSGQETQGPTVWSGPESPLQPKD*E RQE/VGAGASSGVGLSRGRAGGPSSAWEVAAMLLLLRHGSHSEL TDLTEAQTSQH  5716 1711 1370 RVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD *LPK*GPGYIQHFHCDSNILCILYNISFNLFSYSF*GVARYAC* RCPLVL*SGFFTIIVGGYSCCMPLKT  5717 44 1489 LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD		j		VWRWIPLE*LGLSRETGQATRRGLVWISPGRAAAACVACAOALE
GLT/GVPGTDPKRGGRKPGQSGQETQGPTVWSGPESPLQPKP*E RQE/VGAGASSGVGLSRGRAGGPSSAWEVAAMLLLRHGSHSEL TDLTEAQTSQH  5716 1711 1370 RVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD *LPK*GPGY1QHFHCDSN1LC1LYN1SFNLFSYSF*GVARYAC* RCPLVL*SGFFT11VGGYSCCMPLKT  5717 44 1489 LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD				EGPLRLPGQDRGAQPCSHCPGRAAGQPBPGAGAPCRE/GG*DPT
RQE/VGAGASSGVGLSRGRAGGPSSAWBVAAMLLLERHGSHSEL TDLTEAQTSQH  5716 1711 1370 RVFSLLCEGFGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD *LPK*GFGY1QHFHCDSNILCILYNISFNLFSYSF*GVARYAC* RCPLVL*SGFFT11VGGYSCCMPLKT  5717 44 1489 LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD				GLT/GVPGTDPKRGGRKPGQSGQETQGPTVWSGPESPLOPKD+F
TDLTEAQTSQH  5716 1711 1370 RVFSLLCEGFGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD  *LPK*GPGYIQHFHCDSNILCILYNISFNLFSYSF*GVARYAC*  RCPLVL*SGFFTIIVGGYSCCMPLKT  5717 44 1489 LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD	1			RQE/VGAGASSGVGLSRGRAGGPSSAWRVAAMLILLDHGGHGBT
5716 1711 1370 RVFSLLCEGFGHCYQGAVCREACAAASFGLDSAAEPHRLCEHTD *LPK*GPGYIQHFHCDSNILCILYNISFNLFSYSF*GVARYAC* RCPLVL*SGFFTIIVGGYSCCMPLKT 5717 44 1489 LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD	1 1			
**LPK*GPGYIQHFHCDSNILCILYNISFNLFSYSF*GVARYAC* RCPLVL*SGFFTIIVGGYSCCMPLKT  5717 44 1489 LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD	5716	1711	1370	
RCPLVL*SGFFTIIVGGYSCCMPLKT 5717 44 1489 LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD			~~/~	
5717 44 1489 LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD	1. 1	Ì		
DF TEADRESEWVSE TORCGPROUVPEGES TSPEPSSVDTEDSED	1 5717 - I		7466	
EGPGALVLESDLLLGQDLEFEEEEEEEGDGNSDQLMGFERDSE	1 2,7,	**	1489	
	L			EGPGALVLESDLLLGQDLEFEEEEEEEEGDGNSDQLMGFERDSE

SEQ	Predicted	1 5 31 -	
ID	beginning	Predicted end	
NO:	nucleotide	nucleotide	
	location	location	Totaleanite Acia, February alamina a al.
1		corresponding	M-MASCAULIE, ISISOIPHOIDE V.T
j	corresponding	to first	Deneucine, Memethionine Management
1	to first	amino acid	I * = FIOLINE, Um(illitamine D_n==i=i=i=
	amino acid	residue of	S=Serinc, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	}	\=possible nucleotide insertion)
ļ			GDSLGAPPGLEVGYOPPEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
İ			GDSLGARPGLPYGLSDDESGGGRALSAESEVEEPARGPGEARGE
J	1		The Concord of the Concord of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contornal of the Contor
ļ	1		T STEED THE CONTROL OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PRO
			- THE ANGENCE PROCESSION IN THE PROPERTY OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE PROCESSION OF THE
l	İ	į.	1 MILLEY FOR - EVECAVPERPEDATITIONICS INTODOGRAPS
	1	1	Y COVERRADAULIONHOUS / ST. FDWTCDCCCCCT FRANCE
}		1	TARTON CONCORDIGUES ASSESSED CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONT
1	ł	1	MINITIOGERPERCARCPYASAHI, DNI, VDUODIRMODISTANIA
5718	120		THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE S
- 1-0	120	284	TATABLE PARS YGNDVSMTHPOT, DDTOT, AMD LOTTOT DE COMP
5719			1 CIADFURD
1 3/13	48	428	ELNNGPFQMPLCNGGNLAVTGSWADRSPLHEAASQGRLLALRTL LSOGYNVAVTLDHVID VID
ı	i i	•	LSQGYNVNAVTLDHVTPLHEACLGDHVACARTLLEAGANVNAIT
5556			IDGVTPLFNACSQGSPSCAELLLEYGAKAQP\ESCLPSP
5720	1	1051	LQAFRNASEVPMVLVGTQDAISAA\NPRVYRRTSRARKLSTDLK
į.	l i		\RCT\YYE\TCGTYCIOMUGUGTGTXX
			\RCT\YYE\TCGGTYGLQMWSVSFQDVAQKVVAL\RKKQQ\LAI
	1		GPCK\SLPN\SPSH\SAVSAASIPARAPINQGHE/SGGGSAFSD
			Y\SSSVPSTPSISQRELRIETIAASSTPTPIRKQSKRRSNIFTS
1	1		RKGADP\DREKKAAGCKVDSIGSGRAIPIKQGILLKRSGKSLNK
1			
	l i		1 MALEATAPOISPRANGUSVEDSNITOLOGOMON STONES
			LHSERPLSSSAWAGPRPEGLHQRSCSVSSADQWSEATTSLPPGM QHPASG
5721	97	492	¥1.00
1 !			RHSSPCCSLRRTERSSNAAVST/TTVQQFKRFIENYRRHIGCVA
L			1 ** TALAGGUE LEKAYYYAFAAHHTGTTDTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
5722	88	1043	OTHER TENTIFICKNETTE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE   INDICATE
1		1043	VALU VIAGSSPEEGMAGALLCPRIVICT PAUT PUTA POOLICE
			OULD VOITHWARPARPOGRACIST DEPOSIT OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPE
1 1		i	ADDALWOTO TAKGAKKANNI DEUADOGODOGODODOGO COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANSI COMPANS
1	1	l	OTO TO SAGDE OR OGO CONTROL OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF
1 1	1		THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY O
1	ĺ		TTTTTUOMUTAGSGEEROSODPARTIDI CDORRED DE DE DE DE DE DE DE DE DE DE DE DE D
1 1	}		MI NAME OF THE PROPERTY OF THE PROPERTY AND INC.
5723	88		
	, ,	1043	VALDVLAGSSPGGGMAGALLGPRVHGIRAVLRVARGGVQAPGAP
1		1	COLC VOLUME PARPOGRACIONAL DE DESCRIPTION DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON DE LA COLON
1 1	1	Į.	ZED FERS IS IAKGEKKVSRRI.PPOHDCDDCDDDDDDDGGGGGGGGGGGGGGGGGGGGGGGGGG
1 1	1	1	OWNED PRODUCTION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPER
1 1	į	i	OW THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERT
1 1	ł	ļ	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
j l	1		RPKQAEQQQ\PKRPTPPARGPQSSGDPAMLPQRAGLRTGGLAGT
5724			TOO TREET MILE
	3	1841	FTNEAPPAPLPDASASPLSPHRRAKSLDRRSTEPSVTPDLLNFK
	ľ		MOND + NO 1 DUCUMENT WHEN ALVADOCT DAND DOLLAR FOR A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND
		- 1	
	1	1	MOTATIF T TUEDA LOST DEEKNIKGEGEBBUGDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
1		1:	DPEQKRSRARE\RREGRSKTFDWAEFRPIQQALAQERVGGVGP
1		1 '	WALL OF MACENCING SURKER ARREST DEPONT IN MACHINE
j	!	1:	DAALRMEVDRSPGLPMSDLKTHNVHVEIEQRWHQVETTPLREEK
j	Į.	1.3	RALLOS AUTOOCTORING THE LACTUATION OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART O
l	ĺ	l i	NRLLQDQLRVALGREQSAREGYVLQATCERGFAAMEETHQKKIE
İ		l i	DLQRQHQRELEKLREEKDRLLAEETAATISAIEAMKNAHREEME
1	I	] ]	RELEKSORSOTSSINSDURAL BROWN
1	İ	1 7	RELEKSQRSQISSVNSDVEALRRQYLEELQSVQRELEVLSEQYS
1		13	QKCLENAHLAQALEAERQALRQCQRENQELNAHNQELNNRLAAE
		-	TRERTLETGDGGGEATGSPLAQGKDAYELEVPSGARPCLTQLC
5725	3		APPAGOMMANDIKAAGGTIDIRAAFGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA
1			MONSEE I SUSPINETE PUDENCEUNI CTEVERENT CROSS
1		, -	A A COURT A VINDE TORONT AD LITTLE AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COMPANY AND A COM
	ļ	1 -	WIVE STANDALD LIDER OF THE SECRET TERMS TO THE SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECO
			PE/GAKYNKRPHKWAHNLHLKYMVLHSIISNTVAV\RSQRHFVA

SEO	Predicted	I prodice - 3	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	1	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1.0.	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	_	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
-	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, O=Glutamine, R=Arginine
	amino acid	residue of	S=Serine, T=Threonine, V=Valine
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown *-Ston
j	amino acid	sequence	Codon, /=possible nucleotide deletion
1	sequence	ł	\=possible nucleotide insertion)
		<u> </u>	LQTKSPNRPCQFSSSAPS/VDQRAQ/INQSYAKHSANMNFSNHN
	1		NVRANTAYHLHQRLGPARHGEMWAISPNDRLIPAVTRSTIQRQS
			SVSSTASVNLGDPGSTRRAQIPEGDYLSYREFHSAGRTPPMMPG
-	l		SOPPLSAPTYSIDGENASCREGARDSTATE
1	1		SQRPLSARTYSIDGPNASRPQSARPSINEIPERTMSVSDFNYSR TSP
5726	2	486	
7.20	] -	906	SRSLSMWWNSGLPASSHSSKLPVTVGFSGCVKRLRLHGRPLGAP
		ł	TRMAGVTPCILGPLEAGLFFPGSGGVITL/ESVGAGIPGPSRAG
Ì		1	QGSPGGSGEGPPLSSPSQPLPADLPGATLPDVGLELEVRPLAVT
			GLIFHLGQARTPPYLQLQVTEKQVLLRADDG
5727	21	221	RPILILKETRRLPWATGYAEVINAGKSTHNEDQASCEVLTVKKK
	<u></u>		AGAVTSTPNRNSSKRRSSLPNGE
5728	2	877	GTRNGQFEPRRGRAWEGSAGGLRAPGAAAGGPGVOPRGSG/LPG
1			NAIRAGVNPGRGPASPFWDLSLPWDLWPPPTDHAPGAPDFPAVE
i			GR\PWAGGRPPWPVSGVLGSRVCGPLYSTSPAGPG/SGGLSPSQ
1		I	GGPAGAGGDAG/LPGRCPSAPWRAGSRPAASCPDWIPGPQGLWL
1			HRNPTS/GPPSQIGEGAEQGDEGVADAPQIQCKN/GAEDPPAED
1	1	]	EPPQVPEAGEEDAVPAEEGPGGTPETQADQVRERPEAHLAEGGA
		ł	KGSPRRLADPQDLPAGQMSLAPPFPPVAAVIRSNK
5729	1	1525	AGGAREVLTLQLGHFAGFVGAHWWNQQDAALGRATDSKEPPGEL
	, –	1 223	CDDUL VETCETT LICOETYTERS TO MEN TO SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SE
		j	CPDVLYRTGRTLHGQETYTPRLILMDLKGSLSSLKEEGGLYRDK
1			QLDAAIAWQGKLTTHKEELYPKNPYLQDFLSAEGVLSSDGVWRV.
-		ł	KSIPNGKGSSPLPTATTPKPLIPTEASIRVWSDFLRVHLHPRSI
	1		CMIQKYNHDGEAGRLEAFGQGESVLKEPKYQEELEDRLHFYVEE
1	i		CDYLQGFQILCDLHDGFSGVGAKAAELLQDEYSGRGIITWGLLP
į			GPYHRGEAQRNIYRLLNTAFGLVHLTAHSSLVCPLSLGGSLGLR
į	]		PEPPVSFPYLHYDATLPFHCSAILATALDTVTCS\YRLCSSPVS
Į.			MVHL\ADMLSFCGKKVVTAGAIIPFPLAPGOSLPDSLMOFGGAT
ſ	<b>[</b>		PWTPLSACGEPSGTRCFAOSVVLRGIDRACHTSOLTPGTPPPSA
1	l l		LHACTTGEEILAQYLQOOOPGVMSSSHLLLTPCRVAPPVBHI.FC
			SCSPPGMVLDGSPKGAAVESVPVFG
5730	1258	1713	KKFQAPARETCVECQKTVYPMERLLANQQVFHISCFRCSYCNNK
1	l		LSLGTYASLHGRIYCKPHFNQLFKSKGNYDEGFGHRPHKDLWAT
			KIETEGFWERPRNFENCGRPLKSPGGEDCPSC*GGCPGSNY*AQ
			GSSSREKGGQASWNPKLRVA
5731	122	443	RSHRGELIPKDSCYMRKPPRRPKKRRQG/CALPQGCLTFKDVAI
l i			EFSLEEWKCLNPAQRALYRAVMLENYRNLESVGLTSKDSWYMRK
ŀ			KPGRGRGKQRRQEWFFLRVY
5732	226	772	
	220	114	PPSRSCQSPRRKSRRRAHVTVTLVCGFTSFSFSLPLYLCGCLRF
			PERTCSQLQQADWAPDFGPSSFVPSWGATATGARKFLIAFNI\N
1 1	·		LIGTKEQAHRIALNLREQGRGKDQPGRLKKVQGIGWYLDEKNLA
[			QVSTNLLDFEVTALHTVYEETCREAQELSLPVVGSQLVGLVPLK
F223			ALLDAA
5733	1	460	PALQEVNANALAWGKQYENDARTLFEFTSGVNDTESPIIYRDES
j			MRTACSPDGLCSDGNGLELKCPFTSRDFMKFRLGGFEAIKSAYM
			AQVQYSMWVTRKNAWYFANYDPRMKREGLHYVVIERDEKYM\AS
			FDEI\VP\EFIGKMDEVLSRDPM
5734	3	968	RCNSPESLTSLLVLLTTANNLFVLIPAYSKNRAYAIFFIVFTVI
- [	1		GSLFLMNLLTAIIYSQFRGYLMKSLQTSLFRRRLGTRAAFEVLS
1 1	I		SMVGEGGAFPQAVGVKPQNLLQVLQKVQLDSSHKQAMMEKVRSY
1 . [	ľ		GSVLLSAEEFQKLFNELDRSVVKEHPPRPEYQSPFLQSAQFLFG
	i		HYVEDYLCHI. TALAMI, VOTOUBLUI DADUI DADUI DADUI
1			HYYFDYLGNLIALANLVSICVFLVLDADVLPAERDDFILGILNC
	1		VFIVYYLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS
	İ		TL\VCTDCHTQAGGRRWW/RLLSLWDMTRMLNMLIVFRFLRIIP
5735			SMKPMAVVASTVLGL
2/35	2	540	FFTPCVARAFNFPDQATVKKANYSLPRVGGGTSCGLPQARRISL
}	j		ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNO
] 1			YPVFPWVLTNYESEELDLTLPGNFRDLSKPIGALNPKRAVFYAE
1			RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY
			LKILT
5736	1	382	GTRPSTKKSGYSPQQVAVIHCKGHQKENTAVAHSNQKADSAAQV
	<del>,,,,,</del>		

	- Tab			
	EQ	Predicted	Predicted end	Amino acid segment containing signal peptide
	ID	beginning	nucleotide	
N	: 0	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ľ		location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
ł		corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
		to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1		amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
ł		residue of	amino acid	S=Serine, T=Threonine, V=Valine,
i	- 1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	- 1	sequence	bequence	Codon, /=possible nucleotide deletion
				\=possible nucleotide insertion\
			1	TARLSVTPPNLLPTVSFPQPDLPDNPVYSTTTEKLASDLRANKN
57	37	290		VES " "ILPUSGIFIP *T *TSYLOSTTHI.DDAVI DOLL DD
-	٠. ا	250	1041	KACLHLLSSFLTSNFLFNPLLPDSLYSVEARSORANT GROOM
i	Į.			LOT DWKLAAGE OYSSHKDPSLSAKEKETDVHNEAECDWDCWTG
	ĺ		į.	RIADGSCGRGPDGAHHPGPKSSSWRASRIJ.DGI.GGGWII DATHIO
	- 1		I	TADDECG I PAPEOLE I PPOPRGHPAPT PTGOAGDDDCCDGAGDAG
-			1	EIRPLIDGER*PGVRPVGWTPAHPACTI, DDDCAUDDCUCA COM
57	30			APSPTSQGCCEGRCDAVPKHRAWRTPLCSQ
3'	38	8	460	DTLSLNCTLPETLPMTPSF*LSFL*FPGLARAKSIPTKTYSNEV
	- 1		j	VTLWYRPPDILLGSTDYSTQIDMW*GQVEVWQGPCGKGGGLVTT
				ATQPAAFLFTVPSLPRGVGCIFYEMATGRPLFPGSTVEEQLHFI
				FRILSEEAWALCAVETHR
57:	39	1	1222	SFQRRGIRWNVHTLHPHPRAVWAGIGRGHGS*ALLGRARAPALC
	í			FPTILERIEGI EDDI DAL BANGLUTAN
ļ				FPTLLEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLAEV
	i			SAEVDGPVPGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLKI
	- 1			LQCQGFYQLCGVHQEDVIYLALPLYHMSGSLLGIVGCMGIGATV
ł	- 1	i		VLKSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPPSKAERG
1	- 1			HKVRLAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINY
İ	- 1			1 10QAGAVGAASWLYKHIFPFSI,TRVDIZTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
	1	ı		PGEPGLLVAPVSQQSPFLGYAGGPELAQGKLLKDVFRPGDVFFN
				IRDEDVCDDQGFERFHDRIGDPFRWKGENVATTEVARVERATION
574	10	265	231	I TOTAMA IGATA
	l		231	PAYWLKVPTLCLESKTDLREKASHVSAQLQGEVRGLAGALWM*A
ŀ				I IVIERVINANISKMVHALEOKRHDAGT.GGGMAT OT NIDGE GARLAGE
574	1			1 DESTOSMASGSACGGAD
		~ 1	650	PRKTMRRGVLMTLLQQSAMTLPLWIGKPGDRPPPLCGAIPASGD
	- 1	i		I VARPODRVAARVKAVDGDEOWII.AEVIJSVSUATNIKUDIDATDI
	i	i		I BOKEKHILSKKKVIPLPOWKANPRTDDFALFOVEOLULTI VIDOR
				I TOT I RADIHAPPORPODDYSVI, FEDTSVADGVCDDI ARVA ODJETE I
574	3	2		I ACKEPAKA CKLADSPSPNDTGODSPCDAGTVUTDDI WWW
] ","	-	2	362	TUSVKETLKRNPNVNLTDKDGNTALMTAGVECUMETUOD
1	- 1			IIVMIPDROGDIVLIGAVRGGHVETVRALLOVVADIDIDIDGODOW
574	-			TADIWAVEAGNAIMVRDILOCNPDTETCTKDG
3/4	"	2	415	GKTPEGIDAIEEIEIDLEETERETSDOFMGLEEVENDE
		1		KATGREISPREKTPEVIDATEEIDKDLEETGRREISPEENGPEE
	- 1	i	•	VKPVDEMETDLKTTGREGSSREKTREVIDAABVIETDLEETERE
				ISPOE
574	4	3	703	TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA
1	- 1	ļ	1	VFTTANTCLSLTPSTLPEEATGLLTPEPSKEGPILTAESETVLP
				SDSWSSAESTSADTVLLTSKESKVWDLPSTSHVSMWKTSDSVSS
1				PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP
1		1		SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV
			į	QHGREDEDGLFTL DERGIGING TESQRATRLDY TGDSKNVLNDV
5745	5	1400	599	
		1		GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM
	- 1		1	KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT
i	- {	ł	1	VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE
			ĺ	YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR
i	1		ŀ	EKSEEERSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE
	- 1	İ		KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI
5746		3	821	LGr
	- 1			SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES
	- 1	1	4	MAGERREPCPVCGKRFRFNSILALHLRTHOPERPRORDADITED
				DECRALLIKEAKLGRARSSGGMOATPATEGIAPPOAPCCTAPPOR
1	- 1	1	j	I CAGATATSAERERHLHILHRPNKCGLCSFGSSOFFFI LINGER
	1	1	1	AHGAPERPLAATSAAPPPOPOPOPPPOPEPRSVPOPEPRODER
1	- 1	1		EATPTPAPAAPEEPPAPPEFRCQVCGOSFTOSWFI.KCHMDWUWA
5747		2		SFDHACPV
2.47	- 1	<b>4</b>	1328	DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG
	İ			PSPRGKGISSNYRRSPERPTGDLRERTKNKPODUDTEROKDYME
<u> </u>		L.		ESSSPVRKESSRGRHREKEDIKITKERTPESEEENVEWETNRDD
			-	TO DESCRIPTION OF THE INCOME.

000	17-3:		·
SEQ	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
10.	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
l	corresponding	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ı	to first	to first	L=Leucine, M=Methionine, N=Asparagine,
	amino acid		P=Proline, Q=Glutamine, R=Arginine,
	residue of	residue of	S=Serine, T=Threonine, V=Valine,
	amino acid	1	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
<b>——</b>	Bequence		\=possible nucleotide insertion)
	İ		SDNGDINYDYVHELSLEMKRQKIQRELMKLEQENMEKREEIIIK
l	1		KEVSPEVVRSKLSPSPSLRKSSKSPKRKSSPKSSSASKKDRKTS
1	[	1	AVSSPLLDQQRNSKTNQSKKKGPRTPSPPPPIPEDIALGKKYKE
1			KYKVKDRIEEKTRDGKDRGRDFERQREKRDKPRSTSPAGQHHSP
1		İ	ISSRHHSSSSQSGSSIQRHSPSPRRKRTPSPSYORTLTPPLRRS
ŧ			ASPYPSHSLSSPQRKQSPPRHRSPMREKGRHDHERTSOSHDRRH
Ì	· ·	]	ERREDTRGKRDREKDSREEREYEQDQSSSRDHRDDREPRDGRDR
		<u> </u>	RE
5748	934	473	SEGPQVFYKGLAPTLIAIFPYAGLQFSCYSSLKHLYKWAIPAEG
į	J	1	KKNENLQNLLCGSGAGVISKTLTYPLDLFKKRLQVGGFEHARAA
1			FGQVRRYKGLMDCAKQVLQKEGALGFFKGLSPSLLKAALSTGFM
		1	FFSYEFFCNVFHCMNRTASQR
5749	552	1	GFPVDPRVRGSTLSLAERPKGMIRSGSFRDPTDDVHGSVLSLAS
1		1	SASSTYSSAEERMQSEQIRKLRRELESSQEKVATLTSQLSANAN
		1	LVAAFEQSLVNMTSRLRHLAETAEEKDTELLDLRETIDFLKKKN
		1	SEAQAVIQGALNASETTPKELRIKRQNSSDSISSLNSITSHSSI
		1	GSSKDADA
5750	22	866	IFISICLWNAHLCFLLLPKDCIDQVMKLQNLFVDDSGRYLAIQF
		1	IILEWAYVFLYYYEYRKAKDQLDIAKDISQLQIDLTGALGKRTRF
			QENYVAQLILDVRREGDVLSNCEFTPAPTPQBHLTKNLELNDDT
1		1	ILNDIKLADCEQFQMPDLCAEEIAIILGICTNFQKNNPVHTLTE
		1	VELLAFTSCLLSQPKFWAIQTSALILRTKLEKGSTRRVERAMRQ
i		ĺ	TQALADQFEDKTTSVLERLKIFYCCQVPPHWAIQRQLASLLFEL
1		ł	GCTSSALQIFEKLEMWE
5751	3	751	SCGSALRAWRCGAAALATFPAPALPGLMYRALYAFRSAEPNALA
İ			FAAGETFLVLERSSAHWWLAARARSGETGYVPPAYLRRLQGLEO
1			DVLQAIDRAIEAVHNTAMRDGGKYSLEQRGVLQKLIHHRKETLS
i	1		RRGPSASSVAVMTSSTSDHHLDAAAARQPNGVCRAGFERQHSLP
			SSEHLGADGGLFQIPLPSSQIPPQPRRAAPTTPPPPPVKRRDREA
1			LMASGSGGHNTMPSGGNSVSSGSSVSSCI
5752	3	471	GPVCGVGLSVAWAGPWRGPVHSVGGGGRAALHGAELPCLSGAAT
1	1		VEREMELRHKNEMLRVETEARARAKAERENADIIREQIRLKASE
	] :		HRQTVLESIRTAGTLFGEGFRAFVTDRDKVTATVNIFIKQGWQV
l .	, ,		AEROHVGASWSPRSCPCRLCTAL
5753	34	483	DDSXAIPGGVQAPFGAVRNIYTPRTGHRIRKLDQIQSGGNYVAG
			GQEAFKKLNYLDIGEIKKRPMEVVNTEVKPVIHSRINVSARFRK
			PLQEPCTIFLIANGDLINPASRLLIPRKTLNQWDHVLQMVTEKI
	! !		TLRSGAVHRLYTLEGRLV
5754	14	331	TLVHVVEFAGEHAEAIASREQEVLQGWKELLSACEDARLHVSST
1		===	ADALRFHSQVRDLLSWMDGIASQIGAADKPRCPSSLLGLPASPW
			WPTPATPSPLTAPFSME
5755	3	888	LGDQFYKEAIEHCRSYNSRLCAERSVRLPFLDSQTGVAQNNCYI
]			WMEKRHRGPGLAPGQLYTYPARCWRKKRRLHPPEDPKLRLLEIK
			PRIFI.DI.KADGEAGERIA EVI I DOZGONIA DE PORTO DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL
<b>[</b>			PEVELPLKKDGFTSESTTLEALLRGEGVEKKVDAREEESIQEIQ
			RVLENDENVEEGNEEEDLEEDIPKRKNRTRGRARGSAGGRRRHD
]	]		AASQEDHDKPYVCDICGKRYKNRPGLSYHYAHTHLASEEGDEAQ
į .			DQETRSPPNHRNENHRPQKGPDGTVIPNNYCDFCLGGSNMNKKS
5756	3	621	GRPEELVSCADCGRSAHLGGEGRKEKEAAA
		V41	SSKLQALFAHPI.YNVPEEPPLLGAEDSLLASQEALRYYRRKVAR
i I			WNRRHKMYREQMNLTSLDPPLQLRLEASWVQFHLGINRHGLYSR
{			SSPVVSKLLQDMRHFPTISADYSQDEKALLGACDCTQIVKPSGV
1 1			HLKLVLRFSDFGKAMFKPMRQQRDEETPVDFFYFIDFQRHNAEI
5757		483	AAFHLDRILDFRRVPPTVGRIVNVTKEIL
1 2,3,	3	473	YKDALLLPDNHRQVVFENGTLKLTDVQKGMDEGEYLCSVLIQPQ
į l	İ		LSISQSVHVAVKVPPLIQPFEFPPASIGQLLYIPCVVSSGDMPI
	j		RITWRKDGQVIISGSGVTIESKEFMSSLQISSVSLKHNGNYTCI
F			ASNAAATVSRERQLIVRVPPRFVV
5758	1	474	PRRGAGAERGEHREGERGAAGMGEFKVHRVRFFNYVPSGIRCVA
<u> </u>			YNNQSNRLAVSRTDGTVEIYNLSANYFQEKFFPGHESRATEALC
L			WAEGQRLFSAGLNGEIMEYDLQALNIKYAMDAFGGPIWSMAASP

1D   Degianning   noclectide   location   corresponding to first   main oacid   corresponding to first   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   main oacid   ma	SEQ	Predicted	Drodies	
No. muclectide corresponding to first amino acid sequence corresponding to first amino acid sequence corresponding to first amino acid sequence corresponding to first amino acid sequence corresponding to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to first to fir			Predicted end	
Jocation   Corresponding   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   Lofist   L		nucleotide		
corresponding to first amino acid acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence		location		I CAGCOMILO ROLLI, PEPRENIZIATION O OT
to first anino acid amino e sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence s	1	corresponding		)   Manageruthe,  = SO Angina   V_1
amino acid uence (amino acid acquence (amino acid acquence (amino acid acquence (amino acid acquence (amino acid acquence (amino acid acquence (amino acid acquence (amino acid acquence (amino acid acquence (amino acid acquence (amino acid acquence (amino acid acquence (amino acid acquence (amino acid acquence (amino acid acquence (amino acid acquence (amino acid acquence (amino acid acquence (amino acid acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquence (amino acquenc	- 1			D=Deucine, M=Methionine N-Agrana
residue of amino acid sequence description of the ription of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the acid description of the a				F-F4011HE, O=G HFamine D=N==i=i==
### ### ##############################				descrine, TeThreonine Vevaline
Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence   Seguence	1		1	W=Tryptophan, Y=Tyrosine v_U=
SGROLLYGEORGE (Insertion)  SGROLLYGEORGE (INSERTION)  SGROLLYGEORGE (INSERTION)  SGROLLYGEORGE (INSERTION)  SGROLLYGEORGE (INSERTION)  SGROLLYGEORGE (INSERTION)  SGROLLYGEORGE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (INSERTION)  SERVICE (			sequence	Codon, /=possible nucleotide deleti-
SGSQLVGCEBGSVLFQTTPDKIEV  GNAFAGGGVVFTFHMSDLFSTTNGTVEVVVNNQ1GFTTDF  MARSSSYPTDVARVVNARIFHVNANDPENVIVCSVAARMRNTS  MKDVGADLVCGYRRGHEMBEDEPTPOLHVRIGVPVLKXV  DKLLAGGTVTLOEFBEETAKYDRICEBAYGSKOKKILHIGHU  DSPHOGFFNVDGEPSKHTCATG1FEBMLHIGVADSSSYPLEDE  KIHTGLSRILRGRADMTKNRTVDMALAEYMAFGSLLKEGIHVRI  NGQDVERGTISHHEVLHIDGEVBRTTCTVFHHIGVASSSYPLEDE  KIHTGLSRILRGRADMTKNRTVDMALAEYMAFGSLLKEGIHVRI  NGQDVERGTISHHEVLHIDGEVBRTCTVFHYBODAPTYTCH  SSLSSYGVLOFELGYMARSDNALULWEAQFGDFHNYACGILDOF  SSLSSYGVLOFELGYMARSDNALULWEAQFGDFHNYACGILDOF  SSLSSYGVLOFELGYMARSDNALULWEAQFGDFHNYACGILDOF  SSLSSYGVLOFELGEVTYGFGCOPEFLVQFKNGDGQPKAVRYFCHEB  GYTISGLEPDHYXYKMNLYGFHGGGVOFYSAVGLTAFGKDEMA  FASTEPPITEP FI KRRIESLITUTDATPOSLSTATYPGGREDEP  LVQYKNGDGQPKATRVGGEDRYTI SGLEPDNYXMNLYGFHGG  GRVENGASTAPTVARFT SILBEDNYXMNLYGFHGG  GRVENGASTAPTVARHINGHERGRYUPYSTVQTAPQEDDTFPB  TAPGTAPPPFPEP I KRRIESLITUTDATPOSLSTATYPGGREDSFT  VGCLEPGRYXHGHLIGHTUTGSSDDSLLSHTVPQGREDSFT  VGCLEPGRYXHGHLIGHTUTGSSDDSLLSHTVPQGREDSFT  VGCLEPGRYXHGHLIGHTUTGSSDDSLLSHTVPQGREDSFT  VGCLEPGRYXHGHLIGHTUTGSSDDSLLSHTVPQGREDSFT  TAPGTAPABALAVWITGSPGFGCKAVRCASGRCTVEDFIRHCODON  VDVLKYRHOLD FOR ALOVY  VGCLEPGRYXHGHLIGHTUTGSSDDSLLSHTVPQGREDSFT  TAPGTAPABALAVWITGSPGFGCKAVRCASGRCTVEDFIRHCODON  VDVLKYRHOLD FOR ALOVY  VGCLEPGRYXHGHLIGHTUTGSSDDSLLSHTVPQGREDSFT  TAPGTAPABALAVWITGSPGFGCKAVRCASGRCTVEDFIRHCODON  VDVLKYRHOLD FOR ALOVY  VGCLEPGRYXHGHLIGHTUTGSSDDSLLSHTVPQGREDSFT  TAPGTAPABALAVWITGSPGFGCKAVRCASGRCTVEDFIRHCODON  VDVLKYRHOLD FOR ALOVY  RESPONDENT FOR ALOVY  SSPESIALINGLEVAR MALAGUMARALAVER SELECTION FOR ALOVY  GROADSSAMVEN FOR SERVEN FOR ALOVY  GROADSSAMVEN FOR SERVEN FOR ALOVY  GROADSSAMVEN FOR SERVEN FOR ALOVY  ALELLIGLEKKEN FOR ALOVY  ALELLIGLEKKEN FOR ALOVY  ALELLIGLEKKEN FOR ALOVY  ALELLIGHEKKEN FOR ALOVY  ALELLIGHEKKEN FOR ALOVY  ALELLIGHEKKEN FOR ALOVY  GSGRANGWANG FOR FOR THE ALOVY  ALELLIGHEKKEN FOR ALOVY  ALELLIGHEKKEN FOR ALOVY  ALELLIGHEKKEN FOR ALOVY  ALELLIGHEKKEN FOR ALOVY  ALELLIGHEKKEN FOR ALOVY  ALELLIGHEKKEN FOR ALOVY  ALELLIGHEKKEN FOR ALOVY  ALELLIGHEKKEN FOR ALOVY  ALELLIGHEKKEN FO			<u> </u>	( \=Possible nucleatide incertion)
GNAAFAGGGVYSTFFMSDLPSTTINGTVEVVVNQCIGFTEDE MASSSYPTDIARVANAP EINVANDDEBLYCVVAADARWATE MKOVGADLVCVRREGNEMMEPMFTOPLHYKQITEGEFEETAKVPRICEEROGEVALARWATE MKOVGADLVCVRREGNEMMEPMFTOPLHYKQITEGYEVAADARWATE MKUNGADLVCVRREGNEMMEPMFTOPLHYKQITEGYEVAADARWATE MKUNGADLVCVRREGNEMMEPMFTOPLHYKQITEGYEVAADARWATE KIHTGLSRILAGGAMYKUNTUDALAGTHAGUSVASSYPLEDE KIHTGLSRILAGGAMYKUNTUDALAGAMAGULKEGILYVIL NGQDVERGTTSHEHHYLHDQEVDRRTCVPMHILAPPOAPTVCN SSLSEYGYLGFEIGYAMASPAULUREGOFGRAGOPKAVEVPENEL ISTGGAKWVERNGIVLLIPHGGEGORGPERVAGGGOPTAGEVPENEL ISTGGAKWVERNGIVLLIPHGGGORGPERVAGGOPTAGEVPENEL PASTEPPTPEPPIKRELELTYTDATPOSLSISHTYPEGOPTHE LVQYKNIGGPYAATVPGGGORGPOPKAVEATPOETENTY PASTEPPTPEPPIKRELELTYTDATPOSLSISHTYPEGOPTHE LVQYKNIGGPYAATVPGGGORGPOPKAVEATPOETENTY VGGLEPGRXYKMHLYGHEGGRAUPVTSGLEDHYYMGLYGFHEG CRVGPVGAIGVTAGEFTTYTOTSGSPDELIGHTYPGGFTHEY VGGLEPGRXYKMHLYGHEGRRUOPVTSUGHTAPGKDEDDTPPE TEPGTEAPEPPEPPEPLLGETTYTGSSPDELIGHTYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHITTAGGFTHITTAGGFTHITTAGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPGGFTHYPG	5759	<del> </del>		SGSQLLVGCEDGSVKI,FOTTPDKTDV
NEDVEGADL/VERREGHERMOEPMFTOPLAWS (INCOVENABLE)  NEDVEGADL/VERREGHERMOEPMFTOPLAWS (INCOVENABLE)  DE PHOOF PROTOE EST ANY DE LIEBAYORS KORKI LIH KHIM DES PHOOF PROTOEP STATE JEDEM THE GOVERN SAS SYLEDE KIHTGLSR ILREGRADHT (NERT VERT AF GESLLKES) HIVEL NEGOVERN TS SHEHRIV-HOUGE VERT COVER THE AFTER SELLKES HIVEL NEGOVERN TS SHEHRIV-HOUGE VERT COVER THE AFTER SELLKES HIVEL NEGOVERN TS SHEHRIV-HOUGE VERT COVER THE AFTER SELLKES HIVEL NEGOVERN TS SHEHRIV-HOUGE VERT COVER THE AFTER SELL SHE TYPE OF THE AFTER SELL SHE TYPE OF THE AFTER SELL SHE TYPE OF THE AFTER SELL SHE TYPE OF THE AFTER SELL SHE TYPE OF THE AFTER SELL SHE TYPE OF THE AFTER SELL SHE TYPE OF THE AFTER SELL SHE TYPE OF THE AFTER SELL SHE TYPE OF THE AFTER SELL SHE TYPE OF THE AFTER SELL SHE TYPE OF THE AFTER SELL SHE TYPE OF THE AFTER SELL SHE TYPE OF THE AFTER SHE SHE SHE SHE SHE SHE SHE SHE SHE SHE	1 3,33	2	1240	GNAAFAGQGVVYETFHMSDLDSVTTNGTVUURURRIG
DRU LABOTYTICGEPEEL RAYPRI CEBAS CROKK HILH IHRM DSHROF PRIVIDGEPEEL RAYPRI CEBAS CROKK HILH IHRM DSHROF PRIVIDGEPEEL RAYPRI CEBAS CROKK HILH IHRM RODUBEROTES HILBURUH DO CHORT CHAMILLAND PROPERTY CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND CONTROLLAND C	}	1		T TO THE TENTAL VINAPIPH VNAIDDE ATTRICTORY A TOTAL
DENHOGY FINDER KENTCPATGY PEDIAGNICK HILLIAMS  DENHOGY FINDER KENTCPATGY PEDIALISONASS PLEED  KIHTGLISH LIRGERDMTKNRTVONALAEYMAGESLIKEG HAVEL  NOGDVERGTY SHEMH-HULDEVDRRTCVPMMHLW PEDAP PTVCN  SSLSEYGVLGFELGYAMASINALVLMEAQFGDEHNTAGCI I DOP  SSTGGARWARMINGIVLLIDH-HUMBGMGMGPENSAVELTHAGCI I DOP  SSAYAPAFIKDFZVOL  TORITISHELSISMTVPEQGTDHFLVQFKNGDGDFKAVEVFEHED  GVT1SGLEPDHKYKMINLYGHGGGRGVGFVSAVELTHAGCH I DOP  ANSTEPPTEPP F1 KRELEELTVTDATPEDSISLSWTVPEGGTDHE  LVQYKNGDGOPKATRVPGHEDRVT1SGLEPDHKYKMINLYGFHGG  CRVGDVSAIGVTAAEETPTPTFPEMPEAPPEPPLEGLELTVTDATPEDSISLSWTVPEGGTDHE  LVQYKNGDGOPKATRVPGHEDRVT1SGLEPDHKYKMINLYGHGG  CRVGDVSAIGVTAAEETPTPTFPEMPEAPPEPPLEGLELTVTDATPEDSISLSWTVPEGGTDHE  LVQYKNGDGOPKATRVPGHEDRVT1SGLEPDHKYKMINLYGHGG  CRVGDVSAIGVTAAEETPTPTFPEMPEAPPEPPLEGLESSENTYPEGGTDHE  LVQYKNGDGOPKATRVPGHEDRVT1SGLEPDHKYKMINLYGHGG  SSPDSLSISMTVPGGRFDSTTUTYKDRGGFPQVVKWGGESS BVT  VGGLEPGRAKWHINLYGHGGRGVGGSKVVVKGLESSPSTVLYQARDORDTPSP  TEPGTEAPPEPPEEPPLEGELTVTATATPOGEDSTTUTYKORGGESKLTVKGE  RIGDVSAIGVT  SSPDSLSISMTVPGGRFDSTTUTYKDRGGFPQVXWHALKYGHGSFP  TEPGTEAPPEPPEPPLKGELTVTATATPOGEDSTTUTYKORGGESKLTVKMINLYGHGESSENT  VQYKDRCDROPAVKVGHGGSKVVVRGLESSPSTVAWHLYGHGRFDFT  RIGDVSAIGVT  VQYKDRCDROPAVKVGHGGSKVVVRGLESSPSTVAWHLYGHESPT  VQYKDRCDROPAVKVGHGGSKVVVRGLESSPSTVAWHLYGHESPT  RALGAGIEKTTTREACKDLSGRLEDVATRVAHLYGHGORGVHANA  FFSGGGRARVAVTDHGSP FDLOGFTUTTISHCORGCHANA  FFSGGGRARVAVTDHGSP FDLOGFTVATUKKRCPFHLBSVL  SCHENSKRVYETEFTQEKKAESKEPIBEPTQAGLIKKKKRPMINGT  GERVAEVARVATOHGSPGGGGGGGGREPTFRAFINGTKKRPFT FDRAMTYT  MSSESAANGKKSHAALLEISGKVURSLASLEISHTLATHLISDN  SCHENSKAVAPPERENNAVALLOSGOPRAV I DKRTIDLLAFTSV  SSERIPSDIAKINGHVALLOSGORGERFTFRAFINGTKKYRFFT FDRAMTYT  MSSESAANGKKSHAALLEISGKVURSLASLEITHLATHLISDN  SSERIPSDIAKINGHVALLOSGORGERFTFRAFINGTKYRFT FDRAMTYT  MSSESAANGKKSHAALLEISGKVURSLASLEITHLATHLISDN  SLERIPSDIAKINGHVALLOSGORGERFTFRAFINGTHEFERDGLITV  MSSESAANGKKSHAALLEISGKVURSLASLEITHLATHLISDN  SLERIPSDIAKINGHVALLOSGORGERFTFRAFINGTHEFERDGLITV  MSSESAANGKKSHAALLEISGKVURSLASLEITHLATHLISDN  SLERIPSDIAKINGHVALLOSGORGERFTFRAFINGTHEFERDGLITV  MSSESAANGKK			}	1 MOVGADDYCIKRRGHNEMDEDMETODI MYVOTIMOTER
KIHTGLSRILRGRADMICKNICH JEBDLITHIGSVASSVPLEDB  KIHTGLSRILRGRADMICKNICH JEBDLITHIGSVASSVPLEDB  SSLSEYGUJGFLGYAMAPSNALLULBAGEOPHHTAGCI I LOP  ISTGGAKWARIMGIVLLIPHGMEGAPEHSVAPPGHEBD  1 1221 VRDITSDELSLSTVVEGOFDHFLVGFKINGGOPHATAGCI I LOP  GVII SGLEPHKYKNILVGFHGGGAVEPSAVELTAPGKUDENA  PASTEPPTEPP JERRLEELTVIDATPDGSLSLSTVEGOFDHFLVGFKINGGOPHATAGCI I LOP  RATEPPTEPP JERRLEELTVIDATPDGSLSLSTVEGOFDHFLVGFKINGGOPHATAGCI I LOP  LOVINGOGPARTAVEHBEURT TSLEDHNYKOML VGFHGG  CRVGPVSAIGVTAREETPTPTEP SMEAPEPPEPELI GELTVIG  SSPBSLSLSTVPQGFFFSFTVQVKNGRRQPVSTVGGLSENVT  VGGLEPGRKYKMHLVGLHEGRRVGPVSTVGVTAPQEDVDETPSP  TEPGTAPAPEPPEPPLGELTVTGSSPDSLSLSTVPQGFFGGRAVYMELYGELDGELS  SSPBSLSLSTVPQGFFFSTVQVKNGRRQPVSTVGELSENVT  VGGLEPGRKYKMHLVGLHEGRRVGPVSTVGVTAPQEDVDETPSP  TEPGTAPAPEPPEPPLGELTVTGSSPDSLSLSTVPQGFFGCKAPURGRRQPVSTVGGLESENVT  VGGLEPGRKYKMHLVGLHEGRRVGPVSTGVTAPQEDVDETPSP  TEPGTAPAPEPPEPPLGERVAGAGGRGCTUPDFTHRHCGDON  VGVKNFVGFVKNGALLNTSDTVQHGAVTSLEPRLCGGGGGGGML  RALGAGIEKTTRREACDLSGRRLDUNGRRADMICKMHLDSVALHE  RAKEQKRLEELORKUNFFEGOTGGGSGGFGCKAPARGAGGGGGGGGGGGGGAMARACHAPARGAGAGAKRCPMLGM  ELSTATASGESDDDSSEAPSTGMGFHAPKIGNOMARACHAPARGAGAKRCPMLGM  ELSTATASGESDDDSSEAPSTGMGFHAPKIGNOMARACHAPARGAGAKRCPMLGM  ELSTATASGESDDDSSEAPSTGMGFHAPKIGNOMARACHAPARGAGAKRCPMLGM  ELSTATASGESDDDSSEAPSTGMGFHAPKIGNOMARACHAPARGAGAKRCPMLGM  ELSTATASGESDDDSSEAPSTGMGFHAPKIGNOMARACHAPARGAGAKRCPMLGM  ELSTATASGESGGGGGGGGRRTFRFMFKKKYEFPDPRMYTI  MSSESAAMCKSHAARLEISGKVUSKSALNSLITHLTALHLSDN  SERIESDIALBALLGLUKLUSKALLGSGGFRAFTFRMFKKKYEFPDPRMYTI  MSSESAAMCKSHAARLEISGKVUSKSALNSLITHLTALHLSDN  LOWNNVETPFENDAYGGGGGGGGGRRTFFRMFKKKYEFPDPRMYTI  MSSESAAMCKSHAARLEISGKVUSKSALNSLITHLTALHLSDN  LOWNNVETPFENDAYGGGGGGGGRRTFTFRMFKKKYEFPDPRMYTI  MSSESAAMCKSHAARLEISGKVUSKSALNSLITHLTALHLSDN  LITSIVSASAAGSSFFILLYBGGGGGGGGGRAFTAGAGGGGGGGGGGGGGGGGGGGGGGGG				PAGE TALLOCK ELECT AKADE LOKA ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND ACCOUNTS AND A
NGQDVERGTTSHEHHUDGEVDRRTCVPMILMEPQAPTYCN SSLSEYGVIGFELGYAMASINALVLMEAQFGDEHNTAGCI IDG ISTGQAKWINNOTVLLIPHGMEKMGPEHSSARPERFLQMSNDD ISTGQAKWINNOTVLLIPHGMEKMGPEHSSARPERFLQMSNDD ISTGAKWINNOTVLLIPHGMEKMGPEHSSARPERFLQMSNDD ISTGAKWINNOTVLIPHGMEKMGPEHSSARPERFLQMSNDD ISTGAKWINNOTVLIPHGMEKMGPEHSSARPERFLQMSNDD ISTGAKWINNOTVERGFEDEHIVOTATIONESLAMVVERGHEG GVTISGLEPDHXKWINLIGHGGGRGPUSAVGLTADGKDEMA PASTEPPTEPPEP1KRELELTVOTATIONESLAMVVERGEFEM GVTISGLEPDHXKWINLIGHEGGROUPUSAVGLEEMA ILVOYKNGEGOPKATRVPGHEDRVTI SGLEPDNKYKMGLIKOFHGG GVGLEPGRKKMHLUGHEGRRVQMSTVQVTAPQEGSEVT UGGLEPGRKKMHLUGHEGRRVQMSTVQVTAPQEGSESEVT UGGLEPGRKKMHLUGHEGRRVQMSTVQVTAPQEGSESEVT VOYKDRORPQAVRVGGCESKVTVWGLEPGRKYMHLUGHEGR UGGLEPGRKKMHLUGHEGRRVQMSTVQVTAPQEGSESEVT UGYKDRORPQAVRVGGCESKVTVWGLEPGRKYMHLUGHEGRR HIGPVSALGVT VOYKDRORPQAVRVGGCESKVTVWGLEPGRKYMHLUGHEGRR HIGPVSALGVT VOYKDRORPQAVRVGGCESKVTVWGLEPGRKYMHLUGHEGRR RALGAGIEKTTMREACRDLSGRRLDVMHEKAMAEWKOQABRE AEKEKKLELGLKKLUSPHGCTSGDYGOCHMAERLEBVKGQAASSKWSABISENRKQMPTKSGTDRGASAGKRCFWLGM RALGAGIEKTTMREACRDLSGRRLDVMHEKAMAEWKQQABRE AEKEKKLELGLKKLUSPHGLTSGDYGOCHMAERLEBVKGQABRAAK GWQAASSKWSABISENRKQMPTKSGTDRGASAGKRCFWLGM EELBTLAEGNSESSDDDSEAPSTSGMFRAKIGSMGVEMAAK FPSGSGRARVVNTDHGSPDLGIEVTDSGRHLLEDSCABLGESK GWAASVASHELGLEKLELGLAKLUKGCTLQ DGERVAEVAPEERENVAVAKLQESGPONAVIDKETIDLAFTSV DGERVAEVAPEERENVAVAKLQESGPONAVIDKETIDLAFTSV SABELLGLEEKKKCELMALLKCGTLQ DGERVAEVAPEERENVAVAKLQESGPONAVIDKETIDLAFTSV SLUBHTSLIKUTLARLDVELIGRFTHTITIARDGGGETTGRVEINT LDVANDADAN LDVANDWPTPCKDATVGLARENGESVTDLVAGLANGLINGLETTGVKINV LDVANDAVPTPCKDATVGLARENGESVTDLVAGLANGLINGLINGL SGERANGKKSHWABLEISGKVESLASLUSGLINGLIVIL TVSIVASASARGSTPISLYEGVGVISVARPLDVEGIGIK MPDDPTVRDVALLVGSRRLDVMTVGKSTEMMSGFFLER VARACGEBRGLADSTPISLGVVKSTSTRANDALGGRYFSLER ATAGAGGGCKKEEREPGRKGSSTAAALAAGLKFFT ATAGAGGGCKKEEREPGRKGSSTAAALAAGLKFFT ATAGAGGGCKGKEEREPGRGSGSGRARPAALAAGLKFT ATAGAGGGCKKEEREPGRGSGSGRARPERGTBSHLJUT GGNNGSGAAPEGGRANDALGGRYBERDELGEHLLD OGANKGAABGGSSSPABLAGREDSTCHAGGGGGEBEHLD OGGWKGAABGGSSPABLAGGSSSPABLAGTPSSLGVVAG SCHEKAAPDEGGCMANSTPSTGTPSSLGVVAG SCHEKAAPDEGGCMANGAGSSSPAC	1	l	ļ	TOTAL OF THE ADGEDRASMIC PAIRS I DEDMINITED COMPAGNISH TO THE
SSLSEYEQUARMS PRAILUMENT TO THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONT			İ	KIHTGLSRILRGRADMTKNRTVDWALAEVMAEGGILKGG
SOSSETION PRINTANCE LIDENT PROPRIETION PROPRIETION PROPRIETION SOLVED PROPRIETION PROPRIETION SOLVED PROPRIETION SOLVED PROPRIETION SOLVED PROPRIETION SOLVED PROPRIETION SOLVED PROPRIETION SOLVED PROPRIETION SOLVED PROPRIETION SOLVED PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETION PROPRIETIO		}	İ	NGQDVERGTFSHREHVI.HDOEVDBBTCVDARVIVIA
576C 1 1221 VRDITSDELSISMTVERGGEDENSARPERFIQMENDD SANTPARTNPENGEL  VRDITSDELSISMTVERGGEDENSARVENDENGENAN PASTEPPTREP I KPRILEELTVTDATPDELSISMTVERGGEDENA PASTEPPTREP I KPRILEELTVTDATPDELSISMTVERGGEDENA PASTEPPTREP I KPRILEELTVTDATPDELSISMTVERGGEDENA PASTEPPTREP I KPRILEELTVTDATPDELSISMTVERGGEDENA PASTEPPTREP I KPRILEELTVTDATPDELSISMTVERGEDENGENE CRWGPVSAIGVTAAREETPTPTEPSMEAPPEPPEPPLIGELTVTG SSPBELSISMTVOGGEDSFTYVQYKDRORPQVAVROGESESEVT VGGLEPGRKYKMILYGLHEGRRYGPVSTVGVVROGESESEVT VGGLEPGRKYKMILYGLHEGRRYGPVSTVGVRORPQVROTGESSEVT VGYKDROGERPARVGESEKTVTHGTGERKTYMHILYGLHEGR RIGPVSAIGVT SCHARLERIGERKINDERSTRENGENSTRENGERKTYMHILYGLHEGR RIGPVSAIGVT SCHARLERIGERKINDERSTRENGENSTRENGERKTYMHILYGLHEGR RIGPVSAIGVT VVPUNFFVKCNGALINTSDTVOHAVYSLEPRLIGGKGGFGSMIL RALGGGIGEKTYNREAGROSTGENKROMPTREGRKYMHILYGLHEGR RIGPVSAIGVT RALGGERGERKINDERSTRENGENSTRENGENSTRENGERKRINGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRENGENSTRE	1 :	j		SSLSEYGVLGFELGVAMACDNALWINDA OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE O
STAGE   1   1221   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICATION   SURTIFICA	1			ISTGOAKWURHNGTULI LDUGMEGMGDENGA ANTAQCIIDQF
VEDITEDSLISLWIVERGOPUFFLVOFKNODGOPRAVRVPGHED GVITSGLEPDHKYMBLYGFHGGRVGPVSAVGITAFGKDEMA PASTEPPPTEPP1KPPLKELTVTDATTDSLSISWTVERGOFDHF LVOYKNODGOPRATRVPGHEDRVTISGLEPDHKYMLVGFHGG CRYGPVSAIGVTAREETTTTETESBESSWTVERGOFDHF LVOYKNODGOPRATRVPGHEDRVTISGLEPDHKYMMLVGFHGG SSPDSLSLSWTVPGGFDSFTVQYKDRDGRPDVVRVGGESSEVT VGGLEPGRKYMHLVGLHEGRRVDVTVGVAPDGEVDVETPSP TEPGTEAPEPPEPPLIGELTVTGSSPDSLSLSWTVPGGRDGFT VQYKDRDGRPQARVVGGGSKVTVGLGERGRKYMHLYGLHEGR RIGPVSAIGVT  SCDNAEAAALVWIRGPGGKAVKCASGGCTUPDFIHREGODD VPVENFFVKCNGALINTSDTVOHGAVYSLEPRLCGKGGPGSML RALGAGIEKTTRREACRDLGSRILENDHKAWAPWKQAERE AEKECKRLERLGRKLVEPKHCPTSPDYOOCCHEMABRILEDSVLK GWQAASSKWYSAEISENKKGWPTKSQTDRGASAGKRCFWLGM RELETABGSNSESSDDDSEEAPSTSWGFHAPKIGSNGVEMAA FPGSGQARVVYTDHGSPDQOCHEMABRILEDSVLK GWQAASSKWYSAEISENKKGWPTKSQTDRGASAGKRCFWLGM FPGSGQARVVYTDHGSPDQOCHEMABRILEDSCAELGESK GWGAASSKWYSAEISENKAGENSCHGFHLIGH ELETABGSNSESSDDSEEAPSTGWFHAPKIGSNGVEMAAK FPGSGQARVVTDHGSPDQOCHEMABRILEDSCAELGESK GWGAASSKWYSAEISENKAGENFTKAGENFTKAGENFAKT FPGSGQARVVTDHGSPDQOCHEMABRILEDSCAELGESK GWGAASGARVATDHGSPDQOCHEMABRILEDSCAELGESK ELETABGSNRVTTETETQKKARSKEPHERDSCAELGESK ELETABGSNRVTTETETQKKARSKEPHERDSCAELGESK GWGARVVTDHGSPDQOCHEMABRILEDSCAELGESK SCHENKARPTTETETQKKARSKEPHERDSCAELGESK SELETABGRNVTTETETQKKARSKEPHERDSCAELGESK SELETABGRNVTTETETQKKARSKEPHERDSCAELGESK SELETABGRNVTTETETQKARSKEPHERDSCAELGESK SELETABGRNVTTETETQKARSKEPHERDSCAELGESK SELETABGRNVTTETETQKARSKEPHERDSCAELGESK SLENGEVGAAPGGGGGGGGGGGARTFRAGAGGGCGGGGGARTAGALAGGLKFAS TVAMMAGN  VARAAGGGRGGLAPHIAGGGGGGGGGGAPHERDGLIGVKARS TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAMMAGN TVAM				SDAYPAFTKDFFYCOL
PASTEPPTEP? IRRIEBLITYDTOTPOSLISBYDEGOPHER LVQYKNGDGQPKATRVPGHEDRYTISGEPDIKJKNMLYGFHGG CRVGPVSAIGVTAABEETPTPTEPBLIGELTYTG SSPDSLSISWTVPQGRPBSFTVQYKDRGRPDVYRVGEBSEVT VGGLEPGRYKMHLYGLHEGRRVBAPPEPEPLIGELTYTG SSPDSLSISWTVPQGRPBSFTVQYKDRGRPDVYRVGEBSEVT VGGLEPGGRYKMHLYGLHEGRRVBAPPEPEPLIGELTYTG SSPDSLSISWTVPQGRPBSFTVQYKDRGRPDVYRVGEBSEVT VGGLEPGGRYKMHLYGLHEGRRVBAPPEPPLIGETTYTG SSPDSLSISWTVPQGRPBSFTVQYKDRGRPDVRVVGGESEVT VGGLEPGGRYKMHLYGLHEGRR TEPGTEAPEPPEPPLIGETTYTGSSPDSLSISWTVPQGRPBSFT TEPGTEAPEPPEPPLIGETTYTGSSPDSLSISWTVPQGRPBSFT TEPGTEAPEPPEPPLIGETTYTGSSPDSLSISWTVPQGRPBSFT TEPGTEAPEPPEPPLIGETTYTGSSPDSLSISWTVPQGRPBSFT TEPGTEAPEPPEPPLIGETTYTGSSPDSLSISWTVPQGRPBSFT TEPGTEAPEPPEPPLIGETTYTGSSPDSLSISWTVPQGRPBSFT TEPGTEAPEPPEPPLIGETTYTGSSPDSLSISWTVPQGRPBSFT TEPGTEAPEPPEPPLIGETTYTGSSPDSLSISWTVPQGGRPGMAPK RIGHTYTSTSTVAGASAGKTEPLTYN VENERAL SESSMESSDDDSEEAPSTGGMGFHAPKIGSNOVEMAAK FPSGSQRARVVNTDHGSPBDLQIPVTDSGRHLEDSVLKA EBHESRMYTSTEETQKKAESKEPIEEEPTTYGLKNCKETERT DGERVARVAPEETETQKKAESKEPIEEEPTTYGLKNCKETERT DGERVARVAPEETETQKKAESKEPIEEEPTTYGLKNCKETERT DGERVARVAPEETETQKKAESKEPIEEEPTTYGLKNCKETERT MSSEEAANCKKSHWAELSISGKVESLASLWSLTHLITALHLSDN SLSRIPSDIAKHHNIVYLDLSSNKIR  LDNUDNYPTFCNDALVYLDLSSNKIR  LDNUDNYPTFCNDALVYLDLSSNKIR  LDNUDNYPTFCNDALVYLDLSSNKIR  STAGE LDRUTTTYTAMADGG LTTTSIVSASAFGSYFDLSITEGKVESLSWERLATDEDSSPPNNQ ITYSIVSASAFGSYFDLSITEGKVESLSWERLATDEDSSPPNNQ ITYSIVSASAFGSYFDLSITEGKVESLSWERLATDEDSSPPNNQ ITYSIVSASAFGSYFDLSITEGKVESLSWERLATDEDSSPPNNQ ITYSIVSASAFGSYFDLSITEGKVESLSWERLATDEDSSPPNNQ ITYSIVSASAFGSYFDLSITEGKVESLSWERLATDEDSSPPNNQ ITYSIVSASAFGSYFDLSITEGKVESLSWERLATDEDSSPPNNQ ITYSIVSASAFGSYFDLSITEGKVESLSWERLATDEDSSPPNNQ ITYSIVSASAFGSYFDLSITEGKVESLSWERLATDEDSSPPNNQ ITYSIVSASAFGSYFDLSITEGKVESLSWERLATDEDSSPPNNQ ITYSIVSASAFGSYFDLSITEGKVESLSWERLATDEDSSPPNNQ ITYSIVSASAFGSYFDLSTTTIAACGGGETTGRANGAGGRPNNSTSTSTS AATAGAGCCWKERERKERKKERKERKERKERKERKERKERKERKERT KARLITYNDGGSCORPATTYNGGARAPTOKAGGGSPNSGNSTSTSTS AATAGAGSCCKSKEERKERKERKERKERKERKERVDPLF TTPAPPHV SGCORPATATOKAGGGGASSGGGGRPNNGNSTSTSTS AATAGAGSCCKSKEERKERKERKERKERKERVDPLF TTYPAPPHV S	576C	1	1221	VPDITEDEL CLEWINDROSS
LVOYENGBOGPKATRVPGHEDTVT1SGLEPDNYKMELYGFHOG CRVGPVSAIGVTAAEEETTPTTEPSMEAPEPPEPLIGELTVTC SSPDELSLSWTVPGGPFDSFTVOYBGERDGVTVVVGGESEVT VGGLEPGRKYKMHLVGLHEGRRVGPVSTVGVVAPQGEVSEVT VGGLEPGRKYKMHLVGLHEGRRVGPVSTVGVVAPQGEVSEVT VGGLEPGRKYKMHLVGLHEGRRVGPVSTVGVVAPQGDUETTSSF TEPGTEAPEPPEEPLEPLOELTVTGSSPDSLSINTVPQGFFDSFT VQYKDRDGRPQAVRVGGQESKVTVRGLEPGGKXVMALVGLHEGR IGPVSAIGVT SCDMAEAAALVWIRSPGFGCKAVRCASGRCTVRDPTHRHCODON VPVENFFVKCNGALINTSDTVOHGAVYSLEPBLCGGKGGFGSML RALGG, LEKTTNREACRDLSGGRLWHENAMENVKQOLERE AEKEQKRLERIQRKLVEPRHCFTSPDYOQOCHEMAERILEDSVLK GNQAASSKMVSARISISENRKQMPTKSGTDMSAGKRRCFFUIGM EGLBTAAGGSNSESDDDSEAAPSTSGMSHAPKIGSNGVEMAAK FPSGSGRARVVNTDHGSPEQLQIPVTDSGRHIEDSCAELGESK EHMSRWITTEBETCEKKAESKEPLIEEPTGAGLINKGETERT DGERVAEVAPEERENVAVAKLQESQFONAVINKETIDLLAFTSV AELELLELKLKCELMAIGLKCGTL SGRAANKKSHWAELSISCKVRSLASALMSITHLTALHLISDN SLERIPSDIAKHMLVYLDLSSNKIR  5762 2 344 GSTGOTPLMSGGGGGSGGGRRFTFRGMPKEKYEPPDFRRMYTI MSSEAANKKSHWAELSISCKVRSLASALMSITHLTALHLISDN SLERIPSDIAKHMLVYLDLSSNKIR  5763 3 429 LDKDTGLIMLTARLDYELIGRFTLTITIARDGGETTGRVRINV LDVDDNVPTFGKDAXVGALERNEFUOLVAVRARATBESPPNNO ITTSIVSASAFGSYPDISLYEGYGVISVSRPLDYEQISNGLIYL TVAMADGN ITTSIVSASAFGSYPDISLYEGYGVISVSRPLDYEQISNGLIYL TVAMADGN ITTSIVSASAFGSYPDISLYEGYGVISVSRPLDYEQISNGLIYL TVAMADGN TVARAMDGN FPFGKDAXVGALERNEFUSKVRSTSKDLVRGFSLEEK LRSQLVGOFFVAMMEGKDFNYEYVGRELARVELIFREKDGLGIK MPDPDFTVRDVKLLVGSRRIDVDNTTQKGTEMSBOFVRYYE TPEAQRDKI  5765 3 825 QKILENNSHOPPTSSNSKDCGGRASSGAGATAALADGLKFAS VQASAPQGNISKFETSKSKVRSTSKBLANKSLPSALJEJGIPEIS STCKRGEVGGRGFGATGMSALGGSSGGSGNFNSNSTSTTSTS AATAGGSGGRKEERPGKSQSSRGAKRDKDAGKSRNCHDLLQ GHOMSGSQAPSGCHLYGFGALSNGGGSPFFHGGTGSGSVAAA GEVSKAPDSGLMMSMLVKKEEEEEBSHRIKKKKKTEKVDPLF TPPAPPHUM GENGRG SGLFSVDPASSQAMELSDVTLIEGVGNEWWVAGVAVLTLALVL AALLSTVADBGSNQLLGAIVSAGDTSVLHLGHVDHLVAGGGNPE PTELPHPSEGNDEKABEAGEGGGOSPEFLEHLLD LGGJKRQAGAGSSSPEAPLRSEDSTCLPFSFGLITVYLKFLND TEELAVARPEGTAPGSPGANAFFFGSPGLITFYRFILKFLND TEELAVARPEGTAPPGSAVAFFSALAPSATEPPSELGUTNG SLMWPVVVLLGVVWYFRINYRGFFTAPATVSLVGUTVFPSFLV	l l			GVTISGLEDDHYVVANVINGEROFDEFLVQFKNGDGQPKAVRVPGHED
LVOYKNGBOGPKARTVPGHEDTVPTGELSISTTVPEGGFDHE  LVOYKNGBOGPKARTVPGHEDTVT1SGLEPDNYKNMLYGFHGG CRYGPVSAIGVTAAEETTPTTEPSMEAPEPPEPLIGELTVTC SSPDELSISTSVTVPGGRFDSFTTVOYBGERPOSTVOYKGERSEVT VGGLEPGRKYKMHLYGLHEGRRVGPVSTVGVTAPQEDVDETTSP TEPGTEAPEPPEEPLEPLIGELTVTGSSPDSLSISTVTVPGGFFDSFT VQYKDRDGRPQAVRVGGQESKVTVRGLEPGRKYVMHLYGLHEG HERDEN AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE STEP AND THE	1			1 O T T T T T T T T T T T T T T T T T T
CRVGPVSAIGVTAAGEETPTPTEPSMEAPEPPEPLIGELTVTG SSPDSLSISUTVPGGREDSTVQYKDROERPOVYRVGEBSENT VGGLEPGRKYMHLYGLHEGRRVGPVSTVGYTAPGEDVDETPEP TEGTEAPEPPEPLIGELTVTGSSPDSLSLSWTVPQGREDSFTOT TEGTEAPEPPEPLIGELTVTGSSPDSLSLSWTVPQGREDSFTOT TEGTEAPEPPEPLIGELTVTGSSPDSLSLSWTVPQGREDSFTOT VGVKDRORPQAVVRGQESKVTVRGLEPGRVTXMHLYGLHEGR RIGPVSAIGVT SCHMARAALVWIRGPGFGKAVRCASGRCTVRDFIHRHCQDON VPVEMFFVKCNGALINTSDTVQHGAVYSLEPRLCGGKGGFGSML RALGAQIEKTINREACRDLSGRRLEDVHLKEAMAEVKLOQAERE AEKEQKALERLIQRKLUPEHHCTSPDYQQCHEMABRILEDSVLK GNQAASSKMVASISENRRGNPTKSGTDGRASAGKRRCFHIGM EGLITARGSSNESSDDDSEEAPSTGDFLANGSFTVGMAAK FFRGGQRARVVNTDHGSPDQLQIPVTDGGRHILEDSCAELGESK EMESRIVTETEETDCKKAESKEPIEEPTGGLKNOKETEERT DGERVABVAPEREENVAVALUGSSQFONAVIDKETIDLAFTSV AELBLLLEKLKCELMAIGLKCGSTLQ  5762 2 344 GSTGOTPLHSQGGGGSGGGGRRFFRGMMFKEKYBPPDFRRNYTI MSSEEAANGKKSHWAELSISGKVESLSASLWSLTHILTALHLSDN SLSRIPSDIAKLHNIVYDLISSNIV SLSRIPSDIAKLHNIVYDLISSNIV SLSRIPSDIAKLHNIVYDLISSNIV SLSRIPSDIAKLHNIVYDLISSNIV SLSRIPSDIAKHNIVYDLISSNIV STORTGRGSTGRFFRGMFKEKYBPPDFRRNYTI MSSEEAANGKKSHWAELSISGKVESLSASLWSLTHILTALHLSDN LDNUBMVFTFCKDAVGALRENBESVTOLVRIRATDEDSPPNNQ ITYSIVSASAFGSYFDISLYEGGVISVSRPLDVEGISNGLIYL LDNUBMVFTFCKDAVGALRENBESVTOLVRIRATDEDSPPNNQ ITYSIVSASAFGSYFDISLYEGGVISVSRPLDVEGISNGLIYL TVAMADAGN  5764 19 441 VCARACGEMRQLLRPIDRGRYDENELSDVEEIVSVRGFSLEEK LRSQLYGGFVIAMBGRUPFTYEVQUREALRYBLIFREKDGLGIK MPPDDFTVEDVELLVGSRRLVDVMDVNTQKGTEMSMSOFVRYYE TPAQRDKL  5765 3 825 QKILKINSHOPPTSSNSKDCGGRASSGAGATAALDGLKFAS SCKRGEVGGSGRGREATGMNSALGGSVSGGGSGNNENSTSTTST AATAGAGSCGKSEEKPGKSQSSRGAKRDKDAGKSRDHDLLQ GHQNAGGSGAPSGGHLYGGAAKNGGASPFHCGGTGSGSVAAA GSVSKSAPDGGLMGNSHLVKREEBERHRIKKLKKTEKVDPLF TVPAPPHW TVPAPPHW TUPAPPHW TRELAVARPBDTVGALKSKYPFGGDSGMKLUTGRLUDPARTI ANLSTYVADSGSNOLLGAIVSAGDTSVLHLGHVDHLVAGQGNPE PPTELPHPSGMBKABEAGEGGROSTGEAGAGGVEPSLEILLD LGGLPKRQAGAGSSSPEAGAGRABDLAGASSALPSATEPPELGUNGV SLMWPVVULLGVVWYFRINYRQFFTAPATVSLVGUTVPFSFLV FOMMGR				1 AND A DEFILE DESTRUCKLISE STOTE DATE OF CHARLES OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF COMMENTS OF C
SSPDELSLSEWTYACKETTYOTKERARPPEPEPLICELTUTE  SSPDELSLSEWTYACKETTYOTKERARPPEPEPLICELTUTE  VGGLEPGRKYKMHLYGLHEGRRVOGYVSTVOGTAPOEDVDETPSP TEPEGTEAPEPPEPEPLICELTUTGSSPDSLLLSWTYPOCRFDSFT TEPEGTEAPEPPEPEPLICELTUTGSSPDSLLLSWTYPOCRFDSFT TOTTE TOTT TO THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE				1 ~ VIII GOODFRAIRVPGHEDRVTISCI PONIVVVIANT TOTTE
SOFIOLISM TO VGGLEPGRYYMHLYGLHEGRRYOPVSTVOYTAPORDVDETPSP TEPGTEAPEPPEPLLGELTTTGSSPDSLLSMTVPOGRFDSFT VVGYKPDGRPQAVRVGGGESKVTVRGLEPGRKYKMHLYGLHEGR RIGPVSAIGVT SCDMBEAAALVWIRSPGFGCKAVRCASGRCTVRDF IHRHCDDON VPVENFFVKCKGALINTSDTVQHGAVYSLEPELCGKGGFGSML RALGAQIEKTTNREACRDLSGRRIEDVNHEKAMAEWVKQAERE AEKEQKRLERIQRKLVEPKHCTSDTVQOCHEMAERLEDSVLK GMQAASSKMVSAEISERRKRQWPTKSQTDRGASAGKRCFWLGM EELBTAGGSNESSDDDSEEAPSTSGMGFHARKIGSNAVEMAAK EPSGSQRARVNTHHGSPBCLQIPVTDSGRHLIEDSCAELGESK EHMISRHVTETEETQEKKAESKEPIBEPFTGAGLNKKKETEERT DGERVARVAPERERNVAVARLGSOPGNAVIDKETIDLLAFTSV AELELLGLEKLKCELMALGLKCGGTLQ  5762 2 344 GSTGOTPLHSGGGGGGGGGGGRGRTFRGMPKEKYEPPDPRRMYTI MSSEEAANGKKSHWAELEISGKVRSLSASLMSLTHLTALHLISDN SLSRIPSDIAKHHNLVYLDLSSNKIR  5763 3 429 LDKDTGLIMLIARLDVELIQR FILTIIARDGGEETTGRVRINV LDVNDNVPTFQKDAYVGALRENEPSVTQLVSLRATDEDSPNNQ ITYSIVSASAFGSYPDISLYEGYGVISVSRPLDYEGISNGLIYL TVAMADAGN 5764 19 441 VCARACGEMRQLEPIDRQRYDENEDLSDVEIVSVRGFSLEEK MPDPDFTVRDVXLLVGSRRLVDVMDVNTQKGTEMSMSGFVRYYE TPEAGRAKL MPDPDFTVRDVXLLVGSRRLVDVMDVNTQKGTEMSMSGFVRYYE TPEAGRAKL STOKKQEVQGRPGEATGMNSALGGSVSSGGSGNFNSNSTSTSTS AATAGAGSCGKSKEEKPCKSQSSRGAKRAALADGLKFAS STOKKQEVQGRPGEATGMNSALGGSVSSGGSGVAPNNSTSTSTS AATAGAGSCGKKEEKPCKSQSSRGAKRAALADGLKFAS STOKKQEVQGGRGGGGGATGAALADGLKFAS GEVSKSAPDSGIMGNSMLVKKEEEEESHRRIKKLKTEKUDPLF TPPAPPHY TPAPPPHY 5766 1608 663 SGLFSVDPASSQAMELSDVTLIEGVGNEVWVAGGVVLILALVL AALSTYVADSGSNQLLGAIVSAGGTSPHCGGTGSSVAAA GEVSKSAPDSGIMGNSMLVKKEEEEESHRRIKKLKTEKUDPLF TPPAPPHPPHYGNGERAREAGGGGSGSPESLERBLILD IQGLFKRQAAGSSSPEAPLRSEDSTCLPPSPGLITVURLKELND TEELAVARPEDTVQALKSKFFGQGSSALFPSGLITVURLKELND TEELAVARPEDTVQALKSKFFGQGSSALFPSGLITVURLKELND TEELAVARPEDTVQALKSKFFGGGSSALFPSGLITVURLKELND TEELAVARPEDTVQALKSKFFGGGSSALFPSGLITVURLKELND TEELAVARPEDTVQALKSKFFGGGSSALFPSGLITVURLKELND TEELAVARPEDTVQALKSKFFGGGSSALFPSGLITVQCKLQPARTL RSLMITDNCVIHCHRSPPGSALLPSGLAFPSFLGVNVG SLMYPVVULLGVWYFRINYRGFTAPATVSLVGVTVPFSFLV				QRVGFVSAIGVTAAEEETPTDTEDQMEADDDDDEDDLEGGE
TEPGTEAPEPPEEPLLGELTVIGSSPPSLLSWTVPQGRPDSFT TEPGTEAPEPPEEPLLGELTVIGSSPPSLLSWTVPQGRPDSFT VQYKDRDGRPQAVRVGGQESKVTVRGLEPGRKYKMHLYGLHEGR RIGPVSATGVT SCDMAEAAALVWIRSPGFGCKAVRCASGRCTVRDFIHRHCQDQN VPVENFFVKCKGALINTSDTVQHGAVYSLEPBLCGGKGGFGSML RALGAQIEKTTINREACRLUSRIDVNIEKAMAEWVKQQAERE AEKEQKRLERLQRKLVBPKHCFTSPDYQOQCHEMAERLEDSVLK GMQAASSKMVSAEISERRKROPTKSQTTDRGASAGKRRCFWLGM ESLBTAEGSNSESSDDDSEEAPSTSGMGFHAPKTGSNOVEMAAK FPSGSQRARVVNTDHGSPEDLQTPVTDSGRHILEDSCAELGESK EHMESRNVTETEETQEKKAESKEPIBEEFTGGALKKKETEERT DGERVABVAPEERENVAVAKLQESQPGNAVIDKETIDLLAFTEV AELELLGLEKLKCELMALGLKCGGTI  S762 2 344 GSTGOTPLHSQGGGGGGGGGGRRTTRGGMPKEKYEPPDPRRNYTI MSSEAANGKKSHWAELEISGKVRSLSASLWSLTHLTALHLSDN SLSRIPSDIAKLINLVYLDLISNKIR  5763 3 429 LDKUTGLIMLIARLDYELISONKIR  LDVNDAVPTFOKDAYVGALRENEPSVTQUXBLARTDEDSPDNQ ITYSIVSASAFGSYFDISLYEGYGVISVSRPLDYEQISNGLIYL TVMAMDAGN 1TYSIVSASAFGSYFDISLYEGYGVISVSRPLDYEQISNGLIYL TVMAMDAGN 5764 19 441 VCARACGEMROLLRPIDRQRYDENEDLSDVEEIVSVRGFSLEEK LRSQLVQGPFVHAMGGKDFNYEYVQREALRVPLIFREKDGLGIK MPDPDFTVRDVKLLVGSRRLVDVMDVTQKGTEMSMSGFVRYYE LRSQLVQGPFVHAMGGKDFNYEYVQREALRVPLIFREKDGLGIK MPDPDFTVRDVKLLVGGSRRLVDVMDVTQKGTEMSMSGFVRYYE STGKRQEVQGRGGATGMNSALGQSVSSGGSGRNNNSTSTSTS AATAGAGSCGKKEEKPGKSQSSRGARTDALDGLKFAS STGKRQEVQGRGGATGMNSALGQSVSSGGSGRNNNSTSTSTS AATAGAGSCGKKEEKPGKSQSSRGARTDALAGCKFRDNHDLLQ GRONSGSGAPASGGLHLYGFGAKSNGGGASFFKGGTGGSGSVADA GEVSKSAPDSGLMGNSMLVKKEEEEESHRRIKKLKTEKVDPLF TTPAPPPHV 5766 1608 663 SGLFSVDPASSQAMELSDVTLIEGVGNEVMVVAGVVULILALVL AWLSTYVADGSSNLLGALVSAGGGSFFKGAGGGGGGGGGGGGGSGVADA GEVSKSAPDSGAMGNSMLVKKEEEEESHRRIKKLKTEKVDPLF TTPLPHPSEGMDEKREREESGGGTGSGCSVADA GEVSKSAPDSGAMGRSDVLIGGRUFGLVAGGAGGGPSLUGGDARGGOPSLEHLLD IQGLPKRQAGAGSSSPPARDLSDVTLIEGVGNEVMVVAGQONPE PTELPHPSEGMDEKREREEGEGGTGGGGGGGGGDGDART RELAVARPEDTVGALKSKYFPGQESMKLIVQGRLQDAPRTL RSLNITDNCVIHCHRSPGGSAGLAPGAGGGVPSLEHLLD IQGLPKRQAGAGSSSPPARDFSSSLAPSATEPSLGVNVG SLMYPVEVULLGVVWYFRINYRGFTAPATVSLVGVTVPFSFLV	1 1			1 33 FD 3 D 3 D 3 D 3 D 3 D 3 D 3 D 3 D 3
TOTAL TOP PROPRIES TO THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF TOTAL STATES OF THE TOTAL STATES OF TOTAL STATES OF TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES OF THE TOTAL STATES	1			T TOOLE GREAT KINNEY GLIBEGER VCDVCTVCVTX DOUDY TO THE
S761 3 1275 SCDMAEAAALWU RGGGESKUTVRGLEFGRKYKMHLYGLHEGR VEVENFFVK.CNGALINTSDTVOHGAVYSLEPILCGKGGFGSML RALGAO I EKTTNREACRDLSGRRIEDWHERAMAEWVROQAERE AEKEQKRLERLQRKLVEPKHCFTSPDYQOCCHEMAERLEDSVLK GMQAASSKMVSAEI SENRKROWPTKSQTDRGASAGKRRCFWLGM ESLETAEGSNESSDDDSEEAPSTSGMGFHAPKIGSNGVBMAAA FPSGGRRAVVNTDHGSPDQLQI PVTDSGRHILEDSCAELGESK EHMESRWTETEETQEKKAESKEPIEEPTGAGANKOKETEERT DGERVAEVAPEERENVAVAKLQESQPONAVUDKETIDLLAFTSV AELELLCLEKLKCEIMALGKGGTLQ STGOTPIHSGGGGGSGGGRRTFRGMPKEKYEPPDPRRMYTI MSSEAANGKKSWAELEISGKVRELSASLWSITHHTAHHLSDN SLSRI PSDIAKLMILVYLDLSSNKIR  10 LDWDTGLIMLIARLDYBLIORFTITIIARDGGGEFTTGRVRINV LDWDNVPTFCVDAYVGALREPSVTOLVRLRATDEDSPPNNQ LTYSIVSASAFGSYFDISLYEGYGVISVSRPLDYBCISNGLIYL TVAMADAGN VORRGGBMRQLLRPIDRQRYDENEDLSDVEEIVSVRGFSLEEK LRSQLYQGFVHAMEGGDRYVDENEDLSDVEEIVSVRGFSLEEK LRSQLYQGFVHAMEGGDRYVDVINCHARADAGLIYL TPEAQRBOKL TPEAQRBOKL GHQNGSGGAPSGGHLYGFGASGAGATAALADGLKFAS VOASAPQGNSHKETSKSKVRS KTSKDANKSLDSAALYGIPBIS STCKRQEVQGRPGEATGMSALGQSVSSGGSCNPNSNSTSTSTS AATAGASGCGKSKEEKPGKSQSSGAKARAALADGLKFAS VOASAPQGSHKETSKSKVRS KTSKDANKSLDSAALYGIPBIS STCKRQEVGGRRGEAFGMSALGQSVSSGGSCNPNSNSTSTSTS AATAGAGSCGKSKEEKPGKSQSSGAKARAALADGLKFAS VOASAPQGSHKETSKSKVRS KTSKDANKSLDSAALYGIPBIS STCKRQEVGGRRGEAFGMSALGQSVSSGGSCNPSNSTSTSTS AATAGAGSCGKSKEEKPGKSQSSGAKARAALADGLKFAS VOASAPQGSHKETSKSKVRS KTSKDANKSLDSAALYGIPBIS STCKRQEVGGRRGEAFFGMSALGQSVSSGGSCNPSNSTSTSTS AATAGAGSCGKSKEEKPGKSQSSGAKARAALADGLKFAS TVPAPPPHV SCHORGSGAPSGGHLYGFGAKGGGASPFLGGTGGSSVAAA GEVSKSAPDSGLMGNSMLVKKEEEEESHRRIKKLKTEKVDPLF TTPAPPPHY JPELPPPSEGNDEKAEEGEGGGGSTGGTGGTGGSGAVAA AGSVSKSAPDSGLMGNSMLVKKEEEEESHRRIKKLKTEKVDPLF TTPLPPPSEGNDEKAEEGEGGGGSTGGARGATELDLIQDFARTL RSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLCUVNG SLMVPVEVVLLGGVWYFRINYRQFFTAPATVSLUGVTVPFSFLV SLMVTPVVLLGGVWYFRINYRQFFTAPATVSLUGVTVPFSFLV	1 1	[		TEEGIEMPERFEEPLIGELTVTGGGDDGLGLGWWYDAAA
SCHMERARALVWIRGEGEGKAVRCASGRCTVRDFIHRHCODON VDVENFFVKCNGALINTSDTVQHGAVYSLEPRLCGKGGGGSML RALGAQIEKTTHREACRDLSGRRIRDVNHEKAMAEWVKQQAERE AEKEQKRLERLQRKLVEPHICFTSDDYQQCCHEMBERLEDSVLK GQQAASSKNVSABISENRKRQWFTKSGTDEGASAGKRRCFWLGM EGLETAGEGISESSDDDEAPSTSGMGFHAPKIGSNOVEMAAK FPSGSQRARVUNTDHGSPEQLQIPVTDSGRHILEDSCAELGESK EHMESRMVTETEETQEKKAESKEPIEEFTGAGLINKDKETEERT DGERVAEVAPEERENVAVAKLQESQPGNAVIDKETIDLLAFTSV AELELLGLEKLKCEIMALGLKCGGTLQ  5762 2 344 GSTGOTPLISGGGGGGGGGGGRGTFRGMFKEKYEPPDPRRMYTI MSSEBAANGKKSHWAELEISGKVRSLSASLWSITHITALHLSDN SLSRIPSDIAKLHULVILDLSSNKIR  LRUNDSDYTGKDAYVGALRENEFSVTQLVRLRATDEDSPPNNQ LIYSIVSASAFGSYFDISLYEGGYGISVGSPLDVEQISNGLIYL TVVAMDAGM 1YYSIVSASAFGSYFDISLYEGGYGISVGSPLDVEQISNGLIYL TVVAMDAGM VCARACGEMRQLLRPIDRORYDENEDLSDVEIVSVRGFSLEEK MPDPDFTVRDVKLLVGSRRLVDVMDVINGTEMSMSQFVRYYE STEAQRBKL STEKQEVGGREGEATGMNSALGGSVSGGGSGFNSNSTSTSTS AATAGAGSCGKSKEEKREGSSRGAKRDKHDLLQ GHONGSGSQAPSGGHLYGFGAKSNGGSAFFRIKKLKTEKVDPLF TYPAPPHY TYPAPPHY 5766 1608 663 SGLFSVDPASSQAMBLSDVTLIEGVGNEVMVAGVVVLILALVL AALLSTVANDSGSNQLAGAVSCAGGGGLEBHLLD LQGLPKRQAGASSSPEAPLRSEDSTCLPPSPGLITVRLKFLND TEELAVARPEDTVGALKSKYFPGQESQMKLIYGGRLUDPARTI, RSLNITDNCVIHCHRSPPGSAVPGFSASLAPSATEPSSLGVNUG SLMYPVFVVLLGVVWYFRINYRQFFTAPATVSLVGVVTVFFSFLV	1 1			T VALADROGREVAVROGGOESKOTORGI EDGDROVMUT VOT TEDGE
SUMMARAALVMIRGFGFGCKAVRCASGRCTVRDFIRHECDDON VPVENFFVKCNGALINTSVOHGAVYSLEPRLCGKKGGFGSML RALGAQIEKTTRREACRDLSGRRIRDVNHEKAMAEWYKOQAERE AEKEOKRLEPLQRKLVEPRHCFTSDYQOQCHEMAERLEDSVIK GMQAASSKWVSAEISENRRKQWPTKSGTDRGASGKRRCFWLGM ESLETAEGSNSESSDDDSEEAPSTSGMGFHAPRIGSNGVEMAAK FPSGSQRARVAVNTDHGSPLOQTVPTDSGRHILEDSCAELGESK EHMESRMVTETETQEKKAESKEPIEEETJAGLINDKETEERT DGERVAEWAPEERENVAVAKLQESQFGNAVIDKETIDLLAFTSV AELELLGLEKUKCEMALGKCGGTLQ AELELLGLEKUKCEMALGKCGGTLQ STGOTPLHSQGGGGGGGGRRFTFRGMPKEKYEPPDPRRMYTI MSSEEAANGKKSHWAELEISGKVRSLSASLWSLTHLTALHLSDN SLSRIPSDIAKLHNLVYLDLSSNKIR LDVNDNVPTFCKDAYVGALREDESVTOLVRIRATDEDSPPNNQ LTYSIVSASAFGSYFDISLYEGYGVISVSRPLDTEQISNGLIYL TVAMDAGAN 1TYSIVSASAFGSYFDISLYEGYGVISVSRPLDTEQISNGLIYL TVAMDAGAN VCARACGEMRQLLRPIDRQRYDENEDLSDVEEIVSVRGFSLEEK LRSQLYGGDFWHAMEGKDFNYEYVQREALRVELIFREKDGLGIK MPPDPTTVRDYKLLVGSRRLVDVNTQKGTEMSMSGFYRRYE TPEAQROKL VQASAPQGNSHKETSKSKVKRSKTSKDANKSLSSAALYGIPEIS STCKRGEVQGRPGGBATGMNSALGGSVSSGGSGNPNSNSTSTSTS AATACAGSCCKSKEEKPGKSQSSRGSKRAKDKHDLLQ GHONGSGSQAPSGGHLYGFGAKSNGGGSPHCGGTGSGVAAA GEVSKSAPDSGLMGNSMLVKKEEFEEBSHRIKKLKTEKVDPLF TVPAPPPHV 1TYPAPPHYD 1GGLFKRQAGAGSSSPEAPLGEGGSGVABFLEHLLD LQGLFKRQAGAGSSSPEAPLREEDSTCLPFSPGLITVRIKFLND LQGLFKRQAGAGSSSPEAPLREEDSTCLPFSPGLITVRIKFLND TEELLAVARPEDTVGALKSKYFPQGESQMKLIVYGGRLUOPARTI RSLNITDNCVIHCHRSPPGSAVPGFSASLAPSATEPPSELVHVG SLMYPVFVVLLGVWWFRINYRQFFTAPATVSLVGVVVFFSFLV	5761	3	1275	- regr ADVITAAT
RALGAQI EKTTRREACRDLSGRRIADVINERAMAEWKQOAERE AEKEQKRLERLORKLVEPKHCFTSPDYQQQCHEMAERLEDSVLK GMQASSKMVASAEI SENRKRQWPTKSQTDRGASGKRRCFWIGM EGLETAEGSNSESSDIDSEAPSTSGMGFHAPKIGSNGVMAAK FPSGSGRARVVNTDHGSPEQLQIPVTDSGRHILEDSCAELGESK EHMESRMVTETEETDEKEKEKEKPI BEEPTGAGLINKDKETEERT DGERVAEVAPEERENVAVAKLQESQFGNAV IDKETTLDLAFTSV AELELLGLEKKKCETHAGLKCGGTLQ  5762 2 344 GSTGOTPLHSQGGGGGGGGRRFTFRGMFKEKYEPPDPRRMYTI MSSEBAANGKKSHWAELEISGKVRSLSASLWSITHLTALHLSDN SLSRIPSDIAKLHNLVYLDLSSNKRR  5763 3 429 LDKDTGLIMLTARLDYELIQRFTLTTIANDGGGEETTGRVRINV LDVNDNVPTFCKDAYVGALRENEPSVTQLVRLRATDESSPPNNQ ITYSIVSASAFGSYPDLSLYEGYGVISVERPLDVEQISNGLIYL TVMAMDAGN  5764 19 441 VCARACGEMRQLLRPIDRGRYDENEDLSDVEEIVSVRGFSLEEK LRSQLYGGBFVHAMEGKDFNYEYVQREALRVPLHFREKDGLGIK MPDPDPTVRDVKLLVGSRRLVDVMDVNTQKGTEMSMSQFVRYYE LRSQLYGGBFVHAMEGKOSSGRGAKRDKDAFKSRKOKFNYEY TPEAQRBKL  5765 3 825 QKILRINNSHOPPTSSSNSKDCGGFASSGAGATAALADGLKFAS VOASAPOGNSHKETSKSKVKRSKTSKDANKSLJSAALYGIPEIS STGKRQEVQGRPGEATGMNSALGGSVSSGGGSGNNSNSTSTSTS AATAGAGSCCKSKEEKPGSSFRAKRKDAKSLJSAALYGIPEIS STGKRQEVQGRPGEATGMNSALGGSVSSGGGSGNNSNSTSTSTS AATAGAGSCCKSKEEKPGSSFRAKRKDAKGKRKDKHDLLQ GHONGSGSQAPSGGHLYGFGAKSNGGGASPFHCGGTSSGSVAAA GEVSKSAPDSGIMMSNLVKKEEEEESHRRIKKLKTEKVDPLF TVPAPPPHU  5766 1608 663 SGLFSVDPASSQAMBLSDVTLIEGVGNEVWVAGVVVLILALVL AALLSTVADSGSNQLLGAIVSAGGTSVLHLGHVDHLVAGGGNPE PTELPHPSEGNDEKAEEAGEGRGDSTCEAGAGGGVEPSEHLLD IQGJEKRQAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLIND TEELLAVARPEDTVGALKSKYSFPQGESQMKLIYQGRILQDPARTL RSLNITDNCVIHCHRSPPGSAVPGFSASLAPSATEPSLGVINUS SLMYPVFVVLLGVWWYFRINYRQFFTAPATVSLVGVTVFFSFLV	1 1		12/3	SCDMAEAAALVWIRGPGFGCKAVRCASGRCTVRDFIHRHCODON
AEKEÇKELERLQRKLVSPKHCFTSPDYQQQCHEMAERLEDSVLK GMQAASSKWVSABISENRKRQWPTKSQTDRGASAGKRRCFWLGM EGLBTAEGSNSESSDDDSERSPTSGMGFHAPKIGSNGVEMAAK FPSGSQRARVVNTDHGSPEOLOIPVTDGSGHILEDSCAELGESK EHMESRMVTETEETQEKKAESKEPIBEEFTGAGLNKDKETEERT DGGRVAEVAPEERENVAVARLQBSQFGRAVIDKETIDLLAFTSV AELELLGLEKLKCELMALGLKCGGTLQ  5762  344  GSTGOTPLHSQGGGGGGGGGRGRTFRGMPKEKYEPPDPRRMYTI MSSEAANGKKSHWAELEISGKVRSLASZKSLITHLTALHLSDN SLSRIPSDIAKLHNLVYLDLSSNKIR  LDKVDINVPTFOKDAYVGALENEPSVTQLVRLRATDEDSPPNNQ LTYSIVSASAFGSYPDISLYEGGYGUSVSRPLDVEQISNGLIYL TVHAMDAGN  5764  19  441  VCARACGEMRQLLRPIDRQRYDENEDLSDVEEIVSVRGFSLEEK LRSQLYQGDFVHAMEGKDFNYEVQREALEVPLIFREKDGLGIK MPDPDFTVRDVKLLVGSRRLVDVMDVNTQKGTEMSMSOFVRYYE TPEAQRIKL  5765  3 825  QKILRINNSHQPFTSSSNSKDCGGPASSGAGTAALADGLKFAS VQASAPQGNSHKETSKSKVRSKTSKDANKSLSAALJGIPEIS STGKRGEVQGRPGEATGMRALGQSVSSGGSKOPNSNSTTSTS AATAGAGSCGKSKEEKPGKSQSSRGAKRDKDAGKSRKDKHDLLQ GHQNGSGSQAPSGGHLYGFGAKSNGGSSPPNSNSTTSTS AATAGAGSCGKSKEEKPGKSQSSRGAKRDKDAGKSRKDKHDLLQ GHQNGSGSQAPSGGHLYGFGAKSNGGSSPPNSHDTSTTSTS AATAGAGSCGKSKEEKPGKSQSSRGAKRDKDAGKSRKDKHDLLQ GHQNGSGSQAPSGGHLYGFGAKSNGGSSPPNSHDTSTTSTS AATAGAGSCGKSKEEKPGKSQSSRGAKRDKDAGKSRKDKHDLLQ GHQNGSGSQAPSGGHLYGFGAKSNGGGSPPNSNSTTSTS AATAGAGSCGKSKEEKPGKSQSSRGAKRDKDAGKSRKDKHDLLQ GHQNGSGSQAPSGGHLYGFGAKSNGGGSPPNSNSTTSTS AATAGAGSCGKSKEEKPGKSQSSRGAKRDKDAGKSRKDKHDLLQ GHQNGSGSQAPSGGHLYGFGAKSNGGGSPPNSNSTTSTS AATAGAGSCGKSKEEKPGKSQSSRGAKRDKDAGKSRKDKHDLLQ GHQNGSGSQAPSGGHLYGFGAKSNGGGSPPNSNSTLSTS AATAGAGSCGKSKEEKPGKSQSSRGAKRDKDAGKSRKDKHDLLQ GHQKSKAPPPPHV  5766  1608  663  SGLFSVDPASSQAMELSDVTLIEGVGNEVMVVAGVVVLILALVL AWLSTYVADSGSNOLLGAIVSAGDTSVLHLGHVUPHLVAGQGNPE PTELPHPSEGNDEKAEEAGEGGGDSTGEAGAGGVEPSLEHLLD LQGLFKRQABGSSSPPAPLRSDSTCLPFSFGLTVRLKFLND TEELAVARPEDTVGALKKYFPGQESQMKLIYQGRLLQDPARTIL RSLMITUDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNNG SLMVPVFVVLLGVVWYFRINYRGFFTAPATVSLVGVTVFFSFLV	1 1	i		1 VEVEN FEVEN CHICALINES DEVONE AND COCKERS
GMQAASSKWVABISERRKRQWPTKSQTDRGASGKRCFWLGM EGLETAEGSNESSDDDSEEAPSTSGMGFHAPKIGSNGWEMAAK FPFSGSQRARVVNTDHGSPGLIPVTDSGRHLLEDSCAELGESK EHMESRMVTETEETQEKKAESKEPIEEBPTGGEINDKKETEERT DGERVAEVAPEERENVAVAKLOESQPGNAVIDKETIDLLAFTSV AELELLGLEKLKCELAHAGLKCGGTLQ  344 GSTGOTPLHSQGGGGSGGGRRTFRGMPKEKYEPPDPRRMYTI MSSEEAANGKKSHWABLEISGKVVSLSASLWSLTHLTALHLSDN SLSRIPSDIAKLHNLVDLISSNKIR  5763 3 429 LDKDTGLIMLIARLDYELIQRFTLTIIARDGGEETTGRVRINV LDVNDNVPTFCKDAVVGALRENEPSVTQLVVRLRATDEDSPPNNQ ITYSIVSASAFGSYFDISLYEGYGVISVSRPLDVEQISNGLIYL TVAMMDAGN  5764 19 441 VCARACGEMRQLLRPIDRQRYDENEDLSDVEETVSVRGFSLEEK LRSQLYQGDFVHAMEGKDFNYEVQREALRVPLIFREKDGLIJK MPDPDFTVRDVKLLVGSRRLVDVMDVNTQKGTEMSMSOFVRYYE TPEAQRRKL MPDPDFTVRDVKLLVGSRRLVDVMDVNTQKGTEMSMSOFVRYYE TPEAQRKL GGWSASAPGGNSHKETSKSKVKRSKTSKDANKSLPSAALYGIPEIS STGKRGEVQGRPGEATGMNSGLGSVSSGGSGRPNSNSTSTSTS AATAGGSGCKSKEEKPGKSQSSRGKRRDKHDLLQ GHQNGSGSQAPSGGHLYGFGAKSNGGGSPFHCGGTGSGSVAAA GEVSKSAPDGGHGNSMLVKKEEEEESHRRIKKLKTEKVDPLF TVPAPPPHV  5766 1608 663 SGLFSVDPASSQAMELSDVTLIEGVGNEVMVVAGVVVLILALVL AMLSTYVANDSSNOLLAGIVSAGDTSVLHLGHVDHLVAGQGNPE PTELPHPSEGNDEKAEEAGEGGGOSTGEAGAGGGVPSIEHLLD LQGLPKRQADGSSSPPAPLRSEDSTCLPPSPGLTVVRLKFLND TEELAVARPEDTVGALKSVFPQOESQMKLIYQGRLLQDPARTL RSLMITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG SLMVPVFVVLLGVVWYFRINYRQFFTAPATVSLVGVTVFFSFLV	1			T AND AND TENTINKEACROLSGROUND TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN TO THE COLUMN
EGLETAGGSNEESSDDESEAPSTSGMGFHAPKIGSNGVEMAAK FPSGSQRARVUNTDHGSPEOLQIPVTDSGRHILEDSCAELGESK EHMESRMVTETEETQEKKAESKEPIEEEFTGAGLNKDKETEERT DGERVAEVAPEERENVAVAKLQESQPONAVIDKETIDLLAFTSV AELELLGLEKLKCELMALGLKCGGTLQ  5762 2 344 GSTGOTPLHSQGGGGGGGRRTFREMPKEKVEPPDPRRMYTI MSSEEAANGKKSHWAELEISGKVRSLSASLWSLTHLTALHLSDN SLSRIPSDIAKLHNLVYLDLSSNKIR  LDWDNDVPTPCKDAYVGALRENEPSYTOLVRLARTDEDSPPNNQ ITYSIVSASAFGSYFDISLYEGYGVISVSRPLDYEGISNGLIYL TVMMDAGN  5764 19 441 VCARACGEMROLLRPIDRQRYDENEDLSDVEEIVSVRGFSLEEK LRSQLYQGDFVHAMEGKDFNYEYVQREALRVPLIFREKDGLGIK MPDPDFTVRDVKLLVGSRRLVDVMDVNTQKGTEMSMSOFVRYYE LRSQLYQGDFVHAMEGKDFNYEYVQREALRVPLIFREKDGLGIK MPDPDFTVRDVKLLVGSRRLVDVMDVNTQKGTEMSMSOFVRYYE  5765 3 825 QKILRILMNSHQPPTSSSNSKDCGGPASSGAGATAALADGLKFAS VQASAPQGNSHKETSKSKVRRSKTSKDANKSLPSAALYGIPEIS STGKRQEVQGRPGBATGMMSALGGSVSGGSGNPNSNSTSTST AATAGAGSCGKSKEEKPGKSQSSRGAKRDKDAGKSRKDKHDLLQ GHONGSGQAPSGGHLYGFGAKSNGGGASPFHCGGTGSGSVADA GEVSKSAPDGGIMMSMLVKKEEEEESHRRIKKLKTEKVDPLF TVPAPPPHV  5766 1608 663 SGLFSVDPASSQAMELSDVTLIEGVGNEVMVVAGVVULILALUL AWLSTTVADSGSNQLLGAIVSAGDTSULHLGHVDHLVAGQGNPE PTELPHPSEGNDEKAEEAGEGRGDSTGEAGAGGVEPSLEHLLD IQGLPKRQAAGAGSSSPEAPLRSEDSTCLPESPGLITVRLKFLND TEELAVARPEDTVGALKSKYFFGGESGMKLIYQGRLLQDPARTIL RSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGWNG SLMYPVFVVLLGVWYFRINYRQFFTAPATVSLVGVTVPFSFLV				L TOTAL CARLOCK LIVE PROPERTY TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY
FPSGSQRARVNTHDGSPEOLQIPVTDSGRHILEDSCAELGESK EHMESRMVTETEETQEKKAESKEPIEEPTGAGLINKDKETEERT DGERVAEVAPEERENVAVAKLQESQERONAVIDKETIDLLAFTSV AELELLGLEKLKCESIMAGLKCGGTLQ  5762 2 344 GSTGGTPLHSQGGGGGGGGRRTFRGMPKEKYEPPDPRRMYTI MSSEEAANGKKSHWAELEISGKVRSLSASLWSLTHLTALHLSDN SLSRIPSDIAKLHNVIDLSSNKIR SLSRIPSDIAKLHNVIDLSSNKIR LDVWDNVPTFGKDAYVGALRENEPSVTQLVRLRATDEDSPPNNQ LTVSIVSASAFGSYFDISLYEGYGVISVSRPLDYEQISNGLIYL TVMAMDAGN  5764 19 441 VCARACGEMRQLLRPIDRQRYDENEDLSDVEEIVSVRGFSLEEK LRSQLYQGDFVHAMEKFNYEYVQREALRVELIFREKDGLGIK MPDPDFTVRDVKLLVGSRRLVDVMDVNTQKGTEMSMSQFVRYYE TPEAQRDKL  5765 3 825 QKILRLNNSHQPPTSSNSKDCGGPASGAGATAALADGLKFAS VQASAPQGNSHKETSKSKVKRSKTSKDANKSLPSAALYGIPEIS STGKRQEVQGRPGEATGMNSALGQSVSSGGSGNPNNSTSTSTS AATAGAGSCGKSKEEKPPGKSQSSRGAKPBKDAGKSRKDHDLLQ GHQNGSGSQAPSGGHLYGFGAKSNGGGASPFHCGGTGSGSVAAA GEVSKSAPDSGLMGNSMLVKKEEEEEBSHRRIKKLKTEKVDPLF TVPAPPPHV  5766 1608 663 SGLFSUDPASSQAMELSDVTLIEGVGNEVMVVAGVVVUILALVIL AMLSTYVADSGSNQLLGAIVSAGDTSVLHLCHVDHLVAGQGNPE PTELEHPPSEGNDEKAEEAGEGRGDSTGEAGAGGGVEPSLEHLLD LQGLPKRQAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLND TEELAVARPEDTVGALKSKYFFGQESQMKLIYQGRLLQDPARTIL RSLNITDNCV IHCHRSPPGSAVPGPSASLAPSATEPPSLGWNG SLMVPVFVVLLGVVWYFRINYRQFFTAPATVSLVGVTVFFSFLV		1		1 CHAMMONNIVORGISENREROWDTECOTODON CACESTO CONTRA
### STANGON TO THE SPECT OF THE STANGON THE SPECT OF THE STANGON THE SPECT OF THE STANGON THE SPECT OF THE STANGON THE SPECT OF THE STANGON THE SPECT OF THE STANGON THE SPECT OF THE STANGON THE SPECT OF THE STANGON THE SPECT OF THE STANGON THE SPECT OF THE STANGON THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE SPECT OF THE	1 1	f		1 DODA TABOON DESSION SERA DETERMORDATIVE ACCESSOR TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROP
DGERVAEVAPERENVAVAKLQESQFONAVIDKETIDALAFTSV AELELLGLEKLKCE:MALGLKCGGTLQ  STGQTPLHSQGGGGGGGRRTFRGMPKEKYEPPDPRRMYTI MSSEEAANGKKSHWABLEISGKVRSLSASLWSLTHLTALHLSDN SLSRIPSDIAKLHNLVYLDLSSNKIR  LDKDTGLIMLIARLDYELIORFTLITIARDGGGEETTGRVRINV LDWNDNVPFPCKDAYVGALRENEPSVTQLVRLRATDEDSPPNNQ ITYSIVSASAFGSYPDISLYEGYGVISVSRPLDVEQISNGLIYL TVMMDAGN  ST64  19 441 VCARACGEMRQLLRPIDRQRYDENEDLSDVEEIVSVRGFSLEEK MPDPDFTVRDVKLLVGSRRLVDVMDVNTQKGTEMSMSOFVRYYE LRSQLYQGFPVHAMEGKDFNYEYVQREALRVPLIFREKDGIIK MPDPDFTVRDVKLLVGSRRLVDVMDVNTQKGTEMSMSOFVRYYE TPEAQRDKL  S765 3 825 QKILRLNNSHQPPTSSSMSKDCGGFASSGAGATAALADGLKFAS VQASAPQGNSHKETSKSKVKRSKTSKDANKSLPSAALYGIPEIS STGKRQEVQGRPGEATGMNSALGQSVSSGGSGNPNSNSTSTSTS AATAGAGSCGKSKEEKPGKSQSSRGAKRDKHDLLQ GHQNGSGSQAPSGGHLYGFGAKSNGGGAPFHCGGTGSGSVAAA GEVSKSAPDSGLMGNSMLVKKEEEEEESHRRIKKLKTEKVDPLF TVPAPPPHV  5766 1608 663 SGLFSVDPASSQAMELSDVTLIEGVGNEVMVVAGVVVLILALVIL AWLSTYVADSGSNQLLGAIVSAGDTSVLHLGHVDHLVAGQGNPE PTELPHPSEGNDEKAEEAGEGRGDSTGEAGAGGGVEPSLEHLLD IGGLPKRQAGAGSSSPPAPLRSEDSTCLPFSPELITVRLKFLND TEELAVARPEDTVGALKSKYPFQGESQMKLIYQGRALCDPARTIL RSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG SLMVPVFVVLLGVVWYFRINYRQFFTAPATVSLVGVTVFFSFLV	1			1 Troopy Control WITDHGSPEOT OT DUMP DECEMBER TO DOOR TO THE
5762 2 344 SELELLGLEKLKCELMALGLEKCGSTLQ  STGOTPLHSQGGGGSGGGRRTFRGMPKEKYEPPDPRRMYTI  MSSEBAANGKKSHWABLEISGKVRSLSASLWSLTHLTALHLSDN  SLSRIPSDIAKLHNLVYLDLSSNKIR  LDKDTGLIHLIARLDYELIQRFTLTIIARDGGGETTGRVRINV  LDVMDNVPFPQKDAYVGALRENEPSVTQLVRLRATDEDSPPNNQ  ITYSIVSASAFGSYPDISLYEGYGVISVSRPLDYEQISNGLIYL  TVMMMDAGN  VCARACGEMRQLLRPIDRQRYDENEDLSDVEEIVSVRGFSLEEK  LRSQLYQGFPVHAMEGKDFNYEYVQREALRVPLIFREKDGLGIK  MPDPDFTVRDVKLLVGSRRLVDVMDVNTQKGTEMSMSQFVRYYE  TPEAQRDKL  STGKRQEVQGRPGEATGMNSALGQSVSSGGGRPNSNSTSTSTS  AATAGAGSCGKSKEEKPGKSQSSRGAKRBKDAGKSRKDKHDLLQ  GHQNGSGSQAPSGGHLYGFGAKSNGGGSSPFHGGTGSGSVAAA  GEVSKSAPDSGLMGNSMLVKKEEEEESHRRIKKLKTEKVDPLF  TVPAPPPHV  5766 1608 663 SGLFSVDPASSQAMELSDVTLIEGVGNEVMVAGVVVLILALVL  AWLSTTVADSGSNQLLGAIVSAGDTSVLHLGHVDHLVAGQGNPE  PTELPHPSEGNDEKAEEAGEGRGDSTGEAGAGGGVEFSLEHLLD  IQGLPKRQAGAGSSSPPAPLRSEDSTCLPPSPGLITVRLKFLND  TEELAVARPEDTVGALKSKYPPGQESQMKLIYQGRALIVQBPARTIL  RSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG  SLMVPVFVVLLGVVVYFRINYRQFFTAPATVSLVGVTVFFSFLV	1	1		TO THE TEXT OF THE PROPERTY OF A STREET COMMENTS OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPER
5762 2 344 GSTGGTPLHSQGGGGGGGGGRRTPRGMPKEKYEPPDPRRMYTI MSSEEAANGKKSHWAELEISGKVRSLSASLWSLTHLTALHLSDN SLSRIPSDIAKLHNLVYLDLSSMKIR LDKDTGLIMLTARLDYELIQRFTLTIIARDGGGETTGRVRINV LDVNDNVPTPCKDAYVGALRENEPSVTOLVRLKRATDEDSPPNNQ ITYSIVSASAFGSYFDISLYEGYGVISVSRPLDYEQIGNGLIYL TVMAMDAGN  5764 19 441 VCARACGEMRQLLRPIDRQRYDENEDLSDVEEIVSVRGFSLEEK LRSQLYQGDFVHAMEGKDFNYEYVQREALRVPLIFREKDGLGIK MPDPDFTVRDVKLLVGSRRLVDVMDVNTQKGTEMSMSQFVRYYE LRSQLYQGDFVHAMEGKDFNYEYVQREALRVPLIFREKDGLGIK MPDPDFTVRDVKLLVGSRRLVDVMDVNTQKGTEMSMSQFVRYYE TPEAQRDKL STGKRQEVQGRPGEATGMSALGQSVSSGGSGNPNSNSTSTSTS STGKRQEVQGRPGEATGMSALGQSVSSGGSGNPNSNSTSTSTS AATAGAGSGCKSKEEKPGRSQSSRGAKRDKDAKKRKHDLLQ GHQNGSGSQAPSGGHLYGFGAKSNGGGASPFHCGGTGSGSVAPA GEVSKSAPDSGLMGNSMLVKKEEEEEESHRRIKKLKTEKVDPLF TVPAPPPHV  5766 1608 663 SGLFSVDPASSQAMELSDVTLIEGVGNEVMVVAGVVVLILALVL AWLSTTVADSGSNQLLGAIVSAGDTSVLHLGHVDHLVAGQGNPE PTELPHPSEGNDEKAEEAGEGGGDSTGEAGAGGGVEPSLEHLLD IQGLPKRQAGASSSPEAPLRSEDSTCLPPSPGLITVRLKFLND TEELAVARPEDTVGALKSKYFPGQESQMKLIYQGRLQOPPARTL RSLNITDDCVJHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG SLMVPVFVVLLGVVWYFRINYRQFFTAPATVSLVGVTVFFSFLV	1 1	1		1 DODA AD VALLE KENVAVAKI OESODOMAUT DVERT DE LA SELLE
GSTGGTPLHSGGGGGGGGGRRTTFRGMPKEKYEPPDPRRMYTI  MSSEEAANGKKSHWAELEISGKVRSLSASLWSLTHLTALHLSDN  SLSRIPSDIARLHNLVYLDLSSNKIR  LDKDTGLIMLIARLDYELIQRFTLITIARDGGGEETTGRVRINV  LDVMDNVPTFÇKDAYVGALRENEPSVTQLVRLRATDEDSPPNNQ  ITYSIVSASAFGSYFDISLYEGYGVISVSRPLDYEQISNGLIYL  TVMAMDAGN  S764  19  441  VCARACGEMRQLLRPIDRQRYDENEDLSDVEEIVSVRGFSLEEK  LRSQLYGGPFVHAMEGKDFNYEYVQREALRVPLIFREKDGLGIK  MPDPDFTVRDVKLLVGSRRLVDVMDVNTQKGTEMSMSQFVRYYE  TPEAQRDKL  5765  3  825  QKILRLINNSHQPPTSSSNSKDCGGPASSGAGATAALADGLKFAS  VQASAPQGNSHKETISKSKVRSKKTSKDANKSLPSAALYGIPEIS  STGKRQEVQGRPGEATGMNSALGQSVSSGGSGNPNSTSTSTST  AATAGAGSCGKSREEKPGRSQSSRGAKRDKDAGKSRKDKHDLLQ  GHQNGSGSQAPSGGHLYGFGAKSNGGGASPFHCGGTGSGSVAAA  GEVSKSAPDSGLMGNSMLVKKEEEEEESHRRIKKLKTEKVDPLF  TVPAPPPHV  5766  1608  663  SGLFSVDPASSQAMELSDVTLIEGVGNEVMVVAGVVVLILALVL  AWLSTIVADSGSNQLLGAIVSAGDTSVLHLGHVDHLVAGQGNPE  PTELPHPSEGNDEKAEEAGEGGGDSTGEAGAGGGUPSLEHLLD  LQGLPKRQAGAGSSPPEAPLRSEDSTCLPPSPGLITVRLKFLND  TEELAVARPEDTVGALKSKYFFGQESQMKLIYQGRLLQDPARTL  RSLNITDDCVJHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG  SLMVPVFVVLLGVVWYFRINYRQFFTAPATVSLVGVTVFFSFLV	5762	3		1 - MADDE DE RURCE MALGUE (CRITTA
SLSRIPSDIAKLHNILVYLDLSSNKIR  SLSRIPSDIAKLHNILVYLDLSSNKIR  129 LDKDTGLIMLIARLDYELIQRFTLTIIIARDGGGEETTGRVRINV LDVNDNVPTFQKDAYVGALRENEPSVTQLVRLRATDEDSPPNNQ LTYSIVASAAFGSYFDISLYEGYGVISVSRPLDYEQISNGLIYL  TVMMDAGN  VCARACGEMRQLLRPIDRQRYDENEDLSDVEEIVSVRGFSLEEK LRSQLYQGDFVHAMEGKDFNYEYVQREALRVPLIFREKDGLGIK MPDPDFTVRDVKLLVGSRRLVDVMDVNTQKGTEMSMSQFVRYYE  TPEAQRDKL  OKILRLNNSHQPPTSSSNSKDCGGPASSGAGATAALADGLKFAS VQASAPQGNSHKETSKSKVKRSKTSKDANKSLPSAALYGIPEIS STGKRQEVQGRPGEATGMNSALGQSVSSGGSGNPNSNSTSTSTS AATAGAGSCCKSKEEKPGKSQSSRGAKRDKDAGKSRKDKHDLLQ GHQNGSGSQAPSGGHLYGFGAKSNGGGASPFHCGGTGSGSVAAA GEVSKSAPDSGLMGNSMLVKKEEEEESHRRIKKLKTEKVDPLF TVPAPPPHV  5766 1608 663 SGLFSVDPASSQAMELSDVTLIEGVGNEVMVVAGVVVLILALVL AWLSTYVADDSGSJOLIGAIVSAGDTSVLHLIGHVDHLVAGQGNPE PTELPHPSEGNDEKAEEAGEGRGDSTGEAGAGGGVEPSLEHLLD LQGLPKRQAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLND TEELAVARPEDTVGALKSKYFPGQESQMKLIYQGRLLQDPARTL RSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG SLMVPVFVVLLGVWYFRINYRQFFTAPATVSLVGVTVFFSFLV FGMYGR		- 1	344	GSTGQTPLHSQGGGGGGGGGRPPTPBCMDVEVVPDPDDDDDD
19 441 VCARACGEMROLLEDISMKIR  S764 19 441 VCARACGEMROLLEDISMEDISMEDISMEDISMEDISMEDISMEDISMEDISM	1	i		I MOSESAANGRASHWAELEISGKVPQI.CACI.MCI mitt ma - 115 and
LDKDTGLIMLIARLDYELIQRFTLTIIARDGGGEETTGRVRINV LDVNDNVPTFQKDAYYGALRENEPSVTQLVRLRATDEDSPPNNQ ITYSIXSASAFGSYFDISLYEGYGVISVSRPLDYEQISNGLIYL TVMAMDAGN  S764  19  441  VCARACGEMRQLLRPIDRQRYDENEDLSDVEEIVSVRGFSLEEK LRSQLYQGDFVHAMEGKDFNYEYVQREALRVPLIFREKDGLGIK MPDPDFTVRDVKLLVGSRRLVDVMDVNTQKGTEMSMSQFVRYYE TPEAQRDKL  S765  3  825  QKILRLNNSHQPPTSSSNSKDCGGPASSGAGATAALADGLKFAS VQASAPQGNSHKETSKSKVKRSKTSKDANKSLPSAALYGIPEIS STGKRQEVQGRPGEATGMNSALGQSVSSGGSGNPNSNSTSTSTS AATAGAGSCGKSKEEKPGKSQSSRGAKRDKDAGKSRKDKHDLLQ GHQNGSGSQAPSGGHLYGFGAKSNGGGASPHCGGTGSGSVAAA GEVSKSAPDSGLMGNSMLVKKEEEEESHRRIKKLKTEKVDPLF TVPAPPPHV  5766  1608  663  SGLFSVDPASSQAMELSDVTLIEGVGNEVMVVAGVVVLILALVL AWLSTYVADSGSNQLLGAIVSAGDTSVLHLGHVVDHLUVAGQGNPE PTELPHPSEGNDEKAEEAGEGGDSTGEAGAGGGVEPSLEHLLD IQGLPKRQAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLND TEELAVARPEDTVGALKSKYFPGQESQMKLIYQGRLLQDPARTL RSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG SLMVPVFVVLLLGVVWYFRINYRQFFTAPATVSLVGVTVFFSFLV FGMYGR	5763			1 ODOVIEDDINKTHNIVALIIII'GGMALD
1TYSIVSASAFGSYFDISLYEGYGVISVSRPLDYEQISNGLIYL  TVMAMDAGN  19  441  VCARACGEMRQLLRPIDRQRYDENEDLSDVEEIVSVRGFSLEEK LRSQLYQGDFVHAMEGKDFNYEYVQREALRVPLIFREKDGLGIK MPDPDFTVRDVKLLVGSRRLVDVMDVNTQKGTEMSMSQFVRYYE  TPEAQRDKL  5765  3  825  QKILRLNNSHQPPTSSNSKDCGGPASSGAGATAALADGLKFAS VQASAPQGNSHKETSKSKVKRSKTSKDANKSLPSAALYGIPEIS STGKRQEVQGREGEATGMNSALGQSVSSGGSGNPNSNSTSTSTS AATAGAGSCGKSKEEKPGKSQSSRGAKRDKKDAGKSRKDKHDLLQ GHQNGSGSQAPSGGHLYGFGAKSNGGASPFHCGGTGSGSVAAA GEVSKSAPDSGLMGNSMLVKKEEEEESHRRIKKLKTEKVDPLF TVPAPPPHV  5766  1608  663  SGLFSVDPASSQAMELSDVTLIEGVGNEVMVVAGVVVLILALVL AWLSTYVADSGSNQLLGAIVSAGDTSVLHLGHVDHLVAGQGNPE PTELPHPSEGNDEKAEEAGEGRGDSTGEAGAGGGVEPSLEHLLD IQGLPKRQAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLND TEELAVARPEDTVGALKSKYFFGQESQMKLIYQGRLLQDPARTL RSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG SLMVPVFVVLLGVVWYFRINYRQFFTAPATVSLVGVTVFFSFLV FGMYGR	3783	3	429	LDKDTGLIMLIARLDYELIORETLTTIARDCCCER
TVMMDAGN  19 441 VCARACGEMRQLLRPIDRQRYDENEDLSDVEEIVSVRGFSLEEK LRSQLYQGDFVHAMEGKDFNYEYVQREALRVPLIFREKDGLGIK MPDPDFTVRDVKLLVGSRRLVDVMDVNTQKGTEMSMSQFVRYYE TPEAQRDKL  3 825 QKIRLINNSHQPPTSSSNSKDCGGPASSGAGATAALADGLKFAS VQASAPQGNSHKETSKSKVKRSKTSKDANKSLPSAALYGIPEIS STGKRQEVQGRPGEATGMNSALGQSVSSGGSGNPNSNSTSTSTS AATAGAGSCGKSKEEKPGKSQSSRGAKRDKHDAGKSRKDKHDLLQ GHQNGSGSQAPSGGHLYGFGAKSNGGGASPFHCGGTGSGSVAAA GEVSKSAPDSGLMGNSMLVKKEEEEEESHRRIKKLKTEKVDPLF TVAPPPHV  5766 1608 663 SGLFSVDPASSQAMBLSDVTLIEGVGNEVMVVAGVVVLILALVL AMLSTYVADSGSNQLLGAIVSAGDTSVLHLGHVDHLVAGQGNPE PTELPHPSEGNDEKAEEAGEGRGDSTGEAGAGGVEPSLEHLLD IQGLPKRQAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLND TEELAVARPEDTVGALKSKYFPGQESQMKLIYQGRLLQDPARTL RSLNITDNCV IHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG SLMVPVFVVULIGVVWYFRINYRQFFTAPATVSLVGVTVFFSFLV FGMYGR	į į			LEGITION OF THE VIOLATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF T
19 441 VCARACGEMRQLLRPIDRQRYDENEDLSDVEEIVSVRGFSLEEK LRSQLYQGDFVHAMEGKDFNYEYVQREALRVPLIFREKDGLGIK MPDPDFTVRDVKLLVGSRRLVDVMDVNTQKGTEMSMSQFVRYYE TPEAQRDKL  S765 3 825 QKILRLNNSHQPPTSSSNSKDCGGPASSGAGATAALADGLKFAS VQASAPQGNSHKETSKSKVKRSKTSKDANKSLPSAALYGIPEIS STGKRQEVQGRPGEATGMNSALGQSVSSGGSGNPNSNSTSTSTS AATAGAGSCGKSKEEKPGKSQSSRGAKRDKDAGKSRKDKHDLLQ GHQNGSGSQAPSGGHLYGFGAKSNGGGASPFHCGGTGSGSVAAA GEVSKSAPDSGLMGNSMLVKKEEEEEESHRRIKKLKTEKVDPLF TVPAPPPHV  5766 1608 663 SGLFSVDPASSQAMELSDVTLIEGVGNEVMVVAGVVULILALVL AWLSTYVADSGSNQLLGAIVSAGDTSVLHLGHVDHLVAGQGNPE PTELPHPSEGNDEKAEEAGEGRGDSTGEAGAGGGVEPSLEHLLD IQGLPKRQAGGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLND TEELAVARPEDTVGALKSKYFPGQESQMKLIYQGRLLQDPARTL RSLNITDNCV IHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG SLMVPVFVVULLGVVWYFRINYRQFFTAPATVSLVGVTVFFSFLV FGMYGR	[ [			~ 101 VOASAFGS IF DISLYEGYGVISVSDDI.DVDOTENOT TVV
VCARACGEMRQLLRPIDRQRYDENEDLSDVEEIVSVRGFSLEEK LRSQLYQGDFVHAMEGKDFNYEYVQREALRVPLIFREKDGLGIK MPDPDFTVRDVKLLVGSRRLVDVMDVNTQKGTEMSMSQFVRYYE TPEAQRDKL  S765 3 825 QKILRINNSHOPPTSSSNSKDCGGFASSGAGATAALADGLKFAS VQASAPQGNSHKETSKSKVKRSKTSKDANKSLPSAALYGIPEIS STGKRQEVQGRPGEATGMNSALGQSVSSGGSGPNSNSTSTSTS AATAGAGSCGKSKEEKPGKSQSSRGAKRDKDAGKSRKDKHDLLQ GHQNGSGSQAPSGGHLYGFGAKSNGGGASPFHCGGTGSGSVAAA GEVSKSAPDSGLMGNSMLVKKEEEEEESHRRIKKLKTEKVDPLF TVPAPPPHV  S766 1608 663 SGLFSVDPASSQAMELSDVTLIEGVGNEVMVVAGVVVLILALVL AWLSTYVADSGSNQLLGAIVSAGDTSVLHLGHVDHLVAGQGNPE PTELPHPSEGNDEKAEEAGEGRGDSTGEAGAGGGVEPSLEHLLD IQGLPKRQAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLND TBELAVARPEDTVGALKSKYFFGQESQMKLIYQGRLLQDPARTL RSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG SLMVPVFVVLLGVVWYFRINYRQFFTAPATVSLVGVTVFFSFLV FGMYGR	5764			2 (1221DAGN
### STORY VHAMEGRUFNY EY VOREALR VPLIFREK DGLGIK #### MPDDPTVRDVKLLVGSRRLVDVMDVNTQKGTEMSMSQFVRYYE ###################################	2,04	13	441	VCARACGEMRQLLRPIDRORYDENEDI.SDVERTVCVDG
TPEAQRDKL  S765  3  825  QKILRINNSHOPPTSSSNSKDCGGFASSGAGATAALADGLKFAS VQASAPQGNSHKETSKSKVKRSKTSKDANKSLPSAALYGIPEIS STGKRQEVQGRPGEATGMNSALGQSVSSGGSGPPNSNSTSTSTS AATAGAGSCGKSKEEKPGKSQSSRGAKRDKDAGKSRKDKHDLLQ GHQNGSGSQAPSGGHLYGFGAKSNGGGASPFHCGGTGSGSVAAA GEVSKSAPDSGLMGNSMLVKKEEEEEESHRRIKKLKTEKVDPLF TVPAPPPHV  5766  1608  663  SGLFSVDPASSQAMELSDVTLIEGVGNEVMVVAGVVVLILALVL AWLSTYVADSGSNQLLGAIVSAGDTSVLHLGHVDHLVAGQGNPE PTELPHPSEGNDEKAEEAGEGRGDSTGEAGAGGGVEPSLEHLLD IQGLPKRQAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLND TEELAVARPEDTVGALKSKYFFQQESQMKLIYQGRLLQDPARTL RSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG SLMVPVFVVULIGVVWYFRINYRQFFTAPATVSLVGVTVFFSFLV FGMYGR	, ,	j		STORE AND
S765 3 825 OKILRINNSHOPPTSSSNSKDCGGFASSGAGATAALADGIKFAS VQASAPQGNSHKETSKSKVKRSKTSKDANKSLPSAALYGIPEIS STGKRQEVQGRPGEATGMNSALGQSVSSGGSGNPNSNSTSTSTS AATAGAGSCGKSKEEKPGKSQSSRGAKRDKDAGKSRKDKHDLLQ GHQNGSGSQAPSGGHLYGFGAKSNGGGASPFHCGGTGSGSVAAA GEVSKSAPDSGLMGNSMLVKKEEEEEESHRRIKKLKTEKVDPLF TVPAPPPHV  SGLFSVDPASSQAMELSDVTLIEGVGNEVMVVAGVVVLILALVL AWLSTYVADSGSNQLLGAIVSAGDTSVLHLGHVDHLVAGQGNPE PTELPHPSEGNDEKAEEAGEGRGDSTGEAGAGGGVEPSLEHLLD IQGLPKRQAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLND TEELAVARPEDTVGALKSKYFFGQESQMKLIYQGRLLQDPARTL RSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG SLMVPVFVVULLGVVWYFRINYRQFFTAPATVSLVGVTVFFSFLV FGMYGR	ľ	l	í	MPDPDFTVRDVKLLVGSRRLVDVMDVDTOVCTBMCMC
QKILRLNNSHQPPTSSSNSKDCGGPASSGAGATAALADGLKFAS VQASAPQGNSHKETSKSKVKRSKTSKDANKSLPSAALYGIPEIS STGKRQEVQGRPGEATGMNSALGQSVSSGGSGNPNSNSTSTSTS AATAGAGSCGKSKEEKPGKSQSSRGAKRDKDAGKSRKDKHDLLQ GHQNGSGSQAPSGGHLYGFGAKSNGGGASPFHCGGTGSGSVAAA GEVSKSAPDSGLMGNSMLVKKEEEEEESHRRIKKLKTEKVDPLF TVPAPPPHV  5766 1608 663 SGLFSVDPASSQAMELSDVTLIEGVGNEVMVVAGVVVLILALVL AWLSTYVADSGSNQLLGAIVSAGDTSVLHLGHVDHLVAGQGNPE PTELPHPSEGNDEKAEEAGEGRGDSTGEAGAGGGVEPSLEHLLD IQGLPKRQAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLND TEELAVARPEDTVGALKSKYFPGQESQMKLIYQGRLLQDPARTL RSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG SLMVPVFVVLLGVVWYFRINYRQFFTAPATVSLVGVTVFFSFLV FGMYGR	-576E			2: 121DXD
STGKRQEVQGRPGEATGMNSALGQSVSSGSGRPRNSTSTSTS AATAGAGSCGKSKEEKPGKSQSSRGAKRDKDAGKSRKDKHDLLQ GHQNGSGSQAPSGGHLYGFGAKSNGGGASPFHCGGTGSGSVAAA GEVSKSAPDSGLMGNSMLVKKEEEEEESHRRIKKLKTEKVDPLF TVPAPPPHV  5766  1608  663  SGLFSVDPASSQAMELSDVTLIEGVGNEVMVVAGVVVLILALVL AWLSTYVADSGSNQLLGAIVSAGDTSVLHLGHVDHLVAGQGNPE PTELPHPSEGNDEKAEEAGEGRGDSTGEAGAGGGVEPSLEHLLD IQGLPKRQAGASSSPEAPLRSEDSTCLPFSPGLITVRLKFLND TEELAVARPEDTVGALKSKYFFGQESQMKLIYQGRLLQDPARTL RSLNITDNCV HCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG SLMVPVFVVLLGVVWYFRINYRQFFTAPATVSLVGVTVFFSFLV FGMYGR	2,05	3	825	
ATAGAGSCGKSKEEKPGKSQSSSGGSGNPNSNSTSTSTS AATAGAGSCGKSKEEKPGKSQSSRGAKRDKDAGKSRKDKHDLLQ GHQNGSGSQAPSGGHLYGFGAKSNGGGASPFHCGGTGSGSVAAA GEVSKSAPDSGLMGNSMLVKKEEEEESHRRIKKLKTEKVDPLF TVPAPPPHV  5766 1608 663 SGLFSVDPASSQAMELSDVTLIEGVGNEVMVVAGVVULILALVL AWLSTYVADSGSNQLLGAIVSAGDTSVLHLGHVDHLVAGQGNPE PTELPHPSEGNDEKAEEAGEGRGDSTGEAGAGGGVEPSLEHLLD IQGLPKRQAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLND TELLAVARPEDTVGALKSKYFPGQESQMKLIYQGRLLQDPARTL RSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG SLMVPVFVVULLGVVWYFRINYRQFFTAPATVSLVGVTVFFSFLV FGMYGR	Ī	j		VQASAPQGNSHKETSKSKVKPGVTQVDANKQVDANKQV
GHQNGSGSQAPSGGHLYGFGAKSNGGASPFHCGGTGSGSVAAA GEVSKSAPDSGLMGNSMLVKKEEEEESHRRIKKLKTEKVDPLF TVPAPPPHV  5766  1608  663  SGLFSVDPASSQAMELSDVTLIEGVGNEVMVVAGVVVLILALVL AWLSTYVADSGSNQLLGAIVSAGDTSVLHLCHVDHLVAGQGNPE PTELPHPSEGNDEKAEEAGEGRGDSTGEAGAGGGVEPSLEHLLD IQGLPKRQAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLND TEELAVARPEDTVGALKSKYFPGQESQMKLIYQGRLLQDPARTL RSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG SLMVPVFVVVLLGVVWYFRINYRQFFTAPATVSLVGVTVFFSFLV FGMYGR	J			STGKROEVOGRPGEATGMNSALGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
GEVSKSAPDSGLMGNSMLVKKEEEEESHRRIKKLKTEKVDPLF TVPAPPPHV  SGLFSVDPASSQAMELSDVTLIEGVGNEVMVVAGVVVLILALVL AWLSTYVADSGSNQLLGAIVSAGDTSVLHLGHVDHLVAGQGNPE PTELPHPSEGNDEKAEEAGEGRGDSTGEAGAGGGVEPSLEHLLD IQGLPKRQAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLND TEELAVARPEDTVGALKSKYFPGQESQMKLIYQGRLLQDPARTL RSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG SLMVPVFVVVLLGVVWYFRINYRQFFTAPATVSLVGVTVFFSFLV FGMYGR	1		l	AATAGAGSCGKSKEEKPGKGGGGGGSGNENSTSTSTS
TVPAPPPHV  SGLFSVDPASSQAMELSDVTLIEGVGNEVMVVAGVVVLILALVL AWLSTYVADSGSNQLLGAIVSAGDTSVLHLGHVDHLVAGQGNPE PTELPHPSEGNDEKAEEAGEGRGDSTGEAGAGGGVEPSLEHLLD IQGLPKRQAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLND TEELAVARPEDTVGALKSKYFFGQESQMKLIYQGRLLQDPARTL RSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG SLMVPVFVVULLGVVWYFRINYRQFFTAPATVSLVGVTVFFSFLV FGMYGR	Ţ	1		GHONGSGSOA PSCGUL VCROA VCVC
TVPAPPPHV  SGLFSVDPASSQAMELSDVTLIEGVGNEVMVVAGVVVLILALVL AWLSTYVADSGSNQLLGAIVSAGDTSVLHLGHVDHLVAGQGNPE PTELPHPSEGNDEKAEEAGEGRGDSTGEAGAGGGVEPSLEHLLD IQGLPKRQAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLND TEELAVARPEDTVGALKSKYFFGQESQMKLIYQGRLLQDPARTL RSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG SLMVPVFVVULLGVVWYFRINYRQFFTAPATVSLVGVTVFFSFLV FGMYGR	1		}	GEVSKSAPDSGIMGNEMI INVESTIGATION OF THE GET GET GET GET GET GET GET GET GET GE
SGLFSVDPASSQAMELSDVTLIEGVGNEVMVVAGVVVLILALVL AWLSTYVADSGSNQLLGAIVSAGDTSVLHLGHVDHLVAGQGNPE PTELPHPSEGNDEKAEEAGEGRGDSTGEAGAGGGVEPSLEHLLD IQGLPKRQAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLND TEELAVARPEDTVGALKSKYFPGQESQMKLIYQGRLLQDPARTL RSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG SLMVPVFVVVLLGVVWYFRINYRQFFTAPATVSLVGVTVFFSFLV FGMYGR			1	TVPAPPPHY
AWLSTYVADSGSNQLLGAIVSAGDTSVLHLGHVDHLVAGQGNPE PTELPHPSEGNDEKAEEAGEGRGDSTGEAGAGGGVEPSLEHLLD IQGLPKRQAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLND TEELAVARPEDTVGALKSKYFPGQESQMKLIYQGRLLQDPARTL RSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG SLMVPVFVVLLGVVWYFRINYRQFFTAPATVSLVGVTVPPSFLV FGMYGR	5766	1608	663	
PTELPHPSEGNQLLGAIVSAGDTSVLHLGHVDHLVAGQGNPE PTELPHPSEGNDEKAEEAGEGGGDSTGEAGAGGGVEPSLEHLLD IQGLPKRQAGAGSSSPAPLRSEDSTCLPFSPGLITVRLKFLND TEELAVARPEDTVGALKSKYFPGQESQMKLIYQGRLLQDPARTL RSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG SLMVPVFVVLLGVVWYFRINYRQFFTAPATVSLVGVTVFFSFLV FGMYGR	1	i	1	AMI STYLD COCKOT TO THE STYLD CONTROL OF THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE STYLD COCKOT TO THE S
IQGLPKRQAGAGSSSPAPLRSEDSTCLPFSPGLITVRLKFLND IQGLPKRQAGAGSSSPAPLRSEDSTCLPFSPGLITVRLKFLND TEELAVARPEDTVGALKSKYFPGQESQMKLIYQGRLLQDPARTL RSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG SLMVPVFVVLLGVVWYFRINYRQFFTAPATVSLVGVTVFFSFLV FGMYGR			İ	ANDS I VADSGSNOLLGAIVSAGDTSVI.HI.GUUDUI VAGGOVER
TEELAVARPEDTVGALKSKYFPGQESQMKLIYQGRLLQDPARTL RSLNITDNCV HCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG SLMVPVFVVLLGVVWYFRINYRQFFTAPATVSLVGVTVFFSFLV FGMYGR	1		1	FILDERPSEGNOEKAEEAGEGRGDSTGEAGAGGGUEDGT DITT -
RSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG SLMVPVFVVULGVVWYFRINYRQFFTAPATVSLVGVTVFFSFLV FGMYGR	İ		1	TYGHPARQAGAGSSSPEAPLRSEDSTCI, PPSDCI, TYMDI WDI AND
SLMVPVFVVLLGVVWYFRINYRQFFTAPATVSLVGVTVFFSFLV FGMYGR	ļ	1	1	TECHNORIES TO THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES OF THE TECHNORIES O
FGMYGR FGMYGR	1		· · · · · · · · · · · · · · · · · · ·	ASSIST TONCY INCHRSPPGSAVPGPSASTADEATERNOT CORRECT IN
5767 TOMBR			ì	ODM F V F V V D DG V V WY FRINYROFFTAPATVSI.VGVTV PPC PL 17
892 INDEXEDDRESS	5767	<del></del>		10/10R
MFRATPRPPTRPELRTGTEVII.WVI.DWPAIMVPWPWWWANTVILLE		4	-	NFRATPRPPTRPELRTGTEVILWYLDWRALMKRKRMKANIKLVG
SCIPLESSULDUSLTEEIDEKIGFRADAMEDWOMWADEDDAGGO	J	i	1 .	SGFPLPSSDLDDSLTEEIDEKIGFRNDANEDWONGA DERDA GGG
LTEVKVEEEERDPQSPEFEIEEEEEMLSSVIPDSRRENELPDFP	L	<u></u>		LTEVKVEEEERDPQSPEFEIEEEEEMLSSVIDDSDENELDE

SEO	Predicted	18-37-5-3	
ID	beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
""	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
i	residue of	li .	S=Scrine, T=Threonine, V=Valine,
į	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion,
<b></b>	sequence		\=possible nucleotide insertion)
1	į		HIDEFFTLNSTPSRSAYDEPHLLVNIEKQKLELEKRRLDIEAER
			LQVEKERLQIEKERLRHLDMEHERLQLEKERLQIEREKLRLQIV
	ŀ		NSEKPSLENELGQGEKSMLOPODIETEKIKI,ERERI.OLEVORI.O
5768	<del> </del>		FLKFESEKLQIEKERLQVEKDRLRIOKEGHLO
3/88	3	476	SSRSRLSVSVSPPPPGIVELGPPFAWEFCSRLGSAVTSQRAGPA
1			AAMVAKDYPFYLTVKRANCSLELPPASGPAKDAEEPSNKRVKDI.
i			SRVTSLANLIPPVKATPLKRFSQTLQRSISFRSESRPDILAPRP
			WSRNAAPSSTKRRDSKLWSETFDVC
5769	38	667	TKTKKGVKEKATDQSVKAFAEHCPELQYVGFMGCSVTSKGVIHL
			TKLRNLSSLDLRHITELDNETAMEIVKRCKNLISLNLCLNWTIN
	1	j	DRCVEVIAKEGQNLKELYLVSCKITDYALIAIGRYSMTIETVDV
1	1	Ì	GWCKEITDQGATLIAQSSKSLRYLGLMRCDKVNEVTVEOLVOOV
L			PHITFSTVLQDCKRTLERAYQMGWTPNMSAASS
5770	1	484	DSRRYDVKTRKWSFLLEEHSKLIAKVRCLPQVQLDPLPTTLTLA
	1		FASQLKKTSLSLTPDVPEADLSEVDPKLVSNLMPFQRAGVNFAI
i			AKGGRLLLADDMGLGKTIQAICIAAFYRKEWPLLVVVPSSVRFT
L			WEQAFLRWLPSLSPDCINVVVTGKDRLTA
5771	168	741	GLLPSACLRARSWREASEGPSSRACSNGSQDTFEACYSGTSTPS
			FHGSHCSGSDHSSLGLEQLQDYMVTLRSKLGPLEIQQFAMLLRE
	[		YRLGLPIQDYCTGLLKLYGDRRKFLLLGMRPFIPDQDIGYFEGF
1	J j		LEGVGIREGGILTDSFGRIKRSMSSTSASAVRSYDGAAQRPEAQ
			AFHRLLADITHDIE
5772	148	383	EFNLALVSPSHPQIKAEDDQPLPGVLLSLSGGLFRSNLLTQDNG
L			ILTFSNLVTCSAIYHLPVFPEREPGCSMRDLRVA
5773	2	723	PRVRSKHNFCFMEMNTRLQVEHPVTEMITGTDLVEWQLRIAAGE
1			KIPLSQEEITLQGHAFEARIYAEDPSNNFMPVAGPLVHLSTPRA
1 :			DPSTRIETGVRQGDEVSVHYDPMIAKLVVWAADRQAALTKLRYS
l i			LRQYNIVGLHTNIDFLLNLSGHPEFEAGNVHTDFIPQHHKQLLL
			SRKAAAKESLCQAALGLILKEKAMTDTFTLQAHDQFSPFSSSSG
			RRLNISYTRNMTLKDGKNSK
5774	. 2	592	FVEBENIRVVRCGGSELNFRRAVFSADSKYIFCVSGDFVKVYST
1 1			VTEECVHILHGHRNLVTGIQLNPNNHLQLYSCSLDGTIKLWDYI
1 1			DGILIKTFIVGCKLHALFTLAQAEDSVFVIVNKEKPDIFQLVSV
1	l		KLPKSSSQEVEAKELSFVLDYINQSPKCIAFGNEGVYVAAVREF
			YLSVYFFKKETTSRVTLSSS
5775	3	538	SSGCCDPAAPSSLAEAATMPVSKCPKKSESLWKGWDRKAQRNGL
1			RSQVYAVNGDYYVGEWKDNVKHGKGTQVWKKKGAIYEGDWKFGK
1 !			RDGYGTLSLPDQQTGKCRRVYSGWWKGDKKSGYGIQFFGPKEYY
1	ł		EGDWCGSQRSGWGRMYYSNGDIYEGQWENDKPNGEGMLRLSQNP
L !	ĺ		RP
5776	2	484	RLPQDCVCQNLSESLGTLCPSKGLLFVPPDIDRRTVELRLGGNF
1 1	1		IIHISRQDFANMTGLVDLTLSRNTISHIQPFSFLDLESLRSLHL
	ŀ		DSNRLPSLGEDTLRGLVNLQHLIVNNNQLGGIADEAFEDFLLTL
1	Į.		EDLDLSYNNLHGPAVGLRGDAWVQPSTS
5777	2	949	GODPEPGODLFQPEREVDPSWGRGREPRLGKLRFQNDHLSVLKO
ļ			WANTE OF TANK DOOR DOOR DOOR OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF
<u> </u>			VXKLEQALKDGSAGLDPQLPGTCYSPHCPPDKAEAGSTLPENLG GGSGSEVSQRVHPSDLEGREPTPELVEDRKGSCRRPWDRSLENV
į l	1		ADCCECCOARDETABL DADDDAERA GEORGECKELANDESTENA
			YRGSEGSPTKPFINPLPKPRRTFKHAGEGDKDGKPGIGFRKEKR
]	ļ	İ	NLPPLPSLPPPPLPSSPPPSSVNRRLWTGRQKSSADHRKSYEFE
! !			DLLQSSSESSRVDWYAQTKLGLTRTLSEENVYEDILDPPMKENP
i i		i	YEDIELHGRCLGKKCVLNFPASPTSSIPDTLTKQSLSKPAFFRQ
5778	1	1210	NSERRNV OPPOCUSED I I DURI I EDDA EDGI ESTA
	- 1	1210	QRRQSVSRLLLPVFLLEPPAEPGLEPPPEEEGGEPAGVAEEPGS
i J			GGPCWLQLEEVPGPGPLGGGGPLRSPSSYSSDELSPGEPLTSPP
	i		WAPLGAPERPEHLLNRVLERLAGGATRDSAASDILLDDIVLTHS
			LFLPTEKFLQELHQYFVRAGGMEGPEGLGRKQACLAMLLHFLDT
ļ	-	Ĭ	YQGLLQEEEGAGHIIKDLYLLIMKDESLYQGLREDTLRLHQLVE
	1	İ	TVELKIPEENQPPSKQVKPLFRHFRRIDSCLQTRVAFRGSDEIF
į	į	]	CRVYMPDHSYVTIRSRLSASVQDILGSVTEKLQYSEEPAGREDS
	<del></del>		LILVAVSSSGEKVLLQPTEDCVFTALGINSHLFACTRDSYEALV

S	EO	Predicted		
	(D	beginning	Predicted end	
	0:	nucleotide	nucleotide	
1 -		location	location	Cidentic ACIG, Faphenvialaning G of
ļ			corresponding	I "-" Totaliane, Island Policina V. T
- 1		corresponding to first	to first	D-Deucine, Mamerijonino Managera,
			amino acid	***** Ottober Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligion   Deligi
		amino acid	residue of	S=Serine, T=Threonine, V=Valine,
		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1		amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>		sequence	1	\=possible nucleotide insertion)
				PLPEFIOUS PEDITETURE INSERTION)
				PLPEEIQVSPGDTEIHRVEPEDVANHLTAFHWELFRCVHELEFV DYVFHGE
57	79	138	1671	
- 1			1	EAVQVLIKHSADVNARDKNWQTPLHVAAANKAVKCAEVIIPLLS
			1	TO THE ODING REPORTED TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE P
				1 THE TOTAL VALLINEGATOR COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPANY TO A COMPAN
	- 1		1	INVINITION TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF
	- 1		1	1 THE MINGE I PUNEAAASTHGALCLET, TANKER DURIT COMOS
j	ı		ļ	1 TATALIGRE IRSUILIONGGE I DOWN TOWN TOWN TOWN TO THE
	- 1		Í	LEDINI DI ISGADIAKCGI HSMFPI, HI, A AI, NAUCDOODEST I GOO
	- 1		}	2 CLUB TO DE SNEHVLSAGFEIDTPDKFGPTCLUBBBBCGTCC-
1	- 1		1	THE COST OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF TH
	- 1		1	DIDDIGGIAGRIAAASDMDRNKTII.GNAUDNOEDI DDADDI
			1	LATE CHEFT LUNDANDS I RDKEGYNG THVA A A VCIDOGE DE TETT
578	10			RINDGI SESUSGATKSPI,HI,AVÇEMD
3/6	,,	154	624	QFFRVITCLPFKGPDYRLYKSEPELTTVAEVDESNGEEKSEPVS
	- 1			EIETSVVKGSHFPVGVVPPRAKSPTPESSTIASYVTLRKTKKMM
	- 1			DLRTERPRSAVEQLCLAESTRPRMTVEEQMERIRRHCQACLREK
578				KKGLNVIGASDQSPLQSPSNLRDNP
3/8		19	941	RGSLGGHPWRPPMRAASQGCLPVSFVTGPHQERAYGGRGPGGAF
	- 1			PAPPVSGTCPPDLIYAPTPEKAEGGSQKNHQPPPGERAAHRDGE
1	i			QAPCRAGPTRKVAVAPRPPSCP*GPE\PGEEPRRPLDRSPPLGQ
1	ŀ			VOPHETSODAKSAEDEA DORUK GIVE PREPERPLDRSPPLGQ
1				VQPHFTSQDAKSAEDEAPSRHLGKHQPRSAQVGSRLDALQGPKT
				QHSIHTVTCKSPRQKEDRSPKPPQAPKHPERHGRQS\QAPPPLP
1	- 1	- 1		VAPSRTCGGC*TWDPALLVSP/PQGDSTPELPAP\QQPTGGPSR
				CRQALPPQG*RQQPRQRPR/PTGASRSHPAKAKGCQGPPKIRNY NIMD
578:	2	5176	1237	
	- 1	1		DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPPTMPPLPPEE
1	- 1			I FENTER DEPEREPRECIPAL PEROCATION ENTERINGENESS TO THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF THE PROCESS OF
	- 1	ľ		I SEPER SOSEISE SAVETOYS VSA SODS VITTO DE ATTENDA DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DEL COMPANIO DE LA COMPANIO DE LA COMPANIO DEL COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DEL COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DEL COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DE LA COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPA
ł	- 1	1		* DE DOOT I DI PVOSAVVAKEHEVA/DED DA TOMONIO DE DE LE LE LE LE LE LE LE LE LE LE LE LE LE
1	İ	[		I TO DO F TO DELACTED SMRASCHVA CEVOTOT T TO STORE TO THE
1	- 1	į.	1	DOLDEF FARAPESSAMAVIESSAVTVI.FCCTIMITE POOR
	- 1	1		D. SVVIVEEPPVVAEPDYVTIPVPVVQAI.EDGVDVV nnavena -
	- 1	1		1 * OF A VOLES VOVOES IV IVSEDAUTICE OTO UT DEPOSIT TO THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF TH
1		Į.	l	TELEGRAPHICS:IVINGEINLSS(i)()NI,ADRTGMORTAT MAGES
1	- 1			DIGOUT INSTRUMENTAL TAKENGUMBURAN A CORP.
1	- 1	ľ	1	TODERTOFISEIRORTVLDTVDCVQFADACEmr gaman======
	i			ATO TERRETER LIASTESEVNKVDVDI.GI.TTOODTITIES
		ł	i	OCCUPANTE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROP
i	- 1	1	1	
	- 1	1	1	DIRE VOSERI WINVERSPRACILI ECDITION CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CO
	- }	<u> </u>		
}		l		EKEKKRUSSEKSKSKRSKSSEHKSPKI TCTCDCDADVDGCTCTT
	1	ĺ		THE QUINGROKS/KDRRRRSSRSRSRSRSRSPORTED COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNTY TO THE COUNT
	- 1	i		NORSKER ARKKSSSRDNRKTVRARSPTDCDDCDCttmpcppp 1
			1	O TORREST STORKESKT PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSPD COMPONDATION OF THE PSRRSRTPSP
	-	1	1	MIL DARGE I PORRERSES VORRESES I S DUDI DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE DE CERTE
	1	İ	1	THE TENNESSEERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESPERGESP
	- 1		!	OF DEFNORPAPPPTIEEKVAKKSGCATTERITERVOYOTA COM-
	- 1	į		DDD I INKERVOUEREEPPFYHHDEKI.GEDVDTERNILATTATA
	1	į		TITING QUILLIABEPVSSGSOHRKKENDQUVQQQQQQQQQQ
	J	!	ł ·	TOURING SINDESERVILSTAMSERALAOVDI CENTROLI DOLINGO
	1	İ	Į,	DINGS PRODUCT TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY
	1	•		KKDQFLRAAPVTGGMGAVLMRKMGWREGEGLGKNKEGNKEPILV
		ŀ	i i	DFKTDRKGLVAVGERAQKRSGNFSAAMKDLSGKHPVSALMEICN
			1 1	KRRWQPPEFLLVHDSGPDHRKHFLFRVLINGSAYQPNCMFFLNR
FRAS	+		1	Y DEVIES OF DERIVED INGSAYQPNCMFFLNR
5783	1	1693		= (
	1			DSGLRVAFTMEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFM
			1 5	ZALGEGIGVNVI MKRSPRGI SHSDWAUVVIAID FOADUUR
	$\perp$		1 4	WINDERKIERSEHHPNIVGYRAFTFANDGGI CI AMERICANIA
				DLIEE/PI*SQ/PKILFQQP/LILKVALNMARGLKYLHQEKKL

٢.
•
٠.
٠,
•
1,4
4-

CEO	I Donadiahad		
SEQ ID	Predicted beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ı	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence	ł	\=possible nucleotide insertion)
			LHGDIKSSNVVIKGDFETIKICDVGVSLPLDENMTVTDPFACVI
1			GTEPWKPKEAVEENGVITDKADIFAFGLTLWEMMTLSIPHINIS
İ		}	NDDDDEDKTFDESDFDDEAYYAALGTRPPINMEELDESYOKVIE
			LFSVCTNEDPKDRPSAAHIVEALETDV
5784	2669	1388	PRVRPRVRTDHNYYISRIYGPSDSASRDLWVNIDQMEKDKVKIH
ļ			GILSNTHRQAARVNLSFDFPFYGHFLREITVATGGFTYTGEVYH
			RMLTATQYIAPLMANFDPSVSRNSTVRYFDNGTALVVQWDHVHL
	·		QDNYNLGSFTFQATLLMDGRIIFGYKBIPVLVTQISSTNHPVKV
			GLSDAFVVVHRIQQIPNVRRRTIYEYHRVELQMSKITNISAVEM
			TPLPTCLQFNRCGPCVSSQIGFNCSWCSKLQRCSSGFDRHRQDW
ł			VDSGCFEESKEKMCENTEPVET\FLEPPQP*ERQPPSSGS*LPP E/DAVTSQFPTSLPTEDDTKIALHLKDNGASTDDSAAEKKGGTL
1	J		HAGLIVGILILVLIVATAILVTVYMYHHPTSAASIFFIERRPSR
			WPAMKFRRGSGHPAYAEVEPVGEKEGFIVSEQC
5785	2669	1388	PRVRPRVRTDHNYYISRIYGPSDSASRDLWVNIDQMEKDKVKIH
			GILSNTHRQAARVNLSFDFPFYGHFLREITVATGGFIYTGEVVH
1			RMLTATQYIAPLMANFDPSVSRNSTVRYFDNGTALVVQWDHVHL
			QDNYNLGSFTFQATLLMDGRIIFGYKEIPVLVTOISSTNHPVKV
f			GLSDAFVVVHRIQQIPNVRRRTIYEYHRVELOMSKITNISAVEM
	}		TPLPTCLQFNRCGPCVSSQIGFNCSWCSKLORCSSGFDRHRODW
1			VDSGCPEESKEKMCENTEPVET\FLEPPOP*EROPPSSGS*LPP
İ			E/DAVTSQFPTSLPTEDDTKIALHLKDNGASTDDSAAEKKGGTI.
<b>!</b>			FAGLIVGILILVLIVATAILVTVYMYHHPTSAASIFFIERRPSR
5786	2532	1674	WPAMKFRRGSGHPAYAEVEPVGEKEGFIVSEQC
	l	10/4	SYKLPAAERRASSCSQPPTPTRRRWPAPGRTSRGHRPQM*SGTP
i			APRPPARSTVSPASPLPKPRAGRCGSRPRSACSTFRPC*SLN*M S*H*KRNLSQRSSSMSRRPLSCARPHR**RQGLTVAARLPTWAK
			SPPLACSFCQAAQKSQSLSSGRSTR*PERMSFRP\SPPGNPAIP
			SLAPSSRP/PKGRPQCTWIPSRWPASPTAPPTTT*APTSSPGST
1			GRSMMTCPTRWTATPWSARASSRPRNWPTP*WRPSGRLSTV*RA
			TGGSTATAPPKRFPRNWNPMMAE
5787	2	1460	MASAASVTSLADEVNCP\ICQGTLKEAGSLSNCG/HKNFCRACL
			T\RYCEIP\GPD\LEESP\TCP\LCKEPFRP\GSFRPNWOLD\\\\
}	1		VENIERLQLVSTLGLGEEDVCOEHGEKIYFFCEDDEMOLCVVCP
f	1		EAGEHATHTMRFLEDAA\APYREQIHKCLKCLIKEREEIQEIQS
1			RENKRMQVLLTQVSTKRQQVISEFAHLRKFLEEQQSILLAQLES
			QDGDILRQRDEFDLLVAGEICRFSALIEELEEKNERPARBLLTD
}	<b>!</b>		IRSTLIRCETRKCRKPVAVSPELGQRIRDFPQQALPLQREMKMF
	į	·	LEKLCFELDYEPAHISLDPQTSHPKLLLSEDHQRAQFSYKWQNS PDNPQRFDRATCVLAHTGITGGRHTWVVSIDLAHGGSCTVGVVS
1 1			EDVQRKGELRLRPEEGVWAVRLAWGFVSALGSFP\TRLTLKEQP
1 1			RQVRVSLDYEVGWVTFTNAVTREPIYTFTASFTRKVIPFFGLWG
			RGSSFSLSS
5788	2	6860	EHSVSGRSSAYGDATAEGHPAGPGSVSSSTGAISTTTGHQEGDG
j l			SEGEGEGETEGDVHTSNRLHMVRLMLLERLLOTLPOLRNVGGVR
[ ]			AIPYMQVILMLTTDLDGEDEKDKGALDNLLSOLIAELGMDKKDV
]		j	SKKNERSALNEVHLVVMRLLSVFMSRTKSGSKSSICESSSLISS
Į į			ATAAALLSSGAVDYCLHVLKSLLEYWKSQQNDEEPVATSOLLKP
			HTTSSPPDMSPFFLRQYVKGHAADVFEAYTOLLTEMVLRLPYOT
Ì	Ī		KKITDTNSRIPPPVFDHSWFYFLSEYLMIQQTPFVRRQVRKLLL
			FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVTA
			SPOSALQYDTLISLMEHLKACAEIAAQRTINWQKFCIKDDSVLY
		j	FLLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSSAS
	1		SSPAPVAASSGQATTQSKSSTKKSKKEEKEKEDGETSGSQEDQ
	1	!	LCTALVNQLNKFADKETLIQFLRCFLLESNSSSVRWQAHCLTLH
	1	1	IYRNSSKSQQELLLDLMWSIWPELPAYGRKAAQFVDLLGYFSLK
1	l	İ	TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI
1	İ	1	GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA
[	ļ.	1	RWHKAKKVQLTPGQTEVKIDLPLPIVASNLMIEFADPYENYQAS
		ļ	TETLQCPRCSASVPANPGVCGNCGENVYQCHKCRSINYDEKDPF
	<u></u>		

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	The second of the second second in the second second in the second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second secon
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	
j	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
i	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
ŀ	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
ł	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	Deguence	Codon, /=possible nucleotide deletion,
		<del></del>	\=possible nucleotide insertion)
j		i	LCNACGFCKYARFDFMLYAKPCCAVDPIENEEDRKKAVSNINTL
- [	1		LDKADRVYHQLMGHRPQLENLLCKVNEAAPEKPQDDSGTAGGIS
1			STSASVNRYILQLAQEYCGDCKNSFDELSKIIQKVFASRKELLE
- 1			1 DLQQREAATKSSRTSVOPTFTASOYRALSVI.CCGHTGCTVCVC
			CASAVTEHCITLLRALATNPALRHILVSOGLIRELEDYNLARCA
	]		AAMREEVRQLMCLLTRDNPEATOOMNDLIIGKVSTALKGHWAND
1	1		DLASSLQYEMLLLTDSISKEDSCWELRLRCALSLFLMAUNITYD
1	1	Ì	VVVENITLMCLRILQKLIKPPAPTSKKNKDVPVEALTTVXPVCN
ľ	1		ETHAQAQLWLKRDPKASYDAWKKCLPIRGIDGNGKADGKGDIDU
- 1	1		LYLTEKYVWRWKQFLSRRGKRTSPLDLKT.GHNNWT.DOUT.PUDAM
- 1			QAARQAACTIVEALATIPSRKOOVLDLLTSYLDELSTAGECARE
1		l	ILALIQKL_TSAHWKVYLAARGVLPYVGNI.TTKETARI.LAI.PRA
İ	1	[	TLSTDLQQGYALKSLTGLLSSFVEVESIKRHFKSPINGTVI NOV
-			LCLRKLVVQRTKLIDETODMLLEMLEDMTTGTEGETVAEMANGT
ļ			ETAKKINLDDYRTPVFIFERLCSIIYPERNEVTEFEVTLEKDDO
}			Q&D=LQGRMPGNPYSSNEPGIGPLMRDIKNKICODCDLVALLED
i	1		DSGMELLVNNKIISLDLPVAEVYKKVWCTTNEGEDMDTUVDMDC
1	. [		LLGDATEEFIESLDSTTDEEEDEEEVYKMAGVMAOCGGLECMIN
· I	1		RLAGIRDFKQGRHLLTVLLKLFSYCVKVKVNPOOLUKT EMMTELM
İ	1		VMLGTLNLALVAEOESKDSGGAAVAEOVI,SIMPI\ IOA PRANTER
1	1		LSEDKGNLLLTGDKDOLVMLLDOINSTEVRSNDSVI.CGI.DIID
ŀ			I IDSEGRATER TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY O
ł	1		IAAGIK \NNSNGHOL\KDL\ILOKGITONAID\VMVVUID (CAR
	1		RIWDADI WKSFCLRPALPFILRLIRGLATOHPGTOVI.TGTDGT
j	1 1		PNEHKLEQVS\SDEGIGTLA\ENI.\LESI.REUDDUNKKIDA\AD
1	1 (		RETRAEKKRMAMAMROKALGTLG\MTTNEKGOVAD\TPTALLER
			DWEELIEEP \GLTCCICREGYKFOPTKVIGTVTPTKPMIT COM
	1		ENKPRETSRATSTVSHFNIVHYDC\HLA\AVSLADGDEEUEGAA
ŀ	1 1		LQNANTKCNGLLPVWGPHVPESAFATCLARHNTYLQECTGQREP
[	1		1 TIQUNIADIKLLFLRFAMEOSFSADTGGGGRRGWINI TRYTTUM
	l- 1		GLIVENTTRATSREEKNLOGFLEOPKEKWVESAFEVOCDVVERV
1	1		LALATEPPEQWRATRVEILRRLLVTSOARAVAPGGATDITTDVALL
	1		KDYSAYRSSLLFWALVDLIYNMFKKVPTSNTFCGWCCGLARVID
	1		HNDMPIYEAADKALKTFQEEFMPVETFSEFLDVAGLLSEITDPE
F200			SFLKDLLNSVP
5789	1	2407	LPLHAVEKTGRPGQPALKMPGKLRSDAGLESDTAMKKGETLRKQ
1			TEEKEKKEKPKSDKTEEIAEEEETVFPKAKQVKKKAEPSEVDMN
1			SPKSKKAKK\KEEPSQNDISPKTKSLRKKKEPIEKKVVSSKTKK
İ	l i		VTKNEEPSEEEIDAPKPKKMKKEKEMNGETREKSPKLKNGFPHP
			EPDCNPSEAASEESNSEIEQEIPVEQKEG\AFSNFPISEETIKL
1 1			LKGRGVTFLFPIQAKTFHHVYSGKDLIAOAPTGTGVTFGFAIDT
1	1		TEXTHG \ELQURKRGRAPOVLVLAPTRELANOVSKDESDTERVET
	<b>]</b>	J	SVACFYGGTPYGGQFERMRNGIDILVGTPGRTKDHTONGVIDI m
[	1	1	KLNHVVLDEVDQMLDMGFADOVEEILSVAVKKDSEDNBOTTI DE
1 1			ATCPHWVFNVAKKYMKSTYEOVDLIGKKTOKTATTURULATUCH
			WTQRAAVIGDVIRVYSGHQGRTIIFCETKKEAQELSQNSAIKQD
	ļ	1	AUSLHGDIPQKQREITLKGFRNGSFGVLVATNVAAPGLDIDEVD
, l		1	LVIQSSPPKDVESYIHRSGRTGRAGRTGVCICEVOHKEEVOLVO
jĺ	İ	1	VEQUAGI KEKRIGVPSATEIIKASSKDAIRIIDSVDDTAIGURV
		J	QSAEKLIEEKGAVEALAAALAHISGATSVDORSI.TNSNIGGTURM
1		ļ	ILQCSIEMPNISYAWKELKEQLGEEIDSKVKGMVFLKGKLGVCF
, 1	1	1	DVPTASVTEIQEKWHDSRRWQLSVATEQPELEGPREGYGGFRGQ
[ ]	l	}	REGSRGFRGQRDGNRRFRGQREGSRGPRGQRSGGGNKSNRSQNK
<u> </u>			GQKRSFSKAFGQ
5790	3786	1585	ARRORDPLOALRRRNOELKOOVDSLLSESQLKEALEPNKROHIY
[	İ		QRCIQLKQAIDENKNALQKLSKADESAPVANYNQRKEEEHTLLD
	1	1	KLTQQLQGLAVTISRENITEVGAPTEEEBESESEDSEDSGGEEE
!!!	į	i	DAEEEEEKEENESHKWSTGEEYIAVGDFTAQQVGDLTFKKGEI
		]	LLVIEKKPDGWWIAKDAKGNEGLVPRTYLEPYSEEEEGQESSEE
		1.	GSEEDVEAVDETADGAEVK\QRTDPHWSAVQKAISEAGIFCLVN
		f:	HVSFCYLIVLMRNRMETVEDTNGSETGFRAWNVQSRGRIFLVSK
			- I DO THOUSE THE WANT VUSRGET FLVSK

D.   Beginning muclecited   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Coc	SEQ	Predicted	1 Dec 25 1 1 1	
NO: nucleotide corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence of the first amino acid residue of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of amino acid sequence of a			Predicted end	Amino acid segment containing signal peptide
corresponding to first anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid				(A=Alanine, C=Cysteine, D=Aspartic Acid F-
corresponding to first a mino acid amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence se	1.0.	ì		Glutamic Acid, F=Phenylalanine, G=Glycine
to first amino acid residue of amino acid amino acid amino acid amino acid amino acid sequence  Percoline, Gentromine, Neurginine, Mathematic, Section, Thromine, Neurginine, Mathematic, Section, Thromine, Neurginine, Mathematic, Section, Proposible nucleotide deletion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide insertion Neuropsible nucleotide inser	'			H=H1Stidine, I=Isoleucine K=Ivsine
amino acid residue of amino acid amino acid sequence    Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptophan, Y=Tyrosine, X=Unknown, *=sto   Veryptopha	İ			L=Leucine, M=Methionine, N=Asparagine,
xeridue of amino acid sequence	İ			P=Proline, Q=Glutamine, R=Arginine
amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid				S=Serine, T=Threonine, V=Valine
Sequence    Codon, /=possible nucleotide deletion,		1	i e	W=Tryptophan, Y=Tyrosine, X=Unknown, *-Stop
PVLOGINITUDITYMGAI PAGENESTISGLEEGNOFERNYF FELMPSQLARRIDIMMDATEGTITESREPRISGLIZEGNOFERNYF FELMPSQLARRIDIMMDATEGTITESREPRISGLIZITIMSKORE GUTRILLPCLLDGDCFIRSNSASPDLGILFELGISTYIRNSTGE ELSCGWVPLIKPRAGOFFIRSNSASPDLGILFELGISTYIRNSTGE ELSCGWVPLIKPRAGOFFIRSNSASPDLGILFELGISTYIRNSTGE ELSCGWVPLIKPRAGOFFIRSNSASPDLGILFELGISTYIRNSTGE ELSCGWVPLIKPRAGOFFIRSNSASPDLGILFELGISTYIRNSTGE ELSCGWVPLIKPRAGOFFICIAL STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET S	i		sequence	Codon, /=possible nucleotide deletion
PVLCOINTOPULTIMES I FAGERESTIS GLIEBENOFRANDE  PRIMESCIA PROMINDMATE TERREPRIS ILLILIUS COME IN MISTOVILS RHUNGLISH PROPERTY IN STORE  GMSIQUIS RHUNGLISH PROSPOLIC ILLEGIS IN STORE  ELSCGWYELKLEPASGUP I PARTYELF LINGGTPYEKG I EUDPS  BRARHGSYPYOLTMERROPOLIVKIRSI MIRRIS THIS THE BESCGWYELKLEPASGUP I PARTYELF LINGGTPYEKG I EUDPS  BRARHGSYPYOLTMERROPOLIVKIRSI MIRRIS HILLISH PRIMITAFFE LEOPDYMBALRS PROG I LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LINGGAN LI		sequence		\=possible nucleotide insertion)
FELM'S CILAR PLONDATE OT TRERPER IS LILILUS COMITY IN CONTROL POLICY STRENGT ON THE VARIANCE PROMISE AND CONTROL POLICY STRENGT ON THE PLANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE OF THE VARIANCE	1			PVLQQINTVDVLTTMGAIPAGFRPSTLSQLLFFGNOFPANVELO
OWSIGUESHURICEDORKVLSNIHTVENTMOGREPHEGISVIRNSTORS  GUTTELIPECLEGOFFIENDSSEPHLAITPEGISVIRNSTORS  ELSCGNVFH.KLFDASGVPIPAKTELFILNGGTPYERGISVES  SRRAHGSVYGIMTMRGOPGLUKKERSINGSENVISLLEPETI  GMMCSIHLLIFYRGILGDVLKRDRAMSLGSTDLISHPHLAITFP  LEOPDVMDALASSWAGGGES, VLKRESER, PERLKVPFFLLVV  \GCVLPHL/HTPTRIPPERMAEERITARMKVITDFLKONGEN  GALQALLSPOOVIEPPDLISEGTVDFLGRENGKAPEKLKVPFFLLVV  \GCVLPHL/HTPTRIPPERMAEERITARMKVITDFLKONGEN  GROUPLENGE TO THE STANKEN TO THE STANKEN TO THE STANKEN TO THE STANKEN TO THE STANKEN TO THE STANKEN TO THE STANKEN TO THE STANKEN TO THE STANKEN TO THE STANKEN TO THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE STANKEN THE	1			PELMPSQLAFRDLMWDATEGTIPSPDSPTSLTLTLWSGVMTPLD
STREEDER JAKENDASSUPICITIFELGISTIRNSTORE ELSCGAVUR LKFDASSUPICITIFELGISTIRNSTORE SRRAHGSVYQIHTMEROPOLLVKLRSILNERSINVISILLERIT GNMCSIHLLI FYROLIGUPULKDRMIGLOSTISHPMLATFP LEQPDVMBALRSSWAGQES\TLKRSEKR\PKSEKRVKPFLLVY GOMCSIHLLI FYROLIGUPULKDRMIGLOSTISHPMLATFP LEQPDVMBALRSSWAGQES\TLKRSEKR\PKSEKRVKTTDFLKONGEN GALQALLSPDOVIERPBLSEGTTDFLGBMRNAN  SOLOGECHILL'WERTGHGLEKSGLOTHERAPARIBEIGLKSGLOAPALSV GN/GKQL/AMSQGSDDEQIKERNIRSINTSGHVGFESLPDOL NRSIQGGFCRILLCVBETGIGKSTLIDTLINTNFEDVESSHF NVKLKAQTYELQESNVOLKJITVITVGFGOJNIKERSYGJIVO IDAQFFAALQBELKK KRSLFTYBDSRIHLVTHFISPTGHLST- NVKLKAQTYELQESNVOLKJITVITVGFGOJNIKERSYGJIVO IDAQFFAALQBELKK KRSLFTYBDSRIHLVTHFISPTGHLST- DLITMMLDSKVYII IVVIAKADIVSKTELQKFKILKMSELVSN VQIYOFPTDDDTIAKVNAAMNGQLPFAVCLYFISPTGHLST- DLITMMLDSKVYII IVVIAKADIVSKTELQKFKILKMSELVSN VQIYOFPTDDDTIAKVNAAMNGQLPFAVCLYFISTGHGHEKK RYPMGUVQVENENKELTERSAFREJOKAFFHLKKLHGERNMLEE RRILEEEI IAFSKKAATSETHSOSFFALTSHEGGROKKEE MKOMFVQRVKEKEALLKEARRELOAKFHLKKLHGERNMLEE RRILEEEI IAFSKKAATSETHSOSFFALTSHEGGROKKEE KRULEEVINGHAMAN SAMANDON FVKQKVPEHRRSSSOAMFIKKLEVCEDFAV.CFTTSIFGEOD FVKQKVPEHRRSSSOAMFIKKLEVCEDFAV.CFTTSIFGEOD FVKQKVPEHRRSSSOAMFIKKLEVCEDFAV.CFTTSIFGEOD FVKQKVPEHRRSSSOAMFIKKLEVCEDFAV.CFTTSIFGEOD FVKQKVPEHRRSSSOAMFIKKLEVCEDFAV.CFTTSIFGEOD FVKQKVPEHRRSSSOAMFIKKLEVCEDFAV.CFTTSIFGEOD FVKQKVPEHRRSSSOAMFIKKLEVCEDFAV.CFTTSIFGEOD FVKQKVPEHRRSSSOAMFIKKLEVCEDFAV.CFTTSIFGEOD FVKQKVPEHRRSSSOAMFIKKLEVCEDFAV.CFTTSIFGEOD FVKQKVPEHRRSSSOAMFIKKLEVCEDFAV.CFTTSIFGEOD FVKQKVPEHRRSSSOAMFIKKLEVCEDFAV.CFTTSIFGEOD FVKQKVPEHRRSSSOAMFIKKLEVCEDFAV.CFTTSIFGEOD FVKQKSVPHKRSSTELPLTVYNDLVSLOGERVFUHKDETVSKYFTT FVKYVPKKTSHNOGTLAVIYFLAGARNIOLOGERVFUHKDETVSKYFT FVKYVPKKTSHNOGTLAVIYFLAGARNIOLOGERVFHINGOAVYSLO FFGFSKADABEVKGIFTTSHLAGARNIOLUGURVFHINGOAVYSLO FVGFGSKADABEVKGIFTTSHLAGARNIOLUGURVFHINGOAVYSLO FVGFGSKADABEVKGIFTTSHLAGARNIOLUGURVFHIPDIFTSKYFT FVKYVPKKTRINGTIAVIYFLATHFYNAFHILDFOTSHLVUN FVKYSPKKTRINGTIAVIYFLAGARNIOLUGURVFHIPHITTYPHOFTAKAGARNIOLUGURVFHIPHITTYPHITTHOOAVYSLO FVGFGSKADABEVKGIFTTRHINGAAKGGCASGGGGKGCHOOK FVKYSTAMFICHTOR FVKYSTAMFICHTOR FVKYSTAM			1	GMSIQVLSRHVRLCLFDGNKVLSNTHTVDATWODKKDKTETTDGD
ELSGGWYELKIPASGVPIPAKTYELFINGGTPYERGIEVDES SRRAHGSVYCJIMTMRGOPQLUKKESINVISLIEPTI GNMCSIHLLIFYRGIJGDVLLKDRMSLGSTDLISHPMLATFPE LEGPDVMDALASSMAGGGS,VLKRSERK PERKLYPFILLY \GCVLPELL/HTPTRLPPRWAEEETTARMKVITDFLKONGEN \$791  3 1636  LRVAEFAGTSK/JGAGLIGPHRAPARDHGLEGGAAPALGVS GN/GKGL/AMSGGSDDE/GTVPELGRMVGFESLPDGI NRSIQGGFCFNILCVGETGIGKSTLIDTLFNTTHFEDYESSHFC NRSIGGGFCFNILCVGETGIGKSTLIDTLFNTTHFEDYESSHFC NRSIGGGFCFNILCVGETGIGKSTLIDTLFNTTHFEDYESSHFC NRSIGGGFCFNILCVGETGIGKSTLIDTLFNTTHFEDYESSHFC NRSIGGGFCFNILCVGETGIGKSTLIDTLFNTTHFEDYESSHFC NRSIGGGFCFNILCVGETGIGKSTLIDTLFNTTHFEDYESSHFC NRSIGGGFCFNILCVGETGIGKSTLIDTLFNTTHFEDYESSHFC NRSIGGGFCFNILCVGETGIGKSTLIDTLFNTTHFEDYESSHFC NRSIGGGFCFNILCVGETGIGKSTLIDTLFNTTHFEDYESSHFC NRSIGGFCVGARMANGGLIPPAVCSMBEVKYCHTHSPTHSLKT DLITMRNLDSKVII PUT KARDTVSKTELGKERNICHTHSLESSHFC NRSIGHTSMALAMMGGLIPPAVCSMBEVKYCHTHSPTHSLKT DLITMRNLDSKVII PUT KARDTVSKTELGERFTHISERGTHFEHIS VARCKLERMGFTDVGPENKVSVGOFTVEAKRREPFIGRGKKE MKOMFVGRVKVEKSALIKERAEFICHAMPENKENGTHSTENGTHFEHIS RRLLEEEIIAFSKKKATGETFHSGSFLATGSMLRKDKRMO FVKOKVPHRRSSGAMP IKKLEVCFDFFAVLCFTS IFGEOP LLIFMEKYFQVGGOVISOSE RRLLEEEIIAFSKKKATGETFHSGSFLATGSMLRKDKRMO FVKOKVPHRRSSSGAMP IKKLEVCFDFFAVLCFTS IFGEOP LAARASPARWCGFFVVVVHTCWAVGIVVTFRCGSGDASCIGF VANVSVKKTRINGTICATY FLHARGVLIPMCOVILLVS PLT VANVSVKKTRINGTICATY FLHARGVLIPMCOVILLVS PLT VANVSVKKTRINGTICATY FLHARGVLIPMCOVILLVS PLT VANVSVKKTRINGTICATY FLHARGVLIPMCOVILLVS PLT VANVSVKKTRINGTICATY FLHARGVLIPMCOVILLVS PLT VANVSVKTRINGTICATY FRANCHSPTILDEFGSLIVLVI AGGGAALELMKVKKALOHT FRANCHSPTILDVFRAVNEGESSEX ENATAPHTO JGAMKVLSVLIPPLCVGGAVYSLLINKKASHYSNLINKPRADA SPAKKKSMIGMSTKAVLANGCSSTVVIPPLTHIDDVFRAVNEGESSEX ENATAPHTO TANVSVKTRRBINGTICATY TORVINGIGLIRFWIHMGDAVYSLOG FOFSEKDADEVKKTALOHT TIRGRLDBETGTVTSSERKFEE DTQMKVLSVILNTSTTESHLGAENNIDLVLAVVSERDESKFEE TANVSVKKTRBINGTICATY TIRGRLDBETGTVTSSERKFEE DTQMKVLSVILNTSTTRSHLGAENNIDLVLAVVSERDERSKTEE DTQMKVLSVILNTSTTRSHLGAENNIDLVLAVVSERDERSKTEE DTQMKVLSVILNTSTTRSHLGAENNIDLVLAVVSERDERSKETE DTQMKSSSDAADAUTRIPKRIGLGGGCTGFOFFSEKGA KORGERGIGLGGVTGFFGROGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG			ţ	OVTRILPCI.LDGDCFTPGNGAGDDICTI FRICTGYTDYGDGG
SKRAHGSVPYQIMTMRROPQLIVKERSINRISENTISILLETT GNMCSIHLI IPTROIIGPULKORMIGISTISPHMIATEP LEGPDVMBALRSSWAGGES YTIKKSEKR   PKCELKUPFILLVS (GCUPELI, HTPTRI) PEPRWAEETTETAKWYTTPELKONGE GAUQALLSPDOVIEEPPILSEGTYDFLESMKRIND  5791  3 1636  LEVARPRAGTST / GAGLIOPHRAPAREDIGLASGGAPALISVS GAUQALLSPDOVIEEPPILSEGTYDFLESMKRIND  KRIQGGOTORILGVEGTOLGKSTLIDTLENGGAPARISVS GN / GKQL / AMSGGSDDEQIKKERITRSILTMSGRUGFESLDDOI NKSIQGGOTORILGVEGTOLGKSTLIDTLENFEDVESHEF NVLKAGTYELOESNYOLKIT IVNTVGFGOOLNKEERS VOJTU  IDAOFBAYLOBELKI KRSILTYSIBSTHELYTSPOTHELKT  DLITMKNLDSKVYI IPVIAKADTVSGTELOKEKIKLINGBLUXGE VOJTOPPTDDDTIAKVNAMMGOLPAVUGNOMYKEKS KOYPGOVQUENERHODEVILERMI, LICTMBELLREPHIAKRI KOYPGOVQUENERHODEVILERMI, LICTMBELLREPHIAKRI KOYPGOVQUENERHODEVILERMI, LICTMBELLREPHIAKRI KOYPGOVQUENERHODEVILERMI, LICTMBELLREPHIAKRI KOYPGOVQUENERHODEVILERMI, LICTMBELLREPHIAKRI KOYPGOVQUENERHODEVILERMI, LICTMBELLREPHIAKRI KOYPGOVQUENERHODEVILERMI, LICTMBELLREPHIAKRI KOYPGOVQUENERHODEVILERMI, LICTMBELLREPHIAKRI KOYPGOVQUENERHODEVILERMI, LICTMBELLREPHIAKRI KOYPGOVQUENERHODEVILERMI, LICTMBELLREPHIAKRI KOYPGOVQUENERHODEVILERMI, LICTMBELLREPHIAKRI KOYPGOVQUENERHODEVILERMI, LICTMBELLREPHIAKRI KOYPGOVQUENERHODEVILERMI, LICTMBELLREPHIAKRI KOYPGOVQUENERHODEVILERMI, LICTMBELLREPHIAKRI KOYPGOVQUENERHODEVILERMI, LICTMBELLREPHIAKRI KOYPGOVQUENERHODEVILERMI, LICTMBELLREPHIAKRI KOYPGOVQUENERHODEVILERMI, LICTMBELLREPHIAKRI KOYPGOVQUENERHODEVILERMI, LICTMBELLREPHIAKRI KOYPGOVGOVITATI VANVEVEKTRINGTI, LATI YHARGHUPHOGKOVILLVEHIA KOYPGETEMI, LITTMBETTEBILTVEVINKUS LICTMBELLREPHIAKRI KOYPGETISLADEVIKI KYKKANIMI TIPHIAKRI KOYPGETISLOPEN KOYPGOVITA KOYPGOVILLVEHIAKRI KOYPGETISLOPEN KOYPGOVITA KOYPGOVILLVEHIA KYKKANIMI TIPHIAKRI KOYPGETISLOPEN KOYPGOVITA KYKNIMI KYKNIMI KYKNIMI KYKNIMI KYKNIMI KYKNIMI KYKNIMI KYKNIMI KYKNIMI KYKNIMI KYKNIMI KYKNIMI KYKNIMI KYKNIMI KYKNIMI KYKNIMI KYKNIMI KYKNIMI KYKNIMI KYKNIMI KYKNIMI KYKNIMI KYKNIMI KYKNIMI KYKNIMI KYKNIMI KYKNIMI KYKNIMI KYKNIMI KYKNIMI KYKNIMI KYKNIMI KYKNIMI KYKNIMI KYKNIMI KYKNIMI KYKNIMI KYKNIMI KYKNIMI KYKNIMI KYKNIMI KYKNIM	1	}		ELSCGWVFI.KI.FDASGVDT DAVTVET EL NOCEDIATION
GSMCS.HILLIFYRGILGDVLLKDRMSLGSTDLISHMILATEP LEGPOVMDALSSMAGGGS.VLKRSSER, VERLKYPEILLY \GCULPELL/HTPTRI.PPFRWAEESTTARMKVITDFLKQNGEN \$5791  3 1636  LRVAEFAGTSK/TGAGLIGPHREAPARDHIGLEGGARAPALSVS GN/GKCL/MSGSGDDSCGTTDFLGRMSVGFSELPDCJ NRSIQGGCFNILCVGETGIGKSTLIDTLINTNTPEDYRSSHFC NVKLKAGYTSLGSBNVQLKIT INTVIGGGRUKSFESSHFCIN NRSIQGGCFNILCVGETGIGKSTLIDTLINTNTPEDYRSSHFC NVKLKAGYTSLGSBNVQLKIT INTVIGGGRUKSESSGFT LDAGFEAVLOSELKI KRSLFTYHDSRIHVCLKFISPTGHSLKT DLIMMKNLDSKVII IPVIKADTVKESVGJSTUM GRUPGBVUVQVENRINCDSVIKLRSBLICTNKESSYGTV UGYGPTDDDTTAKNAANNGCLPPAVVSMBEVKGVNAMVK RQYPMSVUVQVENRINCDSVIKLRSBLICTNKESSTGTFTHSL VRKCLLERMGFTDVGPENKRVSVOSTVERARREPHGBROKKE MKOMFVGRVVEKSEALILERARELOAKPEHLARDGTHTRIHVS VRKCLLERMGFTDVGPENKRVSVOSTVERARREPHGBROKKE RKLLEBEIIAFSKKKACSEIFHNOSFLATGSNLARDKORNNO FVKOKVPEHRKSSQANF IKKLEVCFDFAV.CFTISIFGEQP LLIFMEKYFOVGGVISGSE RKLLEBEIIAFSKKKACSEIFHNOSFLATGSNLARDKORNNO FVKOKVPEHRKSSGANF IKKLEVCFDFAV.CFTISIFGEQP LARPKLQL KHISFTTRSILGAENNIDLVJANVEDEPDVBSKFE TUNVSVPKKTRNNGTLVAYI-FHANGULVBROVJULVSPLTI- VMVPKPEINLLTGSSDTQGIEADKKPTSALDEPVSHRPBLA NVANDNFYPGSSLPADVHRYKMIGLGKRYVLYLPEILPDVSKKFE FVKOKVPEHRKYKRLOUTGIFFRGIMMESPGOTVSESERKTEN FVKOKVPHRAVKKKALDMTFRRGIMSEFFFTYNFNTFTIDVFAN ISFMKKKKSNIGMSTKAVLURGFSTVVI FPLFLLDEDGTSLAFK NVANDNFYTGSSLPADVHRYKRALDGTFTVYARPHTFTIDVFAN ISFMKKKKSNIGMSTKAVLURGFSTVVI FPLFLLDEDGTSLAFK FVKOKVPHRAVKKALDMTFRRGIMSEFFTYNFNTFTIDVFAN ITMPTSHRLAGFRDDVVPLVYLVQRWLTVPDVRRVWERGESSYE EKATRAPHTO FVKOKVPHRAVENDALVANIFFTTENHLGAENNIDLVINVSEDFDSKFE TVMVSVPKTRRNIGTLAYAI FPLHRAVLJBWINGCQVHLVSPLTI- TVMVSPKTRRNIGTLAYAI FPLHRAVLJBWINGCQVHLVSPLTI- TVMVSPKTRRNIGTLAYAI FPLHRAVLJBWINGCQVHLVSPLTI- TVMVSPKTRRNIGTLAYAI FPLHRAVLJBWINGCQVHLVSPLTI- TVMVSPKTRRNIGTLAYAI FPLHRAVLJBWINGCQVHLVSPLTI- TVMVSPKTRRNIGTLAYAI FPLHRAVLJBWINGCQVHLVSPLTI- TVMVSPKTRRNIGTLAYAI FPLHRAVLJBWINGCQVHLVSPLTI- TVMVSPKTRRNIGTLAYAI FPLHRAVLJBWINGCQVHLVSPLTI- TVMVSPKTRRNIGTLAYAI FPLHRAVLJBWINGCQVHLVSPLTI- TVMSPKKKSMIGMSTRAVLWRCFSTVVI FLUDGTSSLKKEE DTQMKSLBPHADLFTRANIARGGCASGGGCGCCOCHGV TVMSLAVANADDSSCAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1			SRRAHGSVEYOTMTMPROPOLLUVI DEL VIDAGI PIEKGI EVDPSI
LEUPUMMALRSSWAGGES\TLKRSEKR\PKPTELTYPETLEV	į			GNMCSTHILL TEXPOIL COME A REPORT OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPER
GLOALDSPOUMEPPEDLSGOTYPELGEMENIAV  5791  3 1636  LRVARFAGTSK/ IGAGLIOPLIRAPARDINGLERGAPAIGUS  NRSIQGFCFNILLVGRTGIGKSTLIDTLENNFRUYESSHEF  NRSIQGFCFNILLVGRTGIGKSTLIDTLENNFRUYESSHEF  NRSIQGFCFNILLVGRTGIGKSTLIDTLENNFRUYESSHEF  NRSIQGFCFNILLVGRTGIGKSTLIDTLENNFRUYESSHEF  NRSIQGFCFNILLVGRTGIGKSTLIDTLENNFRUYESSHEF  NRSIQGFCFNILLVGRTGIGKSTLIDTLENNFRUYESSHEF  NRSIQGFCFNILLVGRTGIGKSTLIDTLENNFRUYESSHEF  DLITMKINLSKYNII PU IRADITYSKEPKIKKINSELVSN  GYPMGUVQENDRINCDPVLRBRLITGMEUKPKIKKINSELVSN  GYPMGUVQENDRINCDPVLRBRLITGMEUKPKIKKINSELVSN  KOMPORVKEKBAILKRABELIGAKFEILKKINGENTKHIK  RRLLEBEITAFSKKARSTSIPHSGSTLATGSBILKRUKDRKINSO  FVKGKVPEHRRSSSQANFIKKKLEVCFDFAV.CFITSIFGEGP  LIFFEKKYFOVGGVIYASSE HINGSTLATGSBILKRUKDRKINSO  FVKGKVPEHRRSSSQANFIKKKLEVCFDFAV.CFITSIFGEGP  LIFFEKKYFOVGGVIYASSE HINGSTLATGSBILKRUKDRKINSO  FVKGVPEHRRSSSQANFIKKLEVCFDFAV.CFITSIFGEGP  LARRKLGL/RHSFTTTRSHLGARBIDLVLINVEDFDVESKFE  TVAVSVPKKTRINGTLYAYIILHRAULPBHINGSVPLIVSPLIV  ARGURANDFYFOGSSLPADVHRYMMIQLGKTVHLIPLIPLDFLAFKNI  NAVAANFYPOSSLPADVHRYMMIQLGKTVHLIPLIPLDFLAFKNI  SFRKKKKSMIGMSTKALVMRCFSTVUTYLPLILLDEDTSILLIVI  AGGGALELMKVKKALKHTIFWGLMPEFOFGTYSSEEKKTES  DTQAMKYLSLLIPLCGGAVSLLINILKYKSMYSBLLINSFVNOC  VAPGFLEMLFOLDFVHYKLKSVALLPKAFTYVAFNTFIDDVFAI  LITMFSTRILACFRODVYLVYLYRRHLYVAFNTFIDDVFAI  LARRKLOLVRINSTTELPLITYSYDKVSLGRANDFROMENSESKFE  TVAVSVPKKTRANGTLAXYIFLHHAGVLPMIGGNSTVGTR  RKALDMVINSTTELPLITYSYDKVSLGRALPRHHMODAVYSLOC  FOFSEKDADEVKGIFVUTNLYFLALTFFVAAFHLLIFDLAFKNI  NMADDRVFPGSSLBADVHRYMMIQLGKTVHLIFIDLES  RKVELMVINSTTELPLITYSYDKVSLGRLERPHTHMODAVYSLOC  FOFSEKDADEVKGIFVUTNLYFLALTFFVAAFHLLIFTLAFLDVI  SFRKKKENGIMSTKAVLHRCFSTVUTYSTRALDEPVSHRPFLAL  NMADDRVFPGSSLBADVHRYMMIQLGKTVHLIPLIPLDELS  TYMVSYPKKTRANGTLAXYIFLHRAGVLPPORGTYSESKERVEESK  TYMVSYPKKTRANGTLAXYIFLHRAGVLPPORGTYSESKERVEESK  TYMVSYPKKTRANGTLAXYIFLHRAGVLPPORGTYSESKERVEESK  TYMVSYPKKTRANGTLAXYIFLHRAGVLPPORGTYSESKERVEESK  TYMVSYPKKTRANGTLAXYIFLHRAGVLPPORGTYSESKERVEESK  TYMVSYPKKTRANGTLAXYIFLHRAGVLPPORGTYSESKERVEESK  TYMVSYPKKTRANGTLAXYIFLHRAGVLPPORGTYSESKERVEESK  TYMVSYPKKTRANGTLAXYIFLHRAGVLPPORGTYSESKERVEESK		1	ĺ	LEODDUMDAL REGWACORD THE WARRENCE TO LISHPMLATEPML
S791   3   1636   LRVAEPSCISK   TORGIC   GPLHRAPENICLEGGAAPALSVS   GN/GKQL/MSGQGSDDEQIKENIRSLITMSGHVGFSLOPD  GN/GKQL/MSGQGSDDEQIKENIRSLITMSGHVGFSLOPD  MRSIQQGFCFNILLCVSFGIGKSTILLIFNINFEDVSSHFK   NVKLKAOTYELQESNVQLKLTIVNTVCFGDQINKESSYQFVI   DLLTMKNLDSKVYIIPVIAKADTVSKTELQKFKIKLMSELVSN   VOIYOFPTDDTIAKVAAMMGQLPRAVUGSBLKESYQFVI   DLLTMKNLDSKVYIIPVIAKADTVSKTELQKFKIKLMSELVSN   VOIYOFPTDDTIAKVAAMMGQLPRAVUGSBLKESVGNAWW   GVYMGVVQVENENHCDFVKLEBLICTIMBELRGYHTRINE   YRRCKLEMMSTTUGPENRYDVGVGETVEAKREPHGROKKES   RKULEEEIIAFSKKAATSIFHSQSFLATGSBLKKDKDRNNSO   FVKQKVYBHRSSSQANIKKKLEVGENKILEE   RRLLEEEIIAFSKKAATSIFHSQSFLATGSBLKKDKDRNNSO   FVKQKVYBHRSSSQANIK   KKKLEVCHACVCFTISTFGCOP   LARRPKLQL/RHSFTTTRSHLGAENIDLVIAWSCDPUSSKSE   RRLLEEEIIAFSKKAATSIFHSQSFLATGSBLKKDKDRNNSO   LARRPKLQL/RHSFTTTRSHLGAENIDLVIAWSCDPUSSKSE   TVMVSVPKKTRNNSCTLYAY FILHACVALVGKVUNINSTTELPLTVSYDVKVSLGRIRWIHMQDAVVSLQ   TVMVSVPKYRDNSCTLYAY FILHACVHIGKOVALVSPLT   YMVPKPESINLATGSBDVVANTFYDASHLHDGKOVALVSPLT   YMVPKPESINLATGSBDVVANTFYDASHLHDGKOVALVSPLT   YMVPKPESINLATGSBDVVANTFYDASHLHDGKOVALVSPLT   YMVPKPESINLATGSBDVVANTFYDASHLHDGKOVALVSPLT   SFUKKKKSMIGMSTGAVLUMCCSTVVITPLELDEOTSLLVLVI   AGVGAATELMKVKKSMIGMSTGAVLUMCCSTVVITPLELDEOTSLLVLVI   AGVGAATELMKVKKSMIGMSTGAVLUMCCSTVVITPLELDEOTSLLVLVI   AGVGAATELMKVKKSMIGMSTGAVLUMCCSTVVITPLEDPLAFKN   YAFGFLFMLPQLFVNYKLKSVANLIPKAFTYKAFNYFIDDVFAN   TVMVSVPKKKKSMIGNSTGAVYSLUNIVPRCSVPTVAVYDKRVNEGGSSY   ERATTAPHTD   AAAASSPAMCGVFVVVVVITCWVMYGVYTRPCSGBASCTOP   LARRPKLQL/RHSFTTTSSHLGAENIDLVLNVEDDVSKYRE   ERATTAPHTD   TVMVSVPKKYRNINGTVAY FILHAQLVYSLQC   FVFSSKDADEVKGTFVVVVVHTCWVMYGVYTRPCSGBASCTOP   LARRPKLQL/RHSFTTTSSHLGAENIDLVLNVEDDVSKYRE   ERATTAPHTD   TVMVSVPKKYRNINGTVAY FILHAQLVTKYNSVSULINSFONGV   YAFGFLEMLLDFGSSPCHOEVKGTFVVVVVHTCWVMYGVYTRPCSGBACTOP   TVMVSVPKKYRNINGTVAY FILHADAVTSLQC   FVFSSKDADEVKYNTAVAFTYR FILHACT   FVFTAKKKSMIMSTRAVAT FILHACH KKYSWVSMILINSFONGV   YAFGFLEMLADAPATAVSLQC   FVFTAKKKSMIMSTRAVAT FILHACH KKYSWVSMILINSFONGV   YAFGFLEMLDLAGGACY POPONGPOPPOPPOPPOR CORGON   FVFTAKKSMIMSTRAVAT FILHACH KKYSWVSMILNSFONGV				CCULBIT (MEDIDAL BERGY BERGY BERGY BY BERGY BY BERGY BY BERGY BY BERGY BY BERGY BY BERGY BY BY BY BY BY BY BY BY BY BY BY BY BY
1636 LRVAPPAGTSK/ IGAGLIGDELIRAPADHIGLEGGAPAPALSUS  N/SKGA/JAMSGGGSDDEGI KRENI SILITUTISHINGHUGFES LPDDI  NRSIQGFCFNILLGVGETGIGKSTLIDTLENTNIFEDESSHER  NVLKAGVTELQESNYQLKITIVATUTGOLIKKE SYGJVU  IDAQFEAYLOBELKIKSLFTYHDSRITYCLYFISPTGHEKT  DLITMKNIDSKYJI IPD YRARDTYSKETOKYKIKLUSELUSNI  DLITMKNIDSKYJI IPD YRARDTYSKETOKYKIKLUSELUSNI  GOYPGYUOVQVENENCHOPVKLEMILICTMBOLIKEGTYHKIKUS  KOYPGYUOVQVENENCHOPVKLEMILICTMBOLIKEGTHYKIKU  YRKCKLERMGFTDUGPENKPUSYGETYEAKRHEFHGRGRKEE  MKOMFYGGVKKERAILKRARERLOAKFEHLKKLIDESHMILEE  RRLLEEEI IAFSKKARSTSI PHISGS THAGSSILKKDKDRKINSO  FVKQKYPEHRRSSSGANFI KKKLEVCFDFAVLCTIS IFEGOP  LITPHKSTYPOVGGYJYSGSE  ARAABSPAWWGGVPUVYVUHTCWWYGIVYTFPCSGDASCIOP  ARAPSKPAWGGVPUVYVUHTCHWWYGIVYTFPCSGDASCIOP  TWYDYPPERIILLIGESDTOQI EADKKPTSALDEPVSHKHPRLA  NAVAANFYPOSSILPADHIRYMKNIQLGKTVHYLPILFIDOLIS  RVDLMVINKSTTELPLITYSSDKVSIGREFHIMDDAVYSLO  FGFSKKADADEVKGIFVDTNLYFLALTFFVAAFHLLFPILAPKNI  ISFNKKKKSNIGMSTKALUMKCFSTVJYLELDEOTSLLULV  AGVGAAIELMKVKKALKHTIFWGLMPEFOFGTYSESEKKTEES  DTQAMKYLSLLYPLCVGGAVSLLINI KYKSMYSHLINFYNO  VAPGPLPMLPOLFVYVKLKSVANLIPKKAFTYKAFNTFIDDVFAI  IITMPTSHRLACFRODVYFLVYLYQRWLYPUDKRYNDEGSSY  EKATRAPHTD  AAAASSPAWGGVFUVYVHTCWWYGIVYTFPCSGDASCIOP  ITMYSVPKKTRANGTLAYI FILHBGUNPEDVSHKYMEGGSYY  TWYSVPKKTRANGTLAYI TFLHBGUNPEDVSHKYMEGGSYY  TWYSVPKKTRANGTLAYI TFLHBGUNPEDVSHKYMEGGSYY  TWYSVPKKTRANGTLAYI TFLHBGUNPEDVSHKYMEGGSYY  TWYSVPKKTRANGTLAYI TFLHBGUNPEDFOFGTYSESEKTEES  TWYSVPKKTRANGTLAYI TFLHBGUNPEFOFGTYSESEKTEES  DTQAMKYLSTLIPPLTVSYDKVSLGKWYSMLINSFYMOV  VAFGLERUNGTHYSTLIPPLTVSYDKVSLGKWYSMLINSFYMOV  VAFGLERUNGTHYSTLIPPLTVSYDKVSLGKWYSMLINSFYMOV  VAFGLERUNGTHYSTLIPPLTVSYDKVSLGKWYSMLINSFYMOV  VAFGLERUNGTHYSTLIPPLTVSYDKVSLGKWYSMLINSFYMOV  VAFGLERUNGTHYSTLIPPLTVSYDKVSLGKWYSMLINSFYMOV  VAFGLERUNGTHYSTLIPPLTVSYDKVSLGKWYSMLINSFYMOV  VAFGLERUNGTHYSTLIPPLTVSYDKVSLGKWYSMLINSFYMOV  VAFGLERUNGTHYSTLIPPLTVSYDKVSLGKWYSMLINSFYMOV  VAFGLERUNGTHYSTLIPPLTVSYDKVSLGKETHIMDDAVYSLOQ  FOFGEKDADEVIGHTOTTYSTYDKVSLGKETHIMDDAVYSLOQ  FOFGEKDADEVIGHTOTTYSTYDKVSLGKETHIMDDAVYSLOQ  FOFGEKDADEVIGHTOTTYSTYDSVSLGKETHIMDDAVYSLOQ  FOFGEK			1	CALON LODDOWN DEPTRIME TETARWKVITDFLKQNQENQ
LRYMENATISKY (GAGLIQPHERRADDIGLERGAAPALISUS  ON GROLA /AMSGGGSDEGI KERNIRGHUTISHVOTESELPDOL  NRSIQQGCCPNILCVGETGIGKSTLIDTLENTNIFGHUSESHEF  NRSIQQGCCPNILCVGETGIGKSTLIDTLENTNIFGHUSESHEF  NRSIQQGCCPNILCVGETGIGKSTLIDTLENTNIFGHUSESHEF  DLITMMILDSKYYI I PYLKADITVSKEYKKILLNSELVSN  VQIYGPFDDDTIAKVNAAMNGOLPRAVGSDEWKVGNKMW,  RQYPMGUVQVENENGHOFVKLREMLICVEKKILLNSELVSN  VQIYGPFDDDTIAKVNAAMNGOLPRAVGSDEWKVGNKMW,  RQYPMGUVQVENENGHOFVKLREMLICHREDLREGHTHINT  YRRCKLERMGFTDUGPENRPUSVGETGARREDPHGERGRKEE  RRLLEEEIIAFSKKATSEIPHOG PLATGSNIERDDGRRCKEE  RRLLEEEIIAFSKKATSEIPHOG PLATGSNIERDDGRRCKEE  RRLLEEEIIAFSKKATSEIPHOG PLATGSNIERDDGRRCKEE  RRLLEEEIIAFSKKATSEIPHOG PLATGSNIERDDGRRCKEE  RRLLEEEIIAFSKKATSEIPHOG PLATGSNIERDDGRRCKEE  RRLLEEEIIAFSKKATSEIPHOG PLATGSNIERDDGRRCKEE  RRLLEEEIIAFSKKATSEIPHOG PLATGSNIERDDGRRCKEE  RRLLEEEIIAFSKKATSEIPHOG PLATGSNIERDDGRRCKEEN  LARRKLOLKHSFTTTRSHIGAENNIDLVINVEDFDVESKFE  TVANVEVPKKTENNGTIAYTIFLHAGVUFWTSGLOPULVSPITT  AMPERDEEIILLIGESDTQCIADAKTSHILDEDTSLLULVI  AGVGAALELMKVKKALKHTIFWGLMPEFOGGTYSESERKTEEE  DTQAMKYLSVLLYPLCVGAQVSLLINIKYKSWYSMLINSPINGT  VAFGFLFMLPGLFVYVVLKLSVAHLFKKAFTYKAFNTFIDDVFAI  LITMFTSREKAKSHIGNSTKALVHRCSTVUTYTRPCSGDASCIQFY  VAFGFLFMLPGLFVYVVVHTCWVMGIVYTRPCSGDASCIQFY  VAFFRLACKTOLVHSFTTTRSHLGAENNIDLULNVEDFDVESKFE  TVMVSVPKKRRINGTIAYTFLHRAGVLPFHIDGKOMLVSPLITT  STYNSVPKKRKSHIAGSTLAVTYVVHTCWVMGIVYTRPCSGDASCIQFY  VAFFGLERGAPHTD  AAAASPAWGUFVVVVVHTCWVMGIVYTRPCSGDASCIQFY  VAFFGLERGAPHOLOLVHSFTTTRSHLGAENNIDLULNVEDFDVESKFE  TVMVSVPKKRRINGTLAYTFLHRAGVLPFHIDGKOMLVSPLITT  VMVPKPEEINLLTGSSDTQGARAKHTPLHDDLSFFE  TVMVSVPKKRRINGTLAYTFLHRAGVLPFHIDGKOMLVSPLITT  VMVPKPEEINLLTGSSDTQGARAKHTPHARHTPLDDVFAF  LARRKLOLLYRHSFTTTRSHLGAENNIDLULNVERPPLATKNIP  AAAASPAWGUFVVVVVHTCWVMGGVVYTRPCSGDASCIQFY  TVMVSVPKKRRINGTLAYTFLYSMCVSLGRICHTPHTHDDVFAF  LARRKLOLLYRHSFTTLPTVSTYNCVSLGRICHTPHTHDDVFAF  TVMVSVPKKRRINGTLAYTFLYSMCVSLGRICHTPHTHDDVFAF  TVMVSVPKKRRINGTLAYTFLYSMCVSLGRICHTPHTHDDVFAF  TVMVSVPKKRRINGTLAYTFLYSMCVSLGRICHTPHTHDDVFAF  TVMVSVPKKRRINGTLAYTFLYSMCVSLGRICHTPHTHDDVFAF  TVMVSVPKKRRINGTLAYTFLYSMCVSLGRICHTPHTHDDVFAF	5791	3	1636	GALGALLSPDGVHEPFDLSEQTYDFLGEMRKNAV
GN/GKQL/AMSQGFORLICYGRTGIGKSTUTSFINEDUTSSHEC NRSIQGFOFNILCYGSTGIGKSTUTSFININGEDJOINKESSYGPIUV IDAQFGFANIQGELKIK KRSLETYIBDIFNININGEDJOINKESSYGPIUV IDAQFGANIQGELKIK KRSLETYIBDIFNINGEDSTGIGLKI DLLTMKNLDSKYYII PVIAKADTVSKTELQKFKIKLMSELVSM VOIVOPPTDDDTIAKVRADMYGGLYBVVGKMVWK ROYPMGVUQVENENLCDFVKLREMLICTNMEDLREGTHTRINE YREKKLERMGFTDUGPENKPUSYGETUGAKFEHKREHOGERKMLEE MKOMFVORVKERAILKEAGERLOAAFEHKREHOGERMKLEE RRLLEEEIIAFSKKKATSBIFHSQSFLATGSBIKKDKDRNSO FVKQKVPEHRRSSSGAMFIKKKLEVETPFAVICFITSIGGEP LLIFMEKYFOVGGYISQSE  S792 2263 653 AAAAPSPAWGGUSVVYVVHTCWWYGIVYTRPCSGDASCIOP LARRPKLQL\AHSFTTTRSHLGAENNIDLVINVEDEDVSSKSE TVNSVSYKKTENNOTIVAYIFHHAQULPMIDGKOVHLVSPLT YMVPKPEBINLITGESDTQQIEADKKPTSALDEPVSHMPRRA. NVANDNYPDGSSLPADVHRYKMK UQLKTUPHVAPHLLFODLSY RVKDLMVINRSTTELPLTVSYDKVSLGELRRY HIMODAVYSLO FGSEKDADEVKGIFVDTNLYFLALKYKNYSMLINSFYNO YAFGFLFRILDGEVNYKLKSVAHLPWKAFTYKAFNFTDDVFAI ISSWKKKKSMIGMSTKAVLMRCFSTVVIFFLLDEQTSILVLVI AGGAAILWKVKKALMTIFWRGLWFKFTYNKFRFFTDDVFAI ISSWKKKSMIGMSTKAVLMRCFSTVVIFFLDEDGTSILVLVI AGGAAILWKVKALKMTIFWRGFTYKFRFFTDDVFAI ITMPTSBRLACFRDDVVFLVSLVGYRNLYFRFFTDDVFAI PKATAPHTD TANSVYKTRNINGTIVAYIFHHADGAVYNLKFGSYY EKATRAPHTD TANSVYKKTRNINGTIVAYIFHHADGAVYNLVSLDT YWYPKPEEINLLTGSEDTQOIRADKKFTSALDEPVSHWRPRLAI NWANDNFFDGSSLPADVHRYKKHUPHDGKOVNLVSLDT YWYPKPEEINLLTGSEDTQOIRADKKFTSALDEPVSHWRPRLAI NWANDNFFDGSSLPADVHRYKKHUPHDGKOVNLVSLDT YWYPKPEEINLLTGSEDTQOIRADKKFTSALDEPVSHWRPRLAI NWANDNFFDGSSLPADVHRYKKHUPHDGKOVNLVSLDT YWYPKPEEINLLTGSEDTQOIRADKKFTSALDEPVSHWRPRLAI NWANDNFFDGSSLPADVHRYKKHUPHDGKOVNLVSLDT YWYPKPEINLEGGEDTQOIRADKKFTSALDEPVSHWRPRLAI ISFWKKKKSMIGMSTKAVLWRCFSTVVIFIFLDEPOTSLEVLVVIF AGVGAAIELMKVKKALKHTIFWRGLMPECFOFTYSESERKTEEY DTQAMKYLSYLLVPLCYGGAVYSLLHKKKSWYSMLINSFYNOV YAFGFLEMDDVGLTVYNLYSLTGCGGAYCCHUPT AGVGBPGGFGGACYOPCHOVFLVVLVGRAVYSLURKFTSTTSEDSRKTEEY TTGTTGTGBPGGAGYTGOTGCGGGCCCCCCCCCCCCCCCCCCCCCCCCCCCCC		] -	1030	DRVAEFAGTSK/IGAGLIQPLHRAPARDHGLIRGGAAPALSVSH
NRSIQUSPETNILCVGSTGIGKSTLIDTLTNTFDFDYESSYDJIV INVEKRAQTYELQESNYOLKITIVTUGFGODINKESSYDJIVD IDAQFSAYLQEELKIKRSLETYHDSRIHVCLYFISPTGISLKIK DLIMMKIDSKYVII PVIAKADTVSKTELQKFIKLKNSLYSN VQIYQPFDDDTIAKVRAANNGQLPSAVVGSMBVKVGNKMVK RQYPMGVQVENEKLCDFYKLRSHLCTNMEDLERGTHTHIUS YERCKLEEMGFTDVGPENKPVSVQGTYBARHBEFHGERGRKEE MKOMFVQNKEKEASILKEASILGAKFBHLKRHGEERGKKEE MKOMFVQNKEKEASILKEASILGAKFBHLKRHGEERMKLEE RRLLEEEIIAFSKKKATSEIFHIGSTATGSNIKRKOKRNSO FVKQKVPEHRRSSQANFIKKKLEVCFDFAV.CFITSIFGEQD FVKQKVPEHRRSSSQANFIKKKLEVCFDFAV.CFITSIFGEQD FVKQKVPEHRRSSSQANFIKKKLEVCFDFAV.CFITSIFGEQD LIFMEKYFQVQGGYJYGSSE AAAABSPAWMGGVFVVVVVHTCHVWYGIVYFPCSGDASCTQFY VMPKPESINLICTGSSTOTQLEADKFRYALDEFVSHRRPLAA NVANDNFVPDGSSLPADVHRYMKMIQLGKTVHTLPILFIDQLSI RRYDLMVANTNSTTELPLTYSPKVSLGRLRFWHMQDAVYSLOF FGFSEKDADEVKGIFVDTHILFILAFTLAFKLN ISFWKKKSSMIGMSTKAVLMRCFSTVVIFFLLDEGTSLLVLVV AAGGAA ILMKVKKALKMTIFWGENFYSAADEPFOGTYSESERKTEE DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWSMLINSFVNG YAFGFLENLOLVAHSFTTTRSHLGARNNIDLVLAWDEPDVESKFRE ENKTRAPHTD  5793 2263 653 AAAAPSPAWMGGVFVVVVVHTCWVAYGIVTRPCSGDASCTQFY LARRPKLOLVAHSFTTTRSHLGARNNIDLVLAWDEPDVESKFTT TVNVSVPKKTRNNGTIJAYIFHHAGAVPHHOKCVPILVSPLTT YMVFPESIBLLAGFRDDVVFLVYLYGRULYPDHRKRVEDFDVESKFT TVNVSVPKKTRNNGTIJAYIFHHAGAVPHHOKCVPILVSPLTT YMVFPESIBLLAGFRDDVVFLVYLYGRULYPDHOKCVPILVSPLTT YMVFPESIBLLAGFRDDVVFLVYLYGRULYPDHOKCVPILVSPLTT YMVFPESIBLLAGFRDDVVFLVYLYGRULYPDHOKCVPILVSPLTT YMVSVPKKTRNNGTIJAYIFHHAGAVPHHOKCVPILVSPLTT YMVSVPKKTRNNGTIJAYIFHHAGAVPHHOKCVPILVSPLTT YMVSVPKKTRNNGTIJAYIFHHAGAVPHHOKCVPILVSPLTT YMVSVPKKTRNNGTIJAYIFHHAGAVPHHOKCVPILVSPLTT YMVSVPKKTRNNGTIJAYIFHHAGAPPPOHOKCVPILVSPLTT TVNTSVPKKTRNNGTIJAYIFHHAGAPPPOHOKCVPILVSPLTT TVNTSVPKKTRNNGTIJAYIFHHAGAPPPOHOKCVPILVSPLTT TVNTSVPKKTRNNGTIJAYIFHHAGAPPPOHOKCVPILVSPLTT TVNTSVPKKTRNNGTIJAYIFHHAGAPPPOHOKCVPILVSPLTT TVNTSVPKKTRNNGTIJAYIFHHAGAPPPOHOKCVPILVSPLTT TVNTSVPKKTRNNGTIJAYIFHHAGAPPPOHOKCVPILVSPLTT TVNTSVPKKTRNNGTIJAYIFTTDDVFAF BKATKAPHTD DTQMKYLSYLLVPLCVGGAVYSLLNIKYKWYSKILLNSEVNOV YAFGFLEMLPOLFVNYKLKSVAHLPREFOSTE BKATRAPHTD  5794 1 5016 MPPLISVPROLLUPAGALLLHEBSRAAAKGGCAGGGCKCDCHOV KOQKG	1 .	1	1	GN/GKQL/AMSSQGSDDEOIKRENIRSLTMSGHVGFESI, PDOTA
INVALKACTY ELGESNVOLKLI INTUTGEGODINKES YOP IN  IDAGFEATUGELIK KRSLETYINDSHIHULYETSETGISLKI  DLLTMKINLDSKYJI PYLAKADTVSKTELOKYKIKLASELUSM  VOJYOPTDDDITAKVANAMNGLIP PAVVGSMDEVKYKKKASELUSM  KOYPMGUVQVENEKICDFVKLAVBANTUGERAKHEPHGERGKKEE  RELEEELIAFSKKATSEI PHSGSFLATGSINKEKKORKING  KKOMFVGRVKEKEAILKEARRELOAKPEHLKRLHOCERKILEE  RELLEELIAFSKKATSEI PHSGSFLATGSINKEKKORKING  FVKOKVPEHRRSSGANFIKKLAUSETIAGKENKILKEARREL  RELLEELIAFSKKATSEI PHSGSFLATGSINKEKKORKING  FVKOKVPEHRRSSGANFIKKLAUSETIAGKENKILKEARREL  RELLEELIAFSKKATSEI PHSGSFLATGSINKEKKORKING  FVKOKVPEHRRSSGANFIKKLUSVETOKOKKING  FVKOKVPEHRRSSGANFIKKLUSVETOKOKKOKKING  FVKOKVPEHRRSSGANFIKKLUSVETOKOKKOKKING  FVKOKVPEHRRSSGANFIKKLUSVETOKOKKOKKING  FVKOKVPEHRRSSGANFIKKLUSVETOKOKKOKKING  FVKOKVPEHRRSSGANFIKKLUSVETOKOKKOKKOKKING  FVKOKVPEHRRSSGANFIKKLUSVETOKOKKOKKOKKOK  NAVANDAVSTAVATI  ARABSEPAWIGGVEVVYVVHTICVWYGLVYTRPCSGDASCTOP  ARABSEPAWIGGVEVTOKINGLIK TYKKINGLUSVETOK  FVSEKOLDEVKIT PLUTVUS VIKUSLGRIKFUT HIPOLDIS  RVKDLMVINRSTTELPLTVS VIKUSLGRIKFUT HIPOLDIS  RVKDLMVINRSTTELPLTVS VIKUSLGRIKFUT HIPOLDIS  FVSEKOLDEVKIT PUTVILLYELIA PROTESTISSESEKTEES  DTOAKKYLSVLLYPLCVGGAVYSLLNIKYKSMYSMLINSFYNG  VARGELPHI PQLFVNYKLKSVAHLUSVETOKSKOKTOK  TANNSVEYKTRINGTIAVI FILHERUSTVOK  FVSEKOLDEVKIT PVYKKINGLAVI PLIPLIPLOHDIGKOVHUS PLIT  YMVPKPESIBLLTGSSDTOOLEAKKPTSALDEPVSHRPPLAL  NOMANDYFOGSSLPADVIKT MAY FILHERUSTVAVI FILHEDUS  RVKDLMVINRSTTELPLTVS VIKUSLGRIKFUT HIPOLDIS  RVKDLMVINRSTTELPLTVS VIKUSLGRIKFUT HIPOLDIS  RVKDLMVINRSTTELPLTVS VIKUSLGRIKFUT HIPOLDIS  RVKDLMVINRSTTELPLTVS VIKUSLGRIKFUT HIPOLDIS  RVKDLMVINRSTTELPLTVS VIKUSLGRIKFUT HIPOLDIS  RVKDLMVINRSTTELPLTVS VIKUSLGRIK FILHEDUS  RVKDLMVINRSTTELPLTVS VIKUSLGRIK FILHEDUS  RVKDLMVINRSTTELPLTVS VIKUSLGRIK FILHEDUS  RVKDLMVINRSTTELPLTVS VIKUSLGRIK FILHEDUS  RVKDLMVINRSTTELPLTVS VIKUSLGRIK FILHEDUS  RVKDLMVINRSTTELPLTVS VIKUSLGRIK FILHEDUS  RVKDLMVINRSTTELPLTVS VIKUSLGRIK FILHEDUS  RVKDLMVINRSTTELPLTVS RVKDLMVINKSTTELPLT FILDUS  RVKDLMVINRSTTELPLT FILHEDUS  RVKDLMVINRSTTELPLT FILHEDUS  RVKDLMVINRSTTELPLT FILHEDUS  RVKDLMVINRSTTELPLT F	1			MKSIQQGFCFNILCVGETGIGKSTLIDTLFNTNFEDVESSHEOD
DADPSAYLOSELKI KISLIFTHNOSI HIVCLYFI SPTGISLKT DLITMKNIDSKYJI I PVI KAMDTYSKTELOKFKI KIMSELVSN VOJYOFPTDDTITAKVNAAMNOOL PRAVUSMDEVKUGKMUK ROYPMGVUQVENINCD PVKLEMIL CTNMEDLISEDTTRILING YRRCKLEEMINCD PVKLEMIL CTNMEDLISEDTTRILING YRRCKLEEMINCD PVKLEMIL CTNMEDLISEDTTRILING YRRCKLEEMINCD PVKLEMIL CTNMEDLISEDTTRILING YRRCKLEEMINCO PVENTY VARIAGEMIL CONTROL PROSPECTION YRRCKLEEMIL AFSKKATSEI PHOSS FLATGSNIRKDKORKNOS FVKOKVPEHRRSSSQAIN KKKLEVCEDFAY CFTTS I FGEOP LLIPMSKYPOVGGOVIS GSE  AAAAFSPAMWGGVFVVYVVHTCWWYGI VYTRECSGDASCTOP LARRYLOL, HIRST PTTRSHLEABNI DLVILNVEDEDVESKSEE TVAVSVPKKTRINGTLYAYI PLHAGALVHICKOVHLUSPLT YMVPKPEEINLITGSDTOOLFBAKKFTSALDEPVSHWR PRLA NVAADNFVEGS BLPADVHRWKHIOLGKYVHYLPILFI DLSI RVKDLWAVINSTTELPLTVSVDKVSLGRLEFWI HMODAVYSLO FGFSEKDADEVKG I FVDTNLYFLALTTFVAAPHLIEDTLAFKNI ISFWKKKSMIGMSTRAVLWRCESTVV I PLFLLDEQTSLLVLVI AGVGAA I LIMKVKKSMIGMSTRAVLWRCESTVV I PLFLDLEDCTSLLVLVI AGVGAA I LIMKVKKSMIGMSTRAVLWRCESTVV I PLFLDLEDCTSLLVLVI AGVGAA I LIMKVKKSMIGMSTRAVLWRCESTVV I PLFLDLEDCTSLLVLVI YAFGFLEMIL DLYNVILK SVAHLPRKAFTYKAFNTFI DDVFAF I TIMPTSIRLACFRODVVPLVYLVYRWLVYPUKRVENTEFGESYE EKATRAPHTO AAAAPSPAWGGVPVVVVVWTCAWMYGI VYTTRCCSGDASCTOPY TVAVSVPKKTRNNGTLYAYI FLHAGVLPWHIGKQVHLVSPLTT YWVPKPEEINLITGESDTOOLRADKRYTSALDEPVSHWRRLAL NWAADNFVFDGSS LAPADVHRY WMNI OLGKTVHYL PLFLDLEDG RKVLLMVINNSTTELPLTVS YDKVSLGRLEFWI HMODAVYSLOC FFGSEKDADEVKG I FVDTNLYFLATFYVAAFHLEDPLAFKNI I SFWKKKKSMIGMSTRAVLWRCESTVV I FLFLLDEDGTSLLVLVP AGVGAA I ELMKVKKAKAMTI FROMPFPOGTOT SESERKTEEY DTQAMKYLSYLLY PLCVGGAVYSLIN IKY KSWYSWLINSPUNCV YAFGFLEMLPOLFVNYKLKSVAHLPWKAFTYKAPNTFIDDVFAF I I TMPTSHRLACFRDDVVPLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD SO16 MPRILSWULLLEARALLLHEEHSRAAKGGCAGSGCKCDCHGV KOQKGERGLERLOGVIGFFOMOGPEGOPPOOKOTIGEBGLEGG GPLGPPGLEGFAGNPOPPCLI PGMKGDOPE LIGHVPGMLLKGERG FFGTGPFGFGFFGFFGFFGFFGFFGFFGFFGFFGFFGFFGFFGF	1		1	NVKLKAQTYELQESNVQLKLTIVNTVGFGDOINKEESVOOTVDV
DLITMINDSKYTITPVIAKADTVSKTELQKFKIKIMSELVSN VQTYQFTDDDTIAKNDAMNOLFAVUGMBUKVQKMYMKY RQYFMGVVQVENENHCDFVKLREMLICTNMEDLREGTHTRING YRKCKLEMENFTUOGPENKPUGDTEMKRHEFHGERQFKEE MKOMFVQRVKEKEAILKEAERELQAKFEHLKELHGEEMKLEE RRLLEEEIIAFSKKKATSEIFHGGSFLATSSNLRKDKDRKNSO FVKQKVPEHRRSSSGANFIKKLEVCEDFAVICTITSIFGEQD LLIFMEKYFQVGGQVISGSE  AAAAFSPAMWGCVPVVYVHTGWVMYGIVYTRFCSGDASCTQF LARRPKLQL\RHSFTTTSHGAENNIDLVINVEDEDVESKFE TVNVSVPKKTRNNGTLYAYIFHAGLPHDDCKQVHLVSPLT YMVPKDEEINLITGESDTQQIEABVKFTSALDEFVSHMFPRLA NVADADFVPDGSSLDADVHRYMKMIQLGKTVYLVEILEIDQLSI FOFSEEDADDEVKGIFVDTNLYFLALTFFVAAFHLLFDFLAFKNI 1SFWKKKSMSMIGMSTKAVLWRCFSTVVIFLLEDGTSLLVIV AGVGAAIELMKVKKALKMTIFWRGLMPEFOFGTYSESRRYEE DTQAMKYLSYLLYPLCVGGAVYSLIKYKSWSMLINSFYNGV VAFGFLFFILPQLFVNYKLKSVAHLPMKAFTYKAFNTFIDDVFAI IITMPTSHRLAGFRDDVVFLVVYVTTCWNWYGIVYTRPCSGDASCTOP EKATRAPHTD  AAAAFSPAWWGVFVVVVVTTCWNWYGIVTRPCSGDASCTOP LARRRKLOL\RHSFTTTRSHLGAENNIDLVLNVEDFDVESKFEE TVNVSVPKKTRNNGTLYAYIFLHHAGVLPWHDGKCVHLVSPLTI YWVPKPEINLLTGESTQQIEABKTTSALDEVSHWPRLAI NVMANDFVPDGSSLPADVHRYMKMIQLGKTVHYPLFILDLEGTSLLVLVP RVEDLWYNTNSTTELPLTVSYDRVSLGKHTSHIMODAVYSLQC FGFSEKDADEVKGIFVUTNLYFLALTFFVAAFHLLFDFLAFKNI 1SFWKKKKSMIGMSTKAVLWRCFSTVYIFLILDEGTSLLVLVP AVWARDFEINLLTGESTQQIEABKTTSALDEVSHWPRKAFT PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE PRITE				IDAQFEAYLQEELKIKRSLFTYHDSRIHVCLYFTSPTGHSLKTT.
VOLTOPTDDTTAKVNAAMNCQLPFAVVGSMOEVKGKKMVK RQYPMGVQVQUENERMLGPVKLREMLICTNMEDLERGTHTRIHEY YRRCKLERMFTDVGPENKPVSVQETVEAKRHEFHGERGRKEE MKQMFVQRVEXEERLIKERERLQAKPEHLKRLHQEERMKLEE RRLLEEEIIAFSKKKATSEIFHGSFLATGSBLRKCKDRKNSQ FVKCKVPEHRRSSSQANFIKKKLEVCEDFAVICFITSIGEOP LLIFMEKYPOVGGOYISGSE AAAAPSPAWWCGVFVVYVVHTCWVMYGIVYTRCSGGDASCIGP TVAVSVPKKTRNNGTLYAYIFLHRAGVLPWHDGKQVHLVSPLT TVAVSVPKKTRNNGTLYAYIFLHRAGVLPWHDGKQVHLVSPLT AVMPKDEEINLLTGESDTQQIEADKKPTSALDEFVSHWRPRLA NVMADNFVPDGSSLPADVHRYMKNIQLGKTVHYLPILFIDDLSR RVXDLMVINRSTTELPHITVSYDKVSLGRLRFWIHMGDAVYSLQ FGFSECDADEVKGIFVDTNIYTHIFTVAAPHLLPGFLAFWIH ISFWKKKKSMIGMSTKAYLWRCFSTVVIFFLDEGTSLVLIVI AGGGAJIELWKVKKALKWTIFWGAWPFGFGYSESERKTEE DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNG YAFGFFMLPQLFVNTYLKSVAHLPWKAFTYKAFWTFIDDVFAI IITMPTSKRLACFRDDVVFLVYLYQKWLYPVKKRVNFFGESYV EKATRAPHTD  5793 2263 653 AAAAPSPAWWCGVFVVVVVHTCWVMYGIVTRCSGDASCIOPP LARRPKLQL/RHSFTTTSSHLGAENNIDL/LAVEDFDVESKFE DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKWSWSFERSV EKATRAPHTD  AAAAPSPAWWCGVFVVVVVHTCWVMYGIVTRPCSGDASCIOPP LARRPKLQL/RHSFTTTSSHLGAENNIDL/LAVEDFDVESKFE TVMVSPKKTRNNGTLYAY IFLHAUCVPWHIGKQVHLVSPLTT YWVPKPEEINLLITGSSDTQQIEADKKPTSADLEPVSHWRPILAL NVMADNFVFDGSSLPADVHRYMMIQLGKCHVLVSPLTT VMVVPKPEEINLLTGSSDTQQIEADKKPTSADLEPVSHWRPILAL NVMADNFVFDGSSLPADVHRYMMIQLGKCHVIVPILFIDLSN TVMVSPKKKKKSMIGMSTKAVLJWGTSVUTSVIFLIFTDDLSN RVKLMVNNSTTELPLTVSYDVVSLGRLRFWHIMODAVYSLQC FGFSEKDADEVKGIFVDTNLYFLATFFVAAPHLLFPFLAFKND AGVGAAIELWKVKKSMIGMSTKAVLJWGTSVUTSVIFLDEGTSLLVLVIP AGVGAAIELWKVKKSMIGMSTKAVLJWGTSVUTSVIFLDDLGSTSLVLVLPF AGVGAAIELWKVKKSMIGMSTKAVLJWGTSPGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1 1			DLLTMKNLDSKVYIIPVIAKADTVSKTELOKFKIKIMSELVSNG
ROYPMGVVQVENENLGTVKLERGITGTNREDLREGTHTRING YRRCKLERMSTUDGENKUPVGDEVARRHERSGROKES MKOMFVGRVKEKEAILEREBRLQAKFEHLKRLHQERMKLEE RILLEERILAFSKKATSEIFHOSSTLATGSNIKRUKRKSO FVKQKVPERRSSSQANFIKKKLEVCFDRAV.CFITSIFGEQB FVKQKVPERRSSSQANFIKKKLEVCFDRAV.CFITSIFGEQB LLIPMEKYPQVGGOYISGSE  3AAAPSPAWGGVFVVVVHTCWVMYGIVYTRPCSGDASCIQP LARRPKLQL\RHSFTTTRSHLGABNIDLVINVEDFDVESKSE TVNVSVPKKTRINGTLYAYILHAGGVHUNDLVINVEDFDVESKSE TVNVSVPKKTRINGTLYAYILHAGVLPHUNDKQVHLVSPLIT YMVPKPEEINLLTGESDTQQIEADKKRTSALDEPVSHRRPRLA NVAADHFVPDGSSLPADVHRYMKQLGKTVHYLPILIFIDQLSI RVKDLMVINRSTTELPLTVSYDKVSLGRLRFFHIMQDAVYSLQ FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLFDFLAFKNI 1SFWKKKSMIGMSTKAVLWRCFTVVIFIFLLDEGTSLLVLVI AGGGAAIELWKVKKALKMTIFWRGLMPEFGGTYSESERKTEE DTQAMKYLSYLLYPLCVGGAVYSLMIKKYSMYSHLINSFYNGY YAFGFLFRH.PQLFVNYKLKSVAHLPWKAFTYKAFHTFDDVFAI IIINMFTSIRLACFRDDVVFLVYLVQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5793  2263 653 AAAAPSPAWGGVFVVVVVHTCWVNYGIVYTPCCSGDASCIQPY LARRRKLQL\RHSFTTTRSHLGAENNIDLVLNVEDFDVESKFE TVNVSVPKKTRNNGTLYAYIFLHAGVLPWHGKQVHLVSPLTI YWVPKPEINLLTESSTQQIEADKPTSALDEPVSHRPRLAI NVMANDFVPDGSSLPADVHRYMMMIQLGKTVHYLPLIPIDLSN RVKDLWVINNSTTELPLTVSTYBKGRIFFHHMQDAVYSLQC FGFSEKDADEVKGIFVUTUNLYFLAITFFVAAFHLLFDFLAFKNI ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLLIDEGTSLLVLVP AGVGAAIELWKVKAKMMTIFFRGLMPEFGGTYSESERKTEED DTQAMKYLSYLLYLCUGGAVYSLINIKYKSWYSMLINSFVNOV YAFGFLEMBLQLEVNYKKLSVAHLWKAFTYKANTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEPGESYE DTQAMKYLSYLLYPLCUGGAVYSLINIKYKSWYSMLINSFVNOV YAFGFLEMBLOGLEVNYKKLSVAHLWKAFTYKANTFIDDVFAF IITMPTSHRLACFRODDVFLVYLYQRWLYPVDKRRVNEPGESYE EKATRAPHTD  5794 1 5016 MGPRLSVWLLLLPAALLLHEEHSRAAKGGCAGSGCKCDCHGV KQKGBRGLEGLQGVIGFFGMGDFGPFGPGPFGFGFGFG GPLGPFGLPGFAGNDGPFGLPGMFGPGPFGPFGPFGFGFG GPLGPFGLPGFAGNDGPFGLPGMFGPFGPFGPFGFGFGFGFFGFFGFFGFFGFFGFFGFFFGFFFGFFFGFFFF			1	VQ1YQFPTDDDTIAKVNAAMNGQLPFAVVGSMDEVKVGNKMVKA
YRRCKLEEMG TTO JEBNIK PUT SAKTE ALTER HEIGHERGRIKEE  RKOMFVQRVEK RAILKEAR BELQAKPEILKK HIDEERRIKLEE  RRLIEEE I 1AFSKKKATSEI FHSQS LATGSNLRKDKDRKNSQ FVKGVVPERRESSQANFIKKKLEVCFDFAV: CFITSIFGED  LLIFMEKYPOVOGOYISGSE  JARAFSFAWCGUFVVYVVHTCRVWYGI VYTEFGGDASCTOP LARRPKIC, KRISTTTRSHLGAENNIDLVINVEDFDVESKPE TVANSVPKKTRNNGTI JAYI FLHHAGVLJWHDGKOVHLVS PLT YMVPKPEETNIL HEGSDTOG LEAKKPTSAL DEP VSHWRPRLA  RVKDLMVINRSTTEDPLTVS YDKVSLGKLRFWIHMODAVYSLO RVKDLMVINRSTTEDPLTVS YDKVSLGKLRFWIHMODAVYSLO RVKDLMVINRSTTEDPLTVS YDKVSLGKLRFWIHMODAVYSLO RVKDLMVINRSTTEDPLTVS YDKVSLGKLRFWIHMODAVYSLO RVKDLMVINRSTTEDPLTVS YDKVSLGKLRFWIHMODAVYSLO RVKDLKWKKKKSMIGMSTKAVLWRCFSTVV FLFLLDEOTSLLVLVY AGGAAI ELWKVKKALKWT FRRGLMPEFOGSTYSESRRYEE DTQAMKYLSYLLYPLCVGGAVYSLLNI KYKSWYSWLINSFVNG YARGFLFMLP, DD. FAVYKLKSVANLPWKRVVEFGESY EKATRAPHTD  5793  2263  653  ARAPSPAWWCGVFVVYVVHTCWUMYGIVYTRPCSGDASCTOP LARRPKLOL \RRSFTTTRSHLGAENNI DLVLNWZDFDVESK FER TVNVSYPKKTRNNGTLYAY I FHRIGVLPWHDGKOVHLVSPLTT TVNVSYPKKTRNNGTLYAY I FHRIGVLPWHDGKOVHLVSPLTT TVNVSYPKKTRNNGTLAYA I FHRIGVLPWHDGKOVHLVSPLTT TVNVSYPKKTRNNGTLAYA I FHRIGVLPWHDGKOVHLVSPLTT TVNVSYPKKTRNNGTLAYA I FHRIGVLPWHDGKOVHLVSPLTT TVNVSYPKKTRNNGTLAYA I FHRIGVLPWHDGKOVHLVSPLTT TVNVSYPKKTRNNGTLAYA I FHRIGVLPWHDGKOVHLVSPLTT TVNVSYPKKTRNNGTLAYA I FHRIGVLPWHDGKOVHLVSPLTT TVNVSYPKKTRNNGTLAYA I FHRIGVLPWHDGKOVHLVSPLTT TVNVSYPKKTRNNGTAYA I FHRIGVLPWHDGKOVHLVSPLTT TVNVSYPKKTRNNGTAYA I FHRIGVLPWHDGKOVHLVSPLTT TVNTSYPKKTRNNGTAYA I FHRIGVLPWHDGKOVHLVSPLTT TVNTSPKKKKSMIGMSTRALLWRCFSTVUT FLELLDEOTSLLLVLV AGVGAN I ELWKVKKALKMT I FWRGLMPEFOFTSLEDEOTSLLLVLV AGVGAN I ELWKVKKALKMT I FWRGLMPEFOFTSSERKTEEY DTQAMKYLSVLLVLLPAALLLHEEHSRAAKGGCAGSGCKCDCHGV KGOKGERGLPGLOPUT LVVYLVLKUKSUMDHLKGERG FERTAPHTD  5794  1 5016  MGPRISVMLLLPAALLLHEEHSRAAKGGCAGSGCKCDCHGV KGOKGERGLPGLPGCHGOFTSPEPOFPOFPOFPOFPOFPOFPOFPOFPOFPOFPOFPOFPOFP			1	RQYPWGVVQVENENHCDFVKLREMLICTNMEDLREOTHTPHVET.
### STATES OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF				YRRCKLEEMGFTDVGPENKPVSVOETYEAKRHEFHGERORKEER
FUNCKVPEHRRSSQAMPI KKKLEVCFDFAVICFITSIFGOP LLIIFMERYFQVGGQYISQSE AAAAPSBAWGGVEVVVVHTCWUWYGIVTRPCSGDASCIQP LARRPKLQL\RHSFTTTRSHLGAENNILDLVLINVEDFDVESKFE TUNVSVPKKTRNNSTLYAYIFLHAGVLPWIDGKQVHLVSFLT YMVPKPEINLITGESDTQQIFADKRTFJALDEVSHWRPKLA NVAADMFVPGGSLPADVHRYMKHJQGKTVHYLPILFIDQLSI RVKDLMVINSTTELPLITVSYDKVSLGRLRFWIHMQDAVYSLQ FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLFDFLAFKNI AGGGAAIELWKVKKALMTIFWRGLMPEFGGTYSESERKTEE DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNG VAPGFFFHLPQLFVNYKLKSVAHLPWKAFTYKAPNTFIDDVFAF ITMPTSHRLACFRODVVPLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTO LARRPKLQL\RHSFTTTRSHLGAENNIDLVLNVEDFDVESKFEE TVNVSVPKKTRRNGTLYAYIFHHAGVLPHDCKQHLVSPLTT YWWPKPEINLLTGESDTQQIEADKKFTSALDEPVSHWRPRLAI NWAADMFVPGSSLPADVHRYMKNIQLGKTVHYLPILFIDQLSN RVKDLWINRSTTELPLITVSYDKVSLGRLRFWIHMDADVYSLQQ FGFSEKDADEVKGIFVDTHLYFLAIFFVAAFHLLFDFLAFKND ISFWKKKSMIGMSTKAVLWRCFSTVJIFLFLDEGTSTLVLIVP AGVGAAIELWKVKALKMTIFWRGLMPEFGFGTYSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGG FFFSEKDADEVKGIFVDTHLYFLAIFFVAAFHLFDFLAFKND ISFWKKKSMIGMSTKAVLWRCFSTVJIFLFLDEGTSTLVLIVP AGVGAAIELWKVKALKMTIFWRGLMPEFGFGTYSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGC YAFGPLFMLPQLFVNYKKKVAHLEWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESVE EXATTAPHTIO  5794  1 5016 MGPRLSVWILLLIPAALLLHEEHSRAAKGGCAGSGCGKCDCHGV KOOKGERGLPGLQGVJGFPGMGDFGFELGHUPGMLKGERG GPLGPFGLAGRAGNGPPGLPGGPGPPGLPGREGGM GPLGPFGLAGRAGPPGLPGGPGPPGLPGREGGMG GLSFGGFKGDKGDQGVGGFFGPGPFGPGPPGBEGG GPLGPFGLAGRAGPPGLPGGFGPPGFPGPPGBFG GPLGPFGLAGRAGPPGPPGPPGPPGPPGBEGG GLSFGGFKGDKGDQGVSGPPGPPGDPGPPGPFGPPGBFG FFGGTLPGGFRGFKGFFGFPGFFGFFGFFGFFG FFGGTLPGGFRGFRGFFGFPGFFGFFGFFGFFG FFGGTBFGGFGKGFGFFGFFGFFGFFGFFGFFGFFGFFGFFGFFGF				MKQMFVQRVKEKEAILKEAERELOAKFEHLKRLHOEERMKLEEK
\$792 2263 653 AAAASSPAWWGGVEVUYUVHTCWWWYGIVYTRCSGDASCIQF LIFMERYFCVQGGYISQY LARRPKIQL, RISFITTRSHLGARUNIDLVILINGSDFUESKFE TVINVSVPKKTRINGTIJAYIFLHHAGULPWHDGKQVHLVSPLT YMYKPEEINLLTGESDTQQIEADKKFTSALDEFVSHWRPRLA NUMADNEVPEGSSLPADVTKMINIQGKTVHYLPILEIPLDQLSS RVDLMVINRSTTELPLTVSYDKVSLGRLRFWIHMQDAVYSLQ FGFSEKDADEVKGIFVDTNLYFLALTIFVAAFHHLFDFLAFKNI 1SFWKKKKSMIGMSTRAVLWRCTSTVVIFLFLLDEQTSLLVLVI AGGGAAIELWKVKKALWRTIFWRGLMPEFGFGTYSESERKTEB: DTQAMKYLSYLLYPLCVGGAVSLLNIK KYKSWYSWLLNSFVNG VARGFLFML.PQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAI 1ITMPTSHRLACFRDDVVFLVYLYQRWLYFVDKRRVEFGESYE EKATRAPHTD  5793 2263 653 AAAASSPAWGGVFVVYVVHTCWWYGIVYTRCSGDASCIQPY LARRPKLOL, RHSFTTTRSHLGABRNITLVLVVEDFDVESK FE TVWSVPKKTRNNGTLYAYIFLHAGVLPWHDGKQVHLVSPLTT YMVPKPEINLLTGESDTQQIEADKRTSALDEPVSHWRRLAL NUMADNFVFDGSSLPADVHRYMKMIQLGKTVHLPLLFIDQLSN RVKDLMVINRSTTELPLTVSYDKVSLGRLRFWIHMQDAVYSLQC FGFSEKDADEVKGIFVDTHLYFLALTFFVAAFHLLFDFLAFKND NAKANSTYLLYPLCVGGAVYSLUNIKYKKWSWILINFSVNGV VAFGFLFMLPQLFVWYKLKSVAHLPWKAFTYKAFNTFIDDVFAF 1ITMPTSHRLACFRDDVVFLVYLYQRMLYPVDKRRVNEFGESYE DTQAMKYLSYLLYPLCVGGAVYSLUNIKYKKWSWILINFSVNGV VAFGFLFMLPQLFVWYKLKSVAHLPWKAFTYKAFNTFIDDVFAF 1ITMPTSHRLACFRDDVVFLVYLYQRMLYPVDKRRVNEFGESYE EKATRAPHTD  5794 1 5016 MSPRLSVWLLLLPAALLLHEBHSRAAAKGGCASGGGKCDCHGV VAFGFLEFMLPQLFVWYKLKSVAHLPWKAFTYKAFNTFIDDVFAF 1TTMSTSHRLACFRDDVVFLVYLYQRMLYPVDKRRVNEFGESYE EKATRAPHTD  5794 1 5016 MSPRLSVWLLLLPAALLLHEBHSRAAAKGGCASGGGKCDCHGV VAFGFLEFMLPQLFGFGTGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGP	1		ł	RELLEGITAFSKKKATSEIFHSOSFLATGSNIRKDEDENSOR
5792  2263  653  AAAAPSPAWGGGYVIVYDTCWWMYGIUYTPCSGDASCIQP LARRPKLQL\RHSFTTTRSHLGAENNIDLVLINVEDFDVESKFE TVNVSVPKKTRNGTLYAYITLHHAGULPMIDGKQVHLVSPLT TVNVSVPKKTRNGTLYAYITLHHAGULPMIDGKQVHLVSPLT YMYPKPEEINLLTGESTDQIFADKRTTSALDEVSHMPRILAI NVADMFVPGGSLPADVHRYMKMIQLGKTVHYLPILFIDQLSI RVKDLMVINRSTTELPLITVSYDKVSLGRLRFWIHMQDAVYSLOF FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLFPELAFKN LISTWIKKKSMIGMSTKAVLWRCESTVVIFLFLLDEQTSLLVLVI AGGGAAIELWKVKKALMTIFWRGLMPEFOFGTYSESERKTEEN DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNG YAPGFLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAA LITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVMEFGESYE EKNTRAPHTD AAAAPSPAWGGVFVVVVVHTCWWMYGIVYTRPCSGDASCIQPY LARRPKLQL\RHSFTTTRSHLGAENNIDLVINVEDFDVESKFER TVNVSVPKKTRNNGTLYAYIFLHHAGVLPMHDGKQVHLVSPLTT YWWYRPEEINLLTGESDTQLEADKWFTSALDEPVSHWRPRLAI NVMADNFVPGGSLPADVHRYMKMIQLGKTVHYLPILFIDQLSN RVKDLMVINRSTTELPLTVSYDKVSLGRLFWHHMDAVYSLOF FGFSRKDADEVKGIFVDTHLYFLALTFFVAAFHLLEPFTAFKND LSFWKKKKSMIGMSTKAVLWRCFSTVVIFLFLLDEGTSLLVLWP AGGGAAIELWKVKALKWTLYFRGLMPFFQFTYSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWSWLINSFVNGV YAFGFLFRHDPQLFVNYKLKSVAHLEWKAFTYKAFNTFIDDVFFA- LITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5794  1 5016 MGPRLSVWLLLLPAALLLHEEHSRAAAKGGCAGSGCGKCDCHGV KGQKGERCLPGLQGYIGFFGMGPBFGPGPGPGCGGMCGGEGGFGC GPLGPFGLBPGLBCGFVFGTFGFFGFPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPP				FVKQKVPEHRRSSSQANFIKKKLEVCFDFAVTCFTTSTFGFODO
AAAAPSPAWWCGVFVVYVHTCWWYGIVYTRCSGDASCIQE LARRPKLQL\RHSFTTTRSHLGAENNIDLUJUNDEDFOVESKFE TUNVSVPKKTRNNGTLYAYIFHHAGVLPWHDGKQVGHLVSPLT YMVPKPEINILITGESDTQQIEADKRFTSALDEPVSHWRPKLA NUNADNPVFDGSSIPADVHRYMKMIQLGKTVHYLPILFIDQLSI RVKDLMVINRSTTELPLTVSYDKVSLGRLRFWIHMQDAVYSLQC FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLFFFLAPKNI ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLFLLDGGTSLLVLVI AGGGAAIELWKVKKALKWTIFWRGLMPEFQFGTYSESERKTEE DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNG YAAFGFLFMLPQLFVNYYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5793  2263  653  AAAAFSPAWCGVFVVVVVHTCWUMYGTVTTRCSGDASCIQPY LARRPKLQL\RHSFTTTRSHLGAENNIDLVLLWDEDDVESKFER TVNVSVPKKTRNNGTLAYIFLHHAGVLPWHDGKQVHLVSPLTT YMVPKPEEINLLTGESDTQQIEADKKPTSALDEPVSHWRPRLAL NWADNFVPEGSSLPADVHRYMKNQLGKTVHYLPLFLDGLSN RVKDLMVINRSTTELPLTVSVDKVSLGRLFFHIMDDAVYSLQC FGFSEKDADEVKGIFVUTNLYFLALTFFVAAFHLLFDFLAFKND ISFWKKKKSMIGMSTRAVLMRCFSTVVIFLFLIDECTSLLVLVP AGVGAAIELWKVKALKMTIFWRGLMPBFQGTYTSSERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSMLINSFVNGV YAAFGFLFMLPQLFVNYKLKSVAHLPWKAFTYKANTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLLQRMLYPVDKRRVNGFGESYE EKATRAPHTD  5794  1 S016  MOPRISVWLLLLPAALLLHEEHSRAAKGGCAGSGCGKCDCHGV KGQKGERGLPGJQGVGFFGMGFEGFGGPPGPFGPFGFGFGFGFGFGGGGGGGGGG				LLIFMEKYFQVQGQYISQSE
TUNNSVPKKTENNERI LYJ FLHHAGVLPHDEKGVOVLUSPLT TUNNSVPKKTENNERI LYJ FLHHAGVLPHDEKGVOVLUSPLT YMVPKPEEINLLTGESDTQQIEADKKPTSALDEPVSHWRRLAL NVMADNFVFDGSSLPADVHRYKMIQLGKTVHYLPLIFIDQLSI RVKDLMVINRSTTELPLTVSYDKVSLGRIFFUHMODAVYSLOV FGFSEKDADEVKGIFVUTNLYFLALTFFVAAFHLLFDFLAFKNI ISFWKKKKSMIGMSTKAVHWRCFSTVVIFLFLLDEOTSLLVLVI AGVGAAIELWKVKKALKOTTIFWRGLMPEPOFGTYSESERKTEEI DTQAMKYLSYLLYPLCVGGAVYSLINIKYKSWYSWLINSFVNG YAPGFLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAH IIINPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYK EKATRAPHTD  5793  2263  653  AAAAPSPAWWCGVFVVVVVHTCWVMYGIVYTRPCSGDASCIOPY LARRPKLOLNHSFTTTRSHLGAENNIDLVLNVEDFDVESKFER TVMVSVPKKTRNNGTLXAYIFLHHAGVLPWHHDGKQVHLVSPLTT YMVPKPEEINLLTGESDTQQIEADKKPTSALDEPVSHWRPRLAL NVMANDFVPDGSSLPADVHRYMKNIQLGKTVHYLPILFIDQLSN RVKDLMVINRSTTELPLTVSVDKVSLGRLRFWIHMQDAVYSLQC FGFSEKDADEVKGIFVUTNLYFLALTFFVAAFHLLFDFLAFKND ISFWKKKSMIGMSTKAVLWRCFSTVVIFLFLIDEGTSLLVLVP AGVGAAIELWKVKALKMTIFWRGLMPBFQFGTTYSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV YAFGPLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMFTSHRLACFRDDVVFLVYLVQRWLYPDVKRRVNEFGESYE EKATRAPHTD  5794  1 5016  MGPRLSVWLLLLPAALLLHEEHSRAAKGGCAGSGCGKCDCHGV KGQKGERGLPGLQGVTGFFGMQGPEGFQGPPGGPRGNGKGRG GPLGPFGLJPGFAGNPGPFGFGFGPFGPFGPFGPFGPFGPFGERGEKG GPLGPFGLJPGFAGNPGPGLJGGMKGDDGEILGHVPGMLKGERG FPGIPGTPGPPGLPGLQGVTGFFGMGGPEGFGPFGPFGPFGERGEKG GPLGPFGLJPGFAGNPGPFGLPGGNGREGFGPFGPFGPGPFG PGFRGFGFGFGFGFGFGFGFFGFFGFGFGFGFGFFGFFGFG GPLGPFGLPGFGFGFGFGFFGFFGFFGFGFGFGFGFGFGF	5792	2263	653	AAAAPSPAWWCGVFVVYVVHTCWVMYGIVYTRPCSGDASCIODY
TVNVSVPKKTRNGTLYAYIPHHAGVLPWHOGKQHLIVSPLT YMYPKPESINLITGESDTQQIEADKKPTSALDEPVSHWRPRLA NVMADNFVPDGSSLPADVHRYMKMIQLGKTVHYLPILFIDQLSI RVKDLMYINRSTTELPLTVSYDKVSLGRLRFWIHMQDAVYSLQN FGFSEKDADEVKGIFYDTNLYFLALHIFPVAAFHLLFDFLAFKN AGVGAAIELWKVKKALKMTIFPVAAFHLLFDFLAFKN AGVGAAIELWKVKKALKMTIFWRGLMPEFGGTYSESERKTEES DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV YARGFLFMLPQLFVMYKLKSVAHLPWKAFTYKAFNTFIDDVFAH IITMPTSHRLACFRDDVVFLVYLYQRRLYPVDKRRKVNEFGESYE EKATRAPHTD  5793  2263  653  AAAAFSPAWWGGVFVVVVVHTCWMYGIVYTRPCSGDASCIQPY LARRPKLQL\RHSFTTTRSHLGAENNIDLVLNVEDFDVESKFEE TVNVSVPKKTRNNGTLXAYIFLHHAGVLPWHBGKQVHLVSPLTT YMVPKPEEINLLTGESDTQOIFADKKFTSALDEPVSHWRRRLAI NVMADNFVDGSSLPADVHRYMKMIQLGKTVHYLPILFIDQLSN RVKDLMVINRSTTELPLTVSYDKVSLGRLRFWIHMQDAVYSLQQ FGFSEKDADEVKGIFVDTNITYFLALTFFVAAFHLLFPETLAFND ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLFLLDEQTSLLVLVVB PGFSEKDADEVKGIFVDTNITYFLALTFFVAAFHLLFDDVFAF ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLFLLDEQTSLLVLVVB AGVGAAIELWKVKKALKMTIFWRGLMPEFGFGTYSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLINIKYKSWYSWIINSFVNGV YAFGFLFMLPDQLFFVNKLSVAHLPWKAFTYKAPNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNDFGESYE EKATRAPHTD  5794  1  5016  MGPRISVWLLLLPAALLLHEEHSRAAAKGGCAGSGCGKCDCHGV KGQKGERGJPGLQGYIGFPGMQGPEGPGPPGPFGFGFGKGG GPLGPFGGLPGFGAGPGPGFGFGFGFGFGKGG GPLGPFGLPGFAGANGPPGFGFGFGFGFGFGFGFGFGFG FFGIFGTPGPFGVGEKGFDFGFGFGFGFGFGFGFGFGFGFGFG GPLGFFGGTFGGFGFGFGFGFGFGFGFGFGFGFGFGFGFGFG	1			LARRPKLQL\RHSFTTTRSHLGAENNIDLVLNVEDEDVEGVEED
YMVRPEINLLTGESDTQJEADKKPTSALDEPVSHWRPRLAN NVMADNFVPGGS LEPADVHRYMKMIQLGKTVHYLPILFIDQLSI RVKDLMVINRSTTELPLTVSYDKVSLGRLRFWIHMQDAVYSLQI RVKDLMVINRSTTELPLTVSYDKVSLGRLRFWIHMQDAVYSLQI FGFSEKDADEVKGIFVDTNIJYFLALTFFVAAFHLLFDFLAFKNI ISFWKKKKKMIGMSTKAVLWRCFSTVVIFLFLLDEQTSLLVLVI AGVGAAIELWKVKKALKMTIFWRGLMPEFQFGTYSESERKTEEN DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSMYSWLINSFVNGI YARGFLFMLPQLFVMYKLKSVAHLPWKAFTYKAFNTFIDDVFAH IITMPTSHRLACFRDDVVFLVYLYQRULYPVDKRRVNEGGSYN EKATRAPHTD  AAAABSPAWGGVFVVYVVHTCWWYGIVYTRPCSGDASCIQPY LARRPKLQL\RHSFTTTRSHLGAENNIDLVLNVEDFDVESKFER TVMVSVPKKTRNNGTLYAYIFLHHAGGUPWHDGKQVHLVSPLTT YMVPKPEE INLLTGESDTQQIEADKKPTSALDEPVSHWRPRLAL NVMADNFVFDGSSLPADVHRYMKMIQLGKTVHYLPILFTDQLSN RVKDLMVINRSTTELPLTVSYDKVSLGRLRFWIHMQDAVYSLQQ FGFGSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLFDFLAFKND ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLFLDEQTSLLVLVP AGVGAAIELWKVKKALKMTIFFNGLMPEFGFGTYSESRKTEEY DTQAMKYLSYLLYPLGGAVYSLLNIKYKSWYSWLINSFVNGV YAFGPLFMLPQLFVNYKLKSVAHLPKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5794  1 5016  MGPRLSVWLLLLPAALLLHEEHSRAAAKGGCAGSGCGKCDCHGV KGQKGERGIPGLQGVIGFPGMGPEGPPGPPGPRGTKGER GPLGFPGLPGFAGNPGPPGLPGLGGNGDFGTRGER GPLGFPGLPGFAGNPGPPGLPGLGAVVQEKGDFATKEEKGQKG GLSFQGPKGDKGDQGVSGPFGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPG	1 1			TVNVSVPKKTRNNGTLYAYIFLHHAGVI.PWHDGKOVHI.VGDI.TT
NOWADNIVPOGSSLPADVHRYKKMIQLGKTVHYLPILFIDQLSS RYKDIMVINRSTTELPITYSYDKYSLGRIRFWIHMQDAVYSLQG FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLEDFLAFKN ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLEILDEQTSLLVLVI AGVGAAFLELWKVKLKKIFIFWGELMPEFGFGTYSESERKTEES DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNG YAFGFLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFSAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5793  2263  653  AAAAFSPAWGGVFVVYVVHTCWWMYGIVTRPCSGDASCIQPY LARRPKLQL\RHSFTTTRSHLGAENNIDLULNVBDFDUSEKFER TVMVSVPKKTRNNGTLYAYIFLHAGVLPWHDGKQVHLVSPLTT YMVSVPKKTRNNGTLYAYIFLHAGVLPWHDGKQVHLVSPLTT YMVSVPKKTRNNGTLYAYIFLHAGVLPWHDGKQVHLVSPLTT YMVSVPKKTRNNGTLYAYIFLHTFVAAFHLLFDFLAFKND RVKDLMVINRSTTELPLTVSYDKVSLGRLRFWIHMQDAVYSLQC FGFSEKDADEVKGIFVDTMLYFLALTFFVAAFHLLFDFLAFKND ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLFLDEQTSLLVLVP AGVGAAIELWKVKKALKMTIFWRGLMPEFQFGTYSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV YAFGFLFMLPQLFVNYKLKSVAHLPWAFTYKAFNTFIDDVFAAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5794  1  5016  MGPRLSVWLLLLPAALLLHEEHSRAAKGGCAGSGCKCDCHGV KGQKGERGLPGLQGVIGFPGMQGPEGPPGPPGPPGBERGQM GGLSFPGEPGBAGSYPFONPGLLPGIDDGFPGPPSPERGRGCM GGLSFPGEPGBLDGLQGVVGFPGPPGPPGPPGBERGQM GLSFQGPKGDKGDCGVSGFPGVPGQAQVQEKGDFATTKGEKGQKG FPGIFCTPGPBGLPGLQGVGPGPFGPPGPPGPPGBERGQM GLSFQGPKGDKEGDGFPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPG	1 1			YMVPKPEEINLLTGESDTOOIFADKKPTSALDEBUSUMPDB: 31
RVXDLMVINRSTTELPITVSYDKVSLGRIRFWIHMQDAVYSLQ FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLFDFLAFKN ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLFLLDEQTSLLVLVI AGVGAAIELWKVKKALKMTIFWRGLMPEFOFGTYSESERKTEEP DTQAMKVLSYLLYCVGGAVYSLLNIKYKSYSWLINSFVNG YAFGFLFMLPQLFVNYKLKSVAHLEWKAFTYKAFNTFIDDVFAI IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  AAAAPSPAWWCGVFVVVVVHTCWWMYGIVYTRPCSGDASCIQPY LARRPKLQL\RHSFTTTRSHLGAENNIDLVLNVEDFDVESKFER TVNVSVPKKTRNNGTLYAYIFLHHAGVLPWHDGKQVHLVSPLTT YMVPKPEEINLLTGESDTQQIEADKKPTSALDEPVSHWRPRLAL NVMADMFVFDGSSLPADVHRYMKMIQLGKTVHYLPILFIDQLSN RVKDLMVINRSTTELPLTVSYDKVSLGRIRFWHHMQDAVYSLQQ FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLFDFLAFKND ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLFLLDEQTSLLVLVP AGVGAAIELWKVKKALKMTIFWRGLMPEFQFGTYSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWSWLINSFVNGV YAFGELFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5794  1 5016 MGPRLSVWLLLLPAALLLHEEHSRAAAKGGCAGSGCGKCDCHGV KGQKGERGLPGLQGYIGFPGMQGFPGPGPGPGCHGKGPGC GLSFQGPKGDKGDQGVSGPPGPPGPFGPFGPGPG GPLGPFGLPGAROPGPPGPPGPPGPFGPGPGRKGD GLSFQGPKGDKGDQGVSGPPGPPGPGPGPGRKGDG GLSFQGPKGDKGDQGVSGPPGPPGPGPGPGRKGQM GLSFQGPKGDKGDQGVSGPPGPPGPGPGPGPGRKGDG GLSFQGPKGCKEGPGRPGPGRKGKGGKGSGFFGPGPG YFGLIGRQGP\QGEKGEPGFPGPFGRFGRFGKFGKGCKGGFGFPGPFG PGPRGEPGPRGVCEKKEPGKFGRGKGKGGKGSGFGFGEKGD PGPRGEPGPKGFFGLPGQPGPPGPIVIGTGFLGEKGGRKGP PGPRGEPGRSFGFDLPGQPGPPGPGVTGLYGCOPGPP	1 1	i	·	NVMADNEVEDGSSLPADVHRYMKMIOLGKTVUVI DII BIDOLOV
FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLFDFLAFKNI ISFWKKKKSMIGSTKAVLWRCFSTVVIFLFLLDEQTSLLVLVI AGVGAAIELWKVKKALKMTIFWRGLMPEFOFGTYSESERKTEE: DTQAMKYLSYLLYPLCVGGAVYSLLNIKXKSWYSWLINSFVNGV YAFGFLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAI IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  AAAAPSPAWGGVFVVYVVHTCWWMYGIVYTRPCSGDASCIOPY LARRPKLOL\RHSFTTTRSHLGAENNIDLVLNVEDFDVESKFER TVNVSVPKKTRNNGTLYAYIFLHAGVLPWHDGKQVHLVSPLTT YMVPKPEEINLLTGESDTOQIEADKKPTSALDEPVSHWRPRLAI NVMADNFVFDGSSLPADVHRYMKMIQLGKTVHYLPILFIDDLSN RVKDLMVINRSTTELPLTVSYDKVSLGRLRFWIHMQDAVYSLQQ FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLFDFLAFKND ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLFLLDEQTSLLVLVP AGVGAAIELWKVKALKMTIFWRGLMPEFGFGTYSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV YAFGPLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5794  1 5016  MGPRLSVWLLLLPAALLLHEEHSRAAKGGCAGSGGCKCDCHGV KGQKGERGLPGLQGUJGFPGMGPBGPPGPFGPGRGTKGER GPLGPPGLPGAGNPGPPGLPGLGGTYGGTSKGER GPLGPPGLPGAGNPGPPGLPGLGGTYGGTBCGLNG GPLGPPGLPGAGNPGPPGLPGLGGTYGGTBCGLNG GPLGPPGLPGAGNPGPPGPPGPPGPPGPPGPPGPPGPPGREKQM GLSFQGPKGDKGDGGVGSPPPGPPGPPGPPGPPGPPGPFGREKQM GLSFGCPKGDKGDGWGSPPPGPPGPPGPPGPFGREKQM GLSFGCPKGDKGDGWGSPPPGPPGPPGPPGPFGREKGM GPGFPGFKGPDGPGPGPPGPPGPGREKGCMG GPGFPGFKGPGPGFGFGFGFGFGEFGEKGD FPGFGTSLPGDPGPGPPGPPGPFGFGKGGRGGFGGFKGFG FPGIFGTPGPFGPGPFGFGFGFGFGEFGKGD GPGFGFGFGFGFGFGFGFGFGFGFGFGFGFGFGFGFGFG	[			RVKDLMVINRSTTELPITVSYDKVSLGPLPEUTHMODAVYGLGG
ISWKKKKSNIGMSTKAVLWRCFSTVVIFLFLLDEQTSLLVLVI AGVGAAIELWKVKKALKMTIFWRGLMPEFQGGTYSESERKTEST DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNG YAPGFLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAH IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  AAAAPSPAWCGUFVVYVVHTCWWMYGIVYTRPCSGDASCIQFY LARRPKLQL\RHSFTTTRSHLGAENNIDLVLNVEDFDUESKFER TVMVSVPKKTRNNGTLVAYIFLHAGVLPWHDGKQVHLVSPLTT YMVSVPKKTRNNGTLVAYIFLHAGVLPWHDGKQVHLVSPLTT YMVPKPEEINLLTGESDTQQIEADKKPTSALDEPVSHWRPRLAL NVMADMFVFDGSSLPADVHRYMKMIQLGKTVHYLPILFIDQLSN RVKDLMVINNSTELPLTVSYDVSLGRLRFWIHMQDAVYSLQQ FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLFDFLAFKND ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLFLIDEQTSLLVLVP AGVGGAAIELWKVKKALKMTIFWRGLMPEFQFGTYSESERKTEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV YAFGFLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5794  1 5016 MGPRLSVWLLLLPAALLLHEEHSRAAKGGCAGSGCGKCDCHGV KGQKGERGLPGLVGGYFGPFGPPGPPGPPGPPGBPGBPGBPGRPGKGR GPLGPPGLPGLGGPVGPPGLPGLTGDQDPPPGPPGIPGREGKGM GPLGPPGLPGLGGPVGPPGLPGLTGPDPGPPGPPGPPGPPGBPGBPGRPGKGR GPLGPPGLPGLGGPVGPPGPPGPPGPPGPPGPPGPPGPPGPPGPFGPGPGPGP	1 1			FGFSEKDADEVKGI FVDTNI.VFI.AI.TERVAARUI I EDRI ARVAN
AGYGAAIELMKVKKALKMTIFARGLMPEFGFGTYSESERKTEEN DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGG YAFGFIFMLPQLFVMYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSIRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYR EKATRAPHTD  AAAAAPSPAWWCGVFVVYVVHTCWVMYGIVYTRPCSGDASCIQPY LARRPKLQL\RHSFTTTRSHLGAENNIDLVLNVEDFDVESKFFR TVMVSVPKKTRNNGTLYAYIFLHHAGVLPWHDGKQVHLVSPLTT YMWPKPEEINLLTGESDTQQIEADKKPTSALDEPVSHWRPRLAL NVMADNFVFDGSSLPADVHRYMKMIQLGKTVHYLPILFIDQLSN RVKDLMVINRSTTELPLTVSYDKVSLGRLRFWHMQDAVYSLQQ FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLFDFLAFKND 16FWKKKKSMIGMSTKAVLWRCFSTVVIFLFLDEQTSLLVLVP AGVGAAIELWKVKKALKMTIFWRGLMPEFGFGTYSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV YAFGPLFMLPQLFVNYKLKSVAHLPWKAFTSVAFNTFIDDVFAF IITMPTSHRLACPRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5794  1 5016 MGPRLSVWLLLPAALLLHEEHSRAAKGGCAGSGCGKCDCHGV KGQKGRRGLPGLQGVIGFFGMQGPEGPGPGPGDCDFGERGQM GGLSFQGPGLPGLAGVIGGPGFGPFGPFGPFGPGRGGPG TKGTRGPPGASGYPGNPGLPGIJGIGCOPGFFFGPFGPFGRGGRG GFLGFPGLPGFAGNPGPPGLPGFTGPPFGPPFGPFGPFGRGG GLSFQCPKGDKSDQGVSGPPGVFGDAQVQEKGDFATKGEKGQKG GLSFQCPKGDKSDQGVSGPPGVFGDAQVQEKGDFATKGEKGQKG EPGFQGMPGVCEKGEPGKPGRGKPGKDGDKGEKGSPGFTGPE YFGLIGRQGP\QGEKGEAGPPGPFGIVIGTGPLGEKGERGYPGT PGPRGEPGPKGFPGLPGGPGPGPGPFGPPGPPGPPGPPGPPGPPGPPGPPGPPGP	1 1	ĺ		ISFWKKKKSMIGMSTKAVI.WPCFSTWIJEI PLI DEOTGIJI
DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGY YAFGFLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAN 11ITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  AAAAPSPAWWCGVFVVYVVHTCWVMYGIVYTRPCSGDASCIQPY LARRPKLQL\RHSFTTTRSHLGAENNIDLVLNVEDFDVESKFFE TVMVSVPKKTRNNGTLYAY1FLHHAGVLPWHIGKQVHLVSPLTT YMVPKPEEINLLTGESDTQQIEADKKPTSALDEPVSHWRPRLAL NVMADNFVFDGSSLPADVHRYMKMIQLGKTVHYLPILFIDQLSN RVKDLMVINRSTTELPLTVSYDKVSLGRLRFWIHMQDAVYSLQQ FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLFPFLAFKND 15FWKKKKSMIGMSTKAVLWRCFSTVVIFLFLDEQTSLLVLVP AGVGAAIELWKVKKALKMTIFWRGLMPEFGPGTYSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV YAFGFLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF 11TMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5794  1 5016 MGPRLSVWLLLLPAALLLHEEHSRAAKGGCAGSGCGKCDCHGV KGQKGERGLPGLQGVIGFPGMQGPEGPQGPGDKGDTGEPGLPG KGQKGERGLPGLQGVIGFPGMQGPEGPGPGPFGPFGPGFG GPLGPPGLPGFAGNPGPPGLPGMKGDPGEILGHVPGMLLKGERG FPGIFTPGPPCLPGLQGPVGQPAGVQCKGDFATKGEKGQKG EPGFQMPGVCEKGEAGPPGPFGIVIGTGPLGEKGERGYPGT GLSFQCPKGDKGDQGVSGPPGVFGQAQQVQKKGDFATKGEKGQKG EPGFQMMGVGEKGEAGPPGPFGIVIGTGPLGEKGERGYPGT YPGLIGRQGP\QGEKGEAGPPGPFGIVIGTGPLGEKGERGYPGT PGPRGEPGPKGFPGLPGGPGPGPGPGPGPGPGRGKGMG FPGTSLPGGPGPGPGPGPGPGPGPGFGRGKGGKG FPGTSLPGPSGPGPGPGPGPGPGPGFGFGRGKGKG FGFFGTSLPGPSGFGDLPGPGPGSPGGPGGFGGEKGGN FGFFGTSLPGPSGFGDLPGPGPGSPGGPGGFGGEKGGN FGFFGTSLPGPSGFGDLPGPGSFGFFGGFGGEKGD				AGVGAAIELWKVKKALKMTIEWEGIMBEEGEGEVGBEBUKTVP
S793  2263  653  AAAAPSPAWWCGVFVVYVVHTCWVMYGIVYTRPCSGDASCIQPY LARRPKLQL\RHSFTTTRSHLGAENNIDLVLNVEDFDVESKFER TVMVSVPKKTRNNGTLYAYIFLHAGVLPWHDGKQVHLVVPLTI YMVPKPEEINLLTGESDTQQIBADKKPTSALDEPVSHWRPRLAL NVMADNFVPDGSSLPADVHRYMKMIQLGKTVHYLPILFIDQLSN RVKDLMVINRSTTELPLTVSYDKVSLGRLRFWIHMQDAVYSLQQ ISFWKKKKSMIGMSTKAVLWRCFSTVIFLFLDEQTSLLVLVP AGVGAAIELWKVKKALKMTIFFRGLMPEFQFGTYSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLNLNKYKSWYSWLINSFVNGV YAFGPLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5016  MGPRLSVWLLLLPAALLLHEEHSRAAKGGCAGSGCKCDCHGV KGQKGERGLPGLQGVIGFFGMQGPEGPQGPPGQNCGNGTKGER GPLGPPGLPGFAGNPGPFGLPGMKGDPGEILGHVPGMLKKGERG FFGIPGTPGPPGLPGLQGPVGPFGTTPGPPGPPGPPGERGKGQKG GLSFCCPKGDKGDQGVSGPPGVPGQAQVQEKGPPATKGEKQKG EPGFQGMPGVGEKGEPGKPGPRGKPGKDGKGKGSFGFPGEPG YPGLIGRQGP\QCEKGEAGPPGPPGLPGLAEKGERGYPGT PGPRGEPGPKGFPGLPGQPCPPGLPGLAEKGERGYPGT PGPRGEPGPKGFPGLPGQPCPPGLPGQAAPGFFPGERGEKGD RGFFCTSLPGPSGRDGLPGQPCPPGLPGQAAPGFPGERGEKGD RGFFCTSLPGPSGRDGLPGGPFGPPGPCPGTTNGIVECOPGPP	1 1	ſ		DTOAMKYLSYLLVDLCUGGALVGLINTVYVGDIGHT THE
ITTMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  AAAAPSPAWWCGVFVVYVVHTCWWYGIVYTRPCSGDASCIQPY LARRPKLQL\RHSFTTTRSHLGAENNIDLVLNVEDFDVESKFER TVMVSVPKKTRNNGTLYAYIFLHHAGVLPWHDGKQVHLVSPLTT YMVPKPEEINLLTGESDTQQIEADKKPTSALDEPVSHWRPRLAL NVMADNFVPGGSSLPADVHRYMKMIQLGKTVHYLPILFIDQLSN RVKDLMVINRSTTELPLTVSYDKVSLGRLRFWIHMQDAVYSLQQ FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLFDFLAFKND ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLFLLDEQTSLLVLVP AGVGAAIELWKVKKALKMTIFWRGLMPEFQFGTYSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV YAFGFLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5794  1 5016 MGPRLSWILLLPAALLLHEEHSRAAKGGCAGSGCGKCDCHGV KGQKGERGLPGLQGVIGFPGMQGPEGPQGPPGOKGDTGEPGLPG KGQKGERGLPGLQGVIGFPGMQGPEGPGPPGPPGPPGPFGFPGPFGFPGPFGPFGPFGPPGPPGP	1 1			YAFGFLEMI POLEVNIVKI KCVALI DIVA DEVVA DIVINITEDINA
5793  2263  653  AAAASPAWCGVFVVYVVHTCWVMYGIVYTRPCSGDASCIQPY LARRPKLQL\RHSFTTTRSHLGAENNIDLVLNVEDFDVESKFER TVNVSVPKKTRNNGTLXAYIFLHHAGVLPWHDGKQVHLVSPLTT YMVPKPEEINLLTGESDTQQIEADKKPTSALDEPVSHWRRRLAL NVMADNFVFDGSSLPADVHRYMKMIQLGKTVHYLPILFIDQLSN RVKDLMVINRSTTELPLTVSYDKVSLGRIRFWIHMQDAVYSLQQ FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLFDFLAFKND ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLFLDEQTSLLVLVV AGGGAAIELWKVKKALKMTIFWRGLMPEFQFGTYSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV YAFGPLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5794  1  5016  MGPRLSVWLLLLPAALLLHEEHSRAAKGGCAGSGCGKCDCHGV KGQKGERGLPGLQGYIGFPGMQGPFGPPGPPGPPGPPGPPGLPGL KGQKGERGLPGLQGYIGFPGMQGPFGPPGPPGPPGPPGPFGPPGPGPGPGPGPGPGPGPGP	1	•		I I TMPTSHPI A CEPODINEL OUT VORW VERNINGER
AAAAPSPAWWCGVFVVYVVHTCWUMYGIVYTRPCSGDASCIQPY LARRPKLQL\RHSFTTTRSHLGAENNIDLVLNVEDFDVESKFER TVMVSVPKKTRNNGTLYAYIFLHHAGVLPWHNGKQVHLVSPLTT YMVPKPEEINLLTGESDTQQIEADKKPTSALDEPVSHWRPRLAL NVMADNFVFDCSSLPADVHRYMKMIQLGKTVHYLPILFIDQLSN RVKDLMVINRSTTELPLTVSYDKVSLGRLRFWIHMQDAVYSLQQ FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLFDFLAFKND ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLFLIDEQTSLLVLVP AGVGAAIELWKVKALKMTIFWRGLMPEFQFGTYSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV YAFGFLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5794  1 5016  MGPRLSVWLLLLPAALLHEEHSRAAAKGGCAGSGCGKCDCHGV KGQKGERGLPGLQGVIGFPGMQGPEGPQGPGCMGDTGEPGLPG KGQKGERGLPGLQGVIGFPGMKGDPGEILGHVPGMLLKGERG GPLGPPGLPFGASGYPGNPGLPGIPGPGPPGPPGPPGPFGKQM GLSFQGPKGDKGDQSVSGPPGVPGQAQVQEKGDFATKGEKGQKG EPGFQCMPGVEKGEPGKPGPRGKPGKDGDKGEKGSPGFPGEPG YFGLIGRQGP\QBEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT PGPRGEPGFFGFPGPGPGPGPPGLPVPGQAGAPGFPGERGEKGD RGFPGTSLPGPFGFPGPPGPPGPPGPPGPPGPPGPPGPGPGPGREKGPRG RGFPGTSLPGPSGRDCLPGPPGSPGPPGPTNIGTVECOPGPP	1 1	]		EKATPADUTD
LARRPKIQU\RHSFTTTRSHLGAENNIDLVLNVEDFDVESKFER TVNVSVPKKTRNNGTLYAYIFLHHAGVLPWHDGKQVHLVSPLTT YMVPKPEEINLLTGESDTQQIEADKKPTSALDEPVSHWRPRLAL NVMADNFVFDGSSLPADVHRYMKMIQLGKTVHYLPILFIDQLSN RVKDLMVINRSTTELPLTVSYDKVSLGRLRFWIHMQDAVYSLQQ FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLFDFLAFKND ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLFLDEQTSLLVLVP AGVGAAIELWKVKKALKMTIFWRGLMPEFQFGTYSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV YAAFGPLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5016 MGPRLSVWLLLLPAALLLHEEHSRAAAKGGCAGSGCGKCDCHGV KGQKGERGLPGLQGYIGFPGMQGPEGPPGPPGPBGLPGG GGLGFPGLPGLPGLPGLPGLPGLPGDDVFPGPLPGMKGBRG FPGIPGTPGPPGLPGLPGLPGLPGLPGDPGPPGPPGPPGBKGQM GLSFQGPKGDKGDQGVSGPPGVPGQAQVQEKGDFATKGEKGQKG EPGFQGMFGVGEKGEPGKPGFRGKPGKDGDKGEKGSPFPGEPG PGFRGFPGPGPGPGPGPGPGPGPPGPPGPPGPPGPPGPPGPPGP	5793	2263	653	
TVNVSVPKKTRNNGTLYAY1FLHHAGVLPWHDGKQVHLVSPLTT YMVPKPEEINLLTGESDTQQIEADKKPTSALDEPVSHWRPRLAI NVMADNFVFDGSSLPADVHRYMKMIQLGKTVHYLPILFIDQLSN RVKDLMVINRSTTELPLTVSYDKVSLGRLRFWIHMQDAVYSLQQ FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLFDFLAFKND ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLFLLDEQTSLLVLVP AGVGAAIELWKVKKALKMTIFWRGLMPEFGFGTYSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV YAFGFLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5794  1 5016 MGPRLSVWLLLLPAALLHEEHSRAAAKGGCAGSGCGKCDCHGV KGQKGERGLPGLQGYIGFPGMQGPEGPQGPPGDCKGDTGEPGLPG KGQKGERGLPGLQGYIGFPGMQGPEGPQFPGPGPGPGPGFGFGFGFGFGFGFGFGFGFGFGFGFG		ŀ		LARRENTOL DESCRIPTION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE P
YMVPKPEINLLTGESDTQQIEADKKPTSALDEPVSHWRPRLAL NVMADNFVPDGSSLPADVHRYMKMIQLGKTVHYLPILFIDQLSN RVKDLMVINRSTTELPLTVSYDKVSLGRLRFWIHMQDAVYSLQQ FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLFDFLAFKND ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLFLLDEQTSLLVLVP AGVGAAIELWKVKKALKMTIFWRGLMPEFQFGTYSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV YAFGFLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5016 MGPRLSVWLLLLPAALLLHEEHSRAAAKGGCAGSGCGKCDCHGV KGQKGERGLPGLQGVIGFPGMQGPEGPGPPGQKGDTGEPGLPG KGQKGERGLPGLQGVIGFPGMQGPEGPGPPGLPGLPGGPGPGPGPGPGPGPGPGPGPGPGPG		1		TUNISTER AND AND THE TENED OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF TH
NVMADNFVFDGSSLPADVHRYMKMIQLGKTVHYLPILFIDQLSN RVKDLMVINRSTTELPLTVSYDKVSLGRLRFWIHMQDAVYSLQQ FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLFDFLAFKND ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLFLLDEQTSLLVLVP AGVGAAIELWKVKKALKMTIFWRGLMPEFQFGTYSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV YAFGFLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5794  1 5016 MGPRLSVWLLLLPAALLHEEHSRAAAKGGCAGSGCGKCDCHGV KGQKGERGLPGLQGVIGFPGMQGPEGPQGPPGQKGDTGEPGLPG KGQKGERGLPGLQGVIGFPGMQGPEGPQFPGPGPGPGPGPGPGPGPGPGPGPGPGPGPGPGPGPG		İ		VMIDVDEETHILL MCDCCDCCCTBCCTBCCCCCCCCCCCCCCCCCCCCCCCCC
FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLIFDFLAFKND ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLFLLDEQTSLLVLVP AGVGAAIELWKVKKALKMTIFWRGLMPEFQFGTYSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV YAFGPLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5794  1 5016 MGPRLSVWLLLLPAALLHEEHSRAAAKGGCAGSGCGKCDCHGV KGQKGERGLPGLQGVIGFPGMQGPEGPQGPPGQKGDTGEPGLPG KGQKGERGLPGLQGVIGFPGMQGPEGPGPPGPGPGPGPGPGPGPGPGPGPGPGPGPGPGPG	]	l		WIMADNETHINGGE PARTITION OF THE THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY O
FGFSEKDADEVKGI FVDTNLYFLALTFFVAAFHLLFDFLAFKND ISFWKKKKKSMIGMSTKAVLWRCFSTVVIFLFILDEQTSLLVLVP AGVGAAIELWKVKKALKMTIFWRGLMPEFQFGTYSESERKTEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV YAFGPLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5016 MGPRLSVWLLLLPAALLLHEEHSRAAAKGGCAGSGCGKCDCHGV KGQKGERGLPGLQGVIGFPGMQGPEGPGQPPGQKGDTGEPGLPG KGQKGERGLPGLQGVIGFPGMKGDPGEILGHVPGMLLKGERG GPLGPPGLPGFAGNPGPPGLPGNKGDPGEILGHVPGMLLKGERG FPGIPGTPGPPGLPGLQGVVGPPGFTGPPGPPGPPGPRGKGQM GLSFQGPKGDKGDQGVSGPPGVPGQAQVQEKGDFATKGEKGQKG EPGFQGMFGVGEKGEPGKPGPRGKPGKDGDKGEKGSPGFPGEPG YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT PGFRGEPGGPKGFFGLPGQPGPPGLPVPGQAGAPGFPGERGEKGD RGFPGTSLPGPPSGRDCLPGPPGSPGPPGQPGYTNGIVECOPGPP				BUYDI MULADOMBUR DI TURNING MEMIQLIGRITVHYLPILFIDQLSN
ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLFLLDEQTSLLVLVP AGVGAAIELWKVKKALKMTIFWRGLMPEFQFGTYSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV YAFGPLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5016  MGPRLSVWLLLLPAALLHEEHSRAAAKGGCAGSGCGKCDCHGV KGQKGERGLPGLQGVIGFPGMQGPEGPQFPGPGPGLPG KGQKGERGLPGLQGVIGFPGMQGPEGPGPPGPGPGLPGF TKGTRGPPGASGYPGNPGPPGLPGHPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPP	į į	1		EGEGERAL DELIVER THE PLIVEY DEVISION THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPE
AGVGAAIELWKVKKALKMTIFWRGLMPEFQFGTYSESERKTEEY DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV YAFGPLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5016 MGPRLSVWLLLLPAALLLHEEHSRAAAKGGCAGSGCGKCDCHGV KGQKGERGLPGLQGVIGFPGMQGPEGPQGPPGQKGDTGEPGLPG KGQKGERGLPGLQGVIGFPGMQGPEGPQDGPPGPGLPGCNGTKGER GPLGPPGLPGFAGNPGPPGLPGMKGDPGEILGHVPGMLLKGERG GPLGPPGLPGFPGPGPGPGPGPPGPPGPPGPPGPPGPPGEKGQM GLSFQGPKGDKGDQGVSGPPGVPGQAQVQEKGDFATKGEKGQKG EPGFQGMPGVGEKGEPGKPGPPGIVIGTGPLGEKGERGYPGT YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT PGPRGEPGPKGFFGLPGQPGPPGLPVPGQAGAPGFPGERGEKGD RGFPGTSLPGPPGGPFGCPGPPGPPGPPGVPGQAGAPGFPGERGEKGD RGFPGTSLPGPPGGPFGRDELPGPPGSPFGPPGQPGYTNGIVECOPGPP		1		TOTALKUADEVKGIFVDTNLYFLALTFFVAAFHLLFDFLAFKND
DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV YAFGPLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5794  1 5016  MGPRLSVWLLLLPAALLLHEEHSRAAAKGGCAGSGCGKCDCHGV KGQKGERGLPGLQGVIGFPGMQGPEGPGPPGQKGDTGEPGLPG KGQKGERGLPGLQGVIGFPGMQGPEGPGPPGQKGDTGEPGLPG TKGTRGPPGASGYPGNPGLPGIPGODGPPGPPGIPGCNGTKGER GPLGPPGLPGFAGNPGPPGLPGMKGDPGEILGHVPGMLLKGERG FPGIPGTPGPPGLPGLQGPVGPPGPPGPPGPPGPBGPGKGQM GLSFQGPKGDKGDQGVSGPPGVPGQAQVQEKGDFATKGEKGQKG EPGFQGMPGVGEKGEPGKPGPRGKPGKDGKGEKGSPGFPGEPG YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT PGPRGEPGPKGFFGLPGQPGPPGLPVPGQAGAPGFPGERGEKGD RGFPGTSLPGPPGGPFGGPFGGPFGGPFGFFGFFGFFGFRGFKGD RGFPGTSLPGPPGGPFGFFGGPFGGPFGGPFFGFFGFFGFFGFFGFFG				15FWKKKKSMIGMSTKAVLWRCFSTVVIFLFLLDEQTSLLVLVP
DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV YAFGPLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5794  1 5016  MGPRLSVWLLLLPAALLLHEEHSRAAAKGGCAGSGCGKCDCHGV KGQKGERGLPGLQGVIGFPGMQGPEGPGPPGQKGDTGEPGLPG KGQKGERGLPGLQGVIGFPGMQGPEGPGPPGQKGDTGEPGLPG TKGTRGPPGASGYPGNPGLPGIPGODGPPGPPGIPGCNGTKGER GPLGPPGLPGFAGNPGPPGLPGMKGDPGEILGHVPGMLLKGERG FPGIPGTPGPPGLPGLQGPVGPPGPPGPPGPPGPBGPGKGQM GLSFQGPKGDKGDQGVSGPPGVPGQAQVQEKGDFATKGEKGQKG EPGFQGMPGVGEKGEPGKPGPRGKPGKDGKGEKGSPGFPGEPG YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT PGPRGEPGPKGFFGLPGQPGPPGLPVPGQAGAPGFPGERGEKGD RGFPGTSLPGPPGGPFGGPFGGPFGGPFGFFGFFGFFGFRGFKGD RGFPGTSLPGPPGGPFGFFGGPFGGPFGGPFFGFFGFFGFFGFFGFFG		}		AGVGAAIELWKVKKALKMTIFWRGLMPEFQFGTYSESERKTEEY
YAFGFLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5794  1  5016  MGPRLSVWLLLLPAALLHEEHSRAAAKGGCAGSGCGKCDCHGV KGQKGERGLPGLQGVIGFPGMQGPEGPQGPPGQKGDTGEPGLPG KGQKGERGLPGLQGVIGFPGMQGPEGPGPPGLPGLPG KGQKGERGLPGLQGVIGFPGMKGDPGEILGHVPGMLLKGERG GPLGPPGLPGFAGNPGPPGLPGMKGDPGEILGHVPGMLLKGERG FPGIPGTPGPPGLPGLQGPVGPPGFTGPPGPPGPPGEKGQM GLSFQGPKGDKGDQGVSGPPGVPGQAQVQEKGDFATKGEKGQKG EPGFQGMPGVGEKGEPGKPGPRGKPGKDGDKGEKGSPGFPGEPG YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT PGPRGEPGPKGFPGLPGQPGPPGLPVPGQAGAPGFPGERGEKGD RGFPGTSLPGPPGGPGGPGGPFGGPGGPGPPGVFCOPGPP			ł	DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV
IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD  5794  1 5016  MGPRLSVWLLLLPAALLLHEEHSRAAAKGGCAGSGCGKCDCHGV KGQKGERGLPGLQGVIGFPGMQGPEGPQGPPGQKGDTGEPGLPG TKGTRGPPGASGYPGNPGLPGI PGCDGPPGPLPG GPLGPPGLPGFAGNPGPPGLPGMKGDPGEILGHVPGMLLKGERG GPLGPPGLPGFAGNPGPPGLPGMKGDPGEILGHVPGMLLKGERG FPGIPGTPGPPGLPGLQGPVGPPGPFGPPGPPGPBGEKGQM GLSFQGPKGDKGDQGVSGPPGVPGQAQVQEKGDFATKGEKGQKG EPGFQGMPGVGEKGEPGKPGPRGKPGKDGDKGEKGSPGFPGEPG YPGLIGRQGP\QGEKGEAGPPGPPGLVIGTGPLGEKGERGYPGT PGPRGEPGPKGFPGLPGPPGPPGLPVPGQAGAPGFPGERGEKGD RGFPGTSLPGPSGRDCLPGPPGSPGPPGQPGYTNGIVECOPGPP				YAFGPLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF
EKATRAPHTD  MGPRLSVWLLLLPAALLHEEHSRAAKGGCAGSGCGKCDCHGV  KGQKGERGLPGLQGVIGFPGMQGPEGPGCPGCQKGDTGEPGLPG  KGQKGERGLPGLQGVIGFPGMQGPEGPGPPGCHGTKGERG  TKGTRGPPGASGYPGNPGLPG1PGDGPFGPPG1PGCNGTKGERG  GPLGPPGLPGFAGNPGPPGLPGLQGNKGDPGE1LGHVPGMLLKGERG  FPGIPGTPGPPGLPGLQGPVGPPGFTGPPGPPGPPGPPGEKGQM  GLSFQGPKGDKGDQGVSGPPGVPGQAQVQEKGDFATKGEKGQKG  EPGFQGMPGVGEKGEPGKPGPRGKDGDKGEKGSPGFPGEPG  YPGLIGRQGP\QGEKGEAGPPGPPGPPGLVIGTGPLGEKGERGYPGT  PGPRGEPGPKGFPGLPGPPGPPGLPVPGQAGAPGFPGERGEKGD  RGFPGTSLPGPSGRDCLPGPPGSPGPPGQPGYTNGIVECOPGPP				IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE
MGPRLSVWLLLLPAALLLHEEHSRAAAKGGCAGSGCGKCDCHGV  KGQKGERGLPGLQGVIGFPGMQGPEGPQGPPGCKGDTGEPGLPG  TKGTRGPPGASGYPGNPGLPGIPGPGPPGPPGIPGCNGTKGERG  GPLGPPGLPGFAGNPGPPGLPGNKGDPGEILGHVPGMLLKGERG  FPGIPGTPGPPGLPGLQGPVGPPGFTGPPGPPGPPGPPGEKGQM  GLSFQGPKGDKGDQGVSGPPGVPGQAQVQEKGDFATKGEKGQKG  EPGFQGMPGVGEKGEPGKPGPRGKPGKDGDKGEKGSPGFPGEPG  YPGLIGRQGP\QGEKGEAGPPGPPGLVIGTGPLGEKGERGYPGT  PGPRGEPGPYGFPGLPGPGPPGLPVPGQAGAPGFPGERGEKGD  RGFPGTSLPGPSGRDCLPGPPGSPGPPGQPGYTNGIVECOPGPP	E 70.			EKATRAPHTD
KGQKGERGLPGLQGVIGFPGMQGPEGPQGPPGQKGDTGEPGLPG TKGTRGPPGASGYPGNPGLPGIPGCNGTKGER GPLGPPGLPGFAGNPGPPGLPGHCHPGMCDPGEILGHVPGMLLKGERG GPLGPPGLPGFAGNPGPPGLPGHPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPP	5/94	1	5016	MGPRLSVWLLLLPAALLLHEEHSRAAKGGCAGSGCGKCDCUCY
TKGTRGPPGASGYPGNPGLPG1PGQDGPPGPPG1PGCNGTKGER GPLGPPGLPGFAGNPGPPGLPGMKGDPGE1LGHVPGMLLKGERG FPGIPGTPGPPGLPGLQGPVGPPGFTGPPGPPGPPGPPGEKGQM GLSFQGPKGDKGDQGVSGPPGVPGQAQVQEKGDFATKGEKGQKG EPGFQGMPGVGEKGEPGKPGRPGKDGDKGEKGSPGFPGEPG YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT PGPRGEPGPKGFFGLPGQPGPPGLPVPGQAGAPGFPGERGEKGD RGFPGTSLPGPPGSPGDCPPPGQPGYTNGIVECOPGPP	ļ		ļ	KGQKGERGLPGLQGVIGFPGMOGPEGPOGPPGOKGDTGFPGT PG
GPLGPPGLPGFAGNPGPPGLPGMKGDPGEILGHVPGMLLKGERG FPGIPGTPGPPGLPGLQGPVGPPGFTGPPGPPGPPGPEKGQM GLSFQGPKGDKGDQGVSGPPGVPGQAQVQEKGDFATKGEKGQKG EPGFQGMPGVGEKGEPGKPGPRGKPGKDGDKGEKGSPGFPGEPG YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT PGPRGEPGPKGFPGLPGQPGPPGLPVPGQAGAPGFPGERGEKGD RGFPGTSLPGPPGSPGPPGQPGYTNGIVECOPGPP	ļ	<b>!</b>	ſ	TKGTRGPPGASGYPGNPGLPGIPGODGPPGPPGTPGCNCTVCER
FPGIPGTPGPPGLQGPVGPPGFTGPPGPPGPPGEKGQM GLSFQGPKGDKGDQGVSGPFGVPGQAQVQEKGDFATKGEKGQKG EPGFQGMPGVGEKGEPGKPGPKGKGDKGEKGSPGFPGEPG YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYFGT PGPRGEPGPKGFPGLPGQPGPPGLPVPGQAGAPGFPGERGEKGD RGFPGTSLPGPPGSPGPPGQPGYTNGIVECOPGPP	ĺ	1	İ	GPLGPPGLPGFAGNPGPPGT.DGMKGDPGFTTGHRUDGMTTWGGR
GLSFQGPKGDKGDQGVSGPPGVPGQAQVQEKGDFATKGEKGQKG EPGFQGMPGVGEKGEPGKPGPRGKPGKGDKGEKGSPGFPGEPG YPGLIGRQGP\QGEKGEAGPPGPPGLVIGTGPLGEKGERGYPGT PGPRGEPGPKGFPGLPGPPGPPGLPVPGQAGAPGFPGERGEKGD RGFPGTSLPGPPGSPGPPGQPGYTNGIVECOPGPP		1		FPGIPGTPGPPGLPGIOGPVGPPGFTGDDGDDGDDGDDGDDGD
EPGFQGMPGVGEKGEPGKPGKPGKDGDKGEKGSPGFPGEPG YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT PGPRGEPGPKGFPGLPGPPGPPGLPVPGQAGAPGFPGERGEKGD RGFPGTSLPGPPGSPGPPGQPGYTNGIVECOPGPP		j	ļ	GLSFOGPKGDKGDOGVSGDBGVDGONOVORVGDBARVGDV
YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT PGPRGEPGPKGFPGLPGQPGPPGLPVPGQAGAPGFPGERGEKGD RGFPGTSLPGPPGSPGPPGQPGYTNGIVECOPGPP		1	i	EPGFOGMPGVGFKGFBGKPGPBGKPGVGGVGGKGGFATKGEKGQKG
PGPRGEPGPKGFPGLPGQPGPPGLPVPGQAGAPGFPGERGEKGD RGFPGTSLPGPPGSPGPPGQPGYTNGIVECOPGPP	j			VPGLIGPOGEN OCERCENCENCENCENCENCENCENCENCENCENCENCENCENC
RGFPGTSLPGPSGRDGLPGPPGQPGYTNGIVECOPGPP	I	1		DGDDGEDGDVGEDGL DGGDGDGEVGENGYPGT
GDQGPPGIPGQPGFIGEIGEKGOKGESCLICDIDGVRGPPGPDG	j		1	PGEPGTEL POPGER PGLPG PGLPVPGQAGAPGFPGERGEKGD
GDUGPPGIPGQPGFIGEIGEKGOKGESCLICDIDGYPGPDGDGG	1		ļ	CDOCDDGIBGORGE CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL
DDOTTON	Ì	1		DDGFFGTPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGPQG
PPGEIGFPGQPGAKGDRGLPGRDGVAGVPGPQGTPGLIGQPGAK				PYGETGYPGQPGAKGDRGLPGRDGVAGVPGPQGTPGLIGQPGAK

	SEQ			
	ID	Predicted	Predicted en	
	NO:	beginning nucleotide	nucleotide	
	1 40.	location	location	TOTAL MILE ACTO, PEPRANULALANINA O OLI
	1		corresponding	J ( "-" " " " " " " " " " " " " " " " " "
	-1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	İ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	i	amino acid	residue of	S=Scrine, T=Threonine, V=Valine,
	}	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		amino acid	sequence	Codon, /=possible nucleotide deletion,
		sequence		\=possible nucleotide deletion,
	1			GERGREVEDIRI MCDECLIGE Insertion)
	1			GEPGEFYFDLRLKGDKGDPGFPGQPGMPGRAGSPGRDGHPGLPG
	)	i		Out Out VOINGERGEPGGVGPPGCDCCDDCDCCCCCCCCCCCCCCCCCCCCCCCC
	ı			DECEMBER OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF TH
	1	1	ļ	1 - of Soprior For For (PG) / DCRXCAVC (Oncrommon
	1	İ		DODI GDIGEFGI FGRPGFNGI PGNPGVOGOVCEDCVGT DOV
		1		1 - OLL OIF GIFGERGOIGV PGV PGFHCX TCDDCT OGTDGDDGD
	1			1 OUTOURGUERGARGIPEGGOGDDGT CONDOTTONI
	1	i		FPGLDMPGPKGDKGAQGLPGITGQSGLPGLPGQQGAPGIPGFPG
			1	SKGEMGVMGTPGQPGSPGPWGAPGLPGEKGD\HGFPGSSGPRGD
	1	1		PGLKGDKGDVGLPGKPGSMDKVYMGSMKGQKGDQGEKGQIGPIG
	1	İ	İ	EKGSRGDPGTPGVPGKDGQAGQPGQPGPKGDPGISGTPGAPGLP
		i	1	GPKGSVGGMGI.PGTPGPVGVPGTPGPAPGLP
			1	GPKGSVGGMGLPGTPGEKGVPGIPGPGSPGLPGDKGAKGEKGQ
	i	1	!	AGPPGIGIPGLRGEKGDQGIAGFPGSPGEKGEKGSIGIPGMPGS
	i			1 - DAROOF GS VG I FGS FGI PGFKGNKGI DGI DGI DGI WADA A
				1 TOPAGUNGEPGSDG   PGSAGEPGEPGT NARATRANAN
		1		SKODKOL VGE PGLAGSPGI PGSKGPAGEMCDDGDAGAGGT SASS
	1	J		T TO THE REPORT OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERT
	ı	1	j	VIEGAFGVFGFRGDPGF()CMDCTCCCDCTMACVADAMAN
				I WOLLDON TO THE THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE
	l	1		
	1	1		
		į l		I A ATTICK O VINE LITE CHIMNACHINACHINACHIM COMPANIANIANIA
				- \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \
i		1		I TO THE TENTAL CONCINCTION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF
		1		YYANAYSFWLATIERSEMFKKPTPSTLKAGELRTHVSRCQVCMR
	E 200	·		RT
	5795	1192	61	STRSPTVEYTSAHDUTLEMIT VOVO
- 1		i i		STRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHE PLAKIILESMOEPDEENAMI
ı		! 1		PLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVL
- [		1		VADFLEONYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHN
J		]		1 I
		· .		1 100 St T A D TODAY OF VETTER LASS FOR ED ADDES DE LA PRIME TIME -
ſ	5796	2	1078	
1	ſ		1078	GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF
1		ľ		1 - OU TOURDEGROUP IGGENTELCT VINIT COCCUMIT SOCIETIES
1	1	'		THE TOTAL OF TAKNAL RVAEVWMDDVVCUTTATATE OF THE
١	.	1		1 222 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
1	!			1 DIGINICALD V CHOOGPLENHTATT. VDCGCMCDCT ADVOVEDOR
1	Į.	1		1 CAMOTA TABLE TRULK UNSKSRI DOLL DODVINGGA WARRANGE 1
1		i		1
	1	1		EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG OHRDPG
1	5797			1 2
	3/3/	2	891	PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE
İ	- 1	l		VAQVENQLLKMKVESSQEANAEVMREMTKKLYSQYEEKLQEEQR
1	- 1			KHSAEKEALLEETNSEL VATERANISMENT KKLYSQYEEKLQEEQR
ľ	- 1	ì	1	KHSAEKEALLEETNSFLKAIEEANKKMQAAEISLEEKDQRIGEL
ı		1		DRLIERMEKERHOLQLQLLEHETEMSGELTDSDKERYQQLEEAS
L	ļ	ĺ		ASLRERIRHLNDMVHCQQKKVKQMVEEIESLKKKLQQKQLLILQ
L				
Γ	5798	644	115	OZ-OKIKEI WESKUITPITRULEL, TMKKATA
ı	j	· · · · · · · · · · · · · · · · · · ·	113	KILGSRWKSMSNQEKOPYYEEQARLSKIHLEKYPNYKYKPRPKR
	j	1	i	TOT VOGALUATION KOLMRSRROEMPORETUGOODO TRANSCOCIO
l	- 1	J	!	TI GALLINGLI LI PSPOMISDESSTEASDEDEL DULLOCOMUCATURE I
Г	5799	2679		POOR THE MAIN OF DEMENALUDAE DUDGE OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROP
		20/9	1435	DUST I THE INTERESTRATIOGATE ACCOUNT OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PR
	1	l		- LOUVING TO VINI VILLEMPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP
	- 1	Í		DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP
	1	1		PASAGAGNILLYDVEDGRAADDGLGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
	1		1	PASAGAGNILLVDVFDGPAAQPSLGPTPEEAFLSPGPEDIGPPIP
	]	j	1	EADELLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN
	1	[		**** VERSET VVIIEDI: O'ON POUNT ANTON ON
_			1	"TECHADE DIPPLUSVRERYGGADOALTE VE DVOTTVERDO
			<u>i</u> .	AAQDFFQRWKQLSLPQQEAQKIFKANHPMDAEVTKAKLLGFGSA
		4		

SEQ	Predicted	Predicted end	I having agid garant
ID	beginning	nucleotide	Amino acid segment containing signal peptide
	nucleotide		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:		location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucinc, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	saserine, reinfeonine, vevaline,
į.			W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
Ì	sequence	1	\=possible nucleotide insertion)
		1	LLDNVDPNPENFVGAGIIQTKALQVGCLLRLEPNAQAQMYRLTL
	i	1	RTSKEPVSRHLCELLAQOF
5800	2670		
5800	2679	1435	LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL
	1	ĺ	TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL
	!	į.	DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP
1		]	PASAGAGNLLVDVFDGPAAQPSLGPTPEEAFLSPGPEDIGPPIP
] .	i	}	PADELI NVENCIONICII CENICI CENICIE CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CON
}	ł	l	EADELLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN
ľ			KTSVQFQNFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQQVL
		ļ	NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM
i		{	AAQDFFQRWKQLSLPQQEAQKIFKANHPMDAEVTKAKLLGFGSA
		i	LLDNVDPNPENFVGAGIIQTKALQVGCLLRLEPNAQAQMYRLTL
l	{		PROKEDIODIN COLLA COM
5007			RTSKEPVSRHLCELLAQQF
5801	3	1413	FPRLYHLIPDGEITSIKINRVDPSESLSIRLVGGSETPLVHIII
1	1		QHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLLRQP
1	1		CQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEE
1			QLGIKLVRKVDEPGVFIFNVLDGGVAYRHGQLEENDRVLAINGH
1	1		DI BYCCEBEANUI TO A CERTIFICATION OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONTROL OF THE TOTAL CONT
1	1		DLRYGSPESAAHLIQASERRVHLVVSRQVRQRSPDIFQEAGWNS
)	1		NGSWSPGPGERSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVA
}			GGASHREWDLPIYVISVEPGGVISRDGRIKTGDILLNVDGVELT
ì	1		BVSRSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNH
ŀ	<b>!</b> .		NMAPPSDWSPSWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIVG
ł	1		CYEEVICHUDERTYGITTEGERRAINGRATAGSEGFCIVG
			GYEEYNGNKPFFIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSG
			MIHACLARLLKELKGRITLTIVSWPGTFL
5802	3	290	CFSLYQIMERIMDLPTLLRHAFREMFSVGGLFWMFRIRIILCLM
1	1		GAFFYLISPLDFVPEALFGILGFLDDFFVIFLLIYISIMYREV
1	1		ITORLTR
5803	2234	1299	EAQFGTTAEIYAYREEQDFGIBIVKVKAIGRQRFKVLELRTQSD
1			CTOOMIGHT PROTEST PORTEST AND THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PROTEST OF THE PR
	<b>†</b>		GIQQAKVQILPECVLPSTMSAVQLESLNKCQIFPSKPVSREDQC
i	ł .		SYKWWQKYQKRKFHCANLTSWPRWLYSLYDAETLMDRIKKQLRE
1	i 1		WDENLKDDSLPSNPIDFSYRVAACLPIDDVLRIQLLKIGSAIQR
	1		LRCELDIMNKCTSLCCKQCQETEITTKNEIFSLSLCGPMAAYVN
1	<u>}</u>		PHGYVHETLTVYKACNLNLIGRPSTEHSWFPGYAWTVAQCKICA
	i l		SHIGHWEEN TWYDVCDOWENG I TO CALL DESCRIPTION OF CALL
	ļ		SHIGWKFTATKKDMSPQKFWGLTRSALLPTIPDTEDEISPDKVI
			rcr .
5804	2	1707	EMEKQRQEEQRKRTEEERKRRIEQDMLEKRKIQRELAKRAEQIE
i			DINNTGTESASEEGDDSLLITVVPVKSYKTSGKMKKNFEDLEKE
1	, ,		REEKERIKYEEDKRIRYEEQRPSLKEAKCLSLVMDDEIESEAKK
1	l		FST.SDCKT.KI.TEERI EDODORNINANO DEBRANCE
			ESLSPGKLKLTFEELERQRQENRKKQAEEEARKRLEEEKRAFEE
I			ARROMVNEDEENODTAKIFKGYRPGKLKLSFEEMERORREDEKR
1			KAEEEARRRIEEEKKAFAEARRNMVVDDDSPEMYKTISQEFLTP
1			GKLEINFEELLKQKMEEEKRRTEEERKHKLEMEKQEFEQLRQEM
[			GEEEEENETFGLSREYEELIKLKRSGSIQAKNLKSKFEKIGOLS
!			EKEIQKKIEEERARRAIDLEIKEREAENFHEEDDVDVRPARKS
[	1		PADEGUZAMIA DEBOMA VADEGUSAENI HEEDDVDVRPARKS
1			EAPFTHKVNMKARFEQMAKAREEEEQRRIEEQKLLRMQPEQREI
1	. !		DAALQKKREEEEEEGSIMNGSTAEDEEQTRSGAPWFKKPLKNT
]			SVVDSEPVRFTVKVTGEPKPEITWWFEGEILQDGEDYQYIERGE
			TYCLYLPETFPEDGGEYMCKAVNNKGSAASTCILTIESKN
5805	3	776	YISDTLGQVYKSKIRWWIEENGGNGNISVDDLIALLDLAEHASS
			ABYROOOGRAPHITIMETERNOGINGNISVDULTALLDLAEHASS
1			AFKESQQQSEDREYEVKERLYPKSKRRYDTYNIAGYQGEIEVGL
į į	_		YTIQILQLIPFFDNKNELSKRYMVNFVSGSSDIPGDPNNBYKLA
]			LKNYIPYLTKLKFSLKKSFDFFDEYFVLLKPRNNIKQNEEAKTR
}	ļ		RKVAGYFKKYVDIFCLLEESQNNTGLGSKFSBPLQVERCRRNLV
	1		
5806		072	ALKADKFSGLLEYLIKSQEDAISTMKCIVNEYTFLLK
ا مرود ا	1257	877	AVFTFHNHGRTANLYSLHSWLGITTVFLFACQRFLGFAVFLLPW
	! <b>!</b>		ASMWLRSLLKPIHVFFGAAILSLSIASVISGINEKLFFSLKNTT
	<b> </b>		RPYHSLPSEAVFANSTGMLVVAFGLLVLYILLASSWKRP
5807	2267	1302	
1 1		1300	RFSKKTFRRPMAVDIQPACLGLYCGKTLLFKNGSTEIYGECGVC
1 1	f		PRGQRTNAQKYCQPCTESPELYDWLYLGFMAMLPLVLHWFFIEW
; 1	ļ		YSGKKSSSALFQHITALFECSMAAIITLLVSDPVGVLYIRSCRV
	1		LMLSDWYTMLYNPSPDYVTTVHCTHEAVYPLYTIVFIYYAFCLV

SEO	Predicted		
ID	beginning	Predicted end	
NO:	nucleotide	location	(A=Alanine, C=CVSteine, D=Aenartic Acid p
1.	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
J	corresponding	to first	
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
I	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
l	sequence	1	\=possible nucleotide insertion)
			LMMLLRPLLVKKIACGLGKSDRFKSIYAALYFFPILTVLQAVGG
	1		GLLYYAFPYIILVLSLVTLAVYMSASBIENCYDLLVRKKRLIVL
ĺ	1		FSHWLLHAYGIISISRVDKLEQDLPLLALVPTPALFYLFTAKFT
L			EPSRILSEGANGH
5808	2	433	SLPDSGVVEYLSNGGVADNHKDFGELRYNEC_MNFSCNGKNGSS
	1		EGRITHGFQLKSAYENNLMPYTNYTFDFKGVIDYIFYSKTHMNV
ı	1		LGVLGPLDPQWLVENNITGCPHPHIPSDHFSLLTQLELHPPLLP
<u> </u>		1	LVNGVHLPNRR
5809	464	2422	ILVPGFQGILHPGVYCALQSQHQAQELVADIDECEVSGLCRHGG
1	l	1	RCVNTHGSFECYCMDGYLPRNGPEPFHPTTDATSCTEIDCGTPP
			EVPDGYIIGNYTSSLGSOVRYACREGEFSVDFDTVSSCTCLCTV
ĺ	[		ESPKLHCQEINCGNPPEMRHAILVGNHSSRLGGVARYVCQEGFE
			SPGGKLTSVCTEKGTWRESTLTCTEILTKINDVSLENDTCVDWO
			INSRRINPKISYVISIKGORLDPMESVREETVNITTDSPTDEVC
ı	ļ		LALYPGTNYTVNISTAPPRRSMPAVIGFOTAEVDIJEDDGGENT
ŀ	i .		SIFNETCLKLNRRSRKVGSEHMYOFTVLGORWYLANFSHATSEN
}	1		FTTREQVPVVCLDLYPTTDYTVNVTLLRSPKRHSVOTTTATERA
			VKQTISNISGFNETCLRWRSIKTADMEEMYLFHTWGODWYOVER
	i i		AQENTENISSSSRDPEVCLDLRPGTNYNVSI.RAI.SSRI.DIZITET
· ·	Ì		1 TIQITEPPLPEVEFFTVHRGPLPRIRI RKAKEKNGDISEVOVI V
	1		LPLALQSTFSCDSEGASSFFSNASDADGYVAAELLAKDVPDDAM
			EIPIGDRLYYGEYYNAPLKRGSDYCIILRITSEWNKVRRHSCAV
5810	3	1641	WAQVKDSSLMLLQMAGVGLGSLAVVIILTFLSFSAV
1	i i		KVFGTHKDHEVSTLDTAISAVKVQLAEFLENLQEKSLRIEAFVS
[	<b>[</b>		BIESFFNTIEENCSKNEKRLEEQNEEMMKKVLAQYDEKAQSFEE VKKKKMEFLHEQMVHFLQSMDTAKDTLETIVREAEELDEAVFLT
1	i		SFEEINERLLSAMESTASLEKMPAAFSLFEHYDDSSARSDQMLK
			QVAVPQPPRLEPQEPNSATSTTIAVYWSMNKEDVIDSFQVYCME
i i	-		EPODDQEVNELVEEYRLTVKESYCIFEDLEPDRCYQVWVMAVNF
1 }	į		TGCSLPSERAIFRTAPSTPVIRAEDCTVCWNTATIRWRPTTPEA
j			TETYTLEYCRQHSPEGEGLRSFSGIKGLQLKVNLQPNDNYFFYV
	1		RAINAFGTSEQSEAALISTRGTRFLLIRETAHPALHTSSSSTUT
1 1	<b>:</b>		SFGERRRLTEIPSVLGEELPSCGOHYWETTVTDCPAVRLGTCSS
1 1			SAVQAGALGQGETSWYMHCSEPORYTFFYSCTVSDVLUTEDDAD
}			VG1LLDYNNQRLIFINAESEQLLFIIRHRFNEGVHPAFALEKDG
5811			KCTLHLGIKPPDSVRHK
] 3011	1918	851	AAALADPLPEDKWSAEKRRPLKSSLGYEITFSLLNPDPKSHDVY
i I	ļ		WDIEGAVRRYVQPFLNALGAAGNFSVDSOILVVAMIGUNDBEDG
1 1	ļ		ASSSYYLDMHSLPHVINPVESRLGSSAASIYPVINFII.VVDDIA
1 1	1		HSPLYIQDKDGAPVATNAFHSPRWGGTMVVNVDGVTVNAGVT DV
1			RVEVDMVRVMEVFLAQLRLLFGIAQPQLPPKCLLSGPTSEGLMT
1 1	į		WELDRIDWARSVENLATATTTLTSLAOLIGKISNIVIKDDVACE
j l		!	VYKAVAAVQKSAEELASGHLASAFVASQEAVTSSELAFFDPSLL
			HLLYFPDDQKFAIYIPLFLPMAVPILLSLVKIFLETRKSWRKPE KTD
5812	5204	2744	GGRQRCQRGRSCGAREBEVEPGTARPPPAASAMDASLEKIADPT
1	Į.		LAEMGKNLKEAVKMLEDSQRRTEEENGKKLISGDIPGPLQGSGO
]	j	,	DMVSILQLVQNLMHGDEDEEPQSPRIQNIGEQGHMALLGHSLGA
1	1	į	YISTLDKEKLRKLTTRILSDTTLWLCRIFRYENGCAYFHEERE
1 1	j		GLAKICRLAIHSRYEDFVVDGFNVLYNKKPVIYLSAAARPGLGQ
			YLCNQLGLPFPCLCRVPCNTVFGSQHQMDVAFLEKLIKDDIERG
			RLPLLLVANAGTAAVGHTDKIGRLKELCEOVGIWLHVEGUNIAT
			LALGYVSSSVLAAAKCDSMTMTPGPWLGLPAVPAVTLVKHDDDA
į l	İ		LTLVAGLTSNKPTDKLRALPLWLSLOYI.GI.DGFVERIKHACOLC
[ [	İ	[	QRLQESLKKVNYIKILVEDELSSPVVVFRFFOELPGSDDVFKAV
			PVPNMTPSGVGRERHSCDALNRWLGEOLKOLVPASGLTVMDLEA
		ł	EGTCLRFSPLMTAAVLGTRGEDVDOLVACIESKI,PVI,CCTLOLD
	-	ĺ	EEFKQEVEATAGLLYVDDPNWSGIGVVRYEHANDDKSSLKSVBO
1		l	GENIHAGLLKKLNELESDLTFKIGPEYKSMKSCLYVGMASDNVU
	ľ	[	AAELVETIAATAREIEDNSRLLENMTEVVRKGIOEAOVELOKAG
	L.,		EERLLEEGVLRQIPVVGSVLNWFSPVQALQKGRTFNLTAGSLES

Designing   nucleotide   location   corresponding   corresponding   corresponding   cofirst   amino acid   residue of   residue of   amino acid   residue of   amino acid   residue of   amino acid   amino acid   residue of   amino acid   amino acid   amino acid   residue of   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid	SEO	Predicted	Predicted end	
NO: nucleotide corresponding to first amino acid residue of amino acid residue of amino acid sequence corresponding to first amino acid residue of amino acid sequence corresponding to first amino acid sequence corresponding to first amino acid sequence corresponding to first amino acid sequence corresponding to first amino acid sequence corresponding to first amino acid sequence corresponding to the first amino acid sequence corresponding to the first amino acid sequence corresponding to the first amino acid sequence corresponding to the first amino acid sequence corresponding to the first amino acid sequence corresponding to the first amino acid sequence corresponding to the first amino acid sequence corresponding to the first amino acid sequence corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino acid corresponding to the first amino a	, -	ł	l .	Amino acid segment containing signal peptide
location corresponding to first amino acid residue of acid complete the complete of the complete of amino acid amino acid acid equence residue of amino acid acid equence residue of amino acid acid equence residue of amino acid acid equence residue of amino acid acid equence residue of amino acid acid equence residue of amino acid acid equence residue of amino acid acid equence residue of amino acid acid equence residue of amino acid acid equence residue of amino acid acid equence residue of amino acid acid equence residue of amino acid acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid equence residue of acid eque				(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
corresponding to first amino acid residue of amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequen	1.0.			Glutamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of amino acid anino acid sequence  ##TYPTOPHONE, Y-TYTOSINE, X-DURKNOW, *Stop Codon, *possible nucleotide deletion.  ##TYPTOPHONE, Y-TYTOSINE, X-DURKNOW, *Stop Codon, *possible nucleotide deletion.  ##TYPTOPHONE, Y-TYTOSINE, X-DURKNOW, *Stop Codon, *possible nucleotide disertion  ##TYPTOPHONE, Y-TYTOSINE, X-DURKNOW, *Stop TOPITAPHONE, Y-TYTOSINE, X-DURKNOW, *Stop TOPITAPHONE, Y-TYTOSINE, X-DURKNOW, *Stop TOPITAPHONE, Y-TYTOSINE, X-DURKNOW, *Stop TOPITAPHONE, Y-TYTOSINE, Y-TYTOSINE, X-DURKNOW, *Stop TOPITAPHONE, Y-TYTOSINE, Y-TYTOSINE, Y-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X-TYTOSINE, X		Ī.		H=H1Stldine, I=Isoleucine, K=Lysine,
amino acid residue of amino acid sequence  SSSEXINE. TETRIPECHULES. KEUNGINING. SEGUENCE  AMON ACID SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUENCE  SEGUEN	ĺ			L=Leucine, M=Methionine, N=Asparagine,
xemidue of amino acid asquence codon, /=possible most X=Unknown, *=Stop codon, /=possible most X=Unknown, *=Stop codon, /=possible most ide insertion (	ļ	ł	l .	P=Proline, Q=Glutamine, R=Arginine,
amino acid eequence  Codon, /-possible nucleotide towers to you prossible nucleotide towers to you prossible nucleotide towers to you prossible nucleotide towers to you provide the prossible nucleotide towers to you provide the provided towers to you provide the provided towers to you provide the provided towers to you provided the provided towers to you provided the provided towers to you provided the provided towers to you provided the provided the provided towers to you provided the provided the provided towers to you provided the provided the provided the provided towers to you provided the provided the provided the provided to you provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided the provided th	İ	6		S=Serine, T=Threonine, V=Valine,
sequence    Appose bill		•	1	w=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
TEPTYVYZOGORYVTIPTYSKISTROGIPFORSIARSODA  1 SEYSSYSHILDENVERLESGE DOLTLEASTEGHPGAPSYS  TOPERSONSULDENVERLESGE DOLTLEASTEGHPGAPSYS  TOPERSONSULDENVERLESGE DOLTLEASTEGHPGAPSYS  TOPERSONSULDENVERLESGE DOLTLEASTEGHPGAPSYS  REDEVESGE SERPITORS RYTERASY CONTAINANT COST CONTAINANT COST CONTAINANT COST CONTAINANT COST CONTAINANT COST CONTAINANT COST CONTAINANT COST CONTAINANT COST CONTAINANT COST CONTAINANT COST CONTAINANT COST CONTAINANT COST CONTAINANT COST CONTAINANT COST CONTAINANT COST CONTAINANT COST COST CONTAINANT COST COST COST COST COST COST COST COS			sequence	Codon, /=possible nucleotide deletion,
S813  2936  699  HEDOVSGSLERPITDRSRTGARAQORGHARATAGGSGAPGSRG LIRLLSFCVLLAGLCEGNSVERKIY PLINKTAPCVRLINATROI GCGSSLSGDTGVIHVZKEEDLQWVLTDGPRPPYWVLLESKHFT RDAMERLAGTSTRIGGLASLITKSPAGGSGYRAATAGGSGAPGGAG LIRLLSFCVLLAGLCEGNSVERKIY PLINKTAPCVRLINATROI GCGSSLSGDTGVIHVZKEEDLQWVLTDGPRPPYWVLLESKHFT RDAMERLAGTSTRIGGLASLITKSPAGGSFSPYCDDGGVY SRSTGPRFAHCTELQMNSLUNGLAVYEDVSFFIFLLEDENETSTAT KGCTOPHILGANGAPTFFILAMQLSHMANLSFSTATL\CMRRS SATCHER FRITVCDPLSDYWWANILKGINTTOTLKEDDRWYVTL ROATAGARTH COMMINISTATION FOR THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINISTATION REPORT OF THE COMMINIST	<del> </del>	Jequence		\=possible nucleotide insertion)
5813  2936  699  RREOVESSILERIPTIDESERTEANQORGEMATAGGGSADPGSRG LIRLISPCVLLAGLCCKISVERRIYI PINNTAPCURLINATEOI GCOSSISGOTOVIHVUERELDUMVILTOSPUVLLESKIHT REIMERLKGRTSRIAGLAVSITTPSPASGESPSUCCHOPGEVY SRSYGPEAHCREI (WANSLGHALAVSITTPSPASGESPSUCCHOPGEVY CCCOGHALSONGSAPTPICARQLESHMANLSFSTAT) CHRES SIGSTESINFRIVOPLEDTWANSHLERIHTREDDRVVVA ATRIDSRSFFRINV (APGAESAVASFVTOLAAABALOKAPDVTL PRAVMTVPFGCGTTSV TOSSRWY YDMEKGRYCHEVDSFVELI GCVALAFTSLEIMHTID PVS GKRISVRNOVEDLLATLERSGADV AVILARFAGGSDPPSSLORFFRANTISGVLGHVOSFAPHAVI GCVALAFTSLEIMHTID PVS GKRISVRNOVEDLLATLERSGADV AVILARFAGGSDPPSSLORFFRANTISGVLGHVOSFAPHAVI GSIYDTARRINVSYEBMLEPLKK / STIMPG* (OTTAKLAJAVATV LICAGRIGATY PREDIVAGAGESAVASFVTOLAAABALOKAPDVTL LICAGRIGATY PREDIVAGAGETTOVINGS STROPTIVAVLOVALANI GSIYDTARRINVSYEBMLEPLKK / STIMPG* (OTTAKLAJAVATV LICAGRIGATY PREDIVAGAGETTOVINGS STROPTIVAVLOVALANI GSIYDTARRINVSYEBMLEPLKK / STIMPG* (OTTAKLAJAVATV LICAGRIGATY PREDIVAGAGETAVATVAV SSPINTITVV VLOVALANI GTOTVAULUREDO, ODDE FOR VYTAV SSPINTITV VVLOVALANI LICAGRIGATY PREDIVAGAGETAVA (TAVESTANTARRIFIC LASKELELITLTVOFG ILL FELIVITY CITAKADUL FIRREGGA VSY  5814  8500  432  ALKCERRAVLALIVGEVOPDRAREEGAVAGVORVEDELBERSS GCRAQVYKTHNIVY IP PUGASSAPPOPULARDINOVENSA AAPI ILDSAIGGVAGTIFA \ TGOT\ASKELELITTULGOTYOM KPLI IRBOVARNYVADALTEEVYTTSEMALKATIKGERSRIVGE TRANGSSERATIT FEMILLESSERKESPENCESVENSHINLOTLA GSERAAQTGAAGVRIKKEGCHINRSLEFILGOVIKKLISEDHOVTO GOPHGHSONI * EVPLIBERELLIKAVYKETYMLKSEDHLOTIPO GSERAAQTGAAGVRIKKEGCHINRSLEFILGOVIKKLISENDOVIK KPLI KREDVARNYVADALTEEVYTTSEMALKATIKKERSHINLOFAST AXYMKNITYYNEVSTDEAALIKAYRKETMALKKOLESVENSHINLOTLA GSERAAQTGAAGVRIKKEGCHINRSLEFILGOVIKKLISENDOM KPLI RIBOVARNYVADALTEEVYTTSEMALKATIKKERSHILLOFAS AXYMKNITYYNEVSTDEAALIKAYRKETMALKKOLESVENSHINLOFATA AXYMKNITYYNEVSTDEAALIKAYRKETMALKKOLESVENSHINLOTLA GSERAATGAAGVRIKKEGCHINRSLEFILGOVIKKLISENDOM KRACHOLESVENSHINLOTLANGAR TARVATATATATATATATATATATATATATATATATATAT	J	j		TEPTYVYKAQGAGVTLPPTPSGSRTKQRLPGQKPFKRSLRGSDA
### HRDOVSSLERPITDISKTGAFAQORGMATAGGSGADDGSRG LIKLLSGYCLLAGLGCONSYERVITYIPANTAGCONLANTAGU GOSSISGDTOVHYVEKEELJGWILTDGRNPPYWULLSKRIFT RDLMELKGKTSKIAGLAVSLTFSPBAGSGFSTATL\CMFRE RDLMELKGKTSKIAGLAVSLTFSPBAGSGFSTATL\CMFRE SISGTFSINPKIVCDLEDVRWSLIKEINTTGTLKEDDRVVVA ATRIDERSFFRINVARGAGEAVASFVYLLAGLGKAPDVTIL PRIVMFVFQGETFDVIGSSRWYDMEKGKFPVQLERVDSFVEL GQVALETSELLWHTIDFVSGKBSVRNOVDMELAGAPDVTIL PRIVMFVFQGETFDVIGSSRWYDMEKGKFPVQLERVDSFVEL GQVALETSELLWHTIDFVSGKBSVRNOVDMELAGAPDVTIL PRIVMFVFQGETFDVIGSSRWYDMEKGKFPVQLERVDSFVEL GQVALETSELLWHTIDFVSGKBSVRNOVDMELAGAPDVTIL LGRALVELAGGTHSDTVQADGTVTRLLVG\FLIKANISFGS ILGGRDLSSVLG\FREIPANISTGVUADHSGAFHNYY GSITDTARNINVSYFEMLEFLK\FYNNFG\FRAILAGVATV\ LGRALVELAGGTHSDTVQADGTVTRLLVG\FLIKANISFGS ILGGRDLSSVLG\FREIPANISTESVVLADHSGAFHNYY GSITDTARNINVSYFEMLEFLK\FYNNFG\FRAILAGVATV\ LGRALVELAGGTHSDTVQADGTVTRLLVG\FLIKANISFGS ILGGRDLSSVLG\FREIPANISTESVICHSTRUL LGRALVELAGGODSSVFSENDL\STSWVGGELHSNETDRL RCVSTABLARALSPAFELSGWSSTESVTHTSKALLAGUFIGN RCVSTABLARALSPAFELSGWSSTESVTHTSKALLAGUFIGN RCVSTABLARALSPAFELSGWSTSSTSVTHTSKALLAGUFIGN RCVSTABLARALSPAFELSGWSTSSTSVTHTSKALLAGUFIGN RCVSTABLARALSPAFELSGWSTSSTSVTHTSKALLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLAGUFIGN RCVSTABLA	ı			LSETSSVSHIEDLEKVERLSSGPEQITLEASSTEGHPGAPSPQH
ILICALS CRIST WERE IT I PINATE CALL MATERIA  LIGHAGE CHARGE STATE AND	5873	2936	1	TDQTEAFQKGVPHPEDDHSQVEGPESLR
GCGSSISGOTCVIHVVEREELLGWULTDGRNPPYWULESKHFT RDLMERLKGRFSRIAGLAVSLITPSPAGGSFSTATY CMRES SISGIFERIAGIALVSLITPSPAGGSFSTATY CMRES SISGIFERIAGIALVSLITPSPAGGSFSTATY CMRES SIGSIFSINPKIVCDLEDWRWSHLKRINTTGTLKSDDRVVVA ATRIBGRSFFRWVARGAGSAVSFVULAGKGAPDVTLT PRAVMYVFQGEFFDVIGSSRWVDMEKGKFPVULERVDSFVEL GGVALETSELMHTIDPVSGMESVRNOVELLTEKSGAGVY AVILKRPROSOPLPSSLORFIRARNISGVULADHSCAFHNIYY GSITDTARNINSYFEMLELEKKFATNRFO-OTDRAKLADVATV LGRALIELAGGTHFSDTVOADGTVTELLVG\FLIKANNSWGS ILGGRLESVIG+RGFGHYLAVAVSSPTNITVLKSGMAVV GSITDTARNINSYFEMLELEKKFATNRFO-VUQVALANL LGRALIELAGGTHFSDTVOADGTVTELLVG\FLIKANNSWGS ILGGRLESVIG+RGFGHYLAVAVSSPTNITVLUGVALANL GTVVALITRSCQDDSKVPSENDLYSSWVGOPLHSNETDRLD RCVRSTARLARALSAFFLEGGVSSTSSYNTHEKRIPARIFT LAKELELITLTUGGGILIFSLIVTYCTINKADVLETIARPEGA VAYKRHNINVIYAVDSKSKMFDRVLHGNSTERSIL GSTAVVYKKTHNINVIYAVDSKSKMFDRVLHGNSTERSIL GSTAVVYKKTHNINVIYAVDSKSKMFDRVLHGNSTERSIL GSTAVTHKRHNIVIYAVDSKSKMFDRVLHGNSTERNIVGE TEMBER GRAVYVYKHRNIVIYAVDSKSKMFDRVLHGNSTERNIVGE TEMBER GRAVTYVADLTEVVYTSSMALKKITKGEKSRHYGE TEMBER GRAVTYVADLTEVVYTSSMALKKITKGEKSRHYGE TEMBER GRAVTYVADLTEVVYTSSMALKKITKGEKSRHYGE TEMBER GRAVTYVADLTEVVYTSSMALKKITKGEKSRHYGE TEMBER GRAVTYVADLTEVVYTSSMALKKITKGEKSRHYGE TEMBER GRAVTYVADLTEVVYTSSMALKKITKGEKSRHYGE TEMBER GRAVTYVADLTEVVYTSSMALKKITKGEKSRHYGE TEMBER GRAVTYVADLTEVVYTSSMALKKITKGEKSRHYGE TEMBER GRAVTYVADLTEVVYTSSMALKKITKGEKSRHYGE TEMBER GRAVTYVADLTEVVYTSSMALKKITKGEKSRHYGE TEMBER GRAVTYVADLTEVVYTSSMALKKITKGEKSRHYGE TEMBER GRAVTYVADLTEVVYTSSMALKKITKGEKSRHYGE TEMBER GRAVTYVADLTEVVYTSSMALKKITKGEKSRHYGE TEMBER GRAVTYVADLTEVVTSSMALKKITKGEKSRHYGE TEMBER GRAVTYVADLTEVVTSSMALKKITKGEKSRHYGE TEMBER GRAVTYVADLTEVTSSMALKKITKGEKSRHYGE TEMBER GRAVTYVADLTEVTSSMALKKITKGEKSRHYGE TEMBER GRAVTYVADLTEVTSSMALKKITKGEKSRHYGE TEMBER GRAVTYVADLTEVTSSMALKKITKGEKSRHYGE TEMBER GRAVTYNSTATUR GRAVTYNSTATUR GRAVTYNSTATUR GRAVTYNSTATUR SLEADYDNILLDVEGLERKENSTALDENSTATUR THTTATURSKELLIG KKROPTENSTATUR LBEIDESVCSESDVSSTLDTLSE IBBRANLINGERNYLLSKITKG GRAVENSTATUR AKKROPTURCECKLINGKNSTATUR GRAVTYNSTATUR AKKROPTURCECKLINGKNSTATUR GRAVTYNSTATUR LBEIDESVCSE	3013	2936	699	HRDGVSGSLERPLTDRSRTGAFAQQRGKMATAGGGSGADPGSRG
RDLMEKLKGRTSRIAGLAVSLITESPAGGESSVQCHNGGEVYV SINSYGEPAGCEIQMINISGNICAYEDGF FIFLIGHDENETKVI KQCYQOHNLSQNIGSATTFPLCAMQLFSHMAMLSFSTAT.YCMRGS SIGSTETSINFNIVUQDLSYNWSMLKPITGTGLKPDDRVVVA ATRILDGRSFFNIVLAGAGSAVASFYTQLAAAGALQKAPDVTTL PRINMFVYFQCGTTPUT-GSSKRVYDMEWALKPITGLKPDDRVVVA AVALRENDRSCPHINVLAGAGSAVASFYTQLAAAGALQKAPDVTTL PRINMFVYFQCGTTPUT-GSSKRVYDMEWALKPYQLENDSFYGEL GQVALRTSLELMHITDFVSQKNBSVRNQVQEDLLATLEKSGAQVY AVALRENDRSCPLFFLARRISGNAPOLEKSGAGVY AVALRENDRSCPLFFLARRISGNAPOLENDRSAFRINY GSTUDTAENINVSYBEWLEPLKE/ETWNFG-QDTAKALADVATV LGRALVELLAGGTNESTIVADPOTVTRLVA/LQYALAANL TGTVVALITEGCQDFSKVPSBKNDLYEVSYCHABSGAFNKYY AVALRENDRSCPLSKYLGFRGLFQCHYLTAV/SSPTNTTVY/LQYALAANL TGTVVALITEGCQDFSKVPSBKNDLYEVSYCHABSGAFNKYS ALKCRERRVLAILVGFVQPDEMAEEGAVAVCVRVRPLNSREESL GETAQVYMKTHNNU IYPVDGSKSFNDRVLIGMETPKRYTEA,T AARTIDSAIQCYNSTIFA/YGOT\AGSKYTMGSSDHLGVIPQ GOFIGGFSQKI-EVPLDREFFLLRVSYMEI YMBITTLCGTQMN KPLITEGDVNRNVYVADLTEVVTTSEMALKHTKGEKSRIYGE TKNNQRSSRSHTIFRMILESREKGSPSNCCGSVKVSHLINLDDLA GGSERAQYGAAQVRLEGGCNINNSJEIIGGVKLSDGQVGGFI NYRDSSLTRILQNSLGYBFTRILLCTTPVSPPDTLTALQPAST AKYMKNTFYVINEVSTDEALLKRYRKE HUDKKGLESVSLETRAQ AMEKOQLAQLLEKGLI-QKVQNSKI IFNLTRMLUTSSLTLQO-SIG- KARRRRVTVAVESVTDEALLKRYRKE HUDKKGLESVSLETRAQ AMEKOQLAQLLEKGLI-QKVQNSKI IFNLTRMLUTSSLTLQO-SIG- KARRRRVTUNEVSTDEALLKRYRKE HUDGFFELLERKK KOQBWQLTHEISNLKNLVKHREVYNDOLLENELSSKVELLREKGD CIKKLGEVI TOKQKLINITHGLSYSLSSI EGROKKOTLFDABTV ALDAKRESAFLASENLELKERMELLATTYKQMENDIOLYOSQLG- AKKRQVTUNELDJOLATEGNEMELKLKENMELLASTKYCOMKOTLFDABTV ALDAKRESAFLASENLELKERMELLATTYKQMENDIOLYOSQLG- AKKRQVTUNELLOSANDETTKLTSLITGSCHKOTLLATTO SNYKSTDQFFQNFKKLHMDFFCKYKMVLERNENMOGIVALLGRU- GEGRELHITTSCKKLLGSSTHOTKULLSTLKSGLKFGULLATTO SNYKSTDQFFQNFKKLHMDFFCKYKMVLERNENMOGIVALLGRU- ROSSPLOTVSREKTLLTTEKLQQTLEFUKTLMFMQLLKGGLS ROSSPLOTVSREKTLLTTEKLQQTLEFUKTLMFMCLLKGGLS ROSSPLOTVSREKTLLTTEKLQQTLEFUKTLMFMCLLKGGLS ROSSPLOTVSREKTLLTTEKLQQTLEFUKTLMFMCLLKGGLS ROSSPLOTVSREHLLGORLFFSLOGKNOCKTLDREGULLGELLERLG LKRLQKSFFTERDHLRGVI KR IRRATLCTKREKKJKAHTHLKEPIQE TDELRRSVSEKTAQLI TITTQLEKSKHYLDELKENGENGKTERLKICH AKHELSTERLERINGER	1		i .	LLRLLSFCVLLAGLCRGNSVERKIYIPLNKTAPCVRLLNATHQI
SNSYGPEFAHCREIQNISLGNICLAYEDFSFPIFLICHBEREMENTS KOCYOPHILSONGSAPTPICLANGLESHALLSSTATLOWERS SIGSTESINPKIUCDILSDYNUWBULKPINTTGTLKEDDRUVUK ATRILDERSFFINNUNGEGESANASPYOLLALILERSGAUD ATLIARPROSOPLEPSSLORFILRARNISGOVLADHSGAFHKYY GOYALRTSLELMHITDPYSKINESKONGOPOTRAKLADUATU LGRALJELAGGTNESDTUQADEQUYTRLLYG\FLIKAMISSPOX SIUDTABRINUSYEBULEPILKE/ETMISGOVLADHSGAFHKYY GSIUDTABRINUSYEBULEPILKE/ETMISGOVLADHSGAFHKYY GSIUDTABRINUSYEBULEPILKE/ETMISGOVLADHSGAFHKYY GSIUDTABRINUSYEBULEPILKE/ETMISGOVLADHSGAFHKYY GSIUDTABRINUSYEBULESJOWSTEYSYTYTYV/ULOYALANI. TGTVUKLITREOCODESKUPSENKOLTEXTYV/ULOYALANI. TGTVUKLITREOCODESKUPSENKOLTEXTYV/ULOYALANI. TGTVUKLITREOCODESKUPSENKOLTEXTYV/ULOYALANI. TGTVUKLITREOCODESKUPSENKOLTEXTYV/ULOYALANI. TGTVUKLITREOCODESKUPSENKOLTEXTYV/ULOYALANI. TGTVUKLITREOCODESKUPSENKOLTEXTYV/ULOYALANI. TGTVUKLITREOCODESKUPSENKOLTEXTYV/ULOYALANI. TGTVUKLITREOCODESKUPSENKOLTEXTYV/ULOYALANI. TGTVUKLITREOCODESKUPSENKOLTEXTYV/ULOYALANI. TGTVUKLITREOCODESKUPSENKOLTEXTYV/ULOYALANI. TGTVUKLITREOCODESKUPSENKOLTEXTYV/ULOYALANI. TGTVUKLITREOCODESKUPSENKOLTEXTYV/ULOYALANI. TGTVUKLITREOCODESKUPSENKOLTEXTYV/ULOYALANI. TGTVUKLITREOCODESKUPSENKOLTEXTYV/ULOYALANI. TGTVUKLITREOCODESKUPSENKOLTEXTYV/ULOYALANI. AREGUELAOLTICATEXTYV/ULOYALANI. AREGUELAOLTICATEXTYV/ULOYALANI. AREGUELAOLTICATEXTYV/ULOYALANI. TARGESTETTYRINI. TGTVUKLITREOCODESKUPSENTOLTICATICATICATICATICATICATICATICATICATICA			ŀ	GCQSSISGDTGVIHVVEKEEDLQWVLTDGPNPPYMVLLESKHFT
KOCYOPHNISONGSAPTFPLCAMOLFSHMANISFSTAT/CMRRS SIGSTESIPKIVLUDELSYNVMSMLKEJ NTOTOKRODRVVVA ATRLDERSFFNIVLYDELSYNVMSMLKEJ NTOTOKRODRVVVA ATRLDERSFFNIVLAPCASSAVASPYTOLAAASALOKAPDYTTI. PRIVMFVFFCOGTDTD'I SSSRWYDMSKYDVOLLATLEKSGAGUV AVILRRPROSOPLPFSALORFILARRISSYDOLLATLEKSGAGUV AVILRRPROSOPLPFSALORFILARRISSYDOLLATLEKSGAGUV AVILRRPROSOPLPFSALORFILARRISSYDOLLATLEKSGAGUV AVILRRPROSOPLPFSALORFILARRISSYDOLLATLEKSGAGUV AVILRRPROSOPLPFSALORFILARRISSYDOLLADUATV LIGGRLKSYLG*RGLFORLYLAV\SSPTNTIVV/UQYLLANL TGTVULITECOCOPSKYDSERNKLLEYSUGPLINSTENDL RCVRSTARLARALSPAFELSOMSSTEYSTWTESRWODRALIFERDEP RCVRSTARLARALSPAFELSOMSSTEYSTWTESRWODRALIFERDEP RCVRSTARLARALSPAFELSOMSSTEYSTWTESRWODRALIFE RCVRSTARLARALSPAFELSOMSSTEYSTWTESRWODRALIFE RCVRSTARLARALSPAFELSOMSSTEYSTWTESRWODRALIFE RCVRSTARLARALSPAFELSOMSSTEYSTWTESRWODRALIFE RCVRSTARLARALSPAFELSOMSSTEYSTWTESRWODRALIFE RCVRSTARLARALSPAFELSOMSSTEYSTWTESRWODRALIFE RCVRSTARLARALSPAFELSOMSSTEYSTWTESRWODRALIFE RCVRSTARLARALSPAFELSOMSSTEYSTWTESRWODRALIFE RCVRSTARLARALSPAFELSOMSSTEYSTWTESRWODRALIFE RCVRSTARLARALSPAFELSOMSSTEYSTWTESRWODRALIFE RCVRSTARLARALSPAFELSOMSSTEYSTWTESRWODRALIFE RCVRSTARLARALSPAFELSOMSSTEYSTWTESRWODRALIFERSEL RCVRSTARLARALSPAFELSOMSSTEYSTWTESRWODRALSPAFELS RCVRSTARLARALSPAFELSOMSSTEYSTWTESRWODRALSPAFELSOM RCVRSTARLARALSPAFELSOMSSTEYSTWTESRWODRALSPAFELSOM RCVRSTARLARALSPAFELSOMSSTEYSTWTESRWODRALSPAFELSOM RCVRSTARLARALSPAFELSOMSSTEYSTWTESRWODRALSPAFE RTMROSOMSSTEYSTWTESRWODRALSPAFELSOM RCCLAROLERSKULTONSCRESSTEYSTWTESRWTELLARALSPAFELSOM RCCLAROLERSKULTONSCRESSTEYSTRUCKERNOLLOFSSULTATO RAKKROLAROLERSKULTONSCRESSTVESTARLARALSPAFELSKYELLERSKYELLARALSRALDORSHISSEL RCARSTOTOMSSTATARLARALSPAFELSAMSSTARLARALSPAFELSKYELLERSKYELLARALSRALDORSHISSENGELSKARL RCCLRSTARLARALSPAFELSAMSTARLARALSRALDORSHISSENGELSKARL RCCLRSTARLARALSPAFELSAMSTARLARALSRALDRORSHISSENGELSKARL RCCLRSTARLARALSPAFELSAMSTARROLLARALSRALDRORSHISSENGEL RCCLRSTARLARALSPAFELSAMSTARROLLARALSRALDRORSHITALSRALDRORSHARLARALSRALDRORSHARLARALSRALDRORSHARLARALSRALDRORSHARLARALSRALDRORSHARLARALSRALDRORSHARLARALSRALDRORSHARLARALSRA	Į.		[	RDLMEKLKGRTSRIAGLAVSLTKPSPASGFSPSVQCPNDGFGVY
SIGSTESINPKIUCDELSDYNUMBERDINTIGTLERDDRYUVA ATRILDERSEPINUVA, ACREAGAVAS FYULA BALGKAR PUTTL PRIVMFUFFOGETTDY GSSRMVYDMEKGKPPVOLENUDSFVEL GQVALRISLELMHITDYSVEKUESVKNESVROUDELLATLEKSGAUP AVILRENOSOPLPFSSLORFLRARNISGVULADHSGAFHNIYY GSIYDTAGHINVSYBEWLEPJKLE/ETMBGODDTAKALADUATU LGRALVELAGGTNESDTVQADEQTVIRLLYG\FLIKAMISMFOGE ILQGRLERSYLG+RGLFQM\YLAV\SSPITYVYUVLQYALANL TGTVVMLITEGQODPSKVPSENKDLYSYBWOGPLISMSTORLE RCVBSTARLARLSPAPELSQWSTESYSTYTYVVULQYALANL TGTVVMLITEGQODPSKVPSENKDLYSYBWOGPLISMSTORLE RCVBSTARLARLSPAPELSQWSTESYSTERBWIDTRAIPL LASRELELITLTVGFGILIFSLIVTYCHNAKADVLFIAPREPGA VSY  ALKCRERRVLAILVGFVQDEMABEGGAVVCVRVPELBSRESSL VSY  ALKCRERRVLAILVGFVQDEMABEGGAVVCVRVPELBSRESSL GETAQVVMKYNNVIYPVDGSKSENPDRVLIGGETPKNVYBA\ AAPI IDSAIGQYNGTIFAA\YGOT\ASGKTYTMMGSSBILGVI PO GQFHGHFSGVT.* SVFLDREFLLAVSVMEI VEHTITDLLCGTORM KPLI IREDVNRNVYVADLTEEVVYTSEMALKRITKGERSPIYGL TKNNQRSSRSFRIT PRINLESERKGEPSKORVSHLINUVDLA GSBRAAOTGAAGVRLEGGCNINSISIFILGQVIKKLEDQVGGFT NYRDSKLITRILONSLGGFRETRILICTYTEVPSTITTLLQVSLF TNYRDSSLSFRIT PRINLESERKGEPSKORVSHLINUVDLA GSBRAAOTGAAGVRLEGGCNINSISIFILGQVIKKLEDQVGGFT NYRDSKLITRILONSLGGFRKTRI ICTITYDFSTITTLLQVSLF TNYRDSKLITRILONSLGGFRKTRI ICTITYDFSTITTLLQVSLF TNYRDSKLITRILONSLGGFRKTRI ICTITYDFSTITTLLQVSLF TNYRDSKLITRILONSLGGFRKTRI ICTITYDFSTITTLLQVSLF TNYRDSKLITRILONSLGGFRKTRI ICTITYDFSTITTLLQVSLF TNYRDSKLITRILONSLGGFRKTRI ICTITYDFSTITTLLQVSLF TNYRDSKLITRILONSLGFRKTRI ICTITYDFSTITTLLQVSLF TNYRDSKLITRILONSLGFRKTRI ICTITYDFSTITTLLQVSLF TNYRDSKLITRILONSLGFRKTRI ICTITYDFSTITTLLQVSLF TNYRDSKLITRILONSLGFRKTRI ICTITYDFSTITTLTUSISILL LREDIDSVCSSSOVFSTITTLUSTER ICTITYSSILLEFTING AKKMOVDLERSLOGSBOVFSTITLISHLANGERVONDLERS ILEGER TLONGRAF THE SILLAND TO THE TOTTYTTTTLLSKER ILEGER TLONGRAF THE SILLAND TO THE TOTTYTTTTLLSKER ILEGER TLONGRAF THE SILLAND TO THE TOTTYTTTTLLONGRAF ICTITYSSILLERG ICTITYDFT TADVRIDME I TEGERALLES THE TITLITRICHGET TROTTHTLKS TARROTHAND TO THE TOTTYTT THE TOTTYL THE TOTTYL THE TOTTYL THE TOTTYL THE TOTTYL THE TOTTYL THE TOTTYL THE TOTTYL TADVROME I TEGERAL TOTTYL TOTTYL TOTTYL THE TREBLILINING P	1		1	SNSYGPEFAHCREIQWNSLGNGLAYEDFSFPIFLLEDENETKVI
ATRIDSRSFFNINV\AFGAESAVASFVTQLAAABALQKAPDVTTL PRINTPUPCQGTFDY_GSSRMYVQMESVRNOVEDLIATLEKSGAGUV AVULRRRNOSQFLPPSSLQFFLRARILQ*\LIKANSHQG GQVALRTSLELMMHTDPVSQKWESVRNOVEDLIATLEKSGAGUV AVULRRRNOSQFLPPSSLQFFLRARILQ*\LIKANSHQG LGGRALVELGGTNFSDTVQADPQTTPRLLQ*\LIKANSHQG LIGGRALKSYLG*\RGLEPGH\YTAV\SSPTNTIVV\/LQYALANL TGTVVNLTHEQCQDDSRVPSENDLYSQ*\LIKA\SPTTIVV\/LQYALANL TGTVVNLTHEQCQDDSRVPSENDLYSQ*\LIKANDVLFTAPREFGA RCVRSTARLARALSPAPELSQMSSTEYSTWTESRMKDIRARIFF RCVRSTARLARALSPAPELSQMSSTEYSTWTESRMKDIRARIFF RCVRSTARLARALSPAPELSQMSSTEYSTWTESRMKDIRARIFF RCVRSTARLARALSPAPELSQMSSTEYSTWTESRMKDIRARIFF RCVRSTARLARALSPAPELSQMSSTEYSTWTESRMKDIRARIFF RCVRSTARLARALSPAPELSQMSSTEYSTWTESRMKDIRARIFF RCVRSTARLARALSPAPELSQMSSTEYSTWTESRMKDIRARIFF RCVRSTARLARALSPAPELSQMSSTEYSTWTESRMKDIRARIFF RCVRSTARLARALSPAPELSQMSSTEYSTWTESRMKDIRARIFF RCVRSTARLARALSPAPELSQMSSTEYSTWTESRMKDIRARIFF RCVRSTARLARALSPAPELSQMSSTEYSTWTESRMALKTRARIFF RCVRSTARLARALSPAPELSQMSSTEYSTWTESRMALKTRARIFF RCVRSTARALSPAPELSQMSSTEYSTWTESRMALKTRARIFF RCVRSTARTY VSY  ALKCEPRRVLALLGFVQFQDTRABEEGAVAVCVEVERLARSPETAL ARTHOUT STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUST AND THE STATUS AND THE STATUS AND THE STATUS AN	1	1	1	KQCYQDHNLSQNGSAPTFPLCAMQLFSHMAWLSFSTAT\CMRRS
PRINTEYPROGETERY: GSSRAVYDMERGKFPVOLENDESKGAUP AVILRRENOSOPLEPSSLORFIRARNISGVULGENDESKGAUP AVILRRENOSOPLEPSSLORFIRARNISGVULGENDESKGAUP AVILRRENOSOPLEPSSLORFIRARNISGVULGENDESKGAUP OSITOTABRINDSYBEWLEPLKE/ FURMFG4-ODTAKALADVATV LGRALVELAGGTNEDTVOADPOTTRILYG-\PILKANNSYPOGE ILGGEDLARSYLG-RGLORHYTAVA\SSPTITIVY/ULGYALANI TGTVVNLTREOCODESKYPERNDLYESWOOPLISMETDRID RCVRSTRARLARALSEPS-BLIQONSTYTESWTOEPLISMETDRID RCVRSTRARLARALSEPS-BLIQONSTYTESRWADVIFIAPREPGA VSY  SALKCEPRRVLAILVOFVOPDRWAEEGAVAVVCVRVRPLNSREESL GETAQVYNKTHAVITYVDGSKSRNFDRVLHGNETPKNVYFAA\I AAPIIDSAIQGYNGTIBA YOGT-\ASCHTYMMGSEDDLCU'PO GOPRGIFSQKI-EVFLDREFLIRVSYMEINBTITDLLCGTORM RPHIIREDVNNNVYADLTEEVVVTSSKYHMINTUTDLLCGTORM RPHIIREDVNNNVYADLTEEVVVTSSKYHMINTUTDLLCGTORM RSPLANGVANGAAGVELKEGCINNESLFILIGVIKKLSGCOVGGFI NYRDSKLITTILQUSLGGNPKTRIICTITPVSPPBTLTALQPAST AKYMKNTYVNEVSTDEALLKRYKRE INLKKULGKLESVSLETRAQ AMSKODLAQLLEEKDLIQVONGRIEFILTRMLVTSSSITLQOSL KARKRRVTVLGKSIKMKNSNYADOPINTITTKIKKLSIHL LRBIDESVCSESDVFSNTLDTLSEIBUNPATKLINGENIESERNYK KOOGMOLHEISNIKALVHRRVYNODLENELSSKVELLERKED OIKKLGGVIJDSQKLEBINKHRUNDLSYBELBENYGKTLERKET KOOGMOLHEISNIKALVHRRVYNODLENELSSKVELLERKED OIKKLGGVIJDSQKLEBINKHRUNDLSYBELBENYGKTLERKET KOOGMOLHEISNIKALVHRRVYNODLENELSSKVELLERKED OIKKLGGVIJDSQKLEBINKHRUNDLSYBELBENYGKLERKET AKKNOVOLKRELOSAFNEITKELESILKSLESSVELLERKET OKKEELHIITSEKNELSEKVELKERSVOLLENELERKE KOOGMOLHEISNIKALVHRRVYNODLENELSSKVELLERKED OKKEELHIITSEKNELSEKLESSVELKEREIQD KSEELHIITSEKNELSEKVELKERSVOLLENGLENGLENGLE AKKNOVOLKRELOSAFNEITKELTSILDGKVRKOLLENGLENG KSEELHIITSEKNELSEKVELKERSVOLLENGLENGLENGLE AKKNOVOLKRELOSAFNEITKELTEKLENGLENGLENGLENGLE AKKNOVOLKRELOSAFNEITKELTEKLENGLENGLENGLENGLE AKKNOVOLKRELOSAFNEITKELTEKLORTLERKTÜLCHELEGK KSEELHIITSEKNELSEKLESSVELKEREIQD KSEELKILTERGELKUNGLENGERKOOLLENGLEGLER AKKNOVOLKRELOSAFNEITKELTEKLORTLERKTÜLCHELEGK ANGESELGENGENGENGENGENGLENGLEGLER TORLARSVERMINGENGLENGLENGLENGLEGLER TORLARSVERMINGENGLENGLENGLENGLENGLENGLENGLEGLER TORLARSVERMINGENGLENGENGENTOLT TADVARNEITERGELKINGLEGLENGELKOORNIALKENGENGELINGE TORLARSVERMINGENGERINGENGELENGELENGE OSSK	l l	1		SIQSTFSINPKIVCDPLSDYNVWSMLKPINTTGTLKPDDRVVVA
GGVALRTSLELMMITDPVSGKNESVRNQVEDLIATIEKSGAGUP AVILRRENGSQFLPFSLGFLRARIGY GSIDTAENINVSYFEWLEPLEK/ETWHFG*ODTAKALADVATV LGRALVELAGGTNESDYGAPGATTLYGY-PLIKGNINKSYFQE LLGGRUERSYLG*RGLFQH\YTAV\SSPTNITVY\/LQYALANL TGTVVNLTHEQGODDSEVPSENDLYSSPWQDFLISNETDRIJ RCVRSTARLARALSPAFELSQMSSTEYSTWTESRWDLFRARIFL LASKELELITLTVGFGILIFSLIVTYCINAKADVUFVAPLARIF RCVRSTARLARALSPAFELSQMSSTEYSTWTESRWDLFRARIFL LASKELELITLTVGFGILIFSLIVTYCINAKADVUFVAPLARES VSY  ALKCEPRRVLATLVGFVQPDRMAEEGAVAVVCWVRPLNSREESL GETAQVYMKTHNNVIYPVDGSKSTMFDRVLHGNETPKNVYEA\1 AAPIIDSAIGGYNGTIFA\YGGT\ASGKTTTMMGSEDBLCU'IPQ GOFFGHFSQKI*EVFTLDRFLLRSVYMINSTIDHLCGTQKM KPLIIREDVNRNVVADLTEEVVTSEMALKHITKGEKSRNYGE TKNNQRSSSTHIFRMILESREKGEP GSSVKVSHLHNUDLA GSRRAAQTAAGVELKEGCNINRSLFILGQVIKKLSDGOVGGFI NYRDSKLTHILONSLGGNFKTIICTIVSPPETLTALDPAST AXYMKNTPYVGEVSTDEALLKYRKEIMDLTVSSLTLQQSI MERDQLAQLLEEKDLIGKVOMEK ISTRUTVSPETLTALQCAST AXXMKNTPYVGEVSTDEALLKYRKEIMDLTVSSLTLQQSI KARKREPVTMCLGKINKMKNSNYADQTNIPTNITTKTHKLSIAL LREIDESVCSESDVFSNTLDTLSIEBNPATTLLUTOSSLTLQGSI KARKREPVTMCLGKINKMKNSNYADQTNIPTNITTKTHKLSIAL LREIDESVCSESDVFSNTLDTLSEIBNPATTLLUTOSSLEERKTK KOQEMQLIHEISHKHUNDLSYSLESSVELLEREKED QIKKLGGVIJDSQKLESHKHINDLSYSLESIERKTK KOQEMQLIHEISHKHUNDLSYSLESIERKYMLDEFFRARENTELEKE SLRAYDDALVLUDEGURTFKEEMBLLKKENKELATTKKQMENDIOLOYGGOLE AKKRWOVDLERLGASFREITITLTGLEDKOKNETHDAETV ALDARRESAFLRSENLELKEKKMELATTTKKQMENDIOLOYGGOLE AKKRWOVDLERLGASFREITITKGETSLEEIGKTKDOLATTO SHYKSTDQEFONFKTLHMDFRGYKWAULEENERMOREIVALEKE AQKFDSSLGALKYELSYKYTGLOEKTREDGELEIGKTKDOLATTO SHYKSTDQEFONFKTLHMDFRGYKWAULEENERMOREIVALEKE AGKFDSSLGALKYELSYKYTGLOEKTREDGELEIGKTKDOLATTO SHYKSTDQEFONFKTLHMDFRGYKWAULEENERMOREIVALEKE KISEEVSRNLHMENTGETKDSFOGMVGIDKKOHEINTNTKS KISEEVSRNLHMENTGETKDSFOGMVGIDKKOHEINTNTKS KISEEVSRNLHMENTGETKDSFOGMVGIDKKOHEINTNTKS KISEEVSRNLHMENTGETKDSFOGMVGIDKKOHEINTNTKS KISEEVSRNLHMENTGETKDSFOGMVGIDKKOHEINTNTKS KISEEVSRNLHMENTGETKDSFOGMVGIDKCHENTNTKS KISEEVSRNLHMENTGETKDSFOGMVGIDKCHENTNTKS KISEEVSRNLHMENTGETKDSFOGMVGIDKCHENTNTKS KISEEVSRNLHMENTGETKDSFOGMVGIDKCHENTNTKS CHENDLESSERMELITHTROFTLARGERERELALIHL PROGRETIATURG			1	ATRLDSRSFFWNV\APGAESAVASFVTQLAAAEALQKAPDVTTL
AVILARENOSOPLEPSSLORFIZARNISGVILADHSGAFHNIKYY  OSITOTHARININYSFEWLEPLKE/ FINNEG-OPTAKALADVATV  LGRALVELAGGINFSDTVQADPQTVTRLLYG\PLIKANNSMPOS  ILGGROLKESYLG*RGLFQN\YTAV\SYNTIVV/UQYALANI.  TGTVVNLITEQCQDESKVPSENDLYSYSWYDPLISMETDRLP  RCVBSTRALRARLSPSEPLSQMSSTEWSTWTSENBOLTARAIPL  LASRELELITLIVGFGILIFSLIVTYCINAKADVLFIAPREPGA  VSY  5814  8500  432  ALKCEPRRUALLUGFVQDRRMAESGAVAVUVRVRPLNSREESL  GETAQVYMKTHNWYYPVDGSKSFNFDRVLHGREFTRNVYEA\I  AAPIIDSAIQGYMGTIFA\YGCT\ASKTYMMSGEDHGLOVIPQ  GOPHGHFSQKI-SVFLKUSYWEIVMSTITDLLCCTQKM  KPILIREDVNRNVYADLTEEVVYTSPMALKHITGEGSRIKGE  TKHNGRSSRSHITIFNHILSSREKGEPSNCESSVKSHINLIVDLA  GSBRAAGNAGANGVALKGECNINSELFILGOVIKKLSCQOVGGFI  NYROSKUSTITIRANICGARANITIFNHILSSREKGEPSNCESSVKSHINLIVDLA  GSBRAAGNAGAVALKERGENNSTALICTTTPVSPBFTLTALQFAST  AKMKNTYVNEVSTDEALLKRYKEITDLKKKLSEVSLETRAQ  AMSKOQLAQLLEEKDLIQVONDRIFENITATLOFAST  AKMKNTYVNEVSTDEALLKRYKEITDLKKKLSINLOFAST  KARKRKRYTWCLKSIKKMKNSNYADQPHITNITKTKHKLSINL  LREIDESVCSESDVFSNTLDTLSSIEBNPATKLLNOENIESELN  SLRAVYDMIVLDVEQUETREKEMBLKKENNIDLEFSELBERKYK  KOQEMQLIHEISNIKALVKHRRYVNQDLENEISSKVSLLREKED  OIKKLGEFILDSKLESSHVENDLYSKLESIEDROMNOTHOAPTV  ALDAKRESAFLRSENLELKEKKKELATTYKOMENDIOLYGGLE  AKKMOVDLKRELOSAFNEITKLTSLIDGVENDLKOHLENER  KOQEMQLIHEISNIKALVKHRRSVYNQDLENEISSKVSLLREKED  OIKKLGEFILDSKLESSHVENDLYSKLESSEVSELLREKED  OKKSELLIITSEKKRLSSRVUKESSRVGLLESIEKKTDLLATTQ  SYNKSTOQEFQNNKTLHMDFSQKKSWVLEENBRANGEIVALSKE  AQKFDSSLGVVEREFLISTERLOGVLEEVKLTCHENDLKOLLOSEL  AKKMOVDLKRELOSAFNEITKLTSLIDGKKTREVOREILBEMGLKEGLE  NOSSELGVVEREFLISTERLOGVLEEVKLTCHENDLKOLOSEL  OIERQLKSDIHNTVNMNIDTOGLENSTEVEKEMBOLKHGLOSEL  AKKMOVDLYSERETLITERLOGLEKKEVEKVLTOERDLKOLOSEL  OIERGERITHOOPERLISTERLOGVKENERMIKKTOLLOSEL  NUKNSELNSHMELTELHERFERLELANGENERMEKEVENTOLL  TADVKONEI IEQGRK IFSLIGERKECQONLENGEVERMIKKENER  KLEGEVSKHENDENTSTRUKEURGELKKOOLLINGERMERMOKKINNEIE  NUKNELKNIKELTLEBHERFERLELANGENERMEKEVENSTALTERIUNGE  SOSKOGUSLMMKEKNDETTRITVILVSEMGEVERMSAKHTOLL  ARHLETEEBLIKVAHCCIKEOLOSETINGLINGESKYTERDLINGE  SOSKOGUSLMMKEKNDETTRITVILVSENGEROLKENIKETIOHQ  LEANDALORIUNGETYREEGOLIN KGIGEVVEKWURDE	ł	ł	i	PRNVMFVFFQGETFDYIGSSRMVYDMEKGKFPVQLENVDSFVEL
GSIYDTAENINVSYEWLEPLKE/ETWING-ODTAKALADUATY LGRAUGLAGGUAGENTULGY PILKANISMOGO ILGGRUESGUAG-RGLFGH-VIAV\SSPINITYV/UQYALANI. TGTVUNLTREQCODPSKYPSENNULTSWOGDI-INSHETENILE RCVRSTARLARALSPAFELGWSSTEYSTYTESRWKDIRARIFL LGRELGITLTUGFGILIFSLIVTYCINAKADULFIAREFGR VSY  S814  8500  432  ALKCRPRVUAILVGFULFSLIVTYCINAKADULFIAREFGR VSY  AAPIIDSAIQGNGTIFA\VGOT\ASGKTYTHMGSEDHLGUTPO GOFIGHFSQKI-EVPLDREFLLLAVERTYNETITLILLGTOKM KPLIIREDVINNVYUADLTEEVVYTSEMALKHITKGEKSHHYGE TRINGNSSSSHTIFIRMILESRKERSNEGSKYVSHINLFULL GSERAAQTGAAGVRIKEGGINNSLFILGOVIKKLSGOGGGFI NYRDSKLITILONSLGOMPKTRILTTVSPEDETLIALDFAST AKYMKHTPYVWEVSTDEALLKRYRKEIMDLKKGLEEVSLETRO AMEROLAGLEEUSTATALOFAST AKYMKHTPYVWEVSTDEALLKRYRKEIMDLKKGLEEVSLETRO AMEROLAGLEEUSTALDFASTSILLQUIKKLSCOUGGFI NYRDSKLITILONSLGOMPKTRILTTPVENDETLTALOFAST AKYMKHTPYVWEVSTDEALLKRYRKEIMDLKKGLEEVSLETRO AMEROLAGLEEUSTALTVENSTENTLALOFAST AKYMKHTPYVWEVSTDEALLKRYRKEIMDLKKGLEEVSLETRO AMEROLAGLEGLAGLEEUSTATALOFAST AKYMKHTPYVWEVSTDEALLKRYRKEIMDLKKGLEEVSLETRO AMEROLAGLAGLEEUSTATALOFAST AKYMKYTYOLGININGMKSNYADOFNIPTITITKTHKLISIINL LERIDSVCSSEDVSTSTLDTUSEISTEDPKONKOTLFDAETV ALDAKRESAFIRSENLELKEKKMELLSTRUKDMEDIGLOOGGLE AKKMEVVOLERELGSARNEITKLISLINGVYRDLLCHLEKKED QIKKLGEVIDSQLENGARNEITKLISLINGVYRDLLCHLEKKED AKKMEVVOLERELGSARNEITKLISLINGVYRDLLCHLEEGK ITDLOKELINKSVERNEALREVILLSELKSLGSEVERREREIO KSEELII ITTSEKDELISFEVHKESSEVIGLLEEIGKTKDLAFTG SHYKSTDQEFGNFKTLIMDFEQKYKNVLERNERNOGIVALGEE AKKEDLISTSCHAMPHOONING KSEELII ITTSEKDELISFEVHKISTEVORILMERGUKBOLE NEDSFLOAVERBERLITTSKENGULKOLEEUSKYKDLLAGET SHYKSTDQEFGNFKTLIMGFEQKYKNVLERNERNOGIVALGKE AKKBOOLASDIPHYVMIDTOGOQURNALESLICKHENDLARTO SHYKSTDQEFGNFKTLIMGFEQKYKNVLERNERNOGIVALKEE AKKBOOLASDIPHYMIDTOGOQURNALESLICKHEDLARTOT TADVKINSII EQGRKIFSLIGGKNELOGMESVIAEKEGLIKR CERNICHTISHQEELIKTELGGELKVOLAGENINGTKERGUL KRIEBATERGUKSUTATUTTENGELGGHANTOTILKS CHENKERGUKSTATUTTENGENGENGORMSTIKERUL KRIEBATERGUKSTATOTINTOLEKSKUTETUORKHDENGELIKGUE TOGRAGAGGULMVEKSTENETINTICGETPUHTEGELLD NVKKVSETOSTMMELGLIKTIKEALVALOKEKETETISTIOKO LEKKREGGERSTATKETUNTATUESGEROUTHATERGEKURC EGSGERINTERTUNTETIST	1	l		GQVALRTSLELWMHTDPVSQKNESVRNQVEDLLATLEKSGAGVP
LIGRALYELAGGTNFSDTVQADQTVTRLLYG\FLIKANNSH\CQSELLGS\LGA\LGA\LGA\LGA\LGA\LGA\LGA\LGA\LGA\LGA		l .		AVILRRPNOSQPLPPSSLQRFLRARNISGVVLADHSGAFHNKYY
ILIGERLES/16*RCLFCH(VIAV\SEPTINTITY/VLCYALANL TGTVVNITEQCODPSKYPSSKNYDENETSRKENETORLE RCVESTARLARALSPAFELSGWSSTEYSTWTESRKKDIRARIPL LASKELELITLTVGFGILIFSLIVTYCINAKADVLFIAREPGA VSY  ALKCEPRRVLAILVGFVQPDRMAEEGAVAVCVVVPDLNSREESL GETAQVYWKTHINNIYYDOGSKSFNPDRVLHGNETPERNYTEA]I AAPIIDSATQGTGTIFA\VGOT\ASGKTYTMMGSEDHLGVIPO GOFIGHFSQKI*EVPLDREFLLAWRITYNETYBLILGTORM KPLIIREDVNRNVYADLTEEVVYTSEMALKHITKGEKSKHYGE TKINGRSSKHTIFBMILESREESDCGGSVXVSHLNIVDLA GSERAAQTGAAAVRLKEGCNINRSLFILQVIKKLSGGVGGFI NYRDSKLTRILQNSLGCNIPKRIICTITVSFDTLTALQFFAST AKTMKNTFYVEVEVSTDEALLKRYKKSIMDLKKQLEEVSLETRAQ AMSKOQLAQLLEEKDLIQKVQNEKIENLTTRILLYSSSLTLQQSL KARKRARVTWCLGKINKKMSNNYADNIPTNITTKHKLSINL LREIDESVCSSDVFSNTLDTLSEIEWNPATKLINGENIPSELN SCAPYDRINLVLDYSGLATEKEEMELKEKKHLERTKLINGENIESELN SCAPYDRINLVLDYSGLATEKEEMELKEKKHLERTVLLOGSLEKKK KOQEMGLIHEISNLKNLVKHREVYNODLENELSSKVELLREKED QIKKLGYIDSQKLEFIKEMELKEKKHLEATTYKOMENDIOLVGSGLE AKKKMOVDLEKELGSARNEITKLTSLIDGKVPKDLLCNLELEGK ITDLOKEINKSVEENBALREVILLSBLKSSLPSEVERLEREGO KSSELHIITSSKOKLFSEVVHKESRVQGLLEGKTREDINLATO SYNKSTOGEFNNKVELTHIMDFGCKYKNVLEENERMENDGIVNLSKE AQKFDSSLGALKTELSYKTOGLQETTREVQERLNEMEQINKQLE NDSSPLGYVFEKEKILITEKLGCTLEVENDLEGKDLKGLGSSL QIERDQLKSDIHDTVAMNIDTOGGLRNALBELKKOLLSCLKGLSSL  KISEVSRNLHMEENTGETKOBFOQKWYGIDKKOLLEANTOTTL TADVKUNDIIEQORKTFSLIGENELQOMLESVIAKEGLISR TCDLAEVEEKLKSKOOLOEROGQHKVNIDE NKANDELIEGKTKFSLIGENELQOMLESVIAKEGLISR TCDLAEVEEKLKSKOOLOEROGQHKVNIDE NKANDELIEGKEKKITSSLIGENELQOMLESVIAKEGLISR TCDLAEVEEKLKKSOOLOEROGQHKVNIELERENDL NKANDELIERGKSTATGTUNGEFSTRECHTINLESCHCHERENLI ENKLEVEERLKKNALCUNGESSERVKILORENDLINGELSR  CESCELTINGENDLITICGEDLKOOLOERINERELARINGEL  LEKLEGSFERDHKSYNEKTROLOTHESVIAKEGELSR TCDLAEVEEKLKSKOOLOEROGGDVKNINEI NKANDELKRIELTLEHMETERLELAQKINENYEEVKSITKERKVL KELQKSFETERDHIRGYIREIBATGLTKEELITAHIHLEEHER GSGKGEGSLMMKEKDNETTKIVSEMEGPFKYNGBALLRIEIBENG GSGGEGLSJTKKERDIKTIKTAGESEPTQLEKREKLEGKER OESGEELISJTKERDIKTIKTIKAGEGLEGETQUKKERIKELO LEKKLOGSHDEMSVAKEKDOLOGLOGLOGSHOOLKENITELAKTOG GSGGEGLISTKEREDLINTRICESGEELGUTIKGTESWYTERD LEKKLEGGETOKUNDELTEITNIKGSEENTELGERKREGER LEKKLEGG	]			QSIYDTAENINVSYPEWLEPLKE/ETWNFG*QDTAKALADVATV
TGTVMITTEQCODPSKVPSENKDLYSENWOGPLHSNETDRIP RCVRSTARLARALSPAPELSOSTEYSTWTESEKWRIDTARIFI LASKELELTILTVGFGILIFSLIVTYCINAKADVLFIAPREPGA VSY  ALKCRPRPVLAILVGFVQPDRMAEEGAVAVCVRVPLNSREESL GETAQVYWKTHNNVIYPVDGSKSRNFDRVHGMETPKNVYEA\1 AAPI INSATQGINGTIFA\YGGT\ASGKTYMMSEDHLGVIPQ GQPHGHFSGKI*EVFLDEFFLLRVSYMSIVNSTITDLLCGTQKM KPLI IREDVNRNVYADLTEBVT\SEMALKHITTKGEKSRHYGE TKNNQRSSRSHTIFRNILESREKGFSNCGSVKVSHLNLVDLA GSERAAQTGAAGVRIKEGGCINNFEITLGVYSKKLSGGOVGGI NYRDSKLTRILONSLGSRPKTRIICTITPVSPDETLTALOFAST AKYMKNTPVNDEVSTDEALLKYREIMLKKQLEEVSLETRAQ AMEKDOLAQLLEEKDLIQVQNEKIENLTRMUTTSSLTLQQGL KAKRKRYTWCLGKINKNKNSNYADOPNIPNITTTTKTHKISINL LERIDESVCSESDVPSNTLDTLSSIBNDPATKLINGENSESLIN SLRADVDNLVLDYBCLRTEKEEMBLKKKERNDLDEFEALBRITK KOQEMQLIHEISNLKNLVKHEVDQLEMELSKVELLREED QIKKQGFYIDSQKLENIKMULSYSLESIEDPKOMKOTLEDATV ALDAKRESAFLRSENLELKEEMBLALKEVDQLEEVSLETREED QIKKGGFYDSQKLENIKMULSYSLESIEDPKOMKOTLEDATV ALDAKRESAFLRSENLELKEEMBLALKEVDQLEEVSLETREED QIKKGGFYDSGKLENIKMULSYSLESIEDPKOMKOTLEDATV SNYKSTDQEPQNFKTLIMDEGYSKWAULEBNERMOGIVNLSKE AKKMQVDLEKELGSAFNETTKLTSLIDGKVPKDLLCNLELEGK ITDLOKELNKSVEBREALREEVJCKSHENSENEMBGENTLNLSKE AGKFDSSLGALKTELSVKTGELGKYKMULEBNERMOGIVNLSKE AKKFNOVDLEKELGSAFNETTKLTSLIDGKVPKDLLCNLELEGK KSEELHIITSEKDKLFSEVVHKESRVQGLEEIGKTKDDLATTQ SNYKSTDQEPQNFKTLIMDFGQKYKMVLEBNERMMGETINTLKS KISEEVSNLHMEENTGETKDEFOOKNVGIDKODLEARNTOTL TADVKNNEITEGGKRIFSLIOFACKOMETTNTLKS KISEEVSNLHMEENTGETKDEFOOKNVGIDKODLEARNTOTL TADVKNNEITEGGKRIFSLIOFACKOMETTNTLKS KISEEVSNLHMEENTGETKDEFOOKNVGIDKODLEARNTOTL KENIEMTIENOEERIRLIGDELKKQGEVAROEENMAKTIKHENDE KRUZEVSEKLARKSOOLOFKOOLOKNOCENMERMOKTURIE NLKNELKRELTIEMBTTRLELAQUINNYEVKSITKRKVL KELQKSFFTERDHLRGYIREILEAQUINNYEVEKSITKRKVL KELQKSFFTERDHLRGYIREILEAQUINNYEVEKSITKRKVL KELQKSFFTERDHLRGYIREILEAQUINNYEVEKSITKRKVL KELQKSFFTERDHLRGVIREILERGCFTKKNAUCHSOOLENIKGIV AKHLERBEELKVAHCCLKEQGETINELRYNLGEESTIGKG OSGGEINSLIKGENDRAVGENAERDOLOGEVOOLINNIESIV AKHLERBEELKVAHCCLKEQGETINELRYNLSEKSTEISTIQKQ LEANDKLORKIGEIVEKEGONIKGISSOOLKENIKGIV AKHLERBEELKVAHCCLKEOGETIOLHMILEERGERKYVGER LEANDKLORKIGEIVEKGEGONIKGISSOOLKENIKGIS AKHLERBE				LGRALYELAGGTNFSDTVQADPQTVTRLLYG\FLIKANNSWFQS
RCVRSTARLARALSPAFELSQUSSTEYSTWESRWIDIRARIFL JASKELELITLITUTGGILIFSLIVTYCINAKADVLFIAPREPGA VSY  ALKCRPRVLATLVGFUQPERMAEEGAVAVCURVPRINSREESL GETAQVYWKTHINVIYPVDGSKSRNFDRVLHGRETPKNYYEA\I AAPI IDSAIQGYMGTIFA\YGGT\ASGKTYMMGSEDHLGVIPQ GOFHGHFSQKI FVFLDREFLLRVSYMEIVRBTITDLLGGTOKM KPLITREDVNRNYVADLTEEVVYTSEMALKHTIKGEKSRHYGE TKNNGRSSRSHTIFRMILESSREKGPSNCEGSVKSHLNLVDLA GSBRAAQTGAGAGVRLKEGGNINSLFILGQVIKKLSDQQVGGFI NYRDSKLTRILONSLGGNEKTRILTITPVSPDETLTALOFAST AKYMKNTPYVNEVSTDEALLRYRKEIMDLKKQLEEVSLETRAQ AMEKODLAQLLEEKOLLQKVONERIENLTRALVTSSLTLQOSL KARKRRYTWGLGSKINKMKNSNYDOPENIPNITTTTKHKLSINL LREIDESVCSESDVFSNTLDTLSEIENNPATKLLNOENIESELN SLRADVONLVLDYSQLRYRKEMELKKEKNDLDEFEALER KYK KOQEMGLIHEISNLKNLWHREVYNQDLERELSSKVELLREKED QIKKLQEYIDSQLENIRMLSYLSSIELDKGWKMCHLFBLSKVELLREKED QIKKLGEYIDSQLENIRMLSYLSSIELDKGWKMCLEDGKTKOD AKKKMOVDLEKELDSANEITKLTSLIDGKVPKDLLCHLELGK KOQEMGLHEISNLKNLWHREVYNQDLERELSSKVELLREKED QIKKLGEYIDSQLENIAMLSYLSSIELDKGWKPCDLLCHLELGK KOQEMGLHEISNLKNLWHREVYNQDLERELSSKVELLREKED QIKKLGEYIDSQLENIAMLSYLSSILEGKTKNDLLATO SYNKSTODEFONFKLHMDEFSCKYKMVLEENERMOEIVNLSE AQKFDSSLGALKTELSYKTQELOGKTREVQGRINMEQLKBQLE NDSSPLOTVEREKTLITEKLQGTLEVKTLTVEKDDLKQDEL AKKNOVDLEKSLDSANFILITEKLQGTLEVKTLTVEKDDLKOLGES  VIESEVSINLIMEENTGETKLEFTQOKNVGLEKROLGETINTLKS KISEEVSINLIMEENTGETKLEFTQOKNVGENGKNITLKSE KISEEVSINLIMEENTGETKLEFTQOKNVGLIKGELGRANTOTL VENNEMTIENQEERRILGGYIRGELAQKINDENYEEVKSITKERKVL KELQKSFFTEEDHLRGYIRGIELAQKLINDENYEEVKSITKERKVL KELQKSFFTEEDHLRGYIRGIELAQKLINDENYEEVKSITKERKVL KELQKSFFTEEDHLRGYIRGIELAQKLINDENYEEVKSITKERKVL KELGKSFFTEEDHLRGYIRGIELAQKLINDENKEFKINEKF OSSGEINSLTKERDNLKTIKKALEVKHOLLEKHTEILARIEE SGSKGEGISLTNKEEDNLKTIKKALEVKHOLLEKHTETLARIGE SGSKGEISISTTKEEDNLKTIKALEVKHOLLEKHTETLARIGE SGSKGEISISTKEEDNLKTIKKALEVKHOLLEKHTETLARIGE SGSKGEISISTKEEDNLKTIKKALEVKHOLLEKHTETLARIGE SGSKGESIISTTKEEDNLKTIKALEVKHOLLEKTETSTIQKQ LEARIDGENSTKEENKANGESCEKYOFLKMTLKEIV AKHLETEELKVAAGCLKEGESTINELRVNLSKKETEISTIQKG LEARINGESHDENKSTKEERDUKTYTKALEVKHOLLEKTICTIONG AKHLETEELKVAAGCLKEGESTINELTVALESKETEISTIQKG LEARINGESHDENKSTKERDUKTIKALEREWKEVKOEL	-	į		ILQGRDLRSYLG*RGLFQH\YIAV\SSPTNTIYV/VLQYALANL
TASKELELITLTUGFGILIFSLIVTYCINAKADVLFIAPREPGA VSY  ALKCRPRVLATLUGEVQPDRMAEEGAVAVCURVRPLNSREESL GETAQVWKYHNNVIYPVDGSKSFHORVLHGNETFRAVYEA\I AAPIIDSAIQCYMGTIFA\YGGT\ASGKTYMMSSEDHLCVIPQ GQFHGHFSKRI*EVFLDERFLLRVSYMSIVRSTITDLLGGTQKM KPLIIREDVNRNVYADLTEEVTSEMALKMITKGEKSRHYGE TKMNQRSSRSHTIFRNILESREKGEPSNCEGSVKVSHLHLVDLA GSRBAAQTGAAGVRIKEGGCINAFILIGOVIKKLSDGVVGGFI NYRDSKLTRILQNSLGGNPKTRIICTITPVSFPETLTALQFAST AKYMKNTPYVNEVSTDEALLKRYRKEIMDLKKQLEEVSLETRAQ AMBKDQLAQLLEKOLLQKVONEKIEMITRNLTYSSLTLQGSL KARKRRVTWCLGKINKWKNSNYADQFNIPNITTTTTTKTHKLSINL LERIDSSVCSESDVSPSNTLDTLSENPATKLINGENIESELN KDQBMQLIHEISNLKNLVKHREVYNQDLEBLESKVELLREKED QIKKLQEYIDSQKLENIKMDLYSSLSIEDPKOMKOTLFDABTV ALDAKRESAFLRSENLELKEKMKELATYKQMSNDIQLYGSQLE AKKRWOVLEKKLQSAPNEITKLYTSMDENDIQLYGSQLE AKKRWOVLEKKLOSAPNEITKLYTSMDENDIQLYGSQLE ITDLQKELNKEVESNEALREVULLSELKSEVQELLEEIGKTKDLATTQ KSELLIITSSEKDLSSVVNUKENSPVQGLLEEIGKTKDLATTQ SNYKSTDQEFQNFKTLIMDFEQKYKWULEENERMQGIVNISKE AQKFDSSLGAKTELISKLYGDLOGKTREVVGRINDENDLKGQLE NRDSPLQVVEREKTLITEKLQGVLEVKTLTQEKDDLKQLGSSL QIERDQLKSDIHDTVNNNIDTQEQLKNALESLKOHGETINTLKS KISEBVSNILMBERNTGETXDEFORVATGLKOHOLEANTYOTL TADVKDNSI IEQGRKIFSLIGEKNELQGMLESVIAEKGQLEXDL KRIEMSTINDEELRLIGDELKQQSILVAGEKNHAIKKEGLSR TCDRLAEVERLIKKSQLQEKONVGIDKKODLEANTYOTL TADVKDNSI IEQGRKIFSLIQEKNELQCOLLNVQEEMSEMQKKINEIE NLKNELKHSELTLEHMETTERLELAQKINDRYEVKSITKREKUL KELQKSFFTERDHLRGYIRSIERTGLAQKINDRYEVKSITKREKUL KELQKSFFTERDHLRGYIRSIERTGLAQKINDRYEVKSITKREKUL KELQKSFFTERDHLRGYIRSIERTGLAQKENHAIKKEGELSR TCDRLAEVERLIKKSQLOLEKOOLOLNOLEMSEMOKKINEIE NLKNELKHSELTLEHMETTERLELAQKINDRYEVKSITKREKUL KELQKSFFTERDHLRGYIRSIERTGLAQKENHAIKENEELERMOK GSSGEIKSITKRERDNIKTIKKALEVKHOOLEKHIRETLARIQE SQSKQEGSLIMKEERDNETKTIVSEMERFKROSLAKHILKEHQE TIDELRRSVSEKTAQIITOTDLEKSTREKVLLERENGE GSSGEIKSITKRERDNIKTIKKALEVKHOOLEKHIRETLARIQE SGSKGESIENSITKRERDNIKTIKGELERGVKYNDELKYGFKEHR AKHBSTAGGSTERKWALENDELGERGELORINGERKETEISTIQKQ LEANDKLONKIQEIYEKEEQLINKGISEVQEKVNDELKYGFKEHR KAKBSALOSIESKWALENDLOLEKSGEKSYOFLKWALKKYGFKEHR LEHKLEGESHDEMKSVKENDLOLEKSTERIVANNETORMUCHERE	1	i e		TGTVVNLTREQCQDPSKVPSENKDLYEYSWVQGPLHSNETDRLP
ALKCRPRRVLAILUGEVQPDRMAEEGAVAVCURVRPLINSREESL GETAQVYWKTHNINITY PVDGSKSSIPTPRVLHGNETEKNYYEA\1 AAPI IDSAIGGYMCTIEA\7 VGQT\ASGKTYTMMGSEDHLGVIFQ GOFHGHSQKI*EVFLDREFLLRVSYMEIYNBTITDLLGGTOKM KPLIIREDVARNYYVADLTEEVYYTESMALKMITKGEKSRHYGE TKMNGRSSRSHITFRMILESPEKGEPSNCEGSKVSHIMLIVDLA GSERAAQTGAAGVRLKEGCNINSSLFILGGVIKKLSGGOVGGFI NYRDSKLTRILGNSLGGNPKITCITTPYSPDETITALQOFAST AKYMKNIPYVNEVSTDEALLKRYRKEIMDLKKQLEEVSLETRAQ AMERDQLAQLLEKKDLIQKVONEKIENITMTUTSSSLTLQQGI KAKRKRVTWCLGKINKMSNYADQFNIPTNITTKTHKLSINL LREIDESVCSESDVFSNTLDTLEEIBWNPATKLLNQENIESELN SLRAADVDNIVLDYPGQLFTEKEBLKLKEKNDLESFELBERTKK KOQEMQLIHEISNLKRILVKHREVYNDQLENELSSKVELLREKED QIKKLGEYIDSQKLENIKMIDSYLESIENDFOKMKOTLEPAATV ALDAKRESAFLRSENLELKEKMKELATTYKQMENDIOLYGGQLE AKKMOVDLEKELQSAFNEITKLTSLIDGKVERDLLCALELEGK ITDLQRLNKEVEEREALREEVILLSBLKSLPSEVERLRKEIQD KSEELHIITSEKDKLFSEVVHKESRVGGLLEEIGKTKDDLATTQ SAYKSTDQEFGRKTLHMDFEQKYMVLEENERMNGGIVNISKE AQKFDSSLGALKTELSYKTQELQEKTREVGERLENBENGGIVNISKE AQKFDSSLGALKTELSYKTQELQEKTREVGERLENBENGGIKEGLES NRDSPLQTVERERKTLITERLGPEKYMVLEENERMNGGIVNISKE AQKFDSSLGALKTELSYKTQELQEKTREVGERLENBENGGIKEGLE NRDSPLQTVERERKTLITERLGPEKYMVLEENERMNGGIVKGDLEAKNTOTL TADVKONBIIEQGRKIFGLIGGENELQGMLESVIAEKGUKTDL KENIEMTIENGEERKLILGDELKKQEVIAQEKNHAIKKEGGLER TCRRLAEVERKLKEKSQGLOGFGQQLLAVQEKNHAIKKEGGLER TCRRLAEVERKLKEKSGGLERGCQQLLAVGEKMHAIKKEGGLER TCRRLAEVERKLKEKSGGLERGCQCLLAVGEKMHAIKKEGGLER TCRLAEVERKLKEKSGGLERGCQCLLAVGEKMEMEMENERE OESGEEIKSLTKERNILKTIKEALEVKHDLKEHREE OESGEEIKSLTKERNILKTIKEALEVKHDLKEHREELLEMLG SQSKQEGSINMKEKDNETTKIVSEMEGFKPKDSALLHILEEMLG SQSKGEGSINMKEKDNETTKIVSEMEGFKPKDSALLHEITEMLG LSKRLGESHDEMKSVAKKKDILGEVELGVESDOLKENIKEIV AKHLETEELKVAHCCLKEQEETINELTUREVERFORDLKKREIV LEAINDKLONKIGEIYEKEGGLINKGIEVGESCOLKENIKEIV AKHLETEELKVAHCCLKEQEETINELKTIGEVGEKORDLKORKEIV LEAINDKLONKIGEIYEKEGGLINKIGESCOLKENIKEIV AKHLETEELKVAHCCLKEQEETINELKTIGEVGEKORDLKORKEIN LEAINDKLONKIGEIYEKGGLINKIGESCOLKENIKEIVERDE LEAINDKLONKIGEIYEKEGGLINKIGESCOLKENIKEIVERDE LEAINDKLONKIGEIYEKEGGLINKIGESCENDLKORKEEN	1	1		RCVRSTARLARALSPAFELSQWSSTEYSTWTESRWKDIRARIFL
ALKCRPRVLAILUGFVQPDRMAEEGAVAVCVRVRPLNSREESL GETAQVWKTHNNVITPVDGSKSFNFDRVLHGRETPKNYYEA\I AAPI IDSAIQGVMSTIFA\I YGOV\ASGKTYTMGSEDHLGVIFQ GQPTGHFSQKI*EVFLDREFLLRVSYMEIYNBTITDLLGGTQMW KPLIIRDUNRNVYADLTERVYTSEMALKWITKGEKSRHYGE TKMNQRSSRSHTIFRNILESREKGEPSNCEGSVKVSHLMIVDLA GSERAAQTGAAGVRLKEGCNINRSLFILGVIKKLSDGOVGGFI NYRDSKLTHILONSLGSNFKTRICTITVSPDFEITJALQFAST AKYMKNTPYNDEVSTDEALLKRYKKEINDLKKQLEEVSLETRAQ AMERQLAQLLEKDLIQKVQNEKIENDLTMKLTSSSITLQOSL KARKRRVTWCLGKINKMKNSNYADQFNIPTNITTKTHKLSINL LERIDESVCSESDVFSNTLDEIEBWNDATKLINQENIESELN SLRADVDNIVLDYEQLRTEKEEMELKLKEKNNLDBFEALBERTK KQDEMQLIHEISNLKNIVHLEYSVESIESIEDPKOMKOTLFDAATV ALDAKRESAFLRSENLELKEKMKELATTYKQMENDIOLYOSQLE AKKKMOVDLEKELGSAFNEITLSILDGKVEDLLCLELGK ITDLOKELNKEVEENEBALREEVILLSBLUKSLDSEVERLRKEIQD KSEELHITTSENKLIFSEVVHKESRVQELLEEIGKTKDDLATTQ SNYKSTDQEFQNFKTLHDDFGCKYMVLEEBBERNMGEIVNLSKE AQKFDSSLGALKTELSYKTQELQEKTREVQERLIBEMEGLKRGLES NRDSSDLQTVERRKTLITERLQCTLEEVKTLTGEKDLKOLOSSL QIERQLKSDIHDTVNMNIDTOGOLORNALESLKONGFTINTLKS KISEVSRNLHMEENTGETKDEFQCKMVGLOKKDLEAKNTQTL TADVKDNEIIEQQRKIFSLIQEKREQQULMVQEKNHAIKKEGELSR TCDRLAEVERLKMERSOGLOGECQQULMVQEKMHAIKKEGELSR TCDRLAEVERLKMERSOGLOGECQQULMVQEKMHAIKKEGELSR NLKNELKMELTLEHMETERLELAGKLKANLENEEVEKKMEIE NLKNELKMELTLEHMETERLELAGKLKANLENEEVEKKMEIE NLKNELKMELTLEHMETERLELAGKLKANLENEETHAKEIQE SOSKQEGSINMKEKDNETTKIVSEMEGPKPKDSALLHEIEMLG LSKRICKSFETERPHLKEYSTIC ERSOQLUMVERSEMEMKNEIE NLKNELKMELTLEHMETERLELAGKLKANLEHEITERMLG SOSKGEGSLINKMEKDNETTKIVSEMEGPKPKDSALLHEIEMLG LSKRICGSSHOLKENIKEIVARICE SOCKGEDLIKNIKEIV AKHLETEELKVAHCCLKEQBETINELKUREURGPEKSPCKMCE  SOSKGEGSLINKEKDNETTKIVSEMEGPKPKDSALLHEIEMLG LEKRICGSSHOMKEKDNETTKIVSEMEGPKPKDSALLHEIEMLG LEKRICGSSHOMKEKDNETTKIVSEMEGPKPKDSALLHEIEMLG LEKRICGSSHOMKEKDNETTKRIVSENGEROOLKENIKEIV AKHLETEELKVAHCCLKEQBETINELRUREGEROOLKENIKEIV AKHLETEELKVAHCCLKEQBETINELRUREGEROOLKENIKEIV ELAIDDLKGPKKSCHLEUTRILGESQEKURELKGPKEER KANDSALGISSKMELDINRIGESGEBIQINIKKEEMKRVOGE LGAIDDLKENTKSIVANKKSSOKEYOFLKMITAVMETOEKMCS LEAUDKLORKEEMERVOGE LGAIDDLKENTKSIVANKESSOKEYOFLKMITAVMETOEKMCS	1	] .		TASKEDEDITLTVGFGILIFSLIVTYCINAKADVLFIAPREPGA
GETAQVYMKHNINVIYPUGSKSFNPDRULHGRETPKNYYEA\I AAPIIDSAIGGYMGITJA\TGOT\AGKTYTMMGSEDHLGVIPO GOPHGHPSQKI*EVFLDREPELLRUSVMEIYINBTITDLLGGTQKM KPLIIRBUVRNYVYADLTEEVVYTSEMALKWITKGEKSRHYGE TKMMORSSRSHTIFRMILESREKSPNCEGSVKVSHLMILVDLA GSERAAQTGAAGVRLEGGCNINRSLFILGCVIKKLSDGQVGGFI NYRDSKLITRILQNSLGGNPKTRIICTITPVSPDETLTALQFAST AKYMKNTPYVNEVSTDEALLKRYRKEIMDLKKQLEEVSLETRAQ AMEKDQLAQLLEEKDLIQKVQNEKIENLTRMLVTSSSLTLQQSL KAKRKRVTUCKLINKMKNSNYADQFNIPTNITTKTHKLSINL LREIDESVCSESDVFSNTLDTLSEIEWNPATKLLNQENIESSLIN SLRADVDNLVLDYEQLRTEKEEMELKLKEKNDLDEFEALERKTK KOQEMQLIHEISINKAILVHREVYNDLENEELSSKVELLREED QIKKLQEYIDSQKLENIKMUSYSLESIEDPROMKOTLFDAETV ALDAKRESAFLSSENLELKEVEVYNDLENEELSSKVELLREED QIKKLQEYIDSQKLENIKMUSYSLESIEDPROMKOTLFDAETV ALDAKRESAFLSENLELKEKERNELATTYKQMENDIOLYGSQLE AKKKMQVDLEKELQSAFNEITKLTSLIDGKVPKDLLCALELEGK ITDLOKELNKEVEENEALREEVILLSELKSLESEVERLRKEIQD KSEELHIITSEKDKLFSEVVLGERTREVQERLENGEKTKDLAATQ SNYKSTDQSFQNFKTLHMDFEQKYKNVLEENERMNGEIVNLSKE AQKFDSSLGALKTELSYKVGLGETKREVQERLENGENCHEATQ NRDSPLQTVEREKTLITEKLQQTLEEVKTLTQEKDDLKKQLGESL QIERQLKSDHIDTVNMNIDTQEQLRNALESLKOHGETINTLKS KISEEVSRNLHWEENTGETLOGEKTREVQERLENGMECHKNQLE NRDSPLQTVEREKTLITEKLQQTLEEVKTLTQEKDDLKKQLGESL QIERQLKSDHIDTVNMNIDTQEQLRNALESLKOHGETINTLKS KISEEVSRNLHWEENTGETLOGEKTREVQELLANGLESK KISEEVSRNLHWEENTGETLOGEKTREVQELLANGLEKTRUCKTOL ENNIKMTIENQEELRLLGGELKKOQELVAQEKNHAIKKEGELSR TCDRLAEVEEKLKEKSQQLQEKQQLLNVQERMSHKYNGTL TADVKDNEIIEQQRRIFSLOGKNELQOMLESVIAEKSQLKTDL KENIEMTIENQEERLLLGGELKLAGELKALHHLKEHGE TLDELRSSVSEKTAQIINTQLEKHTALQEEIPVLHEEQELLP NYKKVSTQCTHMELELLTGOLKKHTLARIEMEKF QESQEEIKSLTKERDNLKTIKRALEVKHDQLKEHIRETLAKIQE SQSKGEOSLINMKERDNETTKIVSEMEGPKPKDSALLEITEMLG LSKRLQESHDEMKSVAKKKDOLRIQEVUGSESQLKENIKEIV AKHLSTEELKVAHCLKKQESTINGLRVNLSEKETEISTIQKQ LEANDKLONGITYREVERVARCKERDERVERDERKERVL KELQESTDERKVLKERVARCKERDLIKGILGEVECVENELKGPKEER AKKDSALQSIESRMLEUTNILGESGEEIQIMIKKEEMKRVQEA AKHLSTEEELKVAHCLKKEGESETLINELRVNLSEKETEISTIQKG LEANDKLONKIGETYKKEDENSVYKERDI	5814	8500	432	
APIIIDSAIGGYNGTIFA\YGGT\ASGKTYTMMGSEDHLGVIFQ GOFHGHPSGKI* EVFULDEFLURGYMEIYNBTITDLLCGTQKM KPLIIREDVNRNVYVADLTBEVVYTSENALKHITKGEKSRHYGE TKMNQRSSRSHIT FRMILESREKGEPSKCEGSVKVSHLNIUVDLA GSBEAAGTGAAGVELKBGCNINGSLFILGYUKKLSGQVGGFI NYRDSKLTRILQNSLGENPKTRIICTITPVSFDEFLTALQFAST AKYMKNTPYVNEVSTDEALLKRYRKEIMDLKKQLEEVSLETRAQ AMEKDQLAQLLEEKDLLQKVONBRIENLTRMLVTSSSITLQQSL KARKRRVTMCLGKINKMKNSNYADQFNIPTNITTKTHKLSINL LRBIDESVCSSDVFSHTDTLSBIEMMPATKLLNORNIESENIN SLRADVONLULDVEQLRTBKEEMELKLKKKNDLDEFEALBRKTK KDQBMQLIHEISLKMLVKHREVYNDQLENBLSSKVELLREKED QIKKLGEYIDSQKLENIKMDLSYSLESIEDPKONKOTLFDAETV ALDAKRESAFLRSENLELKEKMKBLATTYKGMENDIOLYQSQLE AKKKMOYDLEKBLQSANDEITKLTSLIDGKVYKNLLEGK ITDLQKELNKEVEENBALREVILLSELKSLPSEVERLREKED KSEELHIISEKDKLFSEVVHKESRVGGLLEEIGKTKDDLATTQ SMYKSTDQEFONFKTLHMDEFSYKKMULEBERMNDEIVNLSKE AQKFDSSLGALKTELSYKTOELQGKTREVGERLWLGCESL QIERDQLKSDIHDTVMNIDTQDECKNALDEBLKKOLDLETINTLKS KISEEVSRILHBEBNGETKDEFOOKNYGIDKKGDLBAKNTOTL TADVKDNEIIELQQRKIFSLOGENNELGOMLEVIAAEKGUKTDL KENIEMTIENQEELRLLGGELKKQGEIVAQEKHAHIKKEGELSS TCDRLAEVEKKLKEKSQCLQEKQOGLLNVQEEMSEMGKKINEIE NIKMELKNELTLEHMETELLAGKILENYEFEMSTKERKVL KELQKSFFTERDHLRGYIREIBAGKINTHEVEFUSITKERKVL KELQKSFFTERDHLRGYIREIBAGKINTHEVEFUSITKERKVL KELQKSFFTERDHLRGYIREIBAGKINTHELGELERLENGEF OSSGEEIKSLTKERDNLKTIKBALEVKHDOLKEHIRETLAKIQE SQSKOEGSINMKEKDNETTKUVSEMEGYFKNDSALLRIEIEMG LSKRLQSHIDEMSVAKEKDDLQRLQEVLOSESDCLKENIKEIV AKHLETEELKVAHCCLKSQEETINELRUNGSEKETEISTIOKQ LEAINDKLONKIGEITYEKESQUENIKGISGVOEKVNLEKEFKERKVL LEALNDKLONKIGUTYEKSEQUENIKILRUNGEKFETEISTIOKQ LEALNDKLONKIGUTYEKSEQUENIKLRUNGEKFETEISTIOKQ LEALNDKLONKIGUTETERSEVGYFKNENSLKEFTEISTIOKQ LEALNDKLONKIGUTETTRICEGELINGLIKGISERGKKREFTEISTIOKQ LEALNDKLONKIGUTYEKSEQUENIKGISGVOEKVNELKGFKEFR KAKDSALOSIESKMLELTNRLQESBEIQIMIKEKEEMIKVOER LEALNDKLONKIGUTYEKSEVGEVOEKVELKEFKERENCE LEALNDKLONKIGUTYEKSEVGEVOEKVELKEFKERENCE LEALNDKLONKIGUTYEKSERGUTKRISTURGEREFTEISTIOKG LEALNDKLONKIGUTETERSETURGUTKRISTURGEREFTEISTIOKG LEALNDKLONKIGUTYEKSTONKTILTURGEREFTEISTIOKG LEALNDKLONKIGUTYEKSTONKTILTURGEREFTEISTIOKG LEALNDKLONKIGUTYEKSTONKTILTURGEREFTEISTIO			132	GETAOUVUUTUUTUUTUUTUUTUUTUUTUUTUUTUUTUUTUUTUU
GOPHGHPSQKI*EVFLDREFLLRVSYMEIYNETITDLLCGTORM KPLIIREDVRNTVVADLEVVTSEMALKWITKGEKSRHYGE TKMMORSSRSHIIFRMILESREKGEPSNCEGSVKVSHLNILVDLA GSERAAQTGAAGVRLKEGCNINRELFILGQVIKKLSDGQVGGFI NYRDSKLTRILQNSLGENKTRICTITPVSPDETLTALQFAST AKYMKNTPYVNEVSTDEALLKRYRKEIMDLKKOLEEVSLETRAQ AMEKDQLAQLLEEKDLI,QVDEKIFRITRALVTSSLTLQQSL KARRKRVTWCLGKINKMKNSNYADQFNIPTNITTKTHKLSINL LREIDESVCSSDVFSNTLDTLSEIBMNPATKLLNQENIESELN SLRADVDNLVDLVDEQLETIKEEMELKLKEKKNDLDEFEALERKTK KOQEMQLIHEISNLKNLVKHREVYNQDLENELSSKVELLREKED QIKKLGFYIDSQKLENIKMDLSYSLESIEDPKOMKQTLFDAETV ALDAKRESAFLRSENLELKKMKELATTYKQMENDIOLYOSGLE AKKKMQVDLEKELQSAFNETTKLTSLIDGKVPKDLLCNLELEGK ITDLGKELNKEVENBRALEVILLSELKSLPSSVERLREKEIDD KSEELHIITSEKDKLFSEVVHKESRVGGLLEEIGKTKDDLATTQ SNYKSTDGEFQNFKTLHMDFQKYKMVLEENBENNQEIVNLSKE AQKFDSSLGALKTELSYKTQELGBKTREVQERLMEMENGLKRQLE NRDSPLQTVEREKTLITEKLQQTLEEVKTTTOEKDDLKQLGESL QIERDQLKSDIHDTVMNIDTDEQLNRALESLKGHOETINTLKS KISEEVSRLHMEENTGETKDEFQQKMVGIDKKQDLEAKNTQTL TADVKLNNEI IEQQRKIFSLIQEKNELQMESVIAEKEGLKT KISEEVSRLHMEENTGETKDEFQQKMVGIDKKQDLEAKNTQTL TADVKLDNEI IEQQRKIFSLIQEKNELQMESVIAEKEGLKT KENIEMTIENGEELRLLGDELKQOEIVAQCEKNHAIKKEGGLSR TCDRLAEVEKLKEKSSGCLQEKQOGLINVQEENSEMGKKINE IE NLKNELKNELTLEHMETELAQKLNENYEEVKSITKERKVL KELQKSFETERDLRGYIRE IEATGLQTKEELKIAHIHLEHQE TIDELRRSVSEKTAGIINTQDLEKSHTKLGEEIFVHEEGELLP NVKWYSTCGETNNELELLTAR TEMBERLNEKF QESGEEIKSLTRERDNLKTIKBALEVHOOLKEHIRETLAKIGE SQSKQEGISHSLTRERDNLKTIKBALEVHOOLKEHIRETLAKIGE SQSKQEGSLNKMEKDNETTKIVSEMECPFRYKDSALIRIEIEMG LSKRLGESHDEMKSVAKEKDDLQRLQEVLOGSESDCLKENIKEIV ARHLETEELKVAHCCLKEGEETINELRVLKSKETEISTIQKG LEALNDKLONKKIOTEYTEKEEDLINKGIEVQFKYKDSALIRIEIEMGE LSKRLGESHDEMKSVAKEKDDLQRLOGVEKVOLKOFKEHR KAKDSALQSIESKMLELTNRLQESGEIQIMIKEKEMERVOGE ARHLETEEELKVAHCCLKEGGEITHIRLGUEKEMERVOGE LEALNDKLONKKIOTEYTEKEEDLINKGIEVGEKVNELKGFKEHR KAKDSALQSIESKMLELTNRLQESGEIQIMIKEKEMERVOGE ARHLETEELKVAHCCLKROETINIRLIQUIHKLEMEMERVYKERD	1			AARI IDCA TOCKNOCKERA VOOM) A GENERALI
RPLITREDVNRNVYADLTEEVYTEEMALKUTKGEKSRHYGE TKMNGRSSRSTHIFMILESREKGEPSDNCGSVEYSHLNLVDLA GSERAAQTGAAGVRLKEGCNINRSLFILGQVIKKLSDGQVGGFI NYRDSKLTRILQNSLGGPBYTRICTITPYSPBETLTALQFAST AKYMKNTPYVNEVSTDEALLKRYRKE INDLKKQLEEVSLETRAQ AMERQDAQLLEEKDLLQKVQNEKIENLTRHLVTSSSLTLQQEL KAKKRRVTWCLGKINKKNSNYADQFNIPTNITKTHKLSINL LREIDESVCSESDYFSNTLDTLSEIEWNPATKLLNQENIBSELN SLRADYDNLVLDYBQLRTEKEEMELKLKEKNDLDEFEALBRATK KOQEMQLIHEISNLKUKHREVYNQDLEMELSSKVELLREKED QIKKLQEYIDSQKLENIKMDLSYSLESIEDPKQMKQTLFDAETV ALDAKRESAFLRSENLELKEKNKELATTYKQMENDIQLYQSQLE AKKKMOVDLEKELQSAFNEITKLTSLIDGKVPKDLLCNLELEGK ITDLQKELNESVEBNEALREBVILLSELKSLPSEVERLKEGD KSEELHIITSEKDKLFSEVVYKESRVQGLLEEIGKYKDDLATTQ SNYKSTDQEFQNFKTLHMDFEQKYMVLEENERMOGIVNLSKE AQKFDSSLGALKTELSYKTQELQEKTREVQERLINEMEQLKEQLE NRDSPLQTVEREKKLISTLQQTLEEVRTLTQEKDDLKQLQESL QIERDQLKSDIHDTVNMNIDTQEQLRNALESLKOHQETINTLKS KISEBVSRNLHMEENTGETKDEFQOKMVGIDKKODLEAKNTOTL TADVKNNEIIEQQRK ISLOGKNELQOMLESVILABKEQLKTDL KRNIEMTIENQEELRLLGDENKLQOMLESVILABKEQLKTDL KRNIEMTIENQEELRLLGDELKKQQLLHVVQEEMSEMQKKINEIE NLKNELKNELTLEHMETERLELAQKLMENYEEVSKITKGRKVL KELQKSFETERDHLRGYIREIBLATQKLMENYEEVSKITKGRKVL KELQKSFETERDHLRGYIREIBLATQKLMENTEETKAITHEME GESGEEIKSLTKERDNIKTIKASHTALQEEIFVLHEEDELLP NYKKYSETQETMMELELLLIEGSTTKDSTTLARIEMERLINEKF QESGEEIKSLTKERDNIKTIKASEWEQPKPKDSALLRIEIEMLG LSKRLQESHDEMKSVAKEKDDLQRLQEVLOSESDCLKENIKETV AKHLETEELKVAHCLKEGEETINELRVNLSEKFTEISTIOKQ LEANDKLONKICGIVEKGUNKITKUSEMEGPFKPSALLRIEIEMLG LSKRLQESHDEMKSVAKEKDDLQRLQEVLOSESDCLKENIKETV AKHLETEELKVAHCLKEGEETINELRVNLSEKFTEISTIOKQ LEANDKLONKICGIVEKGUNKITKUSEMEGPFKPSALLRIEIEMLG LSKRLQESHDEMKSVAKEKDDLORLGEVLOSESDCLKENIKETV AKHLETEELKVAHCCLKEGESTITELRVNLSEKFTEISTIOKQ LEANDKLONKICGIVEKGUNKITKUSEMEGPFKPSALLRIEIEMLG LSKRLGESKMELITNRLQESQEEIQMIKKEKEEMKRVOGEA LQIERDQLKENTKEIVAKMESSOKEYCFLKMTANNETQEKMCE IEHLKEOFFTÖKNLENITETURINISEKFTEISTIOKG		1		COFFICHEON THE PROPERTY AND
TKMMQRSSRSHIT FRMILESREKGEPSNCEGSVKVSHLINLVDLA GSBRAAOTGAAGVRILKGCNINRSLFILGQVIKKLSDGVGGFI NYRDSKLTRILQNSLGGNPKTRIICTITPVSPDETLTALQFAST AKYMKNTPYVNEVSTDEALLKRYRKEIMDLKKQLEEVSLETTAQ AMBERQIAGQLEEKDLVQVONEKIENITEMLVTSSSLTLQQEL KARKRRVTWCLGKINKMKNSNYADQFNIPTNITTKTHKLSINL LREIDESVCSESDVFSNTLDTLSEIBWNPATKLINQENIESELN SLEADYDNILUTVSQLFTEKEEMELKLKEKNDLDEFEALBRKTK KOQEMQLIHEISINLKNLVKHREVYNQDLENELSSKVELLREKED QIKKLQEYIDSQKLENIKMDLSYSLESIEDPKOMKOTLFDAETV ALDAKRESAFLRSENLELKEKMKELATTYKOMENDIOLYOSQLE AKKKMOVDLEKELQSAFNEITKLTSLIDGKVPKDLLCNLELEGK ITDLQKELNKEVEENEALREEVILLSELKSLPSEVERLREIQD KESELHIITSEKDKLFSEVVHKESRVQGLLEEIGKTDLATTQ SNYKSTDQEFQNFKTLHMDFEQKYKMVLEENBEMNGEIVNLSKE AQKFDSSLGALKTELSYKTGELQEKTREVQERLNEMEQLKEQLE NRDSPLQTVEREKTLITEKLQQTLEEVKTLTQEKDDLKQLQESL QIERDQLKSDIHDTVNNNIDTQEQLRNALESLKOHOETINTLKS KISEEVSRNLHMEENTGETKDEFQOKMVGIDKKODLEAKNTOTL TADVKDNEIIEQQRKIFSLIQEKKELQMLESVIAEKCELSKNIE KISEEVSRNLHMEENTGETKDEFQOKMVGIDKKOLEAKNTOTL TADVKDNEIIEQQRKIFSLIQEKKELQMLESVIAEKCELSKTDL KRNIENTIENQEELRLLGDELKKQQEIVAQEKNHAIKKEGELSR TCDRLAEVESKLKEKSGOLEKQQCLUAVQEKNHAIKKEGELSR TCDRLAEVESKLKEKSGOLEKQQCLUAVQEKNHAIKKEGELSR TCDRLAEVESKLKAKSGOLEKQQCLUAVQEKNHAIKKEGELSR TCDRLAEVESKLKAKSGOLEKQQCIVAVGEMSEMENQKKINEIE NLKNELKNKELTLEHMETERLELAQKLNENYBEVKSITKERKVL KELQKSFETERDHLRGYIREIEATICJTKLGEIPULHEGGELLP NVKKVSETQETMNELBLLTEQSTKDSTTLARIEMERLINEKKP GESGEEIKSLTKERDNLKTIKGAETVKLOEIPULHEGGELLP NVKKVSETQETMNELBLLTEQSTKDSTTLARIEMERLINEKKP GESGEEIKSLTKERDNLKTIKABLEVKHOQLKEHIRETLAKIGE SGSKGGGGSIMMKEKDDETXIVSDEMOEPKPNDSALTRIEMLG LEKRLQESHDEMKSVAKEKDDLQRLQEVLQSESQLKENIKETU AKHLETEELKVAHCCLKSGEETINELRVILSEKTETISTIOKQ LEAINDKLONKYQEIVEKEGCLNIKGISEVGEKYOFLKENIKETV AKHLETEELKVAHCCLKSGEETINELRVILSEKTETISTIOKQ LEAINDKLONKYGEIVEKEEGLINIKGISEVGEKOFLKERER KAKDSALGSIESKMLELTNRLQESGEETQIMIKEKEEMKRVQEA LQEINDOKKUTKEIVAKKEISGEKYGFLKMTANNETGEKMCE IEHLKEGFETQKUNLENIETENIRLTGILHENLEEMRSYTKEED	Į.			KDI.TTPED/ADAUGUADI MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANAN MERURUWANA
GSERAAQTGAAQVILKEGCNINRSLFILGQVIKKLSDQVGGFI NYRDSKLTRILQNSLGGPKTRIICTITPVSPDETLTALQPAST AKYMKNTPYVNEVSTDEALLKRYRKEIMDLKKQLEEVSLETRAQ AMEKDQLAQLLEEKDLIQKVQNERIENLTRMLVTSSSLTLQQSL KARKKRKVMCLGKIKMKMSNYADQFNIPTNITTKTHKLSINL LREIDESVCSESDVFSNTLDTLSEIEWNPATKLLNQENIESELN SLRADYDNLVLDYBQLRTEKEMELKLKKKNDLDEFEALERKTK KOQEMQLIHEISNLKNLVKHREVYNDQLENEISSKVELLREKED QIKKLGEYIDSQKLENIKMDLSYSLESIEDPKOMKOTLFDAETV ALDAKRESAPLRSENLELKEKMKELATTYKQMENDIOLYOSQLE AKKKMQVDLEKELOSAFNEITKLTSLIDGKVPKDLLCNLELEGK ITDLQKELNKEVEENEALREEVILLSELKSLPSEVERLEREIQD KSBELHIITSEKDKLESVVHKESRVQGLLEEIGKTKDDLATTQ SNYKSTDQEFQNFKTLHMDFEQKYKMVLEENERMNGEIVNLSKE AQKFDSSLGALKTELSYKTQELOEKTREVQGRLENEMEQLKEQLE NRDSPLOTVSREKKTLEKLQCTLEEVKTLTQEKDDLKQLQESL QIERQLKSDIHDTVNMNIDTQEQLRNALESLKOHOETINTLKS KISEEVSRNLHMEENTGETXGDETQOKNVGIDKKODLEARNTOTL TADVKDNEIIEQQKRIFSLIGENELQCMLESVLAEKEGLKTDL KENIEMTIENQELRLLGDELKKQGIVAQEKNHAIKKEGELSR TCDRLAEVEEKLKEKSQQULNVQEEMSEMQKKINEIE NLKNELKNKELTLEHMETERLLQKLNENYEEVKSITKERKVL KELQKSFETERDHLRGYIREIBATGLQTKEBLKIAHIHLKEHQE TIDELRRSVSEKTAQIINTQDLEKSHTKLQEELPVLHEEQELLP NVKKVSETQETMMELELLITEGSTTKDSTTLARIEMERRILLEG SOSKOFGOSLNMKEKDNTETKIVSEMEDFOKRDSALLRIEIEMLG LSKRLQESHDEMKSVAKEKDDLQRLQEVQSESDQLKENIKEIV AKHLETEEBLKVAHCCLKEQEETINELRVNLSEKETEISTIQKQ LEAINDKLONKIGBIYEREINLIRURJENSEKTEISTIQKQ LEAINDKLONKIGBIYEREGOLNIKGISEVGEKWHELKEIVERL KAKDSALQSIESKMLELTNRLQESQEEIQIMIKEKEMERLYGER KAKDSALQSIESKMLELTNRLQESQEEIQIMIKEKEMERVÇEA		ľ		TKMNOPSSPSUTI FOMIL FSDEVGTBONGBONGS
NYRDSKUTRILQNSLGENPHTRILCTITPUSPDETLIALQFAST AKYMKNTPYVNEVSTDEALLKRYRKE IMDLKKQLEVSLETRAQ AMEKDQLAQLLEEKDLLQKVQNERI ENLTRMLVTSSSLTLQQEL KARKRRVTWCLGKINKKNSNYADQFNI PTNITTKTHKLSINL LREIDESVCSSBOYENLDTLSE IE BWNPATKLLNQENIESELN SLRADYDNLVLDYEQLRTEKEEMELKLKEKNDLDEFEALBRKTK KOQEMQLIHEISNLKNLVKHREYVNQDLENELSSKVELLREKED QIKKLOEYIDSQKLENIKMDLSYSLESIEDPKOMKOTLFDAETV ALDAKRESAFLRSENLELKEKMKELATTYKQMENDIQLYQSQLE AKKKMOVDLEKELQSAFNEITKLTSLIBGKVPKDLLCNLELEGK ITDLQKELNKEVEENEALREEVILLSELKSLPSEVERLRKEIQD KSEELHIITSEKDKLFSEVVHKESRVQGLLEEIGKTKDDLATTQ SNYKSTDQEFQNFKTLHMDFEQKYKMVLEENERMOGEIVNLSKE AQKFDSSLGALKTELSYKTQELQEKTREVGELIBLENEMQLKEQLE NRDSPLQTVEREKTLITEKLQQTLEEVKTLTQEKDDLKQLQESL QIERQLKSDIHDTVNNMIDTDEQLRNALESIKOROETINTLKS KISEEVSRNLHMEENTGETKGEFQOKMYGIDKKODLEAKNTQTL TADVKDNEILEQQRKIFSLIQEKNELQQMLESVIAEKEQLKTDL KENIEMTIENGELRLLGDELKQQEIVAQEKMERMQKKTDL KENIEMTIENGELRLLGDELKQQEIVAQEKMERMCKHTEIE NLKNELKNKELTLEHMETERLBLAGKLNENYEEVKSITKERKVL KELQKSFETERDLRGYIREIBATGLQTKEELKTAHIHLKEHQE TIDELRRSVSEKTAGIINTQDLEKSHTKLQEEIPVHEBGELLD NYKKVSTOETMBLELLITEQSTTKDSTTLARIEMERLRINEKF QESGEIKSLTKERDNLKTIKSALEVKHOOLKEHIRETLAKIQE SQSKOEQSLNMKEKDNETTKIVSEMERYFKPDSALLRIEIELLG LSKRLQESHDEMKSVAKEKDDLQRLQEVLQESDQLKENIKEIV AKHLETEELLKVAHCCLKCGEETIBELRVHLSEKETEISTIQKQ LEAINDKLONKIQEITSEQEETIBELRVHLSEKETEISTIQKG LEAINDKLONKIQEITSEEGLINTGQIEVGEKWELKOFKEFE KAKDSALQSIESKMLELTNRLQESQEEIQIMIKEKEEMERVQEA LEAINDKLONKICEITSEKEELLITTOTLEHNEKEFERSTYTKERD		<u> </u>		GSERALOTGALGUPI. VEGGNINEGI BIL GOVINGI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDINI GRANDI GRANDINI GRANDI GRANDI GRANDINI GRANDINI GRANDINI GRANDINI GRAND
AKYMKNTPYVNEVSTDEALLKRYRKEIMDLKKQLEEVSLETRAQ AMERODAQULEEKDLI_QKVQNEKIENLTRALVTSSLTLQGEL KAKRKRRVTWCLGKINKMKNSNYADQFNIPTNITTKTHKLSINL LREIDESVCSESDVFSNTLDTLSEIEWNPATKLINQENIESELN SLRADYDNLVLDYEQLRTEKEEMELKLKEKDLDEFEALERKTK KQDEMQLIHEISNLKNLVKHEVYNQDLENELSSKVELLREKED QIKKLQEYIDSQKLENIKMDLSYSLESIEDPKQMKQTLFDAETV ALDAKRESAFLRSENLELKEKMKELATTYKQMENDIQLYQSQLE AKKKMQVDLEKELQSAFNEITKLTSLIDGKVPKDLLCNLELGEK ITDLQKELNKEVEENEALREBVILLSELKSLPSBVERLRKEIQD KSEELHIITSEKDKLFSEVVHKESRVQGLLEEIGKTKDDLATTQ SNYKSTDQEFONFKTLHMDFEQKYKMVLEENERNNGEIVNLSKE AQKFDSSLGALKTELSYKTQELQEKTREVQERLNEMEQLKEQLE NRDSPLQTVEREKTLITEKLQQTLEEVKTLTQEKDDLKQLQESL QIENDQLKSDIHDTVMNNIDTQEQURNALESIKGHGETINTLKS KISEEVSRNLHMEENTGETKDEFQQKMVGIDKKQDLEAKNTQTL TADVKDNEIIEQQRKIFSLLQEKKDELQQMLESVIAEKEQLKTDL KENIEMTIENQEELLGBDLKKQCQEIVAQEKNHAIKEGELSR TCDRLAEVEEKLKEKSQQLQEKQQQLLNVQEEMSEMQKKINBIE NLKNELKNKELTLEHMETERLELAQKLNENYEEVKSITKERKVL KELGKSFETERDHLELLGBELKKQCGIVAGEKKIAHIKEHQE TIDELRRSVSEKTAQIINTQDLEKSHTKLQEEIPVLHEQGELLP NVKKVSETQETMNELELLTEQSTTKDSTTLARIEMERLRINEKF GESGEEIKSITKERNIKTIKEALEVKHDQLKEHIRETLAKIQE SQSKQEQSLNMKEKNDETTKIVSEMEQFKPKDSALLRIEIEMLG SQSKQEGSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG SQSKQEGSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIENLG LSKRLQESHDEMKSVAKENDDLQRLQEVLQSESDQLKENIKEIV AKHLETEELKVAHCCLKEQEETINELRVNLSEKETEISTIQKQ LEAINDKLONKIGEIYEKEEQLINKQISEVQEKVNELKQFKEFR KAKDSALQSIESKMLELTNRLQESQEEIQIMIKEKEEMKRVQEA LCERDDLKENTKEIVAKMKESQEKEUTGLKKOFKEFR KAKDSALGSIESKMLELTNRLQESQEEIQIMIKEKEEMKRVQEA LGERDQLKENTKEIVAKMKESQEKEUTGLKKOFTKERC				NYRDSKI TRILONSI GENDYTRI I GTITTOVIGIDATOVI TORI
AMEKDQLAQLLEEKDLLQKVQNEKIENLTRMLVTSSLTLQQEL KARKRRVTWCLGKINKMKNSNYADQFNIPTNITTKTHKLSINL LREIDESVCSESDVFSNTLDTLSEIEMNPATKLLNQENIESELN SLRADYDNIVLDYEQLRTEKEEMELKLKEKNDLDEFEALERKTK KOQEMQLIHEISNLKULVKHREVYNQDLENELSSKVELLREKED QIKKLQEYIDSQKLENIKMDLSYSLESIEDPKQMKOTLFDAETV ALDAKRESAFLRSENLELKEKMKELATTYKQMENDIQLYQSQLE AKKKMQVDLEKELQSAFNEITKLTSLIDGKVPKDLLCNLELEGK ITDLQKELNKEVEENEALREEVILLSELKSLPSEVERLRKEIQD KSEELHIITSEKDKLFSEVVHKESRVQGLLEEIGKTKDDLATTQ SNYKSTDQEFQNFKTLHMDFFQKYKMVLEENERMNQEIVNLSKE AQKFDSSLGALKTELSYKTQELQEKTREVQERLNEMEQLKEQLE NRDSPLQTVEREKTLITEKLQQTLEEVKTLTQEKDDLKQLQESL QIERQDLKSDIHDTWMNIDTQEQLRNALESLKQHQETINTLKS KISEBVSRNLHMEENTGETKDEFQCKMVGIDKKQDLEAKNTQTL ZENIEMTIENQELRILGDELKKQQEIVAQEKNHAIKKEGELSR TCDRLAEVEEKLKEKSQQLQEKQQQLLNVQEEMSEMQKKINBIE NLKNELINKELTLEHMETERLELAQKLNENYEEVKSITKERKVL KELQKSFETERDHLRGYIREIEATGLQTKEELKIAHILKEHGE TIDELRRSVSEKTAQIINTQDLEKSHTKLQEEIPVLHEEGGELLP NVKKVSSTQETMNELELLTEGSTTKDSTTLARIEMERLRINEKF QESQEEIKSLTKERDNLKTIKEALEVKHDOLKEHIRETLAKTQE SQSKQEGSLMMKEKKNNETTKIVSEMEQFKPKDSALLRIEIEMLG LSKRLQESHDEMKSVAKEKDDLQRLQEVLQSESDQLKENIKEIV AKHLETEELLVAHCCLKEQEETINELRVNLSEKETEISTIQKQ LEAINDKLQNKIGEIYEKEGLINKQISEVQEKVNELKOFKEER KAKDSALQSIESKMLELTNRLQESQEEIQIMIKEKEEMKRVQEA LQIERDQLKENTKEIVAKMKESQEEETQFLKMTAVUETQEKNCE IEHLKEQFFTQKLNLENTEITERLTURLTGTLHEHULEEMRSVTKERNCE	1	i		AKYMKNTPY/NEVSTDEALLKDVDVETMDLVVOLEDVOLEDVOL
KARKRRYTWCLGKINKMKNSNYADOFNIPTNITTKTHKISINL LREIDESVCSESDVFSNTLDTLSEIEWNPATKLLNQENIESELN SLRADYDNLVLDYEQLRTBKEEMELKLKEKNDLDEFEALBRKTK KOQEMQLIHEISNLKNLVHREVYNQDLENELSSKVELLREKED QIKKLQEYIDSQKLENIKMDLSYSLESIEDPKOMKQTLFDAETV ALDAKRESAFLRSENLELKEKMKELATTYKOMENDIOLYOSQLE AKKKMQVDLEKELQSAFNEITKLTSLIDGKVPKDLLCNLELEGK ITDLQKELNKEVEENEALREEVILLSELKSLPSEVERLRKEIQD KSEELHIITSEKDKLFSEVVHKESRVQGLLEEIGKKTKDLATTQ SNYKSTDQEFQNFKTLHMDFEQKYKMVLEENERMNQEIVNLSKE AQKFDSSLGALKTELSYKTQELQEKTREVQERLNEMEGLKEQLE NRDSPLQTVERRETLITEKLQQTLEEVKTLTQEKDDLKQLQESL QIERDQLKSDIHDTVNMNIDTQEQLRNALESLKOHQETINTLKS KISEEVSRNLHMEENTGETKDBFOOKMVGIDKKODLEAKNTQTL TADVKONEIIEQORKIFSLIQEKNELQQMLESVIAEKEQLKTDL KENIENTIENQEELRLLGDELKKQQETVAQEKNHAIKKEGELSR TCDRLAEVEEKLKEKSQOLQEKQQQLLNVQEEMSEMQKKINEIE NLKNELKNKELTLEHMETERLELAQKLNENYEEVKSITKERKVL KELQKSFETERBPHLRGYIREIEATGLQTKEELKIAHTHLKEHQE TIDELRRSVSEKTAQIINTQDLEKSHTKLQEEIPVLHEEQELLP NVKKVSETGETMNELELLTEGSTTKDSTTLARIEMERLRLNEKF QESQESIKSITKERDNLKTIKKSALEVKHDQLKEHIRETLAKIQE SQSKQEQSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG LSKRLQESHDEMKSVAKEKDDLQRLQEVLQSESDOLKENIKEIV AKHLETEEELKVAHCCLKEQEETINELRVNLSEKETEISTIQKQ LEAINDKLONKIQETYEKEEQLNIKQISEVQEKVNELKQFKEHR KAKDSALQSIFSKMELTNRLQESQEEIQIMIKEKEEMKRVQEA LQIERDQLKENTKEIVAKMKESQEEYQFKKMTAVNETQEKMCE IEHLKEQFETQKLNLENIETENIRITQILHENLEEMSVSTYKERD		· •		AMEKDOLAOLI EEKDI OKVONEKI ENI TEMI TEMI TEMI OKTO
LREIDESVCSESDVFSNTLDTLSEIEWNPATKLLNQENIESELN SLRADYDNILVLDYEQLRTEKEEMELKLKEKNDLDEFEALERKTK KOQEMQLIHEISNLKNLVKHREVYNQDLENELSSKVELLREKED QIKKLQEVIDSQKLENIKMDLSYSLESIEDPKQMKQTLFDAETV ALDAKRESAFLRSENLELKEKMELATTYKQMENDIOLYQSQLE AKKKMQVDLEKELOSAFNEITKLTSLIDGKVPKDLLCNLELEGK ITDLQKELNKEVEENEALREVILLSELKSLPSEVERLRKEIQD KSEELHIITSEKDKLFSEVVHKSSRVQGLLEEIGKTKDDLATTQ SNYKSTDQEFQNFKTLHMDFEQKYKMVLEENERMIQGIVNLSKE AQKFDSSLGALKTELSYKTQELQEKTREVQERINEMEQLKEQLE NRDSPLQTVEREKTLITEKLQQTLEEVKTLTQEKDDLKQLGESL QIERDQLKSDIHDTVMNNIDTOGQLRNALESLKOHOETINTLKS KISEEVSRNLHMENTGETKDEFQOKMVGIDKKODLEAKNTQTL TADVKDNEIIEQQRKIFSLIGEKNELQQMLESVIAEKEQLKTDL KENIEMTIENGEELRLLGGELKKQQETVAQEKNHAIKKEGELSR TCDRLAEVEEKLKEKSQQLQEKQQQLLNVQEEMSEMQKKINBIE NLKNELKNKELTLEHMETERLELAQKLNENYSESVESTKERKVL KELQKSFETERDHLRGYIREIEATGLQTKEELKIAHIHLKEHQE TIDELRRSVSEKTAQIINTQDLEKSITKLGEIPVLHEGQELLP NYKKVSETQETMNELELLTEQSTTKDSTTLARIEMERLRINEKF QESQEEIKSITKERDNLKTIKBALEVKHDQLKEHIRETLAKTQE SQSKQEGSLMMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG LSKRLQESHDEMKSVARKENDLLQRLQEVLQSESDQLKENIKEIV AKHLETEEELKVAHCCLKEQEETINELRVNLSEKETEISTIQKQ LEAINDKLQNKIQEIYEKEEQLNIKQISEVQEKVBELKQFKEHR KAKDSALQSIESKMELITNRLQESQEEIQIMIKEKEEMKRVQEA LQIERDQLKENTKEIVAKMESQEKEYQFLKMTAVNETQEKMCE	1	1		KAKRKRRYTWCIGKTNKMKNGNYADORNI DENITREPUTER CENTER
SLRADYDNIJULDYECLRTEKEEMELKLIKEKNDIDEFEALERKTK KDQEMQLIHEISNIKNILVKHREVYNQDLENELSSKVELLREKED QIKKLQEYIDSQKLENIKMDLSYSLESIEDPRQMKQTLFDAETV ALDAKRESAFLRSENLELKEKMKELATTYKQMENDIQLYQSQLE AKKKMQVDLEKELQSAFNEITKLTSLIDGKVPKDLLCNLELEGK ITDLQKELNKEVEENEALREPUILLSELKSLPSEVPERLRKEIQD KSEELHIITSEKDKLFSEVUHKESRVQGLLEEIGKTKDDLATTQ SNYKSTDQEFQNFKTLHMDFEQKYKMVLEENERMNOEIVNLSKE AQKFDSSLGALKTELSYKTQELQEKTREVQERLNEMEQLKEQLE NRDSPLQTVEREKTLITEKLQQTLEEVKTLTQEKDDLKQLQESL QIERDQLKSDIHDTVNMNIDTQEQURNALESLKOHOETINTLKS KISEEVSRNLHMEENTGETKDEFQQKMVGIDKKQOLEAKNTQTL TADVKOMEIIEQQRKIFSLIQEKMELQQMLESVIAEKEQLKTDL KENIEMTIENQEELRLLGDELKKQQEIVAQEKNHAIKKEGELSR TCDRLABEVEEKLKEKSQQLQEKQQQLLNVQEEMSEMQKKINEIE NIKKNELKNKELIELMHETERLELAQKLNENYEEVKSITKERKVL KELQKSFETERDHLRGYIREIEATGLQTKEELKIAHIHLKEHQE TIDELRRSVSEKTAQIINTQDLEKSHTKLQEIPVLHEEQELLP NVKKVSETQETMNELELLTEQSTTKDSTTLARIEMERLRIMEKF QESQEEIKSLTKERDNIKTIKBALEVKHOOLKEHITETLAKIQE SQSKQEQSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG LSKRLQESHDEMKSVAREKDDLQRLQEVLQSESDQLKENIKEIV AKHLETEELKAVHCCLKEQEBTINELRVNLSEKETEISTIQKQ LEAINDKLQNKIQEIYEKEEQINIKQISEVQEKVMELKQFKEHR KAKDSALQSIESKMLEHTNRLOESQEEIQIMIKEKEEMKRVQEA LQIERQDLKENTKEIVAKMKESQEKEYQFLKMTAVNETQEKMCE IEHLKEQFETQKKNLENIETEENIRLTQILHENLEEMRSVYKERD		ì		LREIDESVCSESDVFSNTI.DTI.SETEWNDATVLINOPNIRGELN
KOQENQLIHEISNLKNLVKHREYNQDLENELSSKVELLREKED QIKKLQEYIDSQKLENIKMDLSYSLESIEDFKQMKQTLFDAETV ALDAKRESAFLRSENLELKEKMKELATTYKQMENDIQLYQSQLE AKKKMQVDLEKELQSAFNEITKLTSLIDGKVPKDLLCNLELEGK ITDLQKELNKEVEENEALREBVILLSELKSLPSEVERLRKEIQD KSEELHIITSEKDKKLFSEVVHKESRVQGLLEEIGKTKKDLATTQ SNYKSTDQEFQNFKTLHMDFEQKYKMVLEENERMNQEIVNLSKE AQKFDSSLGALKTELSYKTQELQEKTREVQERLNEMEQLKEQLE NRDSPLQTVEREKTLITEKLQQTLEEVKTLTQEKDDLKQLOESL QIERQLKSDIHDTVNMNIDTQEQLRNALESLKQHQETINTLKS KISEEVSRNLHMEENTGETKDEFQQKMVGIDKKODLEAKNTQTL TADVKDNEIIEQQRKIFSLIOEKNELQQMLESVIAEKEQLKTDL KENIEMTIENQEELRLLGGDELKQQETVAQEKNHAIKKEGELSR TCDRLAEVEEKLKEKSQQLOEKQQLLNVQEEMSEMQKKINEIE NLKNELKNKELTLEHMETERLELAQKLNENYEEVKSITKERKVL KELQKSFETERDHLRGYIREIEATGLQTKEELKTAHIHLKEHQE TIDELRRSVSEKTAQIINTQDLEKSHTKLQEEIPVLHEEQELLP NVKKVSETQETMMELELLTEGSTTKDSTTLARIEMERLRINEKF QESQEEIKSLTKERDNLKTIKEALEVKHDQLKEHIRETLAKIQE SQSKQEGSLNMKEKDNETTRIVSEMEQFKPKDSALLRIEIEMLG LSKRLQESHDEMKSVAKEXDDLQRLQEVLQSESDQLKENIKEIV AKHLETEEELKVAHCCLKSQEETINELRVNLSSKETEISTIQKQ LEAINDKLQNKIQEIYEKEEQLNIKQISEVQEKVNELKGFKEHR KAKDSALQSIESKMLELTNRLQESOEEIQIMIKEKEPKERCE LEAINDKLQNKIQEIYEKEEQLNIKQISEVQEKVNELKGFKEHR KAKDSALQSIESKMLELTNRLQESOEEIQIMIKEKEEMKRVQEA LQIERDQLKENTKEIVAKMKESQEKEYQFLKMTAVNETQEKMCE IEHLKEQFETQKLNLENIETETENIRLTQILHENLEEMSSVTKERD	1			SLRADYDNLVLDYEOLRTEKEEMELKIKEKNDI.DEERALEREME
QIKKLQEYIDSQKLENIKMDLSYSLESIEDFKOMKQTLFDAETV ALDAKRESAFLRSENLELKEKMKELATTYKOMENDIOLYQSQLE AKKKMQVDLEKELQSAFNEITKLTSLIDGKVPKDLLCNLELEGK ITDLQKELNKEVEENEALREEVILLSBLKSLPSEVERLRKEIQD KSEELHIITSEKDKLFSEVVHKESRVQGLLEEIGKTKDDLATTQ SNYKSTDQEFQNFKTLHMDFEQKYKMVLEENERMNQEIVNLSKE AQKFDSSLGALKTELSYKTQELQEKTREVQERLNEMEQLKEQLE NRDSPLQTVEREKTLITEKLQQTLEEVKTLTQEKDDLKQLQESL QIERDQLKSDIHDTVNMNIDTQEQLRNALESLKQHOETINTLKS KISEEVSRNLHMEENTGETKDEFQQKMYGIDKKQDLEAKNTQTL TADVKDNEIIEQQRKIFSLIQEKNELQQMLESVIAEKEQLKTDL KENIEMTIENQEELRLLGDELKKQQEIVAQEKNHAIKKEGGLSR TCDRLAEVEEKLKEKSQQLQEKQQLLNVQEEMSEMQKKINEIE NLKNELKNKELTLEHMETERLELAQKLNENYEEVKSITKERKVL KELQKSFETERDHLRGYIREIEATGLQTKEELKIAHIHLKEHQE TIDELRRSVSEKTAQIINTQDLEKSHTKLQEEIPVLHEEQELLP NVKKVSETQETMNELELLTEQSTTKDSTTLARIEMERLRINEKF QESQEEIKSLTKERDNLKTIKEALEVKHDQLKEHIRETLAKIQE SQSKQEQSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG LSKRLQESHDEMKSVAKEKDDLQRLQEVLQSESDQLKENIKEIV AKHLETEEELKVAHCCLKEQEETINELRVNLSEKETEISTIQKQ LEAINDKLONKIQEIYEKEEQLNIKQISEVQEKVNELKQFKEHR KAKDSALQSIESKMLELTNRLQESQEEIQIMIKEKEEMRRVQEA LQIERDQLKENTKEIVAKMKESQEKEYQFLKMTAVNETQEKMCE IEHLKEQFETQKLNLENITETENIRLTQILHENLEEMSSVTKERD		i		KDQEMQLIHEISNLKNLVKHREVYNODLENELSSKVELLDEVED
ALDAKRESAFLRSENLELKEKMKELATTYKQMENDIQLYQSQLE AKKKMQVDLEKELQSAFNEITKLTSLIDGKVPKDLLCNLELEGK ITDLQKELLNKEVEENEALREEVILLSELKSLPSEVERLRKEIQD KSEELHIITSEKDKLFSEVVHKESRVQGLLEEIGKTKDDLATTQ SNYKSTDQEFQNFKTLHMDFEQKYKMVLEENERMNQEIVNLSKE AQKFDSSLGALKTELSYKTQELQEKTREVQERLIMEMEQLKEQLE NRDSPLQVTVEREKTLITEKLQQTLEEVKTLTQEKDDLKQLQESL QIERDQLKSDIHDTVNMNIDTQEQLRNALESLKOHQETINTIKS KISEEVSRNLHMEENTGETKDEFQOKMVGIDKKQDLEAKNTQTL TADVKDNEIIEQQRKIFSLIQEKNELQQMLESVIAEKEQLKTDL KENIEMTIENQEELRLLGDELKKQQEIVAQEKNHAIKKEGELSR TCDRLAEVEEKLKEKSQQLQEKQQQLLNVQEEMSEMQKKINEIE NIKNELKNKELTLEHMETERLELAQKLNENYEEVKSITKERKVL KELQKSFETERDHLRGYIREIEATGLQTKEELKIAHIHLKEHQE TIDELRRSVSEKTAQIINTQDLEKSHTKLQEEIPVLHEEQELLP NVKKVSETQETMNELELLTEQSTTKDSTTLARIEMERLRLINEKF QESQEEIKSLTKERDNLKTIKEALEVKHDQLKEHIRETLAKIQE SQSKQEQSLNNKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG LSKRLQESHDEMKSVAKEXDDLQRLQEVLQSESDQLKENIKEIV AKHLETEEELKVAHCCLKEQEETINELRVNLSEKETEISTIQKQ LEAINDKLQNKIQEIYEKEEQLNIKQISEVQEKVNELKQFKEHR KAKDSALQSIESKMLELTNRQESQEEIQIMIKEKEEMKRVQEA LQIERDQLKENTKEIVAKMKESQEKEYQPLKMTAVNETQEKMCE IEHLKEQFETQKUNLENIETENIRLTQILHENLEEMRSVTKERD	į	i i		QIKKLQEYIDSQKLENIKMDLSYSLESIEDPKOMKOTLEDARTU
AKKKMOVDLEKELQSAFNEITKLTSLIDGKVPKDLLCNLELEGK ITDLQKELNKEVEENEALREEVILLSELKSLPSEVERLRKEIQD KSEELHIITSEKDKLFSEVVHKESRVQGLLEEIGKTKDDLATTQ SNYKSTDQEFQNFKTLHMDFEQKYKMVLEENERMIQEIVNLSKE AQKFDSSLGALKTELSYKTQELQEKTREVQERLINEMEQLKEQLE NRDSPLQTVEREKTLITEKLQQTLEEVKTLTQEKDDLKQLQESL QIERDQLKSDIHDTVNMNIDTQEQRNALESLKQHQETINTLKS KISEEVSRNLHMEENTGETKDEFQOKMVGIJKKQDLEAKNTQTL TADVKDNEIIEQQRKIFSLIQEKNELQQMLESVIAEKEQLKTDL KENIEMTIENQEELRLLGDELKKQQEIVAQEKNHAIKKEGELSR TCDRLAEVEEKLKEKSQQLQEKQQQLLNVQEEMSEMQKKINEIE NLKNELKNKELTLEHMETERLELAQKLNENYEEVKSITKERKVL KELQKSFFTERDHLRGYIREIEATGLQTKEELKHAHIHLKEHQE TIDELRRSVSEKTAQIINTQDLEKSHTKLQEEIPVHHEQELLP NVKKVSETQETMNELELLTEQSTTKDSTTLARIEMERLRLNEKF QESQEEIKSLTKERDNLKTIKEALEVKHDQLKEHIRETLAKIQE SQSKQEQSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG LSKRLQESHDEMKSVAKEKDDLQRLQEVLQSESDQLKENIKEIV AKHLETEELKVAHCCLKEQEETINELRVNLSEKETEISTIQKQ LEAINDKLQNKIQEIVEKEEQLNIKQISEVQEKVNELKQFKEHR KAKDSALQSIESKMLELTURLQESGEEIQIMIKEKEEMKRVQEA LQIERDQLKENTKEIVAKMKESQEKEYQFLKMTAVNETQEKMCE IEHLKEGFETQKLKLENIETERIRITQILHENLEEMRSVTKERD		į		ALDAKRESAFLRSENLELKEKMKELATTYKOMENDIOLYOSOLE
ITDLQKELNKEVENBALREVILLSELKSLPSEVERLRKEIQD KSEELHIITSEKDKLFSEVVHKESRVQGLLEEIGKTKDDLATTQ SNYKSTDQEFQNFKTLHMDFEQKYKMVLEENERMNQEIVNLSKE AQKFDSSLGALKTELSYKTQELQEKTREVQERLNEMEQLKEQLE NRDSPLQTVEREKTLITEKLQQTLEEVKTLTQEKDDLKQLQESL QIERDQLKSDIHDTVNMNIDTQEQLRNALESLKQHQETINTLKS KISEEVSRNLHMEENTGETKDEFQQKMVGIDKKQDLEAKNTQTL TADVKDNEIIEQQRKIFSLIQERKLQQMLESVIAEKEQLKTDL KENIEMTIENQEELRLLGDELKKQQEIVAQEKNHAIKKEGELSR TCDRLAEVEEKLKEKSQQLQEKQQQLLNVQEEMSEMQKKINEIE NLKNELKNKELTLEHMETERLELAQKLNENYEEVKSITKERKVL KELQKSFETERDHLRGYIREIEATGLQTKEELKIAHIHLKEHQE TIDELRRSVSEKTAQIINTQDLEKSHTKLQEEIPVLHEEQELLP NVKKVSETQETMNELELLTEQSTKDSTTLARIEMERLRLNEKF QESQEEIKSLTKERDNLKTIKBALEVKHDQLKEHIRETLAKIQE SQSKQEGSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG LSKRLQESHDEMKSVAKEKDDLQRLQEVLQSESDQLKENIKEIV AKHLETEEELKVAHCCLKEQEBTINELRVNLSEKETEISTIQKQ LEAINDKLQNKIQEIYEKEEQLNIKQISEVQEKVNELKQFKERR KAKDSALQSIESKMLELTNRLQESQEEIQIMIKEKEMERKVQEA LQIERDOLKENTKEIVAKMKESQEKEYQFLKMTAVNETQEKMCE	1	1	j	AKKKMQVDLEKELQSAFNEITKLTSLIDGKVPKDLLCNIFIFGK
KSEELHIITSEKDKLESEVUHKESRVQGLLEEIGKTKDDLATTQ SNYKSTDQEFQNFKTLHMDFEQKYKMVLEENERNNQEIVNLSKE AQKFDSSLGALKTELSYKTQELQEKTREVQERLNEMEQLKEQLE NRDSPLQTVEREKTLITEKLQQTLEEVKTLTQEKDDLKQLQESL QIERDQLKSDIHDTVNMNIDTQEQLRNALESLKOHQETINTLKS KISEEVSRNLHMEENTGETKDEFQQKMVGIDKKQDLEAKNTQTL TADVKDNEI IEQQRKIFSLIQEKNELQQMLESVIAEKEQLKTDL KENIEMTIENQEELRLLGDELKKQQEIVAQEKNHAIKKEGELSR TCDRLAEVEEKLKEKSQQLQEKQQLLNVQEEMSEMQKKINEIE NLKNELKNKELTLEHMETERLELAQKLNENVEEVKSITKERKVL KELQKSFFTERDHLRGYIREIEATGLQTKEELKIAHIHLKEHQE TIDELRRSVSEKTAQIINTQDLEKSHTKLQEEIPVLHEEQELLP NVKKVSETQETMNELELLTEQSTTKDSTTLARIEMERLRLNEKF QESQEEIKSLTKERDNLKTIKEALEVKHDQLKEHIRETLAKIQE SQSKQEQSLNMKEKDNETTKIVSEMEQFFPKDSALLRIEIEMLG LSKRLQESHDEMKSVAKEKDDLQRLQEVLQSESDQLKENIKEIV AKHLETEEELKVAHCCLKEQEBTINELRVNLSEKETEISTIQKQ LEAINDKLQNKIQEIYEKEEQLNIKQISEVQEKVNELKQFKEHR KAKDSALQSIESKMLELTNRLQESQEEIQIMIKEKEMKRVQEA LQIERDQLKENTKEIVAKMKESQEKEYQFLKMTAVNETQEKMCE IEHLKEQFETQKLNLENIETENIRLTQLIHENLEEMRSVTKERD		1		ITDLQKELNKEVEENEALREEVILLSELKSLPSEVERLRKETOD
SNYKSTOQEFQNFKTLHMDFEQKYKMVLEENERMNQEIVNLSKE AQKFDSSLGALKTELSYKTQELQEKTREVQERLNEMEQLKEQLE NRDSPLQTVEREKTLITEKLQQTLEEVKTLTQEKDDLKQLQESL QIERDQLKSDIHDTVNMNIDTQEQLRNALESLKQHQETINTLKS KISEEVSRNLHMEENTGETKDEFQQKMVGIDKKQDLEAKNTQTL TADVKDNEIIEQQRKIFSLIQEKNELQQMLESVIAEKEQLKTDL KENIEMTIENQEELRLLGDELKKQQEIVAQEKNHAIKKEGELSR TCDRLAEVEEKLKEKSQQLQEKQQQLLNVQEEMSEMQKKINEIE NLKNELKNKELTLEHMETERLELAQKLNENYEEVKSITKERKVL KELQKSFETERDHLRGYIREIEATGLQTKEELKIAHIHLKEHQE TIDELRRSVSEKTAQIINTQDLEKSHTKLQEEIPVLHEEQELLP NVKKVSETQETMNELELLTEQSTTKDSTTLARIEMERLRINEKF QESQEEIKSLTKERDNLKTIKEALEVKHDQLKEHIRETLAKIQE SQSKQEQSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG LSKRLQESHDEMKSVAKEKDDLQRLQEVLQSESDQLKENIKEIV AKHLETEELKVAHCCLKEQEETINELRVNLSEKETEISTIQKQ LEAINDKLQKIQEIYEKEEQLNIKQISEVQEKVNELKQFKEFR KAKDSALQSIESKMLELTNRLQESQEIQIMIKEKEEMKRVQEA LQIERDQLKENTKEIVAKMKESQEKEYQFLKMTAVNETQEKMCE IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD	1	]		KSEELHIITSEKDKLFSEVVHKESRVOGLLEEIGKTKDDLATTO
AQKFDSSLGALKTELSYKTQELQEKTREVQERLNEMEQLKEQLE NRDSPLQTVEREKTLITEKLQQTLEEVKTLTQEKDDLKQLQESL QIERDQLKSDIHDTVNMNIDTQEQUNALESLKQHQETINTLKS KISEEVSRNLHMEENTGETKDEFQQKMVGIDKKQDLEAKNTQTL TADVKDNEIIEQQRKIFSLIGEKNELQQMLESVIAEKEQLKTDL KENIEMTIENQEELRLLGDELKKQQEIVAQEKNHAIKKEGELSR TCDRLAEVEEKLKEKSQQLQEKQQQLLNVQEEMSEMQKKINEIE NLKNELKNKELTLEHMETERLBLAQKLNENYEEVKSITKERKVL KELQKSFETERDHLRGYIREIEATGLQTKEELKIAHIHLKEHQE TIDELRRSVSEKTAQIINTQDLEKSHTKLQEEIPVLHEEQELLP NVKKVSETQETMMELELLTEQSTTKDSTTLARIEMERLRLNEKF QESQEEIKSLTKERDNLKTIKBALEVKHDQLKEHIRETLAKIQE SQSKQEQSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG LSKRLQESHDEMKSVAKEKDDLQRLQEVLQSESDQLKENIKEIV AKHLETEEELKVAHCCLKEQEBTINELRVNLSEKETEISTIQKQ LEAINDKLQNKIQEIYEKEEQLNIKQISEVQEKVNELKQFKEHR KAKDSALQSIESKMLELTNRLQESQEIQIMIKEKEEMKRVQEA LQIERDQLKENTKEIVAKMKESQEKEYQFLKMTAVNETQEKMCE IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD	1	1 1		SNYKSTDQEFQNFKTLHMDFEQKYKMVLEENERMNOFIVNISKE
NRDSPLQTVEREKTLITEKLQQTLEEVKTLTQEKDDLKQLQESL QIERDQLKSDIHDTVNNNIDTQEQLRNALESLKQHQETINTLKS KISEEVSRNLHMEENTGETKDEFQQKMVGIDKKQDLEAKNTQTL TADVKDNEIIEQQRKIFSLIQEKNELQQMLESVIAEKEQLKTDL KENIEMTIENQEELRLLGDELKKQQEIVAQEKNHAIKKEGELSR TCDRLAEVEEKLKEKSQQLQEKQQQLLNVQEEMSEMQKKINEIE NLKNELKNKELTLEHMETERLELAQKLNENYEEVKSITKERKVL KELQKSFETERDHLRGYIREIEATGLQTKEELKIAHIHLKEHQE TIDELRRSVSEKTAQIINTQDLEKSHTKLQEEIPVLHEEQELLP NVKKVSETQETMNELELLTEQSTTKDSTTLARIEMERLRLNEKF QESQEEIKSLTKERDNLKTIKEALEVKHDQLKEHIRETLAKIQE SQSKQEQSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG LSKRLQESHDEMKSVAKEKDDLQRLQEVLQSESDQLKENIKEIV AKHLETEEELKVAHCCLKEQEBTINELRVNLSEKETEISTIQKQ LEAINDKLQNKIQEIYEKEEQLNIKQISEVQEKVNELKQFKEER KAKDSALQSIESKMLELTNRLQESQEIQIMIKEKEEMKRVQEA LQIERDQLKENTKEIVAKMKESQEKEYQFLKMTAVNETQEKMCE IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD	i			AQKFDSSLGALKTELSYKTQELQEKTREVOERLNEMEOLKEOLE
QIERDQLKSDIHDTVNMNIDTQEQLRNALESLKQHQETINTLKS KISEEVSRNLHMEENTGETKDEFQQKMVGIDKKQDLEAKNTQTL TADVKDNEIIEQQRKIFSLIQEKNELQQMLESVIAEKEQLKTDL KENIEMTIENQEELRLLGDBELKKQQEIVAQEKNHAIKKEGELSR TCDRLAEVEEKLKEKSQQLQEKQQQLLNVQEEMSEMQKKINEIE NLKNELKNKELTLEHMETERLELAQKLNENYEEVKSITKERKVL KELQKSFETERDHLRGYIREIEATGLQTKEELKIAHIHLKEHQE TIDELRRSVSEKTAQIINTQDLEKSHTKLQEEIPVLHEEQELLP NVKKVSETQETMNELELLTEQSTTKDSTTLARIEMERLRINEKF QESQEEIKSLTKERDNLKTIKBALEVKHDQLKEHIRETLAKIQE SQSKQEQSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG LSKRLQESHDEMKSVAKEKDDLQRLQEVLQSESDQLKENIKEIV AKHLETEEELKVAHCCLKEQEBTINELRVNLSEKETEISTIQKQ LEAINDKLQNKIQEIYEKEEQLNIKQISEVQEKVNELKQFKEER KAKDSALQSIESKMLELTNRLQESQEEIQIMIKEKEEMRSVQEA LQIERDQLKENTKEIVAKMKESQEKEYQFLKMTAVNETQEKMCE IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD	1	1		NRDSPLQTVEREKTLITEKLQQTLEEVKTLTOEKDDLKOLOESI.
KISEEVSRNLHMEENTGETKDEFQQKMVGIDKKQDLEAKNTQTL TADVKDNEI IEQQRKIFSLIDEKNELQQMLESVIAEKEQLKTDL KENIEMTIENQEELRLLGDELKKQQEIVAQEKNHAIKKEGELSR TCDRLAEVEEKLKEKSQQLQEKQQQLLNVQEEMSEMQKKINEIE NLKNELKNKELTLEHMETERLELAQKLNENYEEVKSITKERKVL KELQKSFETERDHLRGYIREIEATGLQTKEELKIAHIHLKEHQE TIDELRRSVSEKTAQIINTQDLEKSHTKLQEEIPVLHEEQELLP NVKKVSETQETMNELELLTEQSTTKDSTTLARIEMERLRLNEKF QESQEEIKSLTKERDNLKTIKEALEVKHDQLKEHIRETLAKIQE SQSKQEQSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG LSKRLQESHDEMKSVAKEKDDLQRLQEVLQSESDQLKENIKEIV AKHLETEEELKVAHCCLKEQEETINELRVNLSEKETEISTIQKQ LEAINDKLQNKIQEIYEKEEQLNIKQISEVQEKVNELKQFKEFRE KAKDSALQSIESKMLELTNRLQESQEEIQIMIKEKEEMKRVQEA LQIERDQLKENTKEIVAKMKESQEKEYQFLKMTAVNETQEKMCE IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD		1		QIERDQLKSDIHDTVNMNIDTQEQLRNALESLKOHOETINTIKS
TADVKONEI IEQQRKIFSLIQEKNELQQMLESVIAEKEQLKTDL KENIEMTIENQEELRLLGDELKKQQEIVAQEKNHAIKKEGELSR TCDRLAEVEEKLKEKSQQLQEKQQQLLINVQEEMSEMQKKINEIE NLKNELKNKELTLEHMETERLELAQKLNENYEEVKSITKERKVL KELQKSFETERDHLRGYIREIEATGLQTKEELKIAHIHLKEHQE TIDELRRSVSEKTAQIINTQDLEKSHTKLQEEIPVLHEEQELLP NVKKVSETQETMNELELLTEQSTTKDSTTLARIEMERLRLNEKF QESQEEIKSLTKERDNLKTIKEALEVKHDQLKEHIRETLAKIQE SQSKQEQSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG LSKRLQESHDEMKSVAKEKDDLQRLQEVLQSESDQLKENIKEIV AKHLETEEELKVAHCCLKEQEBTINELRVNLSEKETEISTIQKQ LEAINDKLQNKIQEIYEKEEQLNIKQISEVQEKVNELKGFKEHR KAKDSALQSIESKMLELTNRLQESQEIQIMIKEKEEMKRVQEA LQIERDQLKENTKEIVAKMKESQEKEYQFLKMTAVNETQEKMCE IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD		1		KISEEVSRNLHMEENTGETKDEFQQKMVGIDKKODLEAKNTOTI.
KENIEMTIENQEELRLLGDELKKQQEIVAQEKNHAIKKEGELSR TCDRLAEVEEKLEKEKSQQLQEKQQQLLNVQEEMSEMQKKINEIE NLKNELKNKELTLEHMETERLELAQKLNENYEEVKSITKERKVL KELQKSFETERDHLRGYIREIEATGLQTKEELKIAHIHLKEHQE TIDELRRSVSEKTAQIINTQDLEKSHTKLQEEIPVLHEEQELLP NVKKVSETQETMNELELLTEQSTTKDSTTLARIEMERLRLNEKF QESQEEIKSLTKERDNLKTIKEALEVKHDQLKEHIRETLAKIQE SQSKQEQSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG LSKRLQESHDEMKSVAKEKDDLQRLQEVLQSESDQLKENIKEIV AKHLETEEELKVAHCCLKEQEBTINELRVNLSEKETEISTIQKQ LEAINDKLQNKIQEIYEKEEQLNIKQISEVQEKVNELKGFKEFR KAKDSALQSIESKMLELTNRLQESQEIQIMIKEKEEMKRVQEA LQIERDQLKENTKEIVAKMKESQEKEYQFLKMTAVNETQEKMCE IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD	(	1		TADVKDNEI IEQQRKIFSLIQEKNELQQMLESVIAEKEOLKTDI.
TCDRLAEVEEKLKEKSQQLQEKQQQLLNVQEEMSEMQKKINEIE  NLKNELKNKELTLEHMETERLBLAQKLNENYEEVKSITKERKVL  KELQKSFETERDHLRGYIREIBATGLQTKEELKIAHIHLKEHQE  TIDELRRSVSEKTAQIINTQDLEKSHTKLQEEIPVLHEEQELLP  NVKKVSETQETMNELBLLTEQSTTKDSTTLARIEMERLRLNEKF  QESQEEIKSLTKERDNLKTIKBALEVKHDQLKEHIRETLAKIQE  SQSKQEQSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG  LSKRLQESHDEMKSVAKEKDDLQRLQEVLQSESDQLKENIKEIV  AKHLETEEBLKVAHCCLKEQEBTINELRVNLSEKETEISTIQKQ  LEAINDKLQNKIQEIYEKEEQLNIKQISEVQEKVNELKQFKEHR  KAKDSALQSIESKMLELTNRLQESQEIQIMIKEKEEMKRVQEA  LQIERDQLKENTKEIVAKMKESQEKEYQFLKMTAVNETQEKMCE  IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD		1	ŀ	KENIEMTIENQEELRLLGDELKKQOEIVAOEKNHAIKKEGELSD
NLKNELKNKELTLEHMETERLBLAQKLNENYEEVKSITKERKVL  KELQKSFETERDHLRGYIREIBATGLQTKEELKIAHIHLKEHQE  TIDELRRSVSEKTAQIINTQDLEKSHTKLQEEIPVLHEEQELLP  NVKKVSETQETMNELELLTEQSTTKDSTTLARIEMERLRLNEKF  QESQEEIKSLTKERDNLKTIKEALEVKHDQLKEHIRETLAKIQE  SQSKQEQSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG  LSKRLQESHDEMKSVAKEKDDLQRLQEVLQSESDQLKENIKEIV  AKHLETEEELKVAHCCLKEQEBTINELRVNLSEKETEISTIQKQ  LEAINDKLQNKIQEIYEKEEQLNIKQISEVQEKVNELKQFKEER  KAKDSALQSIESKMLELTNRLQESQEIQIMIKEKEEMKRVQEA  LQIERDQLKENTKEIVAKMKESQEKEYQFLKMTAVNETQEKMCE  IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD		į	ļ	TCDRLAEVEEKLKEKSQQLQEKQQQLLNVQEEMSEMOKKTNETE
KELQKSFETERDHLRGYIREIEATGLQTKEELKIAHIHLKEHQE TIDELRRSVSEKTAQIINTQDLEKSHTKLQEEIPVLHEEQELLP NVKKVSETQETMNELELLTEQSTTKDSTTLARIEMERLRINEKF QESQEEIKSLTKERDNLKTIKBALEVKHDQLKEHIRETLAKIQE SQSKQEQSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG LSKRLQESHDEMKSVAKEKDDLQRLQEVLQSESDQLKENIKEIV AKHLETEEELKVAHCCLKEQEBTINELRVNLSEKETEISTIQKQ LEAINDKLQNKIQEIYEKEEQLNIKQISEVQEKVNELKQFKEER KAKDSALQSIESKMLELTNRLQESQEEIQIMIKEKEEMKRVQEA LQIERDQLKENTKEIVAKMKESQEKEYQFLKMTAVNETQEKMCE IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD		1		NLKNELKNKELTLEHMETERLELAQKLNENYEEVKSITKERKVI.
TIDELRRSVSEKTAQIINTQDLEKSHTKLQEEIPVLHEEQELLP NVKKVSETQETMNELELLTEQSTTKDSTTLARIEMERLRLNEKF QESQEEIKSLTKERDNLKTIKEALEVKHDQLKEHIRETLAKIQE SQSKQEQSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG LSKRLQESHDEMKSVAKEKDDLQRLQEVLQSESDQLKENIKEIV AKHLETEEELKVAHCCLKEQEETINELRVNLSEKETEISTIQKQ LEAINDKLQNKIQEIYEKEEQLNIKQISEVQEKVNELKQFKEHR KAKDSALQSIESKMLELTNRLQESQEEIQIMIKEKEEMKRVQEA LQIERDQLKENTKEIVAKMKESQEKEYQFLKMTAVNETQEKMCE IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD				KELQKSFETERDHLRGYIREIEATGLOTKEELKIAHIHLKEHOE
NVKKVSETQETMNELELLTEQSTTKDSTTLARIEMERLRLNEKF QESQEEIKSLTKERDNLKTIKBALEVKHDQLKEHIRETLAKIQE SQSKQEQSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG LSKRLQESHDEMKSVAKEKDDLQRLQEVLQSESDQLKENIKEIV AKHLETEEELKVAHCCLKEQEBTINELRVNLSEKETEISTIQKQ LEAINDKLQNKIQEIYEKEEQLNIKQISEVQEKVNELKQFKEHR KAKDSALQSIESKMLELTNRLQESQEEIQIMIKEKEEMKRVQEA LQIERDQLKENTKEIVAKMKESQEKEYQFLKMTAVNETQEKMCE IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD				TIDELRRSVSEKTAQIINTQDLEKSHTKLQEEIPVLHEEOELLP
SQSKQEQSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG LSKRLQESHDEMKSVAKEKDDLQRLQEVLQSESDQLKENIKEIV AKHLETEEELKVAHCCLKEQEBTINELRVNLSEKETEISTIQKQ LEAINDKLQNKIQEIYEKEEQLNIKQISEVQEKVNELKQFKEHR KAKDSALQSIESKMLELTNRLQESQEIQIMIKEKEEMKRVQEA LQIERDQLKENTKEIVAKMKESQEKEYQFLKMTAVNETQEKMCE IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD	}	1		NVKKVSETQETMNELELLTEQSTTKDSTTLARIEMERLRINEKF
LSKRLQESHDEMKSVAKEKDDLQRLQEVLQSESDQLKENIKEIV AKHLETEEELKVAHCCLKEQEBTINELRVNLSEKETEISTIQKQ LEAINDKLQNKIQEIYEKEEQLNIKQISEVQEKVNELKQFKEHR KAKDSALQSIESKMLELTNRLQESQEIQIMIKEKEEMKRVQEA LQIERDQLKENTKEIVAKMKESQEKEYQFLKMTAVNETQEKMCE IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD	1	1		QESQEEIKSLTKERDNLKTIKEALEVKHDQLKEHIRETLAKIQE
AKHLETEEELKVAHCCLKEQEBTINELRVNLSEKETEISTIQKQ LEAINDKLQNKIQEIYEKEEQINIKQISEVQEKVNELKQFKEER KAKDSALQSIESKMLELTNRLQESQEEIQIMIKEKEEBMRRVQEA LQIERDQLKENTKEIVAKMKESQEKEYQFLKMTAVNETQEKMCE IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD	1	1		SQSKQEQSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG
AKHLETEEELKVAHCCLKEQEBTINELRVNLSEKETEISTIQKQ LEAINDKLQNKIQEIYEKEEQINIKQISEVQEKVNELKQFKEER KAKDSALQSIESKMLELTNRLQESQEEIQIMIKEKEEBMRRVQEA LQIERDQLKENTKEIVAKMKESQEKEYQFLKMTAVNETQEKMCE IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD	1			LSKRLQESHDEMKSVAKEKDDLQRLQEVLQSESDQLKENIKEIV
LEAINDKLQNKIQEIYEKEEQLNIKQISEVQEKVNELKQFKEHR KAKDSALQSIESKMLELTNRLQESQEEIQIMIKEKEEMKRVQEA LQIERDQLKENTKEIVAKMKESQEKEYQFLKMTAVNETQEKMCE IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD		1		AKHLETEEELKVAHCCLKEQEETINELRVNLSEKETEISTIOKO
KAKDSALQSIESKMLELTNRLQESQEEIQIMIKEKEEMKRVQEA LQIERDQLKENTKEIVAKMKESQEKEYQFLKMTAVNETQEKMCE IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD	1		]	LEAINDKLQNKIQEIYEKEEQLNIKQISEVOEKVNELKOFKEFR
LQIERDQLKENTKEIVAKMKESQEKEYQFLKMTAVNETQEKMCE IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD			i	KAKDSALQSIESKMLELTNRLQESQEEIQIMIKEKEEMKRVORA
IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD			j	LQIERDQLKENTKEIVAKMKESQEKEYQFLKMTAVNETOEKMCE
DLRSVEETLKVERDQLKENLRETITRDLEKQEELKIVHMHLKEH				IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD
	L	<del>-</del>		DLRSVEETLKVERDQLKENLRETITRDLEKQEELKIVHMHLKEH

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ı	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
- 1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
i	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	(Codon, /=possible nucleotide deletion
<del></del>	Bedacuce		\=possible nucleotide insertion)
- 1	ļ	1	QETIDKLRGIVSEKTNEISNMQKDLEHSNDALKAQDLKIQEELR
[	İ		IAHMHLKEQQETIDKLRGIVSEKTDKLSNMOKDI ENSNAKI OFK
- 1		1	1 OELKANEHQLITLKKOVNETOKKVSEMEOLKKOTKDOSLET SK
į		1	LEIENLNLAQKLHENLEEMKSVMKERDNI.PRVERTI.KI.PRDOIL
1	1		ESLOETKARDLEIQQELKTARMLSKEHKETVDKT.DEKTGEVETA
	1	į.	ISDIQKDLDKSKDELQKKIQELQKKELQLLRVKEDVNMSHKKIN
i i			EMEQLKKQFEPNYLCKCEMDNFQLTKKLHESLEEIRIVAKERDE
1			LRRIKESLKMERDQFIATLREMIARDRQNHQVKPEKRLLSDGQQ
			HLMESLREKCSRIKELLKRYSEMDDHYECLNRLSLDLEKEIEFH
- 1	•		RIMKKLKYVLSYVTKIKEEQHECINKFEMDFIDEVEKQKELLIK
			IQHLQQDCDVPSRELRDLKLNQNMDLHIEEILKDFSESEFPSIK
	i	1	TEFQQVLSNRKEMTQFLEEWLNTRFDIEKLKNGIQKENDRICQV
1	]	1	NNFFNNRIIAIMNESTEFEERSATISKEWEQDLKSLKEKNEKLF
	1		KNYOTI, KTSI A SCAONAIDERODANAISE MEQDLKSLKEKNEKLF
Į		1	KNYQTLKTSLASGAQVNPTTQDNKNPHVTSRATQLTTEKIRELE
	1	1	NSLHEAKESAMHKESKIIKMQKELEVTNDIIAKLQAKVHESNKC
1	1		LEKTKETIQVLQDKVALGAKPYKEEIEDLKMKLGKIDLEKMKNA
			KEFEKEISATKATVEYQKEVIRLLRENLRRSQQAQDTSVISEHT
1	j	•	DPQPSNKPLTCGGGSGIVQNTKALILKSEHIRLEKEISKLKQQN
1			EQLIKQKNELLSNNQHLSNEVKTWKERTLKREAHKQVTCENSPK
İ			SPKVTGTASKKKQITPSQCKERNLQDPVPKESPKSCFFDSRSKS
ŀ	1		LPSPHPVRYFDNSSLGLCPEVQNAGAESVDSQP\GPWARLFQGK DVP\ECKTQ
5815	23	1460	
<b>!</b>		1400	SELVMWTVQNRESLGLLSFPVMITMVCCAHSTNEPSNMSYVKET
1			VDRLLKGYDIRLRPDFGGPPVDVGMRIDVASIDMVSEVNMDYTL
1			TMYFQQSWKDKRLSYSGIPLNLTLDNRVADQLWVPDTYFLNDKK
	1 1		SFVHGVTVKNRMIRLHPDGTVLYGLRITTTAACMMDLRRYPLDE
	1		QNCTLEIESYGYTTDDIEFYWNGGEGAVTGVNKIELPQFSIVDY
1	1 1		KMVSKKVEFTTGAYPRLSLSFRLKRNIGYFILQTYMPSTLITIL
	i i		SWVSFWINYDASAARVALGITTVLTMTTISTHLRETLPKIPYVK
			AIDIYLMGCFVFVFLALLEYAFVNYIFFGKGPQKKGASKQDQSA
1	1		NEKNKLEMNKVQVDAHGNILLSTLEIRNETSGSEVLTSVSDPKA
1	1		IMISIDSASIQYRKPLSSRE\A*GRAPDRHGVPSKGRIPPPAG\
5816	861	191	QUAVAIPULTUVNSIDKWSRMFFPITFSLFNVVVWI.VVVIII
	1 332 1	191	TSSRSRAAAQEGDAETPGSVERRGRRAGAEDGMSQAPGAQPSPP
	1		TVYHERQRLELCAVHALNNVLQQQLFSQEAADBICKRLAPDSRL
	j i		NPHRSLLGTGNYDVNVIMAALQGLGLAAVWWDRRRPLSQLALPQ
	<u>†</u>		VLGLILNLPSPVSLGLLSLPLRRRHLRNPCARL/VTVSYYNLDS
1	1		K\LRAPEGPGGLRTE*GPFLAAALAQGLCEVLLVVTKEVEEKG
5817	851		SWERTD
1 -32.	]	118	RLFRGPGANRGRSCRGCSGGREPSGGALPKRHCPC*PPSPPAAD
	]		VMSNTTVPNAPQANSDSMVGYVLGPFFLITLVGVVVAXAMVVOV
			KKKVDKLRHHLLPMYSYDPAEELHEAEGELLSDMGDDKXX/OAG
1			RVATSTSGCHCWMSRRDLTPLPHPSEPGVLDCLGPCHLLDLLSP
1			GSPCWVLGLHFSLHPPSAASASHALTTTSI,PDGI,I,DEVGUET TA
5818	3		HPQALMGRGFPSGMAAAGRHLCFL
	, ,	3918	QALRDKLWIFLVQSFYAVRHTESWKLMSTDDQQKIQAAAFDKGD
1	1	1	DRRIGKKPIFSSSQQRKOVSDSGDIKIKSWRGNNKKECWEVI.cm
1 .	!		NKKMKSDGLGASGHSSSTNRNSINKTLKODDVKEKDGTKTASKT
			TKELKTGGKNVSGKPKTVTKSKTENGDKARLENMSPROWERSA
	[		TAAAAATGQKNLLNGKGVRNOEGOISGARPKVITGNINVOAKAY
l i	i	ĺ	PLKKATGKDSPCLSIAGPSSRSTDSSMEFSISTECLDEDKENGS
i l			TEEEKPSGHKLSFCDSPGQMMKNSVDSVKNSTVAIKSRPVSRVT
		1	NGTSNKKSIHEQDTNVNNSVLKKVSGKGCSEDVDOATLVVDCTC
[ ]		ļ	NGCTAAQQRTKSTPSNLTKTOGSOGESPNSVKSSVSSPOSDENV
; 1		j	AKLDHNTTTEKQAPKRKMVKQVHTALPKVNAKIVAMPKNLNQSK
1		1	KGETLNNKDSKQKMPPGQVISKTQPSSQRPLKHETSTVQKSMFH
		1	DVRDNNNKDSVSEQKPHKPLINLASEISDAFALOSSCRD\ DDOK
	•	!	PLNDQEKEKLALECQNISKLDKSLKHELESKQICLDKSETKFPN
J Í		]	HKETDDCDAANICCHSVGSDNVNSKFYSTTALKYMVSNPNENSL
l j		1	NSNPVCDLDSTSAGQIHLISDRENQVGRKDTNKQSSIKCVEDVS
L l			LCNPERTNGTLNSAQEDKKSKVPVEGLTIPSKLSDESAMDEDKH
			PARTICION POR LEGIT I PSKUSUESAMDEDKH

SEO	Predicted	Predicted end	Amino poid
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
ĺ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
İ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ı	amino acid	sequence	Codon, /=possible nucleotide deletion,
j	sequence	1	\=possible nucleotide insertion)
	· · · · · · · · · · · · · · · · · · ·		ATADSDVSSKCFSGQLSEKNSPKNMETSESPESHETPETPFVGH
ì	J	1	WNLSTGVLHQRESPESDTGSATTSSDD1KPRSEDYDAGGSQDDD
1	1		GSNDRGISKCGTMLCHDFLGRSSSDTSTPEELKIYDSNLRIEVK
			MKKQSSNDLFQVNSTSDDEIPRKRPEIWSRSAIVHSRERENIPR
	ĺ	į	GSVQFAQEIDQVSSSADETEDERSEAENVAENFSISNPAPQQFQ
1	i ·		GIINLAFEDATENECREFSANKKFKRSVLLSVDECEELGSDEGE
			VHTPFQASVDSFSPSDVFDGISHEHHGRTCYSRFSRESEDNILE
			CKQNKGNSVCKNESTVLDLSSIDSSRKNKQSVSATEKKNTIDVL
1	ļ	}	SSRSRQLLREDKKVNNGSNVENDIQQRSKFLDSDVKSQERPCHL
	İ		DLHQREPNSDIPKNSSTKSLDSFRSQVLPQEGPVKESHSTTTEK
}			ANIALSAGDIDDCDTLAQTRMYDHRPSKTLSPIYEMDVIEAFEQ
1	1		KVESETHVTDMDF*DDQHFAKQDWTLLKQLLSEQDSNLDVTNSV
ı	1		PEDLSLAQYLINQTLLLARDSSKPQGITHIDTLNRWSELTSPLD
	<u> </u>		SSASITMASFSSEDCSPQGEWTILELETQH
5819	1	5557	AAAGLLGALHLVMTLVVAAARAEKEAFVQSESIIEVLRFDDGGL
			LQTETTLGLSSYQQKSISLYRGNCRPIRFEPPMLDFHEQPVGMP
	[	] =	KMEKVYLHNPSSE*TITLVSIFATTSHFHASFFQNRKILPGGNT
	i l		SFDVS/VFLARVVGNVENTLFINTSNHGVFTY\QVFGVGVPNPY
}			RLRPFLGARVTVNSSFSPIINIHNPHSEPLQVVEMYSSGGDLHL
1	i l		ELPTGQQGGTRKLWEIPPYETKGVMRASFSSREADNHTAFIRIK
			TNASDSTEFIILPVEVEVTTAPGIYSSTEMLDFGTLRTODLDKV
			LNLHLLNSGTKDVPITSVRPTPQ\NDAITVHFKPITLKAS\ESK
}			YTKVASISFDASKAKKPSQFSGKITVKAKEKSYSKLEIPYOAFV
			LDGYLGFDHAATLFHIRDSPADPVERPIYLTNTFSFAILTHDVI
1			LPEEAKTMFKVHNFSKPVLILPNESGYIFTLLFMPSTSSMHIDN
			NILLITNASKFHLPVRVYTGFLDYFVLPPKIEERFIDFGVLSAT
[ ]			EASNILFAIINSNPIELAIKSWHIIGDG\LSIELVAVDRGNRTT
1			IISSLPECEKSSSSDQSSVTLASGYF\AVFRVKLTAKKL\EGIH
]	1		DGAIQITTDYEILTIPVK\AVIAVGSLTCSPKHVVI.ppsfpckt
	İ		VHQSLNIMNSFSQKVKIQQIRSLSEDVRFYYKRLRGNKEDLEPG
	1		KKSKIANIYFDPGLQCGDHCYVGLPFLSKSEPKVQPGVAMQEDM
1 1			WDADWDLHQSLFKGWTGIKENSGHRLSAIFEVNTDLQKNIISKI
	Į		TABLSWPSILSSPRHLKFPLTNTNCSS\EEEITLENP/SQDVPV
1 1		İ	YVQFIPLALYSNPSVFVDKLVSRFNLSKVAKIDLRTLEFQVFRN
1 1			SAHPLQSSTGFMEG\LSPHLILNLILKPGEKKSVKVK\FTPVHN
1 1	1	ļ	RTVSSLIIVRNNLTVMDAVMVQGQGTTENLRVAGKLPGPGSSLR
1			FKITEALLKDCTDSLKLREPNFTLKRTFKVENTGQLQIHIETIE
	ľ		ISGYSCEGYGFKVVNCQEFTLSANASRDIIILFTPDFTASRVIR ELKFITTSGSEFVFILNASLPYHMLATCAEALPRPNWELALYII
			ISGIMSALFLLVIGTA\YLEAQGIWBP\FRRRLS\FEASNPPFD
1	1		VGRPFDLRRIVGISSEGNLNTLSCDPGHSRGFCGAGGSSSRPSA
	ľ	1	GSHKQ*GPSGHPHSSHSNRNSADVDDVRAYNSGRTSSMTSAQAA
	i		SSQPANKTRPLVLDSNTGAQGHSAGRKSKGAKQSQHGSQHHAHS
1 1	}	ļ	PLEQHPQPPLPPPVPQPQEPQPERLSPAPLAHPSHPERASSARH
	j		SSEDSDITSLIEAMDKDFDHHDSPALEVFTEQPPSPLPKSKGKG
1		1	KPLCRKVKPPKKQEEKEKKGKGKPQEDELKDSLADDDSSSTTTE
]	1	j	TSNPDTEPLLKEDTEKQKGKQMPEKHESEMSQVKQKSKKLLNI
! !	i		KKEIPTDVKPSSLELPYTPPLESKQRRNLPSKIPLPTAMTSGSK
1	į	1	SRNAQKTKGTSKLVDNRPPALAKFLPNSQELGNTSSSEGEKDSP
1 1	ł	į.	PPEWDSVPVHKPGSSTDSLYKLSLQTLNADIFLKQRQTSPTPAS
	ļ	İ	PSPPAAPCPFVARGSYSSIVNSSSSSDPKIKQPNGSKHKLTKAA
[ [		ļ	SLPGKNGNPTFAAVTAGYDKSPGGNGFAKVSSNKTGFSSSLGIS
			HAPVDSDGSDSSGLWSPVSNPSSPDFTPLNSFSAFGNSFNLTGE
		1	VFSKLGLSRSCNQASQRSWNEFNSGPSYLWESPATDPSPSWPAS
		. 1	SGSPTHTATSVLGNTSGLWSTTPFSSSIWSSNLSSALPFTTPAN
		ľ	TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSPTIGR
			RSSDPWSNSHFPHEN
5820	310	1270	RVSLSGPVSLGVLLCARSSTMGKRDNRVAYMNPIAMARSRGPIO
		t t	SSGPTIQ\VI*IDQGLPGKK*KSN*KRKRK/DSKALAEFEEKMN
			ENWKKELEKHREKLLSGSESSSKKRQRKKKEKKKSW*\DSSSS\
			SSSSDSSSSSSDSEDEDKKQGKRRKKKNRSHKSSESSMSETES
			7.2

SEQ	Predicted	Predicted end	Dmino acid
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ľ	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, E=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
İ	to first	amino acid	P=Proline O-Clubania, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W-Tryptophen V Sweet 1
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence		Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			DSVDGLVVVVVCVDCMDVDVDVDVDVDVDVDVDVDVDVDVDVDVDV
	1		DSKDSLKKKKKSKDGTEKEKDIKGLSKKRKMYSEDKPLSSESIS
1	f		ESEYIEEVRAKKKKSSEEREKATEKTKKKKKKKKKKKKKKKKKKAA
İ			SSSPDSP+H+EKSGFPYKESAMSEEISTVKTTTYLLKCMNFLVF GIIPGLFSSHSDATV
5821	179	915	
1		}	KWRNQSWRWPKPGTNWMLSCSVCWRRVTWTGSVWMRKLGKHPQT
ŀ	1		PT/IKDCSIAATGKRPSARFPHQRRKKRREMDDGLAEGGPQRSN
1			TYVIKLFDRSVDLAQFSENTPLYPICRAWMRNSPSVRERECSPS
			SPLPPLPEDEEG\SEVTNSKSR*CVQACPPTHTPGGQPKNACK\
j	j		SRIPSPLAALRMQGTP*RWSPFEPEPSPSTLIYRNMQRWKRIRQ
5822	454	4379	RWKEASHRNQLRYSESMKILREMYERQ
	į.	12.5	QTLKEMPIVMARDLEETASSSEDEEVISQEDHPCIMWTGGCRRI
			PVLVFHADAILTKDNNIRVIGERYHLSYKIVRTDSRLVRSILTA
			HGFHEVHPSSTDYNLMWTGSHLKPFLLRTLSEAQKVNHFPRSYE
	1		LTRKDRLYKNIIRMQHTHGFKAFHILPQTFLLPAEYAEFCNSYS
1	•		KDRGPWIVKPVASSRGRG\VYLINNPNQISLEENILVSRYINNP
			LLIDDFKFDVRLYVLVTSYDPLVIYLYEEGLARFATVRYDQGAK
1	(		NIRNQFMHLTNYSVNKKSGDYVSCDDPEVEDYGNKWSMSAMLRY LKQBGRDTTALMAHVEDLIIKTIISAELAIATACKTFVPHRSSC
1			FELYGFDVLIDSTLKPWLLEVNLSPSLACDAPLDLKIKASMISD
			MFTVVGFVCQDPAQRASTRPIYPTFESSRRNPFQKPQRCRPLSA
			SDAEMKNLVGSAREKGPGKLGGSVLGLSMEEIKVLRRVKEENDR
1			RGGFIRIFPTSETWEIYGSYLEHKTSMNYMLATRLFQDRMTADG
			APELKI *SLNSKAKLHAALYERKLLSLEVRKRRRSSRLRAMRP
			KYPVITQPAEMNVKTETESEEEEEVALDNEDEEQEASQEESAGF
	ļ		LRENQAKYTPSLTALVENTPKENSMKVREWNNKGGHCCKLETQE
1			LEPKFNLMQILQDNGNLSKMQARIAFSAYLQHVQI\RLMKDSGG
			QTFSASWAAKEDEQMELVVRFLKRASNNLQHSLRMVLPSRRLAL
]	,		LERTRILAHQLGDFIIVYNKETEQMAEKKSKKKVEEEEEDGVNM
ì	İ		ENFQEFIRQASEAELEEVLTFYTQKNKSASVFLGTHSKISKNNN
	ĺ		NYSDSGAKGDHPETIMEEVKIKPPKQQQTTEIHSDKLSRFTTSA
ľ	1		EKEAKLVYSNSSSGPTATLQKIPNTHLSSVTTSDLSPGPCHHSS
	- 1		LSQIPSAIPSMPHQPTILLNTVSASASPCLHPGAQNIPSPTGLP
	f f		RCRSGSHTIGPFSSFQSAAHIYSQKLSRPSSAKAGSCYLNKHHS
1 1	į		GIAKTQKEGEDASLYSKRYNQSMVTAELQRLAEKQAARQYSPSS
1 1			HINLLTQQVTNLNLATGIINRSSASAPPTLRPIISPSGPTWSTQ
1 1			SDPQAPENHSSSPGSRSLQTGGFAWEGEVENNVYSQATGVVPQH
1 1			KYHPTAGSYQLQFALQQLEQQKLQSRQLLDQSRARHQAIFGSQT
i i	1		LPNSNLWTMNNGAGCRISSATASGQKPTTLPQKVVPPPSSCASL
1 1	1		VPKPPPNHEQVLRRATSQKASKGSSAEGQLNGLQSSLNPAAFVP
L			TISSIDPAHIKIMNHKHIEKOPVHHEWVHD
5823	42	2293	LLTALSMEGGGGRDEPSACRAGDVNMDDPKKEDILLLADEKFDF
1 1	ĺ		DLSLSSSSANEDDEVFFGPFGHKERCTAASI.FI.NNDVDBODDID
1 1	İ		TSESPFAWSPLAGEKFVEVYKEAHLLALHTESSSPMOAAOAAVA
1 1	1		EDPRSQGVERFIQESKF\KINLFEKEKEMKKSDTSI.VD DTWYT C
1 1	1		DSPLLGPPVGEPRLLASSPALPSSGAOARLTRAPGPPHGAUATR
i i	j		RESCIAHAASQAATORKPGTKLLLPRAASVPGPGTPGAARVPVVV
1 1			ELPASPSRTKIPAEKESHRDVLPDKPAPGAVANIPARGUI COCK
1		İ	RAIPVP\NKLGLKKTLLKAPGSYSN\I.ORKSSSGA\\WSGASGA
	ļ		CIPQPVAKAKSSEFASIPAN*I,PGI,CPNTSKS\GPMGDAMIDDA
1			L\PAGPVG\ASSWQAKRVDVSELAAFQLTADD\SaspTQDQTDD
			GGG \QWLNSSCAWSESSOLNKTRSIRREDSCINGKTVIMDTDTN
1 1	1		QFKIPKFSIGDS\PDSSTPKLSRAORPOSCTSVCPVTVUcmpvp
		ł	RSSGPAPQSLLSAWRVSALPTPASRRCSGI.PPMTPKTMPPANCE
1			PL/CVPARRRSSEPRKNSAMRTEPTRESNRKTDSR/LVDvcppp
1	1		GSPPSRVPQALNFSPEESDSTFSKSTATEVAREEAKPGGDAADC
ļ l		1	EALLVDIKLEPLAVTPDAASOPLIDIPLIDECOTPEAHVAVCER
j l	İ		SRPLIDLMTNTPDMNKNVAKPSPVVGQLIDLSSPLIQLSPEADK
			ENVDSPLLKF
5824	42		LLTALSMEGGGGRDEPSACRAGDVNMDDPKKEDILLLADEKFDF
	ļ	1	DLSLSSSSANEDDEVFFGPFGHKERCIAASLELMNPVPEQPPLP
L	<u> </u>		TSESPFAWSPLAGEKFVEVYKEAHLLALHIESSSRNQAAQAAKP
			THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY O

SEQ	Predicted	Predicted end	I mino acid
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
		<del></del>	EDPRSQGVERFIQESKF\KINLFEKEKEMKKSPTSLKRETYYLS
i	ĺ		DSPLLGPPVGEPRLLASSPALPSSGAQARLTRAPGPPHSAHALP
ſ	1		RESCTAHAASQAATQRKPGTKLLLPRAASVRGRGIPGAAEKPKK
- 1	1		EIPASPSRTKIPAEKESHRDVLPDKPAPGAVNVPAAGSHLGQGK
			RAIPVP\NKLGLKKTLLKAPGSYSN\LQRKSSSGA\VWSGASSA
1			CTPQPVAKAKSSEFASIPAN*LPGLCPNISKS\GRMGPAMLRPA
		Ì	L\PAGFVG\ASSWQAKRVDVSELAAEQLTAPP\SASPTQPQTPE
			GGG\QWLNSSCAWSESSQLNKTRSIRRRDSCLMSKTKVMFTPTN
ı			QFKIPKFSIGDS\PDSSTPKLSRAQRPQSCTSVGRVTVHSTPVR
	]		RSSGPAPQSLLSAWRVSALPTPASRRCSGLPPMTPKTMPRAVGS
	1		PL\CVPARRRSSEPRKNSAMRTEPTRESNRKTDSR\LVDVSPDR
			GSPPSRVPQALNFSPEESDSTFSKSTATEVAREEAKPGGDAAPS
	1		EALLVDIKLEPLAVTPDAASQPLIDLPLIDFCDTPEAHVAVGSE
	1		SRPLIDLMTNTPDMNKNVAKPSPVVGQLIDLSSPLIQLSPEADK
			ENVDSPLLKF
5825	2	4210	FLQIESASPAPFSSGFLAAHPHSPGGSLATKGRSRLSAPGMLHL
1			SAAPPAPPPEVTATARPCLCSVGRRGDGGKMAAAGALERSEVEL
			SGAERERPRHFREFTVCSIGTANAVAGAVKYSESAGGEVVVESG
			KLFSVTRNRFIHWKTSGDTLELMEESLDINLLNNAIRLKFONGS
	ł		VLPGGVYVSETQNRVIILMLTNQTVHRLLLPHPSRMVRSELAAD
			SQMQSIFTDIGKVDFTDPCNYOLIPAVPGISPNSTASTAWLSSD
1			GEALFALPCASGGIFVLKLPPYDIPGMVSVVELKOSSVMORLTT
			GWMPTAIRGDQSPSDRPLSLAVHCVEHDAFIFALCODHKI.DMWc
	į		YKEQMCLMVADMLEYVPVKKDLRLTAGTGHKLRLAYSPTMGLYL
1	1		GIF\MHAPKRGQFCIFQLVSTESNRYSLDHISSLFTSQETLIDF
	1		ALTSTDIWALWHDAENQTVVKYINFEHNVAGQWNPVFMQPLPEE
	l I		EIVIRDDQDPREMYLQSLFTPGQFTNEALCKALQIFCRGTERNL
	]		DLSWSELKKEVTLAVENELQGSVTEYEFSQEEFRNLQQEFWCKF
1	i		YACCLQYQEALSHPLALHLNPHTNMVCLLKKGYLSFLIPSSLVD
	1		HLYLLPYENLLTEDETTISDDVDIARDVICLIKCLRLIEESVTV
l .	1		DMSVIMEMSCYNLQSPEKAAEQILEDMITIDVENVMEDICSKIQ EIRNPIHAIGLLIREMDYETEVEMEKGFNPAQPLNIRMNLTQLY
1			GSNTAGYIVCRGVHKIASTRFLICRDLLILQQLLMRLGDAVIWG
	l í		TGQLFQAQQDLLHRTAPLLLSYYLIKWGSECLATDVPLDTLESN
	1		LQHLSVLELTDSGALMANRFVSSPQTIVELFFQEVARKHIISHL
			FSQPKAPLSQTGLNWPEMITAITSYLLQLLWPSNPGCLFLECLM
	1 . [		GNCQYVQLQDYIQLLHPWCQVNVGSCRFMLGRCYLVTGEGQKAL
			ECFCQAASEVGKEEFLDRLIRSEDGEIVSTPRLQYYDKVLRLLD
1 1	! !		VIGLPELVIQLATSAITEASDDW\KSOATL\RTCIFKHHI\DIC
1			\HNSQAYGSL*PQIPDSSROLDCLROLVVVI.CERSOLODIATERS
1 1			YVNLHNEVVGIIESRARAVDLMTHNYYELLYAFHIYRHNYRKAG
			TVMFEYGMRLGREVRTLRGLEKOGNCYLAALNCIRLTRDEVAWT
1			VQPVSGAVYDRPGASPKRNHDGECTAAPTNROTETLELEDLEVE
j			CSLARIRLTLAQHD?SAVAVAGSSSAEEMVTLLVOAGI.FDTATS
			LCQTFKLPLTPVFEGLAFKCIKLQFGGEAAOAEAWAWLAANOT.S
1			SVITTKESSATDEAWRLLSTYLERYKVONNLYHHCVINKTLSHG
5826	3		VPLPNWLINSYKKVDAAELLRLYLNYDLLDLTPYQVIRICGC
3020	3	871	KSQLLRDHSAPPPKPCTSVGAMGC*PRQ/SPKEQQRQLKKQKNR
1	1		AAAQRSRQKHTDKADALHQQHESLEKDNLALRKEIQSLQAELAW
1 1	1		WSRTLHVHERLCPMDCASCSAPGLLGCWDQAEGLLGPGPQGQHG
	}		CREQLELFQTPGSCYPAQPLSPGPQPHDSPSLLQCPLPSLSLGP
]	i		AVVAEPPVQLSPSPLLFASHTGSSLQGSSSKLSALQPSLTAQTA
1	İ		PPOPLELEHPTRGKLGSSPDNPSSALGLARLQSREHKPALSAAT
5827	194	2207	WQGLVVDPSPHPLLAFPLLSSAQVHF
ļ <del>.</del> .		2287	GMGSENSALKSYTLREPPFTLPSGLAVYPAVLQDGKFASVFVYK
1 1		1	RENEDKVNKAAKVP**HLKTLRHPCLLRFLSCTVEADGIHLVTE
			RVQPLEVALETLSSAEVCAGIYDILLALIFLHDRGHLTHNNVCL
j i			SSVFVSEDGHWKLGGMETVCKVSQATPEFLRSIQSIRDPASIPP
1 1		i	EEMSPEFTTLPECHGHARDAFSFGTLVESLLTILNEQVSADVLS
		· i	SFQQTLHSTLLNPIPKWRPALCTLLSHDFFRNDFLEVVNFLKSL
			TLKSEEEKTEFFKFLLDRVSCLSEELIASRLVPLLLNQLVFAEP

C 050			
SEQ ID	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid F=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine G=Glycine
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine
	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			(-possible nucleotide insertion)
- 1		İ	VAV\KSFLPYLLGPKKDHAQGETPCLLSPALFQSRVIPVLLQLF
	i		EVHEEHVRMVLLSH1EAYVGALSLREQLKKV\IL\PQVLLG\LR
			D\TSDSIVAITLHSLAVLVSLLGPEVVVGGERTKIFKRTAP\SF
i		1	TK\NTDLSLEGDPFSOPIKFPINGLSDVKNTSFDSFNFDSSSVV
I		ŀ	SEEWPDWSGPE\EPENQTVNI\OIWP\REP\CDDVKSQCTTI.DV
1			BESSWDDCEPSSLDTKVNPGGGITATKPVTSGEQKPIPALLSLT
İ			EESMPWKSSLPQKISLVQRGDDADQIEPPKVSSQERPLKVPSEL
1	1		GLGEEFTIQVKKKPVKDPEMDWFADMIPEIKPSAAFLILPELRT
l			EMVPKKDDVSPVMQFSSKFAAAEITEGEAEGWEEEGELNWEDNN
			W WELL THOUSE AND THE THOUSE WEEK GEEN WEDNN
5828	2	257	
1		43/	AREGGSLGAVAACGELSYSCDFCPARPHTSWLTRFVKMEFQAVV
1		]	MAVGGGSRMTDLTSSIPKPLLPVGNKFLIWYPLNLLERVGFEEV
		ľ	IVVTTRDVQKALCAEFKMKMKPDIVCIPDDADMGTADSLRYIYP
}		1	KLKTDVLVLSCDLITDVALHEVVDLFRAYDASLAMI,MRKGODSI
1	Í		EPVPGQKGKKKAVEQRDFIGVDSTGKRLLFMANEADLDFFLVIV
1			GSILQKHPRIRFHTGLVDAHLYCLKKYIVDFLMENG\SITCIDS
1		Ī	EL\IPYLV/RGKQFSSASSQQGTRKEKEGGSKGKRGLKSFRISV
<b></b>		1	SFY*KEANYTGTGAPY\D\ACWI
5829	260	1259	PDGRLIVSCSEDKTIKIWDTTNKQCVNNFSDSVGFANFVDFNPS
	ł	i	GTCIASAGSDQTVKVWDVRVNKLLQHYQVHSGGVNCISFHPSGN
ļ	ĺ	]	YLITASSDGTLKILDLLKGRLIYTLQGHTGPVFTVSFSKGGELF
l .		1	ASGGADTQVLLWRTNFDELHCKGLTKRNLKRLHFDSPPHLLDIY
j			PRIDUDURE COMMINICACION CONTROL OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERT
		i	PRTPHPHEEKVETVEDFFLHLLRLIQSLR*SICRSLLPLLWISF
f			LLILPQQQKPVVGLCQTRVKRPVDIS*TLP*CHQNVCQQPRKRK
			QKT*VTSPVKVK/VSIPLAVTDALEHIMEQLNVLTQTVSILEQR
5830	4496	21.20	LTLTEDKLKDCLENQQKLFSAVQQKS
3030	1136	3139	GGKMAAPEERDLTQEQTEKLLQFQDLTGIESMDQCRHTLEQHNW
i			NIEAAVQDRLNEQEGVPSVFNPPPSRPLQVNTADHRIYSYVVSR
1			PQPRGLLGWGYYLIMLPFRFTYYTILDIFRFALRFIRPDPRSRV
i	1 .		TDPVGDIVSFMHSFEEKYGRAHPVFYOGTYSOALNDAKDELDEL
		•	LVYLHGDDHQDSDEFCRNTLCAPEVISLINTRMLFWACSTNEDE
	( )		GYRVSQALRENTYPFLAMIMLKDRRE*PV\VGRIEGI.T\ODDDI
	1		INQLTFIMDANQTYLVSERLEREERNOTOVI,ROOODEAVI,ASI,D
	1		ADQEKERKKREERERKRRKKEEVOOOKLAEERPRONLOFFUEDV
	l i		LECLPPEPSPDDPESVKIIFKLPNDSRVERRFHFSOST.TVIUDE
ļ ·	!		LFSLKESP\EKFQIEA\NFPRR\VLPCIPSEE\WPNPPTLQE\A
	<u>                                     </u>		GLSHTEVLFVQDLTDE
5831	71	2897	FCSKDKCCLYLPDSINRSKSCTAKPGAHSQDRHAVMDSERQVKD
	]		TDDIESPKRSIRDSGYIDCWDSERSDSLSPPRHGRDDSFDSLDS
1			FEEDEROTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PORTE PO
			FGSRSRQTPSPDVVLRGSSDGRGSDSESDLPHRKLPDVKKDDMS
		İ	ARRTSHGEPKSAVPFNQYLPNKSNQTAYVPAPLRKKKAEREEYR
			KSWSTATSPAGLGKKALQDYGPRT\PVS\DDAESTSMFDMRCEE
1	ļ Ī		EAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWKSRKRSVS
1			QDLIKKEEERKKMEKLLAGEDGTSERRKSIKTYREIVOEKERRE
]			RELHEAYKNARSQEEAEGILQQYIERFTISEAVLERLEMPKILE
			RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVETTIARAS
} i		*	VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLKTFK
1			VDGKVSVNGETVHREEEKERECPTVAPAHSLTKSQMFEGVARVH
'	1	i	GSPLELKQDNGSIEINIKKPNSVPQELAATTEKTEPNSQEDKND
	1	ļ	GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVEFPSSPQLKND
]	1		ASEEKDOKKDENEWGGKAELAN GOOGHAND AND AND AND AND AND AND AND AND AND
( I	ĺ	ł	VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTFPFLD
	ŀ		KMPEANQLHLPNLNSQVDSPSSEKSPVTTPFKFWAWDPEEERRR
	I		QEKWQQEQERLLQERYQ\KEQDK\LKEE\WEKAQKEVEEEERRY
1		Į.	YEEEP*II\EDPVVPFTVSSSSADQLSTSSSMTEGSGTMNKIDL
1		İ	GNCQDEKQDRRWKKSFQGDDSDLLLKTRESDRLEEKGSLTEGAL.
1			AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPOLAODPSONOOTSN
1 1		l	PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSSCGL
1 !			PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDVRIR
			NGLLNCNDCYMRSRSAGQPTTL
5832	2454	829	PGRRFRHGSCAFQKQCIMLHICQYFLQGECKFGTSCKRSHDFSN
		[	SENLEKLEKLGMSSDLVSRLPTIYRNAHDIKNKSSAPSRVPPLF

SEO	Predicted	Predicted end	I have a second
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
ļ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
İ	residue of	amino acid	W-Trimtonham W Thursday Walling,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	sequence	Dequence	\=possible nucleotide insertion)
			VPOCTERPRESCOVERY CONTROL OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF T
	1		VPQGTSERKDSSGSVSPNTLSQEEGDQICLYHIRKSCSFQDKCH
		Ī	RVHFHLPYRWQFLDRGKWEDLDNMELIEEAYCNPKIERILCSES
		1	ASTFHSHCLNFNAMTYGATQARRLSTASSVTKPPHFILTTDWIW
	į	1	YWSDEFGSWQEYGRQGTVHPVTTVSSSDVEKAYLAY/WYTGV*R
Í	1	i	PGSHLEVPGRKAQLRVRFQSLRSEKPGLWHN*KGLPQTQIR\AP
			QDVTTMQTCNTKFPGPKSIPDYWDSSALPDPGFQKITLSSSSEE
1		į	YQKVWNLFNRTLPFYFVQKIERVQNLALWEVYQWQKGQMQKQNG
1	-	Í	GKAVDERQLFHGTSAIFVDAICQONFDWRVCGVHGTSYGKGSYF
İ			ARDAAYSHHYSKSDTQTHTMFLARVLVGEFVRGNASFVRPPAKE
			GWSNAFYDSCVNSVSDPSIFVIFEKHQVYPEYVIQYTTSSKPSV TPSILLALGSLFSSRQ
5833	170	3289	
1		3203	SILCLLSPCVVQFGKPVVSILSSRSRHSPCTKKGWEGMRKHLHT
1			RQGHK*VHVEISKALWVYRDDYFIRHSISVSAVIVRAWITHKYR
1			GRDWNVKWEENJLHAVAKNYTLLQTIPPFERPFKDHQVCLEWNM
	i		GYIWNLRANRIPQCPLENDVVALLGFPYASSGENTGIVKKFPRF
	1	f	RNRELEATRRORMDYPVFTVSLWLYLLHYCKANLCGILYFVDSN
			EMYGTPSVFLTEEGYLHIQMHLVKGEDLAVKTKFIIPLKEWFRL
	1		DISFNGGQIVVTTSIGQDLKSYHNQTISFREDFHYNDTAGYFII GGSRYVAGIEGFFGPLKYYRLRSLHPAQIFNPLLEKQLAEQIKL
1			YYERCAEVQEIVSVYASAAKHGGERQEACHLHNSYLDLQRRYGR
	1		PSMCRAFPWEKELKDKHPSLFQALLEMDLLTVPRNQNESVSEIG
1			GKIFEKAVKRLSSIDGLHQISSIVPFLTDSSCCGYHKASYYLAV
1	1		FYETGLNVPRDQLQGMLYSLVGGQGSERLSSMNLGYKHYQGIDN
1	1		YPLDWELSYAYYSNIATKTPLDQHTLQGDQAYVETIRIKDDEIL
1			KVQTKEDGDVFMWLKHEATRGNAAAQQRLAQMLFWGQQGVAKNP
1			EAAIEWYAKGALETEDPALIYDYAIVLFKGQGVKKNRRLALELM
ŀ			KKAASKGLHQAVNGLGWYYHKFKKNYA\KAAKYWLKA\EE\MGN
ł			PDASYNLGVLHLDGIFPGVPGRNQTLAGEYFHKAAQGGHMEGTL
			WCSLYYITGNLETFPRDPEKAVVWAKHVAEKNGYLGHVIRKGLN
			AYLEGSWHEALLYYVLAAETGIEVSQTNLAHICEERPDLARRYL
1			GVNCVWRYYNFSVFQIDAPSFAYLKMGDLYYYGHQNQSQDLELS
	ļ .		VQMYAQAALDGDSQGFFNLALLIEEGTIIPHHILDFLEIDSTLH
1		1	SNNISILQELYERCWSHSNEESFSPCSLAWLYLHLRLLWGAILH
1 1			SALIYFLGTFLLSILIAWTVQYFQSVSASDPPPRPSQASPDTAT
			STASPAVTPAADASDQDQPTVTNNPEPRG
5834	17	4020	RFRRGGGRVFPGAFPASPSDSLGQGNSQGPPRTPKPPRT/QECG
1			SAAPGPIPGQSSS+VPLRLEQIQQKADCPLSLELALKPRMAAQV
1	1		TLEDALSNVDLLEELPLPDQQPCIEPPPSSLLYOPNFNTNFEDR
1	j		NAFVTGIARYIEQATVHSSMNEMLEEGQEYAVMLYTWRSCSRAT
1 1			PQVKCNEQPNRVEIYEKTVEVLEPEVTKLMNFMYFORNAIERFC
1 1			GEVRRLCHAERRKDFVSEAYLITLGKFINMFAVLDELKNMKCSV
1		j	KNDHSAYKRAAQFLRKMADPQSIQESQNLSMFLANHNKITQSLQ
] ]			QQLEVISGYEELLADIVNLCVDYYENRMYLTFSEKHMLLKVMGF
1 1		!	GLYLMDGSVSNIYKLDAKKRINLSKIDKYFKQLQVVPLFGDMQI
í I		1	ELARYIKTSAHYEENKSRWTCTSSGSSPQYNICEQMIQIREDHM
1 1	1	i	RFISELARYSNSEVVTGSGRQEAQKTDAEYRKLFDLALQGLQLL
i l	i		SQWSAHVMEVYSWKLVHPTDKYSNKDCPDSAEEYERATRYNYTS
	l.	i	EEKFALVEVIAMIKGLQVLMGRMESVFNHAIRHTVYAALQDFSQ
1	1	Ī	VTLMEPLRQAIKKKKNVIQSVLQAIRKTVCDWETGHEPFNDPAL
1 1	İ	ì	RGEKDPKSG*D1KVPRRAVGPSSTQLYMVRTMLESLIADKSGSK
		}	KTLRSSLEGPTILDIEKFHRESFFYTHLINFSETLOOCCDLSOI.
}	į	}	WFREFFLELTMGRRIQFPIEMSMPWILTDHILETKEASMMEYVI,
[ [	l	j	YSLDLYNDSAHYALTRFNKQFLYDEIEAEVNLCFDQFVYKLADQ
ļ l	]	l	IFAYYKVMAGSLLLDKRLRSECKNQGATIHLPPSNRYETLLKOR
	ļ	İ	HVQLLGRSIDLNRLITQRVSAAMYKSLELAIGRFESEDLTSIVE
j l	ļ	į	LDGLLEINRMTHKLLSRYLTLDGFDAMFREANHNVSAPYGRITL
	ļ	1	HVFWELNYDFLPNYCYNGSTNRFVRTVLPFSQEFORDKOPNAOP
į į	į	1	QYLHGSKALNLAYSSIYGSYRNFVGPPHFQVICRLLGYOGIAVV
, ,	i	j	MEELLKVVKSLLQGTILQYVKTLMEVMPKICRLPRHEYGSPGIL
		İ	EFFHHQLKDIVEYAELKTVCFQNLREVGNAILFCLLIEQSLSLE
			EVCDLLHAAPFQNILPRVHVKEGERLDAKMKRLESKYAPLHLVP

SEQ	Predicted	Predicted end	I Amino poid
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
j	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
· l	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
į.	amino acid	1	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	1		LIERLGTPQQIAIAREGDLLTKERLCCGLSMFEVILTRIRSFLD
1	1	}	DPIWRGPLPSNGVMHVDECVEFHRLWSAMQFVYCIPVGTHEFTV
}		1	EQCFGDGLHWAGCMIIVLLGQQRRFAVLDFCYHLLKVQKHDGKD
Ì	1		EIIKNVPLKKMVERIRKFQILNDEIITILDKYLKSGDGEGTPVE
			HVRCFQPPIHQSLASS
5835	4209	1904	SGNIRMAQGSHQIDFQVLHDLRQKFPEVPEVVVSRCMLQNNNNL
	1		DACCAVLSQESTRYLYGEGDLNFSDDSGISGLRNHMTSLNLDLO
ì		ĺ	SQNIYHHGREGSRMNGSRTLTHSISDGQLQGGQSNSELFOOEPO
i			TAPAQVPQGFNVFGMSSSSGASNSAPHLGFHLGSKGTSSLSQQT
	ļ		PRFNPIMVTLAPNIQTGRNTPTSLHIHGVPPPVLNSPQGNSIYI
			RPYITTPGGTTRQTQQHSGWVSQFNPMNPQQVYQPSQPGPWTTC
	ļ		PASNPLSHTSSQQPNQQGHQTSHVYMPISSPTTSQPPTIHSSGS
ŀ			SQSSAHSQYNIQNISTGPRKNQIEIKLEPPQRNNSSKLRSSGPR
ļ			TSSTSSSVNSQTLNRNQPTVYIAASPPNTDELMSRSQPKVYISA
	ļ		NAATGDEQVMRNQPTLFISTNSGASAASRNMSGQVSMGPAFIHH
-			HPPKSRAIGNNSATSPRVVVTQPNT\EYTFKITVSPNKPPAVSP
	İ		GVVSPTFELTNLLNHPDHYVETENIHHLTDPTLAHVDRISETRK
1			LSMGSDDAAYTQDI*RISNSWLGMVAHACNSSALGGQDGRII*A
			QEFETSWGNIWRLRLYRRF*NYAGMVAHTCSPSYSVD*ALLVHQ
i .			KARMERLQRELBIQKKKLDKLKSEVNEMENNLTRRRLKRSNSIS
			QIPSLEEMQQLRSCNRQLQIDIDCLTKEIDLFQARGPHFNPSAI
	l i		HNFYDNIGFVGPVPPKPKDQRSIIKTPKTQDTEDDEGAQWNCTA
		1	CTFLNHPALIRCEQCEMPRHF
5836	361	2303	FHITMCGICCSVNFSAEHFSQDLKEDLLYNLKQRGPNSSKQLLK
1		·	SDVNYQCLFSAHVLHLRGVLTTQPVEDERGNVFLWNGEIFSGIK
1	1		VEAEENDTQILFNYLSSCKNESEILSLFSEVQGPWSFIYYQASS
			HYLWFGRDFFGRRSLLWHFSNLGKSFCLSSVGTQTSGLANQWQE
			VPAS\DFSELILSLLSFPDALFYNCILGNIFLGRILLKKMLIA*
1 1			VXFQQTYQHLYQR*QMKPNCILKNLLFL*I*CCHKLHWRLIAVI
1			FPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR
	•		DENLTANEVLKTCDRKANVAILFSGGIDSMVIATLADRHIPLDE
1 1			PIDLLNVAFIAEEKTMPTTFNREGNKQKNKCEIPSEEFSKDVAA
1			AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIWNFVEINVSME
1			ELQKLRRTRICHLIRPLDTVLDDSIGCAVWFASRGIGWLVAQEG
	į		VKSYQSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLEGLNKEIM
			MELGRISSRNLGRDDRVIGDHGKEARFPFLDENVVSFLNSLPIW
1 1			EKANLTLPRGIGEKLLLRLAAVELGLTASALLPKRAMQFGSRIA
, ,			KMEKINEKASDKCGRLQIMSLENLSIRKETKL
5837	4792	903	NGNAVAQAPVTNCCYLATGSKDQTIRIWSCSRGRGVMILKLPFL
			KRRGGGIDPTVKERLWLTLHWPSNQPTQLVSSCFGGELLQWDLT
] [			QSWRRKYTLFSASSEGQNHSRIVFNLCPLQTEDDKQLLLSTSMD
1		•	PDVKCWDT ATT ECCUME DOLOGE VOT TOO TOO TOO
1	İ		RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVGDG
] 1			MIRVWNTLS IKNNYDVKNFWQGVKSKVTALCWHPTKEGCLAFGT
	1		DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGPPVPPMSLGGE
1 [	1		GDRPSLALYSCGGEGIVLQHNPWKLSGEAFDINKLIRDTNSIKY
1 1	Ì		KLPVHTEISWKADGKIMALGNEDGSIEIFQ\IPNLKLICTIQQH
] ]	1	i	HKLVNTISWHHE\HGSPAQKLSYL\MPSGSQQCSPFTCHNLKNC
1	ł		P*KAAPESPSDPLQSPYRTPPQGHTAQDYPVWAWEPHIH*WEGL
1 1			VFCFPIDGYSPGCWD\AFPGKEAPVAIFRG\HQGRLLCVAWSPL
1	ļ		DPDCIYSG\ADDFCVHKWLTSMQDHSRPPQGKKSIELEKKRLSQ
]	ĺ		PKAKPKKKKPTLRTPVKLESIDGNEEESMKENSGPVENGVSDQ
1			EGEEQAREPELPCGLAPAVSREPVICTPVSSGFEKSKVTINNKV
			ILLKKEPPKEKPETLIKKRKARSLLPLSTSLDHRSKEELHQDCL
, ,	ļ		VLATAKHSRELNEDVSADVEERFHLGLFTDRATLYRMIDIEGKG
1	İ		HLENGHPELFHQLMLWKGDLKGVLQTAAERGELTDNLVAMAPAA
]			GYHVWLWAVEAFAKQLCFQDQYVKAASHLLSIHKVYEAVELLKS
] [	j		NHFYREAIAIAKARLRPEDPVLKDLYLSWGTVLERDGHYAVAAK
1		ĺ	CYLGATCAYDAAKVLAKKGDAASLRTAAELAAIVGEDELSASLA
1 [			LRCAQELLLANNWVGAQEALQLHESLQGQRLVFCLLELLSRHLE
1 1			EKQLSEGKSSSSYHTWNTGTEGPFVERVTAVWKSIFSLDTPEQY
			QEAFQKLQNIKYPSATNNTPAKQLLLHICHDLTLAVLSQQMASW

Predicted

beginning

location

to first

amino acid

residue of

nucleotide

corresponding

Predicted end

corresponding

nucleotide

location

to first

amino acid

residue of

amino acid

SEQ

ID

NO:

Amino acid segment containing signal peptide

(A=Alanine, C=Cysteine, D=Aspartic Acid, E=

W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop

RKPSDDKHFGQAPSKGTPSDGVSLSNLTQPSLTATDQQQQEEHY RIETRVSSSCLDLPDSTEEKGAPIETLGYHSASNRRMSGEPIQT VESIRVPGKGNRGHGREASRVGWFDLSTSGSSFDNGPSSASELA SLGGGGSGGLTGFKTAPYKERAPQFQESVGSFRSNSFNSTFEHH LPPSPLEHGTPFQREPVGPSSAPPVPKDHGGIFSRDAPTHLPS VDLSNPFTKEAALAHAAPPPPGEHSGIPFPTPPPPPPPGEHSS SGGSGVPFSTPPPPPPPVDHSGVVPFPAPPLAEHGVAGAVAVFP

Glutamic Acid, F=Phenylalanine, G=Glycine,

H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,

P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,

SEQ	15		
	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine C-Cratain and signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
Ī	location	1	Grucamic Acid, F=Phenylalanian C_Cl
	corresponding	corresponding	n-nistidine, i=lsolencine V-turine
ĺ		to first	halleucine, MaMethionine Nahanamagina
J	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ŀ	residue of	amino acid	W=Trontonham w marine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Į	sequence		Codon, /=possible nucleotide deletion,
		<del> </del>	\=possible nucleotide insertion\
1	ł	i	TLPSHSLEHLGPPHGGGGGGGSNSSSGPPLGPSHRDTISRSGII
1	j	1	LRSPRPDFRPREPFLSRDPFHSLKRPRPPFARGPPFFAPKRPFF
- 5045		1	PPRY
5841	1908	762	GLRLFLVLTVWPMMKPSWLSRTEFSKRLLCRTLWCQSGWSSRSY
- 1	İ	ł	TRSMLKMTTGINDBCDMCMXCMDCCKTLWCQSGWSSRSY
ı	İ		TRSMLKMTTSINRRSRTSTKSTRTSARPGLTATVSIGLSDSPTW
ı		ļ	RHCWMTARSCSGEKGGHWAPRQVGVYLLPGRVGCVSSRVSPSFP
		i e	GDGDDSGDARRGSAVSALASGLVEEDMI.CDDFDDFDDFDDFDARA
	ł		SAEDEVSQGFTEFTIEDFHNTFMDIJTEOVEKOTEVADI I ACRIT
	1		Voioning Albert SGYLORESKEFFHFT FGGPTVVFFGO OF
1	ļ.		\VEFNCKESDHIHIIALAOGLORVHPGWEVMGDDDD77 mm\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
ł			FP*CLPSPKVYLLYRPG\HYDILYKIGLGSSPLGCPGCPLLARA
			LGHCYRGFSVVVKWSYFTPFFLSHDPPPMFY
5842	307	1918	OEPTADEKI BETCOCOPEUTED
1	1		QEPTADFKLRSTCGCGREMTCPDKPGQLINWFICSLCVPRVRKL
	i		WSSRPRTRRNLLLGTACAIYLGFLVSQVGRASLQHGQAAEKGP
	1		HRSKUTAEPSFPEIPLDGTLAPPESOCNCSTLOPMANTER BOX
	1 1		ASKAMIRGIVAPKKKKHAVASAABCOEALUCDELODODA \
J	} !		ALME "HLGTLREOTWLRLESDPGGWCGVPF /WPACCED BLANCE
	1		RESNIKI YSESAPSWLSKDDIRRMRITADSAVAGI DDVGGDGG
			RLLVLEGGAPGAVLRCGPSPCGLLKQPLDMSEVFAFHLDRILGL
1			NRTLPSVSRKAEFIQDGRPCPIILWDASLSSASNDTHSSVKLTW
1	1		GTYQQLLKQKCWQNGRVPKPESGCTEIHHHEWSKMALFDFLLQI
1			YNRIDINGGGERRRYERA GUGUGI RELIGIONE PRINCIPLE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CON
	1		YNRLDTNCCGFRPRKEDACVQNGLRPKCDDQGSAALAHIIQRKH
	1		DPRHLVFIDNKGFFDRSEDNLNFKLLEGIKEFPASAVYVLKSQH
	1		LRQKLLQSLFLDKGYWESQGGRQGIEKLIDVIEHRAKILITYIN
5843	500	1453	MIGAKATHME
1	1	1433	GTARLVTCWVLHGQ*VKKPAWEPGVVWL*Q*RCRPKGWGLGAGM
Ì			I AGGREGUERKAOSSCCHFMVKT.I.DDCTPMTDCDVTDTTTTT
1	! i		DADA TENDOKETERKKETTLOBCKOKUDAMIDAKUTER AGMANA 1
	1 1		EEAACPVSAPEEASPKPVLCHQSKERKPSAEM/RQNNHQGSHFL
	Į í		LPPKIPSWRDPPETLEEPQNAPRERPEGPAAAKKPPRHCELVVT
1	1		LGCPEIHGDL P DUDPKPODDC I DCGUT GGODT
1	1 1		LGCPEIHGDLRPWDRKRQPRSLRGSHLGGQRLHGSLCGHISQKP
Ĺ	1		LTAPGTKRQKGPHQEGREVGQLH*GDPRGQELAPNGSESPILPG VQARAPGLGRA
5844	202	2471	FDCAUT CCCCCC
•	1	24,1	FDSAVLSSINVMAVLPGPLQLLGVLLTISLSSIRLIQAGAYYGI
1	1 1	•	VEDEE STEEN WELL TO TO THE PROPERTY
	f [		YIGAGIFADEQIMAEIOPAPRMGKEAVDKKGKEIDLAGIDGOG I
	1	į	FRGEEGPRGPPGLPGHGIPGIKGKPGPCGVDGVCVDCVCV
			PGRPGAMGMPGAKGEIGOKGEIGPMGID* POGDDGDUGI DGTGK
1 .	!		PGGPGLPGQPGPKGDRGPKGLPGPQGLRGPKGDKGFGMPGAPGV
1			KGPPGMHGPPGPVGLPGVGKPGVTGFPGP\QGPLGK\PGAPGEP
1		i	GPOGPIGVPGVOGPPGTPGTGVPGGPGV TTGTPGY
	[		GPQGPIGVPGVQGPPGIPGIGKPGQDG\IPGQPGFPGGKGEQGL
	1		PGLPGPPGLPGIGKPGFPGPKGDRGMGGVPGALGPRGEKGPIGA
1 1			PGIGGPPGEPGLPGIPGPMGPPGAIGFPGPKGEGGIVGPQGPPG
	1		FROM PGLOGE PGKPGFLGEVGPPGMPGFPGDIGDVGPPGOVGTP
1	[	1	GDPGVPGLLGPKGEPGIPGDOGI,OGPPGIPGTGGDGGDTGDGG
1 1	1		FGFAGEFGDFGFPGFPGIGKPGVAGIHCPDGKPGATCDGGGGG
1 1		- 1	PGPGPPGPPAVMPPTPPPOGEVI.PDMGLGTDGVVDDVAVG
1 !		ŀ	AKKGKNGGPAYEMPAFTAELTAPFPPVGAPVKFNKLLYNGRQNY
1	1	İ	NPQTGIFTCEVPGVYYFAYHVHCKGGNVWVALFKNNEPVMYTYD
1 1	]	ŀ	EYKKGFLDOASGCAVI I I PROPRIM CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE C
L		į	EYKKGFLDQASGSAVLLLRPGDRVFLQMPSEQAAGLYAGQYVHS SFSGYLLYPM
5845	215	2061	
, ,		~001	HASNKSASLQDKMANPKEKTAMCLVNELARFNRVQPQYKLLNER
1	i	l	GFARSKIT S VQLSLGEOTWESEGSSTKKAOOAVGNVAT MDOME D
ļ ļ	}		KPI *KPPKSNVNNNPGCITPTVEINGLAMKPG\ VDA TUDDI DOK
į (	{	l l	PEPNINAM INFOVMYNORYHCPI PKI FYVOLTVCMMPPECECE
( Í	i	1	RQAARHNAAMKALQALQNEPIPERSPQNGESGKDMDDDKDANKS
[	ŀ	1	EISLVFETALKPAMPUSEEVIVESSANDUNGESGKDMDDDKDANKS
1		1	EISLVFEIALKRNMPVSFEVIKESGPPHMKSFVTRVSVGEFSAE
[	i		GEGNSKKLSKKRAATTVLQELKKLPPLPVVEKPK\HFFKKRPKT
! İ	}	1	IVKAGPEYGQGMNPISRLAOIOOAKKEKEPDVVI.I.SEPCMDDDD
	ŀ	1.	EFVMQVKVGNEVATGTGPNKKIAKKNAAEAMIJOI.GVVA.CMIV.O
			DQLEKTGENKGWSGPKPGFPEPTNNTPKGILHLSPDVYQEMEAS

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	to first	L=Leucine, M=Methionine, N=Asparagine,
	•	amino acid	P=Proline, Q=Glutamine, R=Arginine
	amino acid	residue of	S=Serine, T=Threonine, V=Valine
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown *-Ston
	amino acid	sequence	Codon, /=possible nucleptide deletion
	sequence		\=possible nucleotide insertion)
			RHKVISGTTLGYLSPKDMNQPSSSFFSISPTSNSSATIARELLM
	ļ		NGTSSTAEAIGLKGSSPTPPCSPVQPSKQLEYLARIQGFQVHYC
1	ł		DRQSGKECVTCLTLAPVQMTFHAIGSSIEASHDQV*YATAILLC
1			YGPARKWKAIKMEAMCAHAALLSLIHYLLAPSARLEKSKLFALG
	1		N.
5846	1126	456	FSKLIMKTFIIGISGVTNSGKTTLAKNLQKHLPNCSVISQDDFF
1	1	-	KPESEIETDKNGFLQYDVLEALNMEKMMSAISCWMESARHSVVS
}	1		TDOESAEFIDII TIECELLENIVADI DETTUMBATSCWMESARHSVVS
	1	1	TDQESAEEIPILIIEGFLLFNYKPLDTIWNRSYFLTIPYEECKR
			RRSTRVYQPPDSPGYFDGHVWPMYLKYRQEMQDITWEVVYLDGT
ł	1	1	KSEEDLFLQVYEDLIQELAKQKCLQVTA*RRNTTNPS/CK*IRK
5847	2769	505	LQGVI
1	.,,,,	305	APEMEDLSSPDSTLLQGGHNLLSSASFQESVTFKDVIVDFTQEE
1	1	1	WKQLDPGQRDLFRDVTLENYTHLVSIGLOVSKPDVISOLFOGTE
1			PWIMEPSIPVGTCADWETRLENSVSAPEPDISEEELSPEVIVEK
}		Į.	EKRDDSWSSNLLESWEYEGSLERQOANOOTLPKEIKVTEKTIPS
	1	1	WEKGPVNNEFGKSVNVSSNLVTQEPSPEETSTKRSIKQNSNPVK
1	1	1	KEKSCKCNECGKAFSYCSALIRHQRTHTGEKPYKCN*/CVEKAF
1	İ	i	SRSENLINHQRIHTGDXPYKCDQCGKGFIEGPSLTQHQRIHTGE
1			KPYKCDECGKAFSQRTHLVQHORIHTGEKPYTCNECGKAFSQRG
	<b>!</b>		HFMEHQKIHTGEKPFKCDECDKTFTRSTHLTOHOKTHTGEKTYK
ı			CNECGKAFNGPSTFIRHHMIHTGEKPYECNECGKAFSOHSNLTO
			HQKTHTGEKPYDCAECGKSFSYWSSLAOHLKIHTGEKPYKCNEC
1	i		GKAFSYCSSLTQHRRIHTREKPFECSECGKAFSYLSNINOHOKT
ļ	]		HTQEKAYECKECGKAFIRSSSLAKHERIHTGEKPYOCHECGKTE
	1		SYGSSLIQHRKIHTGERPYKCNECGRAFNONIHLTOHKRIHTGA
	1		KPYECAECGKAFRHCSSLAQHQKTHTEEKPYQCNKCEKTFSQSS
ŀ			HLTQHQRIHTGEKPYKCNECDKAFSRSTHLTOHORTHTGEKPVK
			HLTQHQRIHTGEKPYKCNECDKAFSRSTHLTOHORTHTGEKPVK
			HLTQHQRIHTGEKPYKCNECDKAFSRSTHLTQHQRIHTGEKPYK CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSALN KHQRLHPGI
5848	22	2961	HLTQHQRIHTGEKPYKCNECDKAFSRSTHLTQHQRIHTGEKPYK CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSALN KHQRLHPGI AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMDAVCK
5848	22	2961	HLTQHQRIHTGEKPYKCNECDKAFSRSTHLTQHQRIHTGEKPYK CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSALN KHQRLHPGI AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMDAVCK
5848	22	2961	HLTOHORIHTGEKPYKCNECDKAFSRSTHLTQHQRIHTGEKPYK CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSA_N KHQRLHPGI AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAI
5848	22	2961	HLTOHORIHTGEKPYKCNECDKAFSRSTHLTOHORIHTGEKPYK CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSA_N KHQRLHPGI AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERKKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVMLLSSMRYTEKOIG
5848	22	2961	HLTOHORIHTGEKPYKCNECDKAFSRSTHLTOHORIHTGEKPYK CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSA_N KHQRLHPGI AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASU
5848	22	2961	HLTOHORIHTGEKPYKCNECDKAFSRSTHLTOHORIHTGEKPYK CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSA_N KHQRLHPGI AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKOSAALCLURLYDTSPDI
5848	22	2961	HLTOHORIHTGEKPYKCNECDKAFSRSTHLTOHORIHTGEKPYK CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSA_N KHQRLHPGI AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAOKNPEFFKTSV
5848	22	2961	HLTOHORIHTGEKPYKCNECDKAFSRSTHLTQHQRIHTGERPYK CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSALN KHQRLHPGI AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLODYTY*FCPGFLGLSVKULBLLOCV
5848	22	2961	HLTOHORIHTGEKPYKCNECDKAFSRSTHLTQHQRIHTGERPYK CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSALN KHQRLHPGI AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVOHSNAKNAVLFEA
5848	22	2961	HLTOHORIHTGEKPYKCNECDKAFSRSTHLTQHQRIHTGERPYK CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSA_N KHQRLHPGI AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNOLGOFLOHRETNLRYIALESMCTLA
5848	22	2961	HLTOHORIHTGEKPYKCNECDKAFSRSTHLTQHQRIHTGERPYK CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSA_N KHQRLHPGI AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVMLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDCHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLOHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRORAVDLLYAMCDRSN
5848	22	2961	HLTOHORIHTGEKPYKCNECDKAFSRSTHLTQHQRIHTGEKPYK CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSA_N KHQRLHPGI AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREEIVIKVAILAEKVAVDYTMI
5848	22	2961	HLTOHORIHTGEKPYKCNECDKAFSRSTHLTQHQRIHTGEKPYK CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSA_N KHQRLHPGI AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEWYRVIQIVINRDDVOGYAAKTVFFALO
5848	22	2961	HLTOHORIHTGEKPYKCNECDKAFSRSTHLTQHQRIHTGERPYK CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSALN KHQRLHPGI AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIOPHLLHSKEHI
5848	22	2961	HLTOHORIHTGEKPYKCNECDKAFSRSTHLTQHQRIHTGERPYK CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSALN KHQRLHPGI AAPRRLERGGDGRTPRFPLPALLRPGPPAEAAPERKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQLVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL CSVPTRALLLSTYIKFVNLFPEVKPTIODVLRSDSOURNADVEL
5848	22	2961	HLTOHORIHTGEKPYKCNECDKAFSRSTHLTQHQRIHTGERPYK CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSALN KHQRLHPGI AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFCHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGGFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEWWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL CSVPTRALLLSTYIKFVNLPPEVKPTIQDVLRSDSQLRNADVEL QQRAVEYLRLSTVASTDLIATVLEEMPPFPERESSILAKLKKKK
5848	22	2961	HLTOHORIHTGEKPYKCNECDKAFSRSTHLTQHQRIHTGERPYK CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSALN KHQRLHPGI AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL CSVPTRALLLSTYIKFVNLPPEVKPTIQDVLRSDSQLRNADVEL QQRAVEYLRLSTVASTDILATVLEEMPPFPERESSILAKLKKKK GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG
5848	22	2961	HLTOHORIHTGEKPYKCNECDKAFSRSTHLTQHQRIHTGERPYK CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSALN KHQRLHPGI  AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLOHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL CSVPTRALLLSTYIKFVNLPPEVKPTIQDVLRSDSQLRNADVEL QQRAVEYLRLSTVASTDILATVLEEMPPFPRESSILAKLKKKK GPSTYTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSFDNFA
5848	22	2961	HLTOHORIHTGEKPYKCNECDKAFSRSTHLTQHQRIHTGERPYK CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSALN KHQRLHPGI AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL CSVPTRALLLSTYIKFVNLFPEVKPTIQDVLRSDSQLRNADVEL QQRAVEYLRLSTVASTDILATVLEEMPPFPERESSILAKLKKKK GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRONLGRMFIFYGNKTSTDEL
5848	22	2961	HLTOHORIHTGEKPYKCNECDKAFSRSTHLTQHQRIHTGERPYK CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSALN KHQRLHPGI  AAPRRLLRGGDGRTPRFPLPALLRPGPPAEAAPERKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL CSVPTRALLLSTYIKFVNLPPEVKPTIQDVLRSDSQLRNADVEL QQRAVEYLRLSTVASTDILATVLEEMPPFPERESSILAKLKKKK GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFL NFTPTLICSDDLQPNLNIQTKPVDPTVEGGAOVOVNITECUSD
5848	22	2961	HLTOHORIHTGEKPYKCNECDKAFSRSTHLTQHQRIHTGERPYK CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSALN KHQRLHPGI AAPRRLERGGDGRTPRFPLPALLRPGPPAEAAPERKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL CSVPTRALLLSTYIKFVNLPPEVKPTIQDVLRSDSQLRNADVEL QQRAVEYLRLSTVASTDILATVLEEMPPFPERESSILAKLKKKK GPSTYTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFL NFTPTLICSDDLQPNLNIQTKPVDPTVEGGAQVQQVVNIECVSD FTEAPVLNIQFRYGGTFONVSVOLPITLNKFFOPTFMASODEFO
5848	22	2961	HLTOHORIHTGEKPYKCNECDKAFSRSTHLTQHQRIHTGERPYK CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSALN KHQRLHPGI AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQLVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL CSVPTRALLLSTYIKFVNLPPEVKPTIQDVLRSDSQLRNADVEL QQRAVEYLRLSTVASTDILATVLEEMPPFPERESSILAKLKKKK GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFL NFTPTLICSDDLQPNLNIQTKPVDPTVEGGAQVQQVVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLFEVDP
5848	22	2961	HLTOHORIHTGEKPYKCNECDKAFSRSTHLTQHQRIHTGERPYK CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSALN KHQRLHPGI AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ CSVPTRALLLSTYIKFVNLPPEVKPTIQDVLRSDSQLRNADVEL QQRAVEYLRLSTVASTDILATVLEEMPFFPERESSILAKLKKKK GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFL NFTPTLICSDDLQPNLNIQTKPVDPTVEGGAQVQQVVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV
			HLTOHORIHTGEKPYKCNECDKAFSRSTHLTQHQRIHTGERPYK CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSALN KHORLHPGI AAPRRLLRGGDGRTPRFPLPALLRPGPPAEAAPERKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFCHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY**FCPGFLGISVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGGFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL CSVPTRALLLSTYIKFVNLPPEVKPTIQDVLRSDSQLRNADVEL QQRAVEYLRLSTVASTDILATVLEEMPPFPERESSILAKLKKKK GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFL NFTPTLICSDDLQPNLNIQTKPVDPTVEGGAQVQQVVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQF
5849	3545	2961	HLTOHORIHTGEKPYKCNECDKAFSRSTHLTQHQRIHTGERPYK CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSALN KHORLHPGI AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY**FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGGFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL CSVPTRALLLSTYIKFVNLPPEVKPTIQDVLRSDSQLRNADVEL QQRAVEYLRLSTVASTDILATVLEEMPPFPERESSILAKLKKKK GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFL NFTPTLICSDDLQPNLNIQTKPVDPTVEGGAQVQQVVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQF  KRREIKETVFHHVAQAGLELLSSNPPSSASRSAGITGMFHOVO
			HLTOHORIHTGEKPYKCNECDKAFSRSTHLTQHQRIHTGERPYK CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSALN KHQRLHPGI  AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ QQRAVEYLRLSTVASTDILATVLEEMPPFPERESSILAKLKKKK GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFL NFTPTLICSDDLQPNLNIQTKPVDPTVEGGAQVQQVVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQF KRREIKETVFHHVAQAGLELLSSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTEEDRFSLEALQTIHKOMDDDKDGGIEVEFS
			HLTOHORIHTGEKPYKCNECDKAFSRSTHLTQHQRIHTGERPYK CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSALN KHQRLHPGI  AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ CSVPTRALLLSTYIKFVNLFPEVKPTIQDVLRSDSQLRNADVEL CSVPTRALLLSTYIKFVNLFPEVKPTIQDVLRSDSQLRNADVEL QQRAVEYLRLSTVASTDILATVLEEMPPFPERESSILAKLKKKK GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFL NFTPTLICSDDLQPNLNIQTKPVDPTVEGGAQVQQVVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQF KRREIKETVFHHVAQAGLELLSSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTEEDRFSLEALQTIHKQMDDDKDGGIEVEES DEFIREDMKYKDATNKHSHLHREDKHITIEDLWKRWKTSEVHNW
			HLTOHORIHTGEKPYKCNECDKAFSRSTHLTQHQRIHTGERPYK CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSALN KHQRLHPGI  AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEWYYRVIQIVINRDDVQGYAAKTVFEALQ CSVPTRALLLSTYIKFVNLPPEVKPTIQDVLRSDSQLRNADVEL QQRAVEYLRLSTVASTDILATVLEEMPPFPERESSILAKLKKKK GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGKSEFRQNLGRMFIFYGNKTSTQFL NFTPTLICSDDLQPNLNIQTKPVDPTVEGGAQVQQVVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQF KRREIKETVFHHVAQAGLELLSSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTEEDRFSLEALQTIHKQMDDDKDGGIEVEES DEFIREDMKYKDATNKHSHLHREDKHITIEDLWKRWKTSEVHNW
			HLTOHORIHTGEKPYKCNECDKAFSRSTHLTQHQRIHTGERPYK CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSALN KHQRLHPGI AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ CSVPTRALLLSTYIKFVNLPPEVKPTIQDVLRSDSQLRNADVEL QQRAVEYLRLSTVASTDILATVLEEMPPFPERESSILAKLKKKK GPSTYTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFL NFTPTLICSDDLQPNLNIQTKPVDPTVEGGAQVQQVVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQF  KRREIKETVFHHVAQAGLELLSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTEEDRFSLEALQTIHKQMDDDKDGGIEVEES DEFIREDMKYKDATNKHSHLHREDKHITIEDLWKRWKTSEVHNW TLEDTLQWLIEFVELPQYEKNFRDNNVKGTTLPRIAVHEPSFMI
		1895	HLTOHORIHTGEKPYKCNECDKAFSRSTHLTQHQRIHTGERPYK CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSALN KHQRLHPGI AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQLVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ QRAVEYLRLSTYIKFVNLPPEVKPTIQDVLRSDSQLRNADVEL QQRAVEYLRLSTYIKFVNLPPEVKPTIQDVLRSDSQLRNADVEL QQRAVEYLRLSTVASTDLLATVLEEMPPFPERESSILAKLKKKK GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFL NFTPTLICSDDLQPNLNIQTKPVDPTVEGGAQVQVVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQF KREIKETVFHHVAQGGLELLSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTEEDRFSLEALQTIHKQMDDDKDGGIEVEES DEFIREDMKYKDATNKHSHLHREDKHITIEDLWKRWKTSEVHNW TLEDTLQWLIEFVELPQYEKNFRDNNVKGTTLPRIAVEPSFMI SQLKISDRSHRQKLQLKALDVVLFGPLTRPPHNWMKDFILTVSI
		1895	HLTOHORIHTGEKPYKCNECDKAFSRSTHLTQHQRIHTGERPYK CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSALN KHQRLHPGI AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ QRAVEYLRLSTYIKFVNLPPEVKPTIQDVLRSDSQLRNADVEL QQRAVEYLRLSTYIKFVNLPPEVKPTIQDVLRSDSQLRNADVEL GGAPPAPAGGPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFL NFTPTLICSDDLQPNLNIQTKPVDPTVEGGAQVQQVVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQF KRREIKETVFHHVAQAGLELLSSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTEEDRFSLEALQTIHKQMDDDKDGGIEVEES DEFIREDMKYKDATNKHSHLHREDKHITIEDLWKRWKTSEVHNW TLEDTLQWLIEFVELPQYEKNFRDNNVKGTTLPRIAVKWTSEVHNW SQLKISDRSHRQKIQLKALDVVLFGPLTRPPHNWKMFIITVSI VIGVGGCWFAYTQNKTSKEHVAKMMKDLESLQTAEQSLMDLOER
		1895	HLTOHORIHTGEKPYKCNECDKAFSRSTHLTQHQRIHTGERPYK CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSALN KHQRLHPGI AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFCHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL CSVPTRALLLSTYIKFVNLPPEVKPTIQDVLRSDSQLRNADVEL QQRAVEYLRLSTVASTDILATVLEEMPPFPERESSILAKLKKKK GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFL NFTPTLICSDDLQPNLNIQTKPVDPTVEGGAQVQQVVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQF  KRREIKETVFHHVAQAGLELLSSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTEEDRFSLEALQTIHKQMDDDKDGGIEVEES DEFIREDMKYKDATNKHSHLHREDKHITIEDLWKRWKTSEVHNW TLEDTLQWLIEFVELPQYEKNFRDNNVKGTTLPRIAVHEPSFMI SQLKISDRSHRQKLQLKALDVVLFGPLTRPPHNWMKDFILTVSI VIGVGGCWFAYTQNKTSKEHVAKMMKDLESLQTAEQSLMDLQER LEKAQEENRNVAVEKQNL*RKMMEINYAKBEACRLRELREGAE
		1895	HLTOHORIHTGEKPYKCNECDKAFSRSTHLTQHQRIHTGERPYK CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSALN KHQRLHPGI AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ QRAVEYLRLSTYIKFVNLPPEVKPTIQDVLRSDSQLRNADVEL QQRAVEYLRLSTYIKFVNLPPEVKPTIQDVLRSDSQLRNADVEL GGAPPAPAGGPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFL NFTPTLICSDDLQPNLNIQTKPVDPTVEGGAQVQQVVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQF KRREIKETVFHHVAQAGLELLSSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTEEDRFSLEALQTIHKQMDDDKDGGIEVEES DEFIREDMKYKDATNKHSHLHREDKHITIEDLWKRWKTSEVHNW TLEDTLQWLIEFVELPQYEKNFRDNNVKGTTLPRIAVKWTSEVHNW SQLKISDRSHRQKIQLKALDVVLFGPLTRPPHNWKMFIITVSI VIGVGGCWFAYTQNKTSKEHVAKMMKDLESLQTAEQSLMDLOER

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
1 .	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ.	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
İ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
ŀ	amino acid	residue of	S=Serine, T=Threonine, V=V=line
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +=c+==
1	amino acid	sequence	Codon, /=possible nucleotice deletion
	sequence		\=possible nucleotide insertion)
1			AHSSSLDEVDHKILEAKKALSELTTCLRERLERWOOTEKTCGEO
			IAHNSGLPSLTSSLYSDHSWVVMPRVSIPPVDTAGGVDDLDPDT
İ	ł		PPIVSQFPGTMAKPPGSLARSSSLCRSRRSTVPSSPOPOPAGIA
1			PHAPHPSHPRHPHHPOHTPHSLPSPDPDILSVSSCPALYRNEEE
	ŀ		EEAIYFSAEKQWEVPDTASECDSLNSSIGRKQSPP/SKPRDIPN
5850	3	1895	IIS/DERYQEMRCP*RIPSGGIL
1	_	1033	KAVLNFSASGSVISLTGSNPMHDASMWHLKKNGIIVYLDVPLLN
1		1	LICRLKLMKTDRIVGQNSGTSMKDLLKFRRQYYKKWYDARVFCE
1			SGASPEEVADKVLNAIKRYQDVDSETFISTRHVWPEDCEQKVSA
			EFFIEAVIEGLASDGGLFVPAKEFPKLSCGEWKSLVGATYVERA QILLERCIHPADIPAARLGEMIETAYGENFACSKIAPVRHLSGN
	1	1	QFILELFHGPTGSFKDLSLQLMPHIFAQCIPPSCNYMILVATSG
			DTGSAVLNGFSRLNKNDKQRIAVVAFFPENGVSDFQKAQIIGSQ
			RENGWAVGVESDFDFCQTAIKRIFNDSDFTGFLTVEYGTILSSA
			NSINWGRLLPQVVYHASAYLDLVSQGFISFGSPVDVCIPTGNFG
			NILAAVYAKMMGIPIRKFICASNONHVWTDFIKTG\HVDI.PCVE
	ł		N*AQTFFTVQ*IFLPNLSNLERHLHLMANKDGOIMTELENDLEG
-			QHHFQIEKALVEKLQQDFVADWCSEGECLAAINSTVNTSGVILD
-			PHTAVAKVVADRVQDKTCPVIISSTAHYSKFAPATMOALKTVET
1			NETSSSQLYLLGSYNALPPLHEALLERTKOOEKMEYOVCAADMN
5851	3120	1802	VLKSHVEQLVQNQFI
	5220	1002	RCYLQFLALLLTSTSARAAAAIAAAEEPAGSPSVMTRAGDHNRQ
1			RGCCGSLADYLTSAKFLLYLGHSLSTWGDRMWHFAVSVFLVELY
			GNSLLLTAVYGLVVAGSVLVLGAIIGDWVDKNARLKVAQTSLVV QNVSVILCGIILMMVFLHKHELLTMYHGWVLTSCYILIITIANI
1			ANLASTATAITIQRDWIVVVAGEDRSKLANMNATIRRIDQLTNI
			LAPMAVGQIMTFGSPVIGCGFISGWNLVSMCVEYVLLWKVYQKT
1 1			PALAVKAGLKEEETELKQLNLHKDTEPKPLEGTHLMGVKDSNIH
1 1			ELEHEQEPTCASQMAEPFRTFRDGWVSYYNOPVF/LCWHGSCEP
1 1			LYDCPGL*LHHHRVRLHSGTEWFHPOYFDGSISVNWNNGNCGEV
5852			LATSKMWFGSDRSDLRIGTAFLFDLVCDLCIHAWKPPGLVPFSF
3032	1	422	KTTFPSSLCPLRQLPEVRGYSGOPLTDPLTSLCPSHKCPCVCWC
1 1			SSSYPSLPALLRARSAPGHCTHRSCGPEWRIDGISDLEMOCADD
			SGWAQAQPTILLLVPRLRKSLPSIWG/SLMGFFITSGPG/WFRQ
] [	1		YYFFISGRH*VLFTESDFYYVAMDFGGHGLSSHYSPGVPYYLQT
1 1			FVSBIRRVVAGKKQSVYFRRCGGCSRAPPLITGGGVGSRKQRWP ESGAWALAPGLPAIHGRSWES
5853	223	1346	PLICICPUVCI UCEN CONTROLLES
1 .	1		RLLGLSRVKGLHGPAASAWISDPETRGDPGGPWGMWRGSDLRPR PVSLTGLTLVCK*AAQGPQV\HSVKLCFGLGG\PCLL\FPIFRP
1			LLLHPRRPRLHPGTRGVAVEPHALRVVHVAHGEEAGIRAAGPGH
[ [	ſ		GGVEIPQG/VGSLGARRGLRPSRPSSRHRNRVPAPPPGRPLATP
			HRRRFPPDPALTCPGLGQDQGPREQQKQGSGRHDTILGDWGESE
i i		i	SRWVRGNFRTGTAATLIGFSRNPTLNGSENWGSLVSTOFFGDDT
			GWEREKRNPAEMGNPORWASPIHTPPLGPEILRAMPEALRAMDE
1			ALGLRPDPATSVPSALS/QTF/PESWPRSCLRNOGETLGMGDVD
5854			LSSLCITESPSQNWTPCLLLLTCPRGLF
5034	86	938	KGRNTAPEKKGAALNNRENASS*NGY/SRWKQDIRRIENHIIQE
			LXHLCAMIKRVLLERLENTRKLRELTEGRTLDWPONRITENSAV
] ]			RQIVTEYREKGKRN*EEKKRDLEGRSRRYNLCTIGIDETEDDAG
1 1		1	GAETIKDLLE/ENFPELKNELDLOMEKAHRIPIKENEKKAN CDU
]	į	]	IRVTFL/KFQRRNILQASSQRKQVTYKGAKVRLTSDFSPAILNA
			RROW/N/PISRVLRENNFEPRIIYSAKLSFLYKGNWKTFLDIQG
5855	536	2391	LEGYINGELSLKILLKOLLQLTENLN
1			LRSYGCKAPSRISHLHK\FLFLLLPSLLMGYSESPPPITDSWAP
			FISLTHHVLSQSQSPLSSNCWICLSTHTQ*FTALPADLLTWTQS NVSLHISYLAIPFLADSFLKPV/L*PGNSAKHLSFKLSSLSMVS
		ļ	GRAVALLHLIASGLTSIQTNTASSKPPIWGY\LSTQTSFISPPP
	ľ	1	LCLSRTYPNPAHATMVGQVPQSLCGLIFTL/RTPCRPSILHPNY
		Ī	KIISTSAWQKVLCFSGSPTIHTSLHLTTGSSFLSFHPIPGFPAA
			NSALYVSSLKGPPGKNVTIPSPVTGT*QPPHRGSN/RLTVDKDN
			ZEFARGSM/ REIVERDN

SEC	Predicted	1 5 22 3	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
ŀ	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	bequence	Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			(-possible nucleotide insertion)
i			FFLSPKPNSLHQLPSQ\TPYQALTGAALAGSYPIWENENTLSWL
	1	į.	PTFTYNFCLSTPSLFFLCDTN*YLCLPANWSGTCTLVFQAPTIN
		i	ILPPNOTILISVEASISSSPIRNKWALHLITLLTGLGITAALGT
			GIAGITTSITSYQTLFTTLSNTVEDMHTSITSLQRQLDFLVGVI LQNWRVLDLLTTEKGGTCIYLQEECCFCVNESGIVHIAVRRLHD
			RAAEL+HQVADSWWQGSSLLRWIPWVAPFLGPLIFLFLLLMIGP
}			CIFNLVSRFISQRLNCFIQASMQKHIDNIFHLCHV*YQSLRGNH
Ì			SEAPEPRP
5856	173	1137	PWLHGLGLSAVFLFYL*/YVTFHLYGGIILLLLIFISIAGILYK
1			FQDVLLYFPEQPSSSRLYVPMPTGIPHENIFIRTKDGIRLNLIL
-			IRYTGDNSPYSPTIIYFHGNAGNIGHRLPNALLMLVNLKVNLLL
j	]	į	VDYRGYGKSEGEASEEGLYLDSEAVLDYVMTSPDLDKTKIYLSG
1			RSLG\GAAAIHLASDNSHRISAIMVENTFLSIPHMASTLFSFFP
1			MRYLPLWCYKNKFLSYRKISQCRMPSLFISGLSDQLIPPVMMKQ
			LYELSPSRTKRLAIFPDGTHNDTWQCQGYFTALEQFIKEVVKSH
L			SPEEMAKTSSNVTII
5857	1597	563	KLIGKVLVLSVVADAMAAFAVEPQGPALGSEPMMLGSPTSPKPG
1			VNAQFLPGFLMGDLPAPVTPQPRSISGPSVGVMEMRSPLLAGGS
1			PPQPVVPAHKDKSGAPPVRSIYDDISSPGLGSTPLTSRPOPMIC
			VMQSPLVGVTSTPGTGOSMFSPASIGOPRKTTI.SPAGI.DBEVTO
			GDSLTSEDH\LDDSWGDCIWGFLKASA\SYILL\OFAOYGGTS*
		!	NMWMSNTGNWMHIRYQSKLQARKALSKDGRIFGESIMTGVKDCT
			DKSVMESSDRCALSSPSLAFTPPIKTLGTPTOPGSTPRISTMPD
FOCO			LATAYKASTSDYQVISDRQTPKKDESLVSKAMEYMFGW
5858	355	1419	PPHQPAAASTSXHQQQQPPPPPPQDSSKPVVAOGPGPAPGVGSAP
			PASSSAPPATPPTSGAPPGSGPGPTPTPPPAVTSAPPGAPPPTP
			PSSGVPTTPPQAGGPPPPPPAAVPGPGPGPKGGKMP
			GGPKPGGGPGLSTPGGHPKPPHRGGGEPRGGRQHHPPYHQQHHQ
			GPPPGGPGGRSEEKISGPRRGFKANLSLLRRPGEKTYTQRCRFC
1	i		LLGIYLLISRRMNSRRLFAKIWENQEKFLSTKAKDSEFIKLESR
i 1			ALA*NCPKFELG*YTP*GGRQLPSSLFPTHACLPLSCSVIFSPF
			MFPQ*NCWGRKPFRPNLGPHLKGAVCNRWDDPWEGPTGKGHCLN
5859	307	1503	FAS .
		1303	GGSSARPRASSRRMLSRKKTKNEVSKPAEVQGKYVKKETSPLLR
1 1	İ		NLMPSFIRHGPTIPRRTDICLPDSSPNAFSTSGDGVVSRNQSFL
1			RTPIQRTPHEIMRRESNRLSAPSYLARSLADVPREYGSSQSFVT
1 1	I		EVSFAVENGDSGSRYYYSDNFFDGQRKRPLGDRAHEDYRYYEYN HDLFQRMPQNQGRHASGIGRVAATSLGNLTNHGSEDLPLPPGWS
1			VDWTMRGRKYYIDHNTNTTHWSHPLBREGLPPGWERVESSEFGT
i (	1	i	YYVDHTNKKAQY\RHPCAPTCTSV*STTSCHI/AS/RQQTERNQ
			SLLVPANPYHTAEIPDWLQVYARAPVKYDHILKWELFQLADLDT
	í		YQGMLKLLFMKELEQIVKMYEAYRQALLTELENRKQRQQWYAQQ
		!	HGKNF
5860	2956	1270	TIRVEEFPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFP
[	1		LLLFSRLCGALAGPIIVEPHVTAVWGKNVSLKCLIEVNETITQI
			SWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLFKNYSLNDATI
1 1		I	TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG
			PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFP
1			NETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFILDI
1	i	1	QYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDG
			QWPDGLLASDNTLHFVHPLTFNYSGVYICKVT\NSPGSKEVTQK
j		]	VHPTFQDPSLPTYPPLPALQFQWASPSTA*TSRD\LATEP*KTA
			PSPLSTL\ATIKGWTQLPTIIA*CSGVGALFIV\LVKCFGLGIF
1		ļ	CYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQQDELDPYPDSV
[		1	KKENKNPVNNLIRKDYLEEPEKTQWNNVENLNRFERPMDYYEDL
			KMGMKFVSDEHYDENEDDLVSHVDGSVISRREWYV
5861	2051	1305	EVCACVQAFWLVASSGDDSQGGDKCGCEVGSWVGSMRVVMARLL
	1		SEGEQGIPTACAAFAQQPAG/EPRRGLAGVGEGGPOCSWVNYRC
1		!	TLEFLVSLLGTDLARGRGNSASGPTAPADSKQL/ML*DVHRRVI
			LE*RMNSGSPARDNAPSQRFCTNLSEGLRFGISPSWREALYGCH
			201001

SEQ	Predicted	Predicted end	1 Devices
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
į.	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
I	to first		L=Leucine, M=Methionine, N=Asparagine,
	1	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
ŀ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown *=Ston
i	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
			A
5862	1556	483	PPFQLIMGEIKVSPDYNWFRGTVPLKKIIVDDDDSKIWSLYDAG
1		i	PRSIRCPLIFLPPVSGTADVFFRQILALTGWGYRVIALQYPVYW
			DHLEFCDGFRKLLDHLQLDKVHLFGASLGGFLAQKFAEYTHKSP
j	}	J	RVHSLILCNSFSDTSIFNQTWTANSFWLMPAFMLKKIVLGNFSS
	İ	· ·	CDUDDMMADA IDEMIDDI DOS COCCIO A COLOR DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CO
1	l,		GPVDPMMADAIDFMVDRLESLGQSELASRLTLNCQNSYVEPHKI
	1		RDIPVTIMDVFDQSALSTEAKEEMYKLYPNARRAHLKTGGNFPY
j	1		LCRSAEVNLYVQIHL/R/RNSMEPNTRPLTHQWSVPRSLRCRKA
i			ALASARRSSSVSLAVNDELTRCVLV*SVASAPVSRPFPSGSSGS
F 6 6 2			PVLTVSGK
5863	2714	249	PFPSRGSLPLAAPREDTMGPLMVLFCLLFLYPGLADSAPSCPQN
1			VNISGGTFTLSHGWAPGSLLTYSCPQGLYPSPASRLCKSSGQWQ
	1		TPGATRSLSKAVCKPVRCPAPVSFENGIYTPRLGSYPVGGNVSF
	·		ECEDGFI\LRGSPVRQCRPNGMWDGETAVCDNGAGHCPNPGISL
1			GP\VRTGFRFGHGDKVRYRCSSNLVLTGSSERECQGNGVWSGTE
1 1	1		PICROPYSYDFFEDVAPALGTSFSHMLGATNPTQKTKESLGRKI
			QIQRSGHLNLYLLLDCSQSVSENDFLIFKESASLMVDRIFSFEI
			NVSVATTTEACED VIII MOUT NEW
1			NVSVAIITFASEPKVLMSVLNDNSRDMTEVISSLENANYKDHEN
1			GTGTNTYAALNSVYLMMNNQMRLLGMETMAW\QEIRHAIILL\T
			DGK\SHMGGSPKTAVDHIREILNINQKRNDYLDIYAIGVGKLDV
	l		DWRELNELGSKKDGERHAFILQDTKALHQVFEHMLDVSKLTDTI
1	1		CGVGNMSANASDQERTPWHVTIKPKSQET\C\RGALISDQWVLT
1			AAHCFRDGNDHSLWRVNVGDPKSQWGKEFLIEKAVISPGFDVFA
			KKNQGIL\EFYGD\DIALL\KLAOKVKM\STHCOGPSCI.P\CTM
			\EANLGFLRETFKGSTCR\DHENEL/VWNKOSV\DAHF\VAI.\N
1			GSKLEHLTLRMGVEWTSCCRGLSPKKKTM\FPNLT\DVRR\VVT
1 1			D\QFL\CS\GPQEDESP\CK*E\SGGA\VFLERRFRLSAGGVWC
			SWGL\YNP\CLGSA\DKNSPKKGPSVAKVPPPTR/DFHIN\LFP
1	1		Q*SPWLRQHPGGMS*IFLPLLANGHLSPFACPARICRPLHFLPS
1 [	<b>1</b>		EWATLETL
5864	173	1013	PLISVPQSLISLPQPLLCFPGGQEPSAPSPCLYSFLWACSFTMG
] [			KLPPSIPPSSPLACVLKNLKPLQLTPDLKPKCLIFFCNTAWPQY
1 1			KLDNDSK*PENGTFEFSILQVLDNSCHKMGKWSEVPDVQAFF\S
[	1		HWSLPSLCSQC/GLIPNLSSFSPFCSFG/PPPQVPSP/TESFFS
1 1			MDSSDI DDSDOARDSARDS SPECSEG/PPPQVPSP/TESFFS
1 1			MDSSDLPPSPQAAPRQAEPGPNSHLASAPPPYNPFITSPPHTWS
	i	Į.	SLQFHSVTSPPPPAQQFTLKKVAGAKGIVKVSAPFSLSQIR*RL
5865	568	1684	GSFSSNIKIQPSSWLIWQQP
1 1	300	T024	CLPGPRWGEGWRAGHTIVGCIFFKTAIISHFKGGMYLCVCMCTC
1 1	1	j	LSVCVCVQVGSWICV/CVSMCACVSLCTC\ICRCISMYTREHAC
1	Í		ACTRV*VYMCMS/VCTCVSTCIDVRVCAHVCVYMCLCLGVA*AC
1			TCV*MCVCMHEHVCMC/VCACSCVLL/CRGHTCM/MCMSAVICI
			/CVYVCVLCVWACMRMSTCVWLVYG*ACTCVWMHM/CSCTCR/C
1			VHVCCMSMHACECLCVYLHICGCAGTRRWWAGSARGSRSCSRIP
	j		CWAPGPGLSLPGPSCPSVEQGLGGGPGQLQGRSGEARLGEHRGW
1			GSPAAVCSRNCTVSPRRGADCFEAPDVPKQPPGWGRASFEERGC
<u> </u>		ł	GGRGWVCAPPLNGPQCCCFSIKPELKAKKKK
5866	98	3197	ARPEVPAPPAWLSRRGAAKMGDKKDDKDSPKKNKGKERRDLDDL
1 1	ł		KKEVAMTEUKMCUPEUKONAMINGUKKUUKUSPKKNKGKERRDLDDL
1 1	ĺ	į	KKEVAMTEHKMSVEEVCRKYNTDCVQGLTHSKAQEILARDGPNA
1		. 1	LTPPPTTPEWVKFCRQLFGGFSILLWIGAILCFLAYGIQAGTED
1 1	1	· 1	DPSGDNLYLGIVLAAVVIITGCFSYYQEAKSSKIMESFKNMVPQ
1 1	ĺ	j	QALVIREGEKMQVNAEEVVVGDLVEIKGGDRVPADLRIISAHGC
] [	ļ	İ	KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFFSNNFVEGTA
1			RGVVVATGDRTVMGRIATLASGLEVGKTPIAIEIEHFIOLITGV
1	1		AVFLGVSFFILSLILGYTWLEAVIFLIGIIVANVPEGLLATVTV
	1		CLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNRM
1 1	}		TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*H/LLGFC
			NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE
1	1	-	RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD
			RCSTILLOGKEODI.DEEMER PONENT DE CO-
			RCSTILLQGKEQPLDEEMKEAFQNAYLELGGLGERVLGFCHYYL
1. 1		}	PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG
			KCRSAGIKVIMVTGDHPITAKAIAKGVGIIFEGNETVEDIAARL

Designing   cotion   corresponding   cofine   corresponding   cofine   corresponding   cofine   corresponding   cofine   corresponding   cofine   corresponding   cofine   corresponding   cofine   corresponding   cofine   corresponding   cofine   corresponding   cofine   corresponding   cofine   corresponding   cofine   corresponding   cofine   corresponding   cofine   corresponding   cofine   corresponding   cofine   corresponding   cofine   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corres	SEQ	Predicted	Predicted end	
No:   mucleotide   location   corresponding to first   corresponding to first   amino acid   residue of   amino acid   residue of   amino acid   sequence   seventh   corresponding to first   amino acid   sequence   seventh   corresponding to first   amino acid   sequence   seventh   corresponding to first   amino acid   sequence   seventh   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   cor				Amino acid segment containing signal peptide
Cocresponding   Coffree   Corresponding   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Co	- 1		· -	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
corresponding to first amino acid serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of serious of		· ·	ł .	Glutamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of amino acid ELIOGHTFIVPAR TSPQOKLIIVESCORGOATAWTOGUNDSPALKADIGUMMST ASSUVSKOADMILLDBNRASIUTCSVEGGILFENKKISTAYTL PRAESIOHKUPPRENTENTININIPLICITITICIDISTENTPAR ASSUVSKOADMILLDBNRASIUTCSVEGGILFENKKISTAYTL PRAESIOHKUPPRENTENTININIPLICITITICIDISTENTPAR ASSUVSKOADMILLDBNRASIUTCSVEGGILFENKKISTAYTL PRAESIOHKUPPRENTENTININIPLICITITICIDISTENTPAR ASSUVSKOADMILLDBNRASIUTCSVEGGILFENKKISTAYTL PRAESIOHKUPPRENTENTININIPLICITITICIDISTENTPAR ASSUVSKOADMILLDBNRASIUTCSVEGGILFENKKISTAYTL PRAESIOHKUPPRENTENTININIPLICITITICIDISTENTPAR ASSUVSKOADMILLDBNRASIUTCSVEGGILFENKKISTAYTL PRAESIOHKUPPRENTENTININIPLICITITICIDISTENTPAR ASSUVSKOADMILLDBNRASIUTCSVEGGILFENKKISTAYTL PRAESIOHKUPPRENTENTININIPLICITITICIDISTENTPAR ASSUVSKOADMILLDBNRASIUTCSVEGGILFENKKISTAYTL PRAESIOHKUPPRENTENTININIPLICITICIDISTENTPORTICITICIDISTENTPAR ASSUVSKOADMILLDBNRASIUTCH AND ASSUVSKOADRENTY PRAESIO PRAESIOHKUPPRENTENTININIPLICITICIDISTENTSVEGGILFENKKISTAYTENTPAR ASSUVSKOADMILLDBNRASIUTCH AND ASSUVSKOADRENTY PRAESIOLIDISTENTPAR ASSUVSKOADMILLDBNRASIUTCH AND ASSUVSKOADRENTY PRAESIO PPSCHALARDSVEGGILFENKKISTAY TANONOMINITATION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION PRAESION		1		H=H1Stidine, I=Isoleucine, K=Lysine,
amino acid residue of amino acid amino acid acquence  Seserine, T-Threcoming, Meangline, acquence  acquence  Residue of amino acid acquence  Residue of amino acid acquence  Residue of acquence  Residue of acquence  Residue of acquence  Residue of acquence  Residue of acquence  Residue of acquence  Residue of acquence  Residue of acquence  Residue of Acquence  Residue of Acquence  Residue of Acquence  Residue of Acquence  Residue of Acquence  Residue of Acquence  Residue of Acquence  Residue of Acquence  Residue of Acquence  Residue of Acquence  Residue of Acquence Acquence  Residue of Acquence  Residue of Acquence Acquence  Residue of Acquence  Residue of Acquence Acquence  Residue of Acquence Acquence  Residue of Acquence Acquence  Residue of Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acquence Acque	]			h=beucine, M=Methionine, N=Asparagine,
maino acid aequence  ### Author	1		i i	P=Proline, Q=Glutamine, R=Arginine,
### ATTYPTOSING, X=DURKNOM, *=Stop adjuance  ### amino acid acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ### acquence  ##		1	(	S=Serine, T=Threonine, V=Valine
acquence    Codon, /-possible nuclectide deletion,		N .		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Apposible nucleotide insertion			seguence	Codon, /=possible nucleotide deletion
NTYPSGOWNRIDAKACUTHGTDLKOPTSEGIDETLONHTETUTE TSPROCKLITUSCORGGATUNTOTICGUNISPALKADIGVAMGE AGSDUSKOARMILLIDDINGSTUTOVEGERIJFENILKKSTATY THE TITPELITHAND IPLINGTUTUSCHEGERIJFENILKKSTATY EARSSDUKKOPRINGTUNIONDOTTUNLESSYSTOMVATSLAN EARSSDUKKOPRINGTUNIONDOTTUNLESSYSTOMVATSLAN EARSSDUKKOPRINGTUNIONDOTTUNLESSYSTOMVATSLAN EARSSDUKKOPRINGTUNIONDOTTUNLESSYSTOMVATSLAN EARSSDUKKOPRINGTUNIONDOTTUNLESSYSTOMVATSLAN EARSSDUKKOPRINGTUNIONDOTTUNLESSYSTOMVATSLAN EARSSDUKKOPRINGTUNIONDOTTUNLESSYSTOMVATSLAN GUSTTLITIKRINKKURTIKKURTIKKURTIKKANKOPPOKALPPYSELITY TOETRILITIKRINKKURTIKKANKOPPOKALDOSKINGKAKVPASKRAPSSYVAKP GUSTTLITIKRINKKURTIKKKARTIKKKARTIKKANKARPOKANAPSYSTATASSYSTOKA GUSTTLITIKRINKKURTIKKKARTIKKKARTIKKANKARPOKANAPSYSTATASSYSTOKA ETSISTOVKGERMPAGKOGASRGSVESSKOMBRARVERTIKASSY ERINKKOTKERTUNGULVOKSOADERKUKKANKA (GOOPHIPPE/TDI  BERNANGTIKERTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTUNIONDOTTU		sequence		\=possible nucleotide insertion)
S869  2122  833  LTAGASHTODASCISTRAKTPARADILVEVINERGILIPINYIE  S869  2122  833  LTAGASHTORASCISTRAKTPARADILVEVINERGILIPINYIE  S869  2122  833  LTAGASHTORASCISTRAKTPARADILVEVINERGILIPINYIE  S869  2122  833  LTAGASHTORASCISTRAKTPARADILVEVINERGILIPINYIE  S869  2122  833  LTAGASHTORASCISTRAKTPARADILVEVINERGILIPINYIE  S869  2122  833  LTAGASHTORASCISTRAKTPARADILVEVINERGILIPINYIE  S869  2122  833  LTAGASHTORASCISTRAKTPARADILVEVINERGILIPINYIE  S869  2122  833  LTAGASHTORASCISTRAKTPARADILVEVINERGILIPINYIE  S869  2122  833  LTAGASHTORASCISTRAKTPARADILVEVINERGILIPINYIE  S869  2122  833  LTAGASHTORASCISTRAKTPARADILVEVINERGILIPINYIE  S869  2122  833  LTAGASHTORASCISTRAKTPARADILVESTISTREDEPISTLAN  LESRY-TWILDIGHILDISTRAKTPARASEPEDPY  TERSASTERRASCISTVERICHESSISTRAKTPARADILVETINGENERGILIPINYIE  S869  2122  833  LTAGASHTORASCISTRAKTPARADILVESTISTREDEPISTLAN  LESRY-TWILDIGHILDISTRAKTPARASEPEDPY  TERSASTERRASCISTVERICHESSISTRAKTPARADILVETINGENERGILIPINYIE  S869  2122  833  LTAGASHTORASCISTRAKTPARADILVETINGENERGILIPINYIE  S869  2122  833  LTAGASHTORASCISTRAKTPARADILVETINGENERGILIPINYIE  S869  2122  833  LTAGASHTORASCISTRAKTPARADILVESTISTREDEPPSILLAN  LESRY-TWILDIGHILDISTALUSTRATIPERPSILLIPINYIE  S869  2122  833  LTAGASHTORASCISTRAKTPARADILVESTISTREDEPPSILLAN  LESRY-TWILDIGHILDISTALUSTRAKTPARASEPEDPY  TERSASTERRASCISTVERICHESSISTRATIPARASEPEDPY  TERSASTERRASCISTVERICHESSISTRATIPARASEPEDPY  TERSASTERRASCISTRATIPARADILVETINGENERGISTRATIPARASEPEDPY  TERSASTERRASCISTRATIPARADILVETINGENERGISTRATIPARASEPEDPY  TERSASTERRASCISTRATIPARADILVETINGENERGISTRATIPARASEPEDPY  TERSASTERRASCISTRATIPARADILVETINGENERGISTRATIPARASEPEDPY  TERSASTERRASCISTRATIPARADILVETINGENERGISTRATIPARASEPEDPY  TERSASTERRASCISTRATIPARADILVETINGENERGISTRATIPARASEPEDPY  TERSASTERRASCISTRATIPARADILVETINGENERGISTRATIPARASEPEDPY  TERSASTERRASCISTRATIPARADILVETINGENERGISTRATIPARASEPEDPY  TERSASTERRASCISTRATIPARADILVETINGENERGISTRATIPARASEPEDPY  TERSASTERRASCISTRATIPARADILVETINGENERGISTRATIPARASEPEDPY  TERSASTERRASCISTRATIPARADILVENERGISTRATIPARASEPEDPY  TERSASTERRASCISTRAT				NIPVSOVNPRDAKACVIHGTDI KDETSEOLDELI ONUMETURE
AGSDVSKQAAMMILLDBARPASITYGVEEGRILIFDMIKKSTATTI  SANSEDIMREQDRNPETDKINNERLISMAYGOIGHIQALGGFFS YEVILLAENGFLEGHTINLCIUDIJMWYPAISLAN EAASSDIMREQDRNPETDKINNERLISMAYGOIGHIQALGGFFS YEVILLAENGFLEGHUNGTURUDETVURDEZQONTTEGRK VUEETCHTAFEVSIVVVOMADLIICKTERNSVEQGGMKNEKLIF GLESTATALAELSYCGMEUNGLAENGPYARDLAINGEVLESSKAPESPVAKF GLESTATALAELSYCGMEUNGLAENGPYARDLAINGEVLESSKAPESPVAKF GLESTATARAENGEGERPAGKOIGSKAPKARPSKRAFSSPVAKF GLESTATARAENGEGERPAGKOIGSKAPKARPSKRAFSSPVAKF GLESTATARAENGEGERPAGKOIGSKAPKARPSKRAFSSPVAKF GLESTATARAENGEGERPAGKOIGSKAPKARPSKRAFSSPVAKF GLESTATARAENGEGERPAGKOIGSKAPKARPSKRAFSSPVAKF GLESTATARAENGELKKAKKARFKASKASEVSKAPASGGGAVVEPKARF DPSOMKAGLERINGEDAKKASAEVSKAPASGGGAVVEPKARG GLESTATARAENGELKAKKAKARFKASKASEVSKAPASGGGAVVEPKARG GLESTATARAENGELKAKKAKARFKASKASEVSKAPASGGGAVVEPKARG GLESTATARAENGELKAKKAKARAENGELGSEGSVELSIVKGARG GLESTATARAENGELKAKKAKARAENGEVAKKAKAGGGGGAVASTAKAGG GLESTATARAENGELKAKKAKARAENGEVAKKAKAGGGGGAVASTAKAGG GLESTATARAENGELKAKKAKARAENGELVOKKAKARAENGAKKAGA ALIANDAKVILFILDHEKKAK ROMGELEVOKKARAENGARGHINGH ALIANDAKVILFILDHEKKAK ROMGELEVOKKARAENGAGATATAA ALIANDAKVILFILDHEKKAK ROMGELEVOKKARAENGAGATATAA ALIANDAKVILFILDHEKKAK ROMGELEVOKKARAENGAGATATAA ALIANDAKVILFILDHEKKAK ROMGELEVOKKARAENGAGATATAA ALIANDAKVILFILDHEKKAK ROMGELEVOKKARAENGAGATATAAAA ALIANDAKVILFILDHEKKAK ROMGELEVOKKARAENGAGATATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1	1		TSPOOKLI TVEGCOROCA TVA IMORDORA TVA IMORDORA TVA
EARSEDIMENGENER TITLLCIDISTOMYPAISIAY EARSEDIMENGENER TO THE TOTAL CONTROL OLLOGETS YEVILLARNOFLEGRILUGITE MINDERTUNDELS YGOGNIT TEGRE YEVILLARNOFLEGRILUGITE MINDERTUNDELS YGOGNIT TEGRE YEVILLARNOFLEGRILUGITE MINDERTUNDELS YGOGNIT TEGRE YEVILTAREN TEGRETALAR LISCUSCHEUR LICKTERREN YER THE GLEET ALAR LISCUSCHEUR LICKTER YER THE DEGRARAGEGELGMEP AGALDGSHOKAK VPASKRAESSEPVAKE GUNTUTRIKHEKKKER PHEKAREVSKEPAS SEPVAKE GUNTUTRIKHEKKKER PHEKAREVSKEPAS SEPVAKE GUNTUTRIKHEKKKER PHEKAREVSKEPAS SEPVAKE GUNTUTRIKHEKKKER PHEKAREVSKEPAS SEPVAKE ETS SOVKGEREN PAGALOGSKEVESKI TOONKE ERINKKITEER TUNDI VERGOI EHEKKRAEN (GODOPHEPR / IDI MEDDUPADA I BERAI GEPARAK TARKOLOGSBESLIJVE GOAF GUTTALALALOCHMUSUP SKEESSENAARVS I VIQVYKCVUNKYKUN TEPVIDYRTAN YESIGI SIDA AGAGELLEV VOKKRAEN KORTON ALINDIKKULF LOHPKKKI RUTTOKY YEPKSOVKSGRES LELLISEK ILOLOVGABELIS IDA AGAGELLEV VOKKRAEN KORTON ALINDIKKULF LOHPKKKI RUTTOKY YEPKSOVKSGRES LELLISEK ILOLOVGABELIS IDA AGAGELLEV VOKKRAEN KORTON ALINDIKKULF LOHPKKKI RUTTOKY YEPKSOVKSGRES LELLISEK ILOLOVGABELIS IDA AGAGELLEV VOKKRAEN KORTON ALINDIKKULF LOHPKKKI RUTTOKY YEPKSOVKSGRES LELLISEK ILOLOVGABELIS I TOONKA THE TERRETTER TOONKA TOONKA THE TERRETTER TOONKA THE TERRETTER TOONKA THE TERRETTER TOONKA THE TERRETTER TOONKA THE TERRETTER TOONKA THE TERRETTER TOONKA THE TERRETTER TOONKA THE TERRETTER TOONKA THE TERRETTER TOONKA THE TERRETTER TOONKA THE TERRETTER TOONKA THE TERRETTER TOONKA THE TERRETTER TOONKA THE TERRETTER TOONKA THE TERRETTER TOONKA THE TERRETTER TOONKA THE TERRETTER TOONKA THE TERRETTER TOONKA THE TERRETTER TOONKA THE TERRETTER TOONKA THE TERRETTER TOONKA THE TERRETTER TOONKA THE TERRETTER TOONKA THE TERRETTER TOONKA THE TERRETTER TOONKA THE TERRETTER TOONKA THE TERRETTER TOONKA THE TERRETTER TOONKA THE TERRETTER TOONKA THE TERRETTER TOONKA THE TERRETTER TOONKA THE TERRETTER TOONKA THE TERRETTER TO THE TERRETTER TOONKA THE TERRETTER TO THE TERRETTER TOONKA THE TERRETTER TO THE TERRETTER TOONKA THE TERRETTER TO THE TERRETTER TO THE TERRETTER TOONKA THE TERRETTER TOONKA THE TERRETTER TOON	1	İ	ı	ACCDUCYCAADMILLADAHAACTUBGUNDSPALKKADIGVAMGI
EARSED IMERGPRIPETIOKLUMERLISMA YOQIGHTOLOGGFFS YEVILLARING FUNDATUMENTUMBERLY COMPUTEORIK UVETCHTAFFEVSIVVVOMADLIICKTERRSVPQOGMKNKLIF GLFSETALARI-SVCCMUNDLARMYLIKESWALPPYSPISLIFV YDEIRKLILRRIPGGWVEKETY  JERRALILRRIPGGWVEKETY  DERRALILRRIPGGWVEKETY  DERRALILRRIPGGWEKETY  FORMANGGELGWFPAGALDGSRAMGKAKVPASKRAPSSEVAKP GVEKTLUTRKKKKKR FMSKAREVSKKPASGGGAVURPPKAPE DPSONNKALGENGAPETIVITSON GERPUTVISON GERPUTVEN FARE ERNKSTHERFINGDIVPSKGE FINITISON GERPUTVEN FARE BENNKSTHERFINGDIVPSKGE INHKKRIKKKKKKKKRYDE JONKKE ETSPOVKGEMPAGKDO EARRGSVPSGSKWIGHAPVPRYKASGT BENNKSTHERFINGDIVPSKGE INHKKRIKKKKKYNEYDE JONKGE GLITAPALALCH WEDDUPADI EAAIGPEAAKLARKOLGGSELSUVKEQAFG GLTAFALALCH GERMAVOLPROSESMARVE INVKKENESHARDERPLLITA PHOLOGDA*GGELSIODAGAMRLYYMVKENESHARDERPLLITA PHOLOGDA*GGELSIODAGAMRLYYMVKENESHARDERPLLITA PHOLOGDA*GGEPAAAAAPLGCGCOSGGGTSGGETS ESWGROWAWC  TERRAPTERDAGSGLVTHARPRALLUSSTSHESPERLIHGKHIFON AVTVYNKPASFFRETPLDLQHRLFMKLISSMISPRARSEPEDDY TERRAPTERDAGSGLVTHLERPRALLUSSTSHEDEPSILLAA LESRV*TWITLDGHALPSLVCUTTKKGPLREYSTSLHIHGKHIFON GCLPVCANNFKCHBLUKHEENGLVFEDSEELAAGLQMLFSNFP PAGKIMOFRANIRESQQLANDESWOTUTLIPWIDT TERSAPTERDAGSGLVTHLERERPALLUSSTSHEDDPSILLAA LESRV*TWIDHANDESSVOTUTLIPWIDT TERSAPTERDAGSGLVTHLERERPALLUSSTSHEDDPSILLAA LESRV*TWIDHANDESSVOTUTLIPWIDT TERSAPTERDAGSGLVTHLERERPALLUSSTSHEDDPSILLAA LESRV*TWIDHANDESSVOTUTLIPWIDT TERSAPTERDAGSGLVTHLERERPALLUSSTSHEDDPSILLAA LESRV*TWINDHANDESSVOTUTLIPWIDT GCLPVCANNFKCHBLVKHEENGLVFEDSEELAAGLQMLFSNFP DPAGKLMOFRKHLESGOLGHOSWGVTUTLIPWIDT TERSAPTERDAGSGLVTHLERERPALLUSSTSHEDDFSILLAA LESRV*TWINDHANDESSVOTUTLIPWINDHANDEN GCLPVCANNFKCHBLVKHEENGLVFEDSEELAAGLQMLFSNFP DPAGKLMOFRKHLESGOLGHOSWGVTUTLIPWIDT TERSAPTERDAGSGLVTHLERERPALLUSSTSHEDDFSILLAA LESRV*TWINDHANDESSVOTUTLIPWINDHANDEN GCLPVCANNFKCHBLVKHEENGLVFEDSEELAAGLQMLFSNFP DPAGKLMOFRKHLESGOLGHOSWGVTUTLIPWIDT TERSAPTERDAGSGLVTHLERERPALLUSSTSHEDDFSILLAA LESRV*TWINDHANDESSVOTUTLIPWINDHANDESDFSILLAA LESRV*TWINDHANDESSVOTUTLIPWINDHANDESDFSILLAA LESRV*TWINDHANDESSVOTUTLIPWINDHANDESSOLGHON VICKLYSLERGENGTHANDHANDHANDHANDHANDHANDHANDHANDHANDHAND	1	1		AGSDVSKQAADMILLEDDNFASIVIGVEEGRLIFDNLKKSIAYTL
1485  1485  1485  1485  1485  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486  1486	<u> </u>	1		-SNIPETIFFELFIMANIPLPLGTITILCIDLGTDMVPAISLAY
WEFTCHTAFFYS: VVVQWADLII CKTRRNSVFQQMKRKILIF GEFETLAAFISVCPGMVECTYY YDEIRKLILRRNPGGWVEKTYY JDEIRKLILRRNPGGWVEKTYY JDEIRKLILRRNPGGWVEKTYY JDEIRKLILRRNPGGWVEKTYY JDEIRKLILRRNPGGWVEKTYY LDERRAKGGRGGFMPPAQALDGSKMGKAKYPASKRAPSSPVAKP GPVKTLTRKNKKKKKRPWKSKAREVSKKPASGGAVVRPPKAPS DPSQNWKALQEMLLKKQSQAPEKPLUTSGKKYEKITQOMKK ETSPQVKGEMPAGKDQEASRGSVPSGSKMDRRAPVFRKASGT BRINKGTRERTIGHIV PREGDIEHKKRAK (GQOPHPPR) / IDI WEDDVDPADIERAIGPEAKKIARIOLGGSEGSVELSILVEQAFG GUTPALALDCEMVLVUPKGEGSMARAVS VKOKEVSKHYKVEV ALEDRUKLJEDHEKKI ENDTOKKYPK KOKGPOPHPRP / IDI WEDDVDPADIERAIGPEAKKIARIOLGGSEGSVELSILVEQAFG GUTPALALDCEMVLVUPKGESMARAVS VKOKEVSKHYKVEV TEPVTYRTAVSGTRPENLKGGEELEVVOKEVABMLKGELUGH ALINDLKVLTJEDHEKKI ENDTOKKYPK KOKGFISHLISEK ILGLQVQCABHCSI DOAQAANKLYVMVKKEWESMARDRPPLLTA PDHGSDDA'ASCPARAAAADLQCCCDSSCOTSFGGSMSGTFF ESMGROVANCY LTAGASHTODASGSTSAKYPAAAONL/CVTNAMREDLADIMYIR AVTVYKKPASFFKETELDLQHRIJERRPALLVSTSWFTEDEDFSILLAA LESRV-T\MTLDGHNIPSILVCVITGKGPLRSFYSRLIHQKHFQH IQVCTPWLEABDYPLLIASADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCANNFRCHEUVKHEENGLVFEDSEELAAQLGMLFSNPP DPAGKLMOFRRNINESQQLRRDESWOYTULPLWMDT TERSAFTERDAGSGLVTRLRSFRALLVSSTSWTEDEDFSILLAA LESRV-T\MTLDGHNIPSILVCVITGKGPLRAGAQLGVCHPSNPP DPAGKLMOFRKULHESNGLVCVITGKGPLRAGAQLGVCHPSNPP DPAGKLMOFRKULHESNGLVCVITGKGPLRAGAQLGVCHPSNPP DPAGKLMOFRKULHESNGLVCVITGKGPLRAGAQLGVCHPSNPP DPAGKLMOFRKULHESNGLVCVITGKGPLRAGAQLGVCHPSNPP DPAGKLMOFRKULHESNGLVCVITGKGPLRAGAQLGVCHPSNPP DPAGKLMOFRKULHESNGLVCVITGKGPLRAGAGAGLDFWKVUDMFG CCLPVCANNFRCHLELVKHERNGLVFEDSEELAAQLGAULFSNPP DPAGKLMOFRKULHESNGLVCVITKKGPLRAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	ł	}	EAAESDIMKROPRNPRTDKLVNERLISMAYGQIGMIQALGGFFS
WEFTCHTAFFYS: VVVQWADLII CKTRRNSVFQQMKRKILIF GEFETLAAFISVCPGMVECTYY YDEIRKLILRRNPGGWVEKTYY JDEIRKLILRRNPGGWVEKTYY JDEIRKLILRRNPGGWVEKTYY JDEIRKLILRRNPGGWVEKTYY JDEIRKLILRRNPGGWVEKTYY LDERRAKGGRGGFMPPAQALDGSKMGKAKYPASKRAPSSPVAKP GPVKTLTRKNKKKKKRPWKSKAREVSKKPASGGAVVRPPKAPS DPSQNWKALQEMLLKKQSQAPEKPLUTSGKKYEKITQOMKK ETSPQVKGEMPAGKDQEASRGSVPSGSKMDRRAPVFRKASGT BRINKGTRERTIGHIV PREGDIEHKKRAK (GQOPHPPR) / IDI WEDDVDPADIERAIGPEAKKIARIOLGGSEGSVELSILVEQAFG GUTPALALDCEMVLVUPKGEGSMARAVS VKOKEVSKHYKVEV ALEDRUKLJEDHEKKI ENDTOKKYPK KOKGPOPHPRP / IDI WEDDVDPADIERAIGPEAKKIARIOLGGSEGSVELSILVEQAFG GUTPALALDCEMVLVUPKGESMARAVS VKOKEVSKHYKVEV TEPVTYRTAVSGTRPENLKGGEELEVVOKEVABMLKGELUGH ALINDLKVLTJEDHEKKI ENDTOKKYPK KOKGFISHLISEK ILGLQVQCABHCSI DOAQAANKLYVMVKKEWESMARDRPPLLTA PDHGSDDA'ASCPARAAAADLQCCCDSSCOTSFGGSMSGTFF ESMGROVANCY LTAGASHTODASGSTSAKYPAAAONL/CVTNAMREDLADIMYIR AVTVYKKPASFFKETELDLQHRIJERRPALLVSTSWFTEDEDFSILLAA LESRV-T\MTLDGHNIPSILVCVITGKGPLRSFYSRLIHQKHFQH IQVCTPWLEABDYPLLIASADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCANNFRCHEUVKHEENGLVFEDSEELAAQLGMLFSNPP DPAGKLMOFRRNINESQQLRRDESWOYTULPLWMDT TERSAFTERDAGSGLVTRLRSFRALLVSSTSWTEDEDFSILLAA LESRV-T\MTLDGHNIPSILVCVITGKGPLRAGAQLGVCHPSNPP DPAGKLMOFRKULHESNGLVCVITGKGPLRAGAQLGVCHPSNPP DPAGKLMOFRKULHESNGLVCVITGKGPLRAGAQLGVCHPSNPP DPAGKLMOFRKULHESNGLVCVITGKGPLRAGAQLGVCHPSNPP DPAGKLMOFRKULHESNGLVCVITGKGPLRAGAQLGVCHPSNPP DPAGKLMOFRKULHESNGLVCVITGKGPLRAGAQLGVCHPSNPP DPAGKLMOFRKULHESNGLVCVITGKGPLRAGAGAGLDFWKVUDMFG CCLPVCANNFRCHLELVKHERNGLVFEDSEELAAQLGAULFSNPP DPAGKLMOFRKULHESNGLVCVITKKGPLRAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG		Ì		YFVILAENGFLPGNLVGIRLNWDDRTVNDLEDSYGQQWTYEQRK
S867  3 1485 LEGRARGGGGGGGGGGGPPAQALDGSINGKAKVPASKRAPSSPVAKF DPSTRIKLILERNPGGWUFEKTYY DPSTRIKLILERNPGGWUFEKTYY DPSTRIKLILERNPGGWUFEKSTARYSPAGGGAVVRPYKAPE DPSQNWKALQEALLKQKSQAPERFLVISOMSKKKPKIJOOMKK ETSJOVKGEREPMAKOQDABRATIARKOLGGORDVRPPFKAPE DPSQNWKALQEALLKQKSQAPERFLVISOMSKKKPKIJOOMKK BETSJOVKGEREPMAKOQDABRATIARKOLGGSVSUSLIVKEQAPG GLTRALALDCEMVGVGPKGESMAARUSIVNQYKCVYDKYVKP HEPDVDPADIALAAGPAVAGGRESMAARUSIVNQYKCVYDKYVKP ALHADLKVLFLDHPKKKIRDTQKKYPKSOVKGGRESIRLLSEK ILGLQVQQABHCSIODAAGMIKLYVWKAPEKABOKYRCKYDKYVKP ALHADLKVLFLDHPKKKIRDTQKKYPKSOVKGGRESIRLLSEK ILGLQVQQAHCSIODAAGMIKLYVWKAPEKABOKYPCHY ALHADLKVLFLDHPKKKIRDTQKKYPKSOVKGGRESIRLLSEK ILGLQVQAHCSIODAAGMIKLYVWKAPEKABOKYPCHY ALHADLKVLFLDHPKKKIRDTQKKYPKSOVKGGRESIRLLSEK ILGLQVQAHCSIODAAGMIKLYVWKAPEKABOKYPCHY PDHCSDDA*QSCPAAAAAPLQCOCQSOGOITSPQSGNSGETFS ESWGRGVANCY  5868  2122  833 LTAGASHTODASGSTSAKYPAAAGNL/CVTRAMBEDLADIWVIT LESRATTERDAGSGLVTRLRERPALLVSSTSWTEDEDPSILLAA LESRATTRADAGSGLVTRLRERPALLVSSTSWTEDEDPSILLAA LESRATTRADAGSGLVTRLRERPALLVSSTSRLHGKWYDMYC CCLPVCANNFKCLHELVKHERNGLVFLOSGDLDFMKVVDMYC TERSATTERDAGSGLVTRLRERPALLVSSTSRLHGKWITGH IQVCTPWLEABDYPLLIGAAGLGVCHTSSSGDLDFMKVVDMYG CCLPVCANNFKCLHELVKHERNGLVFLOSGSSGDLDFMKVVDMYG CCLPVCANNFKCLHELVKHERNGLVFLOSGSSGDLDFMKVVDMYG CCLPVCANNFKCLHELVKHERNGLVFLOSGSSGDLDFMKVVDMYG CCLPVCANNFKCLHELVKHERNGLVFLOSGSSGDLDFMKVVDMYG CCLPVCANNFKCLHELVKHERNGLVFLOSGSSGDLDFMKVVDMYG CCLPVCANNFKCLHELVKHERNGLVFLOSGSSGDLDFMKVVDMYG CCLPVCANNFKCLHELVKHERNGLVFLOSGSSGDLDFMKVVDMYG CCLPVCANNFKCLHELVKHERNGLVFLOSGSSGDLDFMKVVDMYG CCLPVCANNFKCLHELVKHERNGLVFLOSGSSGLDFMKVVDMYG TERSATTERDAGSGLVTRLBERPALLVSTSTSWTEDEDPSILLAA LESRY-TVWILDGHNILERRALLVSTSTSWTEDEDPSILLAA LESRY-TVWILDGHNILERRALLVSTSTSWTEDEDPSILLAA LESRY-TVWILDGHNILERRALLVSTSTWTEDEDPSILLAA LESRY-TVWILDGHNILERRALLVSTSWTWEDEDPSILLAA LESRY-TVWILDGHNILERRALLVSTSTWTEDEDPSILLAA LESRY-TVWILDGHNILERRALLVSTSTWTEDEDPSILLAA LESRY-TVWILDGHNILERRALLVSTSTWTEDEDPSILLAA LESRY-TVWILDGHNILERRALLVSTSTWTEDEPTTC CCGPCKAKIQDBAYCVQCWGDLDPWKVVTRURGKYGFKR FFERRERTERSTTGTGTGKWTWINGTTLESTWTWTTGDELLS SHTDAAAGHTOGGCSTSVTVFTAAAGA			1	VVEFTCHTAFFVSIVVVQWADLIICKTRRNSVFOOGMKNKILTF
TOPERRICILERNINGGWERETTY  DEGRARAGEGGGGFPOALDGSEMGKAKVPASKRAPSSPVAKP GPVKTUTRKNIKKKKRPMKSKAREVSKKPASGGAVPFKADS DEGRAMAGEGLIGMENGADEFKLUTSGMOSKKKKPKIOOMK ETSPOWGEEMPAGKOGEASRGSVPGSKMDRRAPVPPKADSC BENKKGTRERTINGIDIVERGDI EHKRKAK (QOOPHPEN) / IDI WEDDUPAN IEAAIGPEAAKIARVOGSEGSVELSLIVEOARG GLITALALDCEMVOVOD KGESMAANGS VOKSGREBLENGELISK ALHDIKUT, LDHPKKKI ENTOKVEPKENGKGREBLENGELISK ALHDIKUT, LDHPKKKI ENTOKVEPKENGKGREBLENGELISK ALHDIKUT, LDHPKKI ENTOKVEPKENGKGREBLENGELISK ALHDIKUT, LDHPKKI ENTOKVEPKENGKGREBLENGELISK ALHDIKUT, LDHPKKI ENTOKVEPKENGKGREBLENGELISK ALHDIKUT, LDHPKKI ENTOKVEPKENGKGREBLENGELISK ALHDIKUT, LDHPKKI ENTOKVEPKENGKGREBERLISK ALHDIKUT, LDHPKKI ENTOKVEPKENGKGREBERLISK ALHDIKUT, LDHPKKI ENTOKVEPKENGKGREBERLISK ALHDIKUT, LDHPKKI ENTOKVEPKENGKREBERLISK ALHDIKUT, LDHRKI ENTOKVERKENGENGER ENTOK BENGGVANCY  LERGY-TYMILOBAND PSILVOTTOKGEPLERYTSRILHOKHTOH ANTYVIKPASFFKETEDLOGRIFTENSSGLDLEMKVUMMEN CCLPVCANNFECHBLIVKERENGLIVEDSGADGAVCHFSNPP DEAGKLNOPRINLESSOLLERENGLIVEDSGADGAVCHFSNPP DEAGKLNOPRINLESSOLLERENGLIVEDSGELAADIOUHESNPP TERSAFTERDAGSGLIVTELRERPALLVSTSTWTEDEDFS ILLAA LESRY-TYMILDGHALPSLIVCVITOKGEPLERYTSRILHOKHTOH IQVCTPHILEABDYPLLICADALOUCHTRSSGLDLPMKVUMMEN CCLPVCANNFECHBLIVKHENGLIVEEDSGELAADIOUHESNPP DEAGKLNOPRINLESSOLDERINGSHOON TORTOK TERSAFTERDAGSGLIVTELRERPALLVSTSTWTEDEDFS ILLAA LESRY-TYMILDGHALPSLIVCVITOKGEPLERYTSRILHOKHTOH IQVCTPHILEABDYPLLICADALOUCHTRSSGLDLPMKVUMMEN CCLPVCANNFECHBLIVKHENGLIVEEDSGELAADIOUHESNPP DEAGKLNOPRINLESSOLDERINGSWOTVUPIUMDT TERSAFTERDAGSGLIVTELRERPALLVSTSWTEDEDFS ILLAA LESRY-TYMILDGHALPSLIVCVITOKGEPLERYSKILHOKHTOH IQVCTPHILEABDYPLLICADALOUCHTRSSGLDLPMKVUMMEN CCLPVCANNFECHBLIVKHENGLIVEENSCHLIVKHTOH TERSAFTERDAGSGLIVTELRERPALLVSTSWTEDEDFS ILLAA LESRY-TYMILDGHALPSLIVCVITOKGGPLERGAMTRES VIKILA-SLERRY-LUPTI-NOLLT-OSRLEVFRITEPTT CGGCQKAKI ODSLYCANAMALALAYR IDDOKGRTIELHSAI KCMGLIYCYMOPRICHERINGHENDALTOKUT SURKIVERSTATTRES VIKILA-SLERRY-LUPTI-NOLLT-OSRLEVFRITEPTT CGGCCCLPVCANNFECHBLIVKHTUKSTILLITORSFTOHTOPLETS SINTOAALBCCT, VOKARGEKYTY / SGSTELHSSVOIGKRO LKSINLOPSKAR FSENOCROBI				GLFEETALAAFLSYCPGMDVALRMYPLKPSWWFCAFPYSFI.TEV
1485 LEGRARAGGGIGIGIPPAQALDGSINGALVPASKRAPSSPVAKPE  DFSQNMKALQEMLIKKKSKAPUSKAPASGGAVUTPPYKADE  DFSQNMKALQEMLIKKKSKAPUSKAPASGGAVUTPPYKADE  ETSQVKUTERKKIKKKRAPUSKAPASGGAVUTPPYKADE  ETSQVKUTERKKAPKARATISKAPUSKAPASGGAVUTPPYKADE  ENKKGTKERTIGDIVPERGITERKKKAK GOPOPHPPA / 2DT  MEPDUPPAD I EAAT GEPRAKTARKOGGELSUVGENDEN PUPTYKASGT  ENKKGTKERTIGDIVPERGITERKKEKAK GOPOPHPPA / 2DT  MEPDUPPAD I EAAT GEPRAKTARKOGGELSUVGENDEN LEGADE  GLTRALALDCEMUSVOPKGESMAARUS VINOVOKCUTNAVVEN  TEPTOPTOPKTRAVSGTR PENKLAGGELSUVGANGMIKLVAN PENKLADILAN PUTLAT  ALIGLOVCABICISTODA, ADARKILVAN PENKAMBLADILAN PUTLA  BOHCSDDA * 9SCPAAAAP LQROCDOSOGOITS POSGINGETF ESWORGVANCY  SSEGG 2122 833 LTAGASHTODASGSTSAKYPAAGANL / CUTRIMEELADI WYTE  SSEGGRUNAVCY  TERSAFTERDAGSGLVTRLERER PALLVSSTSTETEDEPSILLAA  LESRV-TAMTLDGKINLPSILVOVITGKGAPLERPARGEPPEDEV  TERSAFTERDAGSGLVTRLERER PALLVSSTSTETEDEPSILLAA  LESRV-TAMTLDGKINLPSILVOVITGKGAPLEDIAN PENKAMBLADI PUTLAGAN PENKAMBAN PENKAMBUN PENKAMBENDA PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN PENKAMBAN				YDEIRKLILRRNPGGWVEKETYY
GEVALTURKKKKERPIKSKAREVSKYPAGGEOVURPIKARGE DPSOMMKALQEALLKOKSOAPERPLIJONKK ETSPOVKGEMPAGKDOEASRGVPSGSKMPRAPPPRIVAGGT EMNKGTKERTIGGIV PERGDI IHKRAK (GQDOPHPPRI JDI WFDDVDPADIEAALGPEAKIR KQLGQSEGSVSLSLVKEQAFG GLTPALALDLEWGUGGFGESMANALK (GQDOPHPPRI JDI WFDDVDPADIEAALGPEAKIR KQLGQSEGSVSLSLVKEQAFG GLTPALALDLEWGUGGFGESMANALK (GQDOPHPPRI JDI WFDDVDPADIEAALGPEAKIR KQLGQSEGSVSLSLVKEQAFG GLTPALALDLEWGUGGFGESMANALK (GQDOPHPPRI JDI WFDDVDPADIEAALGPEAKIR KQLGQSEGSVSLSLVKEQAFG ALHBOLKVLFLDHPKKKK KRTDKYKKPGVOKGYGRSELLSEK ALHBOLKVLFLDHPKKKK KRTDKYKKPGVOKGYGRSELLSEK ALHBOLKVLFLDHPKVLFLSPDAGGIVTYDKAKKRETOKYRFELLSEK ILGUVQAEHGSIQDAQAMRLYVMVKKEMEMADRR PLLTA PDHCSDDA GCSCPAAAAPLQRCQDCSQGOTISPQSGNSGETFS ESWGRGWANCY TERSAFTEDDAGGIVTALBERPALLYSTSWFTEDEPSILLADI AVTYVKPASFFKETPLDLQHLFFKLLSMISPPRARSEPEDEV TERSAFTEDDAGGIVTALBERPALLYSTSWFTEDEPSILLADI LESRYTVMTLDGINLDSLVCVTTCKOPLREYYSKLHQKHFQH CCLPVCAVMPKCLHELVKHEEROLVFDSBELAAQLQMLFSNPP DPAGKLMOPERVLRESQQLRWDESWVTVLPLWMDT TERSAFTEDDAGGIVTARREPALLYSTSWFTEDEPSILLAD LESRYTVMTLDGINLDSLVCVTTCKOPLREYYSKLHQKHFQH IQVCTPWLEADDYPLLIGSADLGVCHTSSGOLDPKWVDMFG CCLPVCAVMPKCHELVKHEEROLVFDSSHVFDEDEPSILLAD LESRYTVMTLDGINLDSJALGVCHTGKEPLARUFUNDTUT TERSAFTERDAGSGLVTRIRERPALLVSSTSWTEDEPSILLAD AVTVYDKARSFKKETPLDQHFBKYMSTGDFDSILLAD LESRYTVMTLDGRINLDSJALVCTTGKOPLREYYSRLHQKHFQH IQVCTPWLEADDYPLLIGSADLGVCHTSSGOLDPKWVDMFG CCLPVCAVMPKCHELVKHEEROLVFDSSWFDFARSEPEDPV TERSAFTERDAGSGLVTRIRERPALLVSSTSSTEDEPSILLAD LESRYTVMTLDGRINLDSJALVCTTGKOPLREYYSRLHQKHFQH IQVCTPWLEADDYPLLIGSADLGVCHTSSGOLDPKVVDMFG CCLPVCAVMFKCHELVKHEEROLVFSSKVFDEPSTSLLAD AVTVYDKARSFKKTELDSJALVCTTGKORMSFFFARSEPEDPV TERSAFTERDAGSGLVTRIRERPALLVSSTSSTEDEPSILLAD LESRYTVMTLOGHNLDSJALVCHTSNSGLDDPKCVVDMFG CCLPVCAVMFKCHELVKHEEROLVFSSKVFDEPSTLLAG LESRYTVMTLOGHNLDSJALVCTGKORMSFFFFARSEPEDPV TERSAFTERDAGSGLVTRIRERPALLVSSTSSTEDEPSTLLAG LESRYTVMTLOGHNLDSJALVCTGKORMSFFFFARSEPEDPV TERSAFTERDAGSGLVTRIRERPALLVSSTSTTEDEPSTLLAG LESRYTVMTLOGHNLDSJALVCTGKORMSFFFFFTARSSCOLLAGROP VIKLTGGTGVANAVGARGGVAYFASALLAVERSTOPHTTT CGGDQKAKLODSLVANGKRGKYGFKE TERSAFTERDAGGCLATHRORMSFFFFTCHLESSV	5867	3	1485	LPGRRARGGRGLGWPPAOALDGSRMGKAKVPASKPADSSDVAVD
DPSONMKALQEALLKOKSOAPEKPLUTISOMSIKKRPKIIQONKK ETSPOVKGEMPAGKOBEASRGSVESUKMPRANPPRIKASGT BENNKGTKERTINGDIVERGIDISHKKKRKAK\GOPOPHPRI/IDI WFDDVDPADIEAAIOPEAAKIARKOKOVEAVEKWEAKKG GUTRALALDCEWWGUGKGEESMAARVSIVWOKKGVYDXYVKP TEPVTVPYTAVSGRIP PRINLKQGEELGSGSVESLUKEQAFG GUTRALALDCEWWGUGKGEESMAARVSIVWOKKGVYDXYVKP TEPVTVPYTAVSGRIP PRINLKQGEELGSGSVESLUKEGAFG GUTRALALDCEWWGUGKGEESMAARVSIVWOKKGVYDXYVKP TEPVTVPYTAVSGRIP PRINLKQGEELGVKAVENHKREILVGH ALHADLKVI,FLDHPKKKIRTTOKYKPFKSOVXSGRFSLRLLSEK LIGLOVQCABHCSIODAOAAMELYVKEKMESMARRRPLLIJEK LIGLOVQCABHCSIODAOAAMELYVKEKMESMARRRPLLIJEK PDHGSDDA*QSCGPAAAAAPLQRQCDQSCGOITSPQSGRSGETFS ESWORGWACY  TERSAFTERDAGSGUTTRIRERPALLVSSTSWTEEDEPSILDAA LESRV*T\MTLDGINLESLUCVITTKKEPKALDSSTSWTEEDEPSILDAA LESRV*T\MTLDGINLESLUCVITTKKSPLALGVKHFOH IQVCTPWLEAEDYPLLIGSADLGVCHTSSGLDLPMKVVDMFG CCLPVCANMFKCHLELVKHEEMGLYFEDSEELAADLGMLFSNFP DPAGKLINOPRINLESGOLRMDESSWOTVLPLWMDT TERSAFTERDAGSGIVTRIRERPALLVSSTSWTEEDEPSILLAA LESRV*T\MTLDGINLPSLUCVITTKKSHSFPRANSEEDEPV TERSAFTERDAGSGIVTRIRERPALLVSSTSWTEEDEPSILLAA LESRV*T\MTLDGINLPSLUCVITTKKSHSFPRANSEEDEPV TERSAFTERDAGSGIVTRIRERPALLVSSTSWTEEDEPSILLAA LESRV*T\MTLDGINLPSLUCVITTKKEPLYSYSLLHQKHFOH IQVCTPWLEAEDYPLLIGSADLGVLHTSSSGLDLPMKVVDMFG CCLPVCANMFKCHELVKHEEMGLVFERYSSLLHQHFOH IQVCTPWLEAEDYPLLIGSADLGVLHTSSSGLDLPMKVVDMFG CCLPVCANMFKCHELVKHEEMGLVFERYSSLLHQHFOH IQVCTPWLEAEDYPLLIGSADLGVCHTSSSGLDLPMKVVDMFG CCLPVCANMFKCHELVKHEEMGLVFERYSSLLHQHFOH IQVCTPWLEAEDYPLLIGSADLGVCHTSSSGLDLPKVVDMFG CCLPVCANMFKCHELVKHEEMGLVFERYSSLLHQHFOH IQVCTPWLEAEDYPLLIGSADLGVCHTSSSGLDLPKKVVDMFG CCLPVCANMFKCHELVKHEEMGLVFERYSSLLHQHFOH IQVCTPWLEAEDYPLLIGSADLGVCHTSSSGLDLPKKVVDMFG CCLPVCANMFKCHELVKHEEMGLVFERYSSCLHAGNGAGTSNFF PROFTERLETLASSTTGMSSAMGAAGHTLUSGFFF ILMSGLGKFSTATLASSGNCOMSVT;PVUDDT  S871  3 3465  FFFCRFRIENGSGNAGAAGHTLUSGFFANGAGAGHTLUSGFFF ILMSGLGKRFSTATKSSGNCOMSVT;PVUDDT CVCNEWYNELDGRNVMKGFGKYYY*VPUDDT CVCNEWYNELDGRNVMKGFGKYYY*VPUDDT CVCNEWYNELDGRNVMKGFGKYYY*VPUDDT CVGRNYFANDAGGCSMSVT;PVUDDAHNRRGTCLSLLPRIS SHNYDAALDCTSYPAPALDOVYNALAESGNCOMSVT;PVUDDAHNRDGTLLSGNG PRENGGCGTSMSVT;PVUDDAHNRRGTLLSFRO	1		<u> </u>	GPVKTLTRKKNKKKRFWKSKARFYSKKDASGDGAMGDDVADD
### FTS*CVKGEEMPAGKDGEASRGVPSGSKMDRRAPVFRTKASGG ### BEINKGTKERTINGIV VERGOI FIRKKAK (GOGDH PPR) / IDI ### BEINKGTKERTINGIV VERGOI FIRKKAK (GOGDH PPR) / IDI ### BEINKGTKERTINGIV VERGOI FIRKKAK (GOGDH PPR) / IDI ### BEINKGTKERTINGIV VERGEMERARK (GOGDH PPR) / IDI ### BEINKGTKERTINGIV VERWOKKEV VERVEK VER  ### BEIVTPYRTAVSGTR PENLKOGEELEVVOKEVAEMLKOR ILVGH ALHADLKVI-LDHPKKIK IRTUTKYK PENOV KSGURS ILVGK ### BEIVTPYRTAVSGTR PENLKOGEELEVVOKEVAEMLKOR ILVGH ALHADLKVI-LDHPKKIK IRTUTKYK PENOV KSGURS ILVGK ### BEIVTPYRTAVSGTR PENLKOGEELEVVOKEVAEMLKOR ILVGH ### BEIVTPYRTAVSGTR PENLKOGEELEVVOKEVAEMLKOR ILVGH ### BEIVTPYRTAVSGTR PENLKOGEELEVVOKEVAEMLKOR ILVGH ### BEIVTPYRTAM PENLKOGEELEV VOKEN PENGKATE ### BEIVTPYRTAM PENLKOGEELEV VOKEN PENGKATE ### BEIVTPYRTAM PENLKOGEELEV VOKEN PENGKATE ### BEIVTPYRTAM PENLKOGEELEV VOKEN PENGKATE ### BEIVTPYRTAM PENLKOGEN PENGKATE ### BEIVTPYRTAM PENLKOGEN PENGKATE ### BEIVTPYRTAM PENLKOGEN PENGKATE ### BEIVTPYRTAM PENLKOGEN PENGKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ### BEIVTPYRTAM PENCKATE ##			1	DESONWKALOEWIJKOKSOADEKBIJISOMCKKERASTER
BENNKGTKERTNGDIVERGDIEHKKREAK\GOPGPHPER/IDI WEDDUNDADIEAAIDEPBAKIARKOLGOSEGSUSLIJUKEQAFE GLTALALDCEWUGUGKGESESSAARVSIVUKGKUTUKYUKE TEPPTDYRTNAUSGIR PENLKOGEELEVUKKEVAEMLKGELIJUGH ALIMDLKVI,FLDHPKKKIRTTOKYFEKGOVKAGENLKGILJUGH ALIMDLKVI,FLDHPKKKIRTTOKYFEKGOVKAGENLKGILJUGH ALIMDLKVI,FLDHPKKKIRTTOKYFEKGOVKAGENLKGILJUGH ALIMDLKVI,FLDHPKKKIRTTOKYFEKGOVKAGENLKGERIJUKGH ALIMDLKVI,FLDHPKKKIRTTOKYFEKGOVKAGENLKGER IGLOVGOAGHGSIODAGAARKIYMWKKEMESMADREPLLITA PDHOSDDA GSCGAAAAAPLGRQCDQSQQITSPQSGNSGETFS ESWORGWACY  TERSAFTERDAGSGIVTRLEREPALL/GSTNWTBEDEPSILLAA LESRV-T\MTLDGINLPSIJUCUTTKKGFLKEYSSALHOKHFOH IQVCTPWLEABDYFLLIGSADLGVLTSSGIDLPMKVVDMFG CCLPVCAWFKCLHELVKHEERGIVFEDSEELAADLGMLFSNFP DFAGKLNOFRKNIKESGOLKWBESSWOTVLPJUMDT  TERSAFTERDAGSGIVTRLRERPALLVSSTSWTEDEPSILLAA LESRV-T\MTLDGINLPSIJUCVTTTKKGHSFYSRLTHGHFOH IQVCTPWLEABDYFLLIGSADLGVLTSSGIDLPMKVVDMFG CCLPVCAWFKCHELVKHEERGIVFEDSEELAADLGMLFSNFP DFAGKLNOFRKNIKESGOLRWDESSWOTVLPJUMDT  TERSAFTERDAGSGIVTRLRERPALLVSSTSWTEDEPSILLAA LESRV-T\MTLDGINLPSIJUCVTTTKGERFYSSLIHDGHFGH IQVCTPWLEABDYFLLIGSADLGVLHTSSSGIDLPMKVVDMFG CCLPVCAWFKCHELVKHEERGIVFEDSEELAADLGMLFSNFP DFAGKLNOFRKNIKESGOLRWDESWOTVLPJUMDT  TERSAFTERDAGSGIVTRLRERPALLVSSTSWTEDEPSILLAA LESRV-T\MTLDGINLPSIJUCVTTTKGEPLAYSSLIHDGHFGH IQVCTPWLEABDYFLLIGSADLGVCHTSSSGIDLPKVVDMFG CCLPVCAWFKCHELVKHEERGIVFEDSELAADLGMLFSNFP DFAGKLNOFRKNIKESGOLWBESWOTVLPJUMDT  TERSAFTERDAGSGIVTRLRERPALLVSSTSWTEDEPSILLAA LESRV-T\MTLDGINLPSILVCTTTKGKPIRPSTSDEFSILLAA LESRV-T\MTLDGINLPSILVCTTTKGKPIRPSTSDEFSILLAA LESRV-T\MTLDGINLPSILVCTTTKGKPIRPSTSDEFSILLAA LESRV-T\MTLDGINLPSILVCTTTKGKPIRPSTSDEFSILLAA LESRV-T\MTLDGINLPSILVCTTTKGKPIRPSTSDEFSILLAA LESRV-T\MTLDGINLPSILVCTTTKGKTERFFILMSSTSTEDEFSILLAA LESRV-T\MTLDGINLPSILVTTANTESGOFSALLAYDLTKTTRSFPPD DFAGKLNOFFKKNIKESGOLWFILMSTSGIDLFKVVGDWFG VERSAFTSLEDGFSILLSSWORTHKESGOLFREYSFILMSSTSTEDFSILLSSWORTHKES VIKLL-1SLRRI-LEFTI-NGLIT-CSRLSVFRIKVGSVFFILMS VIKLL-1SLRRI-LEFTI-NGLIT-CSRLSVFRIKVGSVFFILMS VKRILL-1SLRRI-LEFTI-NGLIT-CSRLSVFRIKKGKYGFKR VKRILL-1SLRRI-LEFTI-NGLIT-CSRLSVFRIKKGKYGFKR FREGOYRTSLEDDNRCYYKPAERTYKTRGOTTLATE				ETSPOVKGEEMPAGKDOED CDGGUDGGGKKKPKI I QQNKK
WFDDVPADIEAAIOCEMAKIARQLGSESSUSLIVKEQAFG GLTARIALDCEMWGVPKGESHARARVSIVMOYGKCYDKYVKY TEPVTDVRTAVSGIRPENLKGGELEVVGKVAEMLKGRILVGH ALHADLKVLFUDHPKKKIRDTGKKYFKSOVASGRPENLKLSSK ILGLQVQAAHGSIQDAQAAMRLVYMVKEMESMARDRRPLLTA PHGSDDA*QSCFAAAAAPLQRCCDQSCGITSPQSGNSGETS ESWGRGVAMCY  1746ASHTQDASGSTSAKYPAAAQNL/CVTNAMREDLADIWYIR AVTVYNKPASFFKETPLDLGHRIFMKLGSMISPFRARSPEEDDV TERSAFTERDAGSGLVTRLERERALLVSSTSMTDEEDFSILLAA LESKY*T\MTLGGHNESLVCVITGKGPLREYYSRLHQKHFOH IQVCTPWLEAEDYPLLIGSADLGVCHTSSSGLDLPMKVVDMFG CCLPVCAVWFKCHERLVKHEENGLYCTGKGPLREYYSRLHQKHFOH IQVCTPWLEAEDYPLLUSADLGVCHTSSSGLDLPMKVVDMFG CCLPVCAVWFKCHELVKHEENGLYCTGKSPEEDSELAAQLGMLFSNFP DPAGKLNOPRKRIRESQQLRMDESWVGTVLPLVMDT TERSAFTERDAGSGLVTRLERERALVSSTSWTDEDFSILLAA AVTYYNKPASFFKETPLDLGHRIFMKLGSMISPFRARSPEEDDV TERSAFTERDAGSGLVTRLERERALVCTTGKSPLREYYSRLHQKHFOH IQVCTPWLEAEDYPLLIGSADLGVCHTTSSSGLDLPMKVVDMFG CCLPVCAVWFKCLHELVKHEENGLVFEDSELAAQLGMLFSNFP DPAGKLNOPRKNLRESQQLRMDESWVGTVLPLWNDT TERSAFTERDAGSGLVTRLERERALVSTSWTEDDEFSILLAA LESRY*T\MTLDGHNLPSLVCVTTGKGPLREYYSRLHGKHFOH IQVCTPWLEAEDYPLLIGSADLGVCHTMSSSGLDLPMKVVDMFG CCLPVCAVWFKCLHELVKHEENGLVFEDSEELAAQLGMLFSNFP DPAGKLNOFRKNLRESQQLKDESWVGTVLPLWNDT TERSAFTERDAGSGLVTRLERERALVSTSTWTEDDFSILLAA LESRY*T\MTLDGHNLPSLVCVTTGKGPLREYYSRLHGKHFOH IQVCTPWLEAEDYPLLLGSADLGVCHTTSSSGLDLPMKVVDMFG CCLPVCAVWFKCLHELVKHEENGLVFEDSEELAAQLGMLFSNFP DPAGKLNOFRKNLRESQQLKDESWVGTVLPLWNDT TERSAFTERDAGSGLVTRLERERALLAALGMLFSNFP DPAGKLNOFRKNLRESQQLKDUFSSWTSTWTEDDFSILLAA LESRY*T\MTLDGHNLPSLVCVTTGKGPLREYYSRLHGKHFOH IQVCTPWLEAEDYPLLLGSADLGVCHTTSSSGLDLPMKVVDMFG CCLPVCAVWFKCLHELVKHEENGLVFEDSEELAAQLGMLFSNFP DPAGKLNOFRKNLRESQQLKDUFSTSTSTEDELAAQLGMLFSNFP DPAGKLNOFRKNLRESQQLKDUFSTSTSTSTSTSDEDFSILLAA LESRY*T\MTLDGHNLPSLVCVTTKKERPALLAALGHGFFTLEHSAI KCMGGILTGVKWPADKLAALAYRHIDDGKTHELEHSAI VLLL'LSRRL*LEPTI*NGLLTYKSTLLLYGSPTGGFFFTLYMIDG VFKPMFQAGVGFYGNGCKGKYKY*/SGSTELHSSVCLKKG LKGNGGNGCKGPGFNCTCHSVFNVHTAGDELTSCHLFFFTLYMIDG VFKPMFQAGVGFYGNGCKGKYKY*/SGSTELHSSVCLKKGYGFK FLRGGYKTSLEDDNGCYYKPASIKLFTGGETSTHELEHSAI VKNDAALLPCLSYRAPALDDGVLFGAVALOLGGINERGLGGG PPRIGCGGTKYTPLHTTTTGGAVYVFYYTYTAP				EHMKKGTKERTYCDIVEERODITUKKEVEVA KA RARATVERTKASGT
GUTRALALDCEWGVQPKGESMAARGI LVQKKCYVDKYVKYK  TEPVTDYRTAYSGI FPENLKQGEELEVVQKVAEMIKGRI LVGH  ALHNDLKVL-LDHPKKKI RDTQKYKYPKSQVKSGRPSLIRLLSEK  LIGLQVQAEHGS LQDAQAAMALYWKEMESMAPDRRPLLITA  PDHCSDDA 19.SCPAAAAAPLQRQCDQSQQQITSPQSGNSGETES  ESWQRQWACY  LTAGASHTQDASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR  AVTYVIKPASFFKETPLDLQHRLFMKLGSMISPPFARSEPEDDV  TERSAFTERDASGQLVTRLEREPALVSSTSWTEDEPSILLAA  LESRY-T\MTLDGHNLPSLVCVITGKSPLREYYSRLHQKHFQH  IQVCTPWLBAEDYPLLLGSADLQGVTSSSSGOLLPMVVOMGG  CCLPVCAVMFKCHBLVKHBENGLVFDSEELAAQLQMLFSNFP  DPAGKLMOPKRNLHRSQQLKMDESWVQTVLPLYWDIS  S869  2122  833  LTAGASHTQDASGSTSAKYPAAQONL/CVTNAMREDLADIWYIR  AVTYVIKPASFFKETPLDLQHRLFMKLGSMISPPRARSEPEDDV  TERSAFTERDAGSGLVTRLEREPALLVSTSWTEDDEPSILLAA  LESRY-T\MTLDGHNLPSLVCVITGKGPLREYYSRLHQKHFQH  IQVCTPWLEABDYPLLLGSADLGVCHTSSSGOLLPMKVVDMFG  CCLPVCAVMFKCLHELVKHBENGLVFDSEELAAQLQMLFSNFP  DPAGKLMOPKRNLRESQQLKMDESWQTVLPLWNDT  CCLPVCAVMFKCLHELVKHBENGLVFDSEELAAQLQMLFSNFP  DPAGKLMOPKRNLRESQQLKMDESWQTVLPLWNDT  TERSAFTERDAGSGLVTRLEREPALLVSTSWTEDDEDFSILLAA  LESRY-T\MTLDGHNLPSLVCVITGKGPLREYYSRLHQKHFQH  IQVCTPWLEABDYPLLLGSADLGVCHTSSGDLDLFMKVVDMFG  CCLPVCAVMFKCHELVKHBENGLVFEDSELAAQLQMLFSNFP  DPAGKLMOPKRNLRESQQLKMDESWQTVLPLWNDT  TERSAFTERDAGSGLVTRLEREPALLVSSTSWTEDDEDFSILLAA  LESRY-T\MTLDGHNLPSLVCVITGKGPLREYYSRLHGKHFQH  IQVCTPWLEABDYPLLLGSADLGVCHTSSGDLDLFMVVDMFG  CCLPVCAVMFKCHELVKHBERDLLVFEDSELAQLQMLFSNFP  DPAGKLMOPKNLRESQQLKMDESWQTVLPLWMTTR  AVTYNKPASFFKETPLDLQHRLFMKLGSMISPPRARSEPEDPV  TERSAFTERDAGSGLVTRLEREPALLVSSTSWTEDDEFSILLAA  LESRY-T\MTLDGHNLPSLVCVITGKGPLREYYSRLHGKHFQH  IQVCTPWLEABDYPLLLGSADLGVCHTSSGDLDLFWVVDMFG  CCLPVCAVMFKCHEUVHBERNOLVFEDSELAQLQMLFSNFP  DPAGKLMOPKNLRESQQLRWDESWQTVLPLWVDMTTR  S871  3 3465  FFFCRPLRIYSKTGDRSAMAGAGGLTAEVSWKLERRAFTERS  VLELL-SLRIFL-FEDGAGAGAGALALAYRI DDDKGRTHELEISIAI  KCMGGLVCYWRQADKVQQFKQDPPPTTCLHSVFNVHYGDELLS  YEEYGHQI NAVSLYLLVLVEMISSGQQI YUDLDAHNNRGTLCSLLPRESS  SINTDAALALPCIS YRAFALDDEVLY-YGGSTELMSSVCLKRQ  LKGNGFKYVPLDFQVWGKYCGLVY-YGGSTELMSSVCLKRQ  FFROGSPRVJERGNQCSWSU IVDLDAHNNRGTLCSLLPRESSA  SINTDAALALPCIS YRAFALDDEVLY-YGGSTELMSSVCLKKKYGFKB	ł		i	WEDDING A DIERRO TERRO TERROR ENKREKAK GOPOPHPPR / IDI
ALIMBLEVILFUDHENKKIRDTQKKYEPKSQVKSGREPSIRLLISEK ILGLQVQQAEHCSIQDAQAANGLYVMYKKENESQVKSGREPSIRLLISEK ILGLQVQQAEHCSIQDAQAANGLYVMYKKENESMARDRRPLITA PHCSDDA*QSCCPAAAAAPLQQCCQSGQITSPQSGNSGETFS ESWQRGWAWCY ITAGASHTQDASGSTSAKYPAAAQNL/CVTNAMREDLADIWYTR AVTVYNKPASFFKETPLDLQHRLFMKLGSMHSPFRARS BPEDDV TERSAFTERDAGSGLVTRIRERPALLVSSTSWTEDEDFSILLAA AVTVYNKPASFFKETPLDLQHRLFMKLGSMHSPFRARS BPEDDV TERSAFTERDAGSGLVTRIRERPALLVSTSWTEDEDFSILLAA LESRV*T\MTLDGHNLPSLVCVITGKSPLREYYSRLHQXHFOH IQVCTPWLEAEDYPLLIGSADLGVCHTSSSGLDLPMKVVDMFG CCLPVCAVWFKCHELVKHEENGLVCTTGKSPLREYYSRLHQXHFOH IQVCTPWLEAEDYPLLUSADLGVCTTGKSPLREYSRLHQXHFOH IQVCTPWLEAEDYPLLIGSADLGVCTTGKSPLREYSRLHQXHFOH IQVCTPWLEAEDYPLLIGSADLGVCTTGKSPLREYSRLHQXHFOH IQVCTPWLEAEDYPLLIGSADLGVCTTGKSPLREYSRLHQXHFOH IQVCTPWLEAEDYPLLIGSADLGVCTTSSSGNLDPMKVVDDFG CCLPVCAVWFKCHELVKHEEMGLVFEDSEELAAQLQMLFSNFP DPGKLMOPRKNLRESQQLRNDESWQTVLPLWNDT AVTVYNKPASFFKETPLDLQHRLFWKLGSMHSPFRARSEPEDPV TERSAFTERDAGSGLVTTRILERPALIVSSTSWTEDEDFSILLAA LESRV*T\MTLDGHNLPSLVCVTTGKGPLREYYSRLHQKHFOH IQVCTTPWLEAEDYPLLIGSADLGVCHTTSSSGLDLPMKVVDDFG CCLPVCAVWFKCLHELVKHEEMGLVYEDSEELAAQLQMLFSNFP DPGKLMOPKRNLRESQQLRNDESWQTVLPLWNDT AVTVYNKPASFFKETPLDLQHRLFWKLGSMHSPFRARSPEEDPV TERSAFTERDAGSGLVTTRILERPALIVSSTSWTEDEDFSILLAA LESRV*T\MTLDGHNLPSLVCVTTGKGPLREYYSRLHQKHFOH IQVCTTPWLEAEDYPLLIGSADLGVCHTTSSSGLDLPMKVVDDFG CCLPVCAVWFKCLHELVKHEENGLVYEDSELAAQLQMLFSNFP DPGKLMOFRNLRESQQLRNDESWQTVLPLWAMDTHATKS LLSINLPRPDNETLMDKLDHYRIVSSLLLYLVGSPTGGFPTKT CGGQCKARIQDSLYCAAGAAALAARRIDDGKRTHLEISIAI KCMGISLIVCYMFQABLAAARRIDDGKTHELEISIAI KCMGISLIVCYMFQABLAAARRIDDGKTHELEISIAI KCMGISLIVCYMFQABLAAARRIDDGKTHELEISIAI KCMGISLIVCYMFQABLAAARRIDDGKTHELEISIAI KCMGISLIVCYMFQABLAAARRIDDGKTHELEISIAI KCMGISLIVCYMFQABLAAARRIDDGKTHELEISIAI KCMGISLIVCYMFQABLAAARRIDDGKTHELEISIAI KCMGISLIVCYMFQABLAAARRIDDGCCCCLDKVVFRKKKKYGFKR FLRGGYRTSLEDDNRCYYKPABIKLFTGGEPTFTLYMMIDG VYRGMPKGVQFYQDLYVGYYYYVATYYVPADFVGYYE KNNDSORFFSNCGROBKLFTITGGALYTITAKLADELISKGI DPVRGTVPLGCQGRYGTRITTEGDTFTYNAQDVFLID DPVRGTVPLGCQGRYGTRITTEGDTFTYNAGQDFYTILIDALAA LKKGIIGGVKVPDRCGTTTTGGAVVGCDFTTSTTEELGLISFGCI	Į.		j	WFDDVDPADIEAAIGPEAAKIARKQLGQSEGSVSLSLVKEQAFG
ALHNDLKVL*LDHEKKKIROTQKYRFYKSQVKSGRSELRLLSK  ILGLQVQQABELSQQAAAAPLQRQCDQSQGITSPQSGNSGETFS  ESWQRGWAWCY  LTAGASHTQDASQGTSAKYPAAAQNL/CVTNAMREDLADIWYIR  AVTYDKRASFFKETPLDLQHRLFMKLGSHISPFRARSBEDDV  TERSAFTERDAGSGLVTRLRERPALLVSSTSWTBEDEPSILLAA  LESRV*I^MTLDGHNLPSLVCVITKGGPLREYYSRLHCKHFCH  GVCTPPHLAEADYPLLIGSADLGVCLHTSSSGLDLPMKVVDMFG  CCLPVCAVMFKCLHELVKHEENGLVFEDSEBLAAQLGMLFSNFP  DPAGKLNOFKRKLRESQQLRMDESWVOTVLPLWDT  TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA  AVTYVKPASFFKETPLDLQHLFMKLGSMISPFRARSBEDDV  TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA  LESRV*I^MTLDGHNLPSLVCVITKGGPLREYYSRLHCKHFCH  1QVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLFMKVVDMFG  CCLPVCAVMFKCLHELVKHEENGLVFEDSELAAQLQMLFSNFP  DPAGKLNOFKRKLRESQQLRMEKIGSMHSPFRARSBEDFDV  TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA  LESRV*I\MTLDGHNLPSLVCVITKGGPLREYYSRLHKKHFCH  S870  2122  833  LTAGASHTODASGSTSAKYPAAAQNL/CVTMAMREDLADIWYIR  AVTVYNKPASFFKETPLDLQHRKLGSMHSPFRARSBEDEDV  TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA  LESRV*I\MTLDGHNLPSLVCVITKGGPLREYYSRLHKKHFCH  LESRV*I\MTLDGHNLPSLVCVITKGGPLREYYSRLHKKHFCH  LESRV*I\MTLDGHNLPSLVCVITKGGPLREYYSRLHKKHFCH  LESRV*I\MTLDGHNLPSLVCVITKGGPLREYYSRLHKKHFCH  LESRV*I\MTLDGHNLPSLVCVITKGGPLREYYSRLHKKHFCH  LESRV*I\MTLDGHNLPSLVCVITKGGPLREYYSRLHKHFCH  AVTVYNKPASFFKETPLDLQHRCGSMSVTVLPLVMDT  TERSAFTERDAGSGLVTRLRERPALLVSSTSWFUEDEDFSILLAA  LESRV*I\MTLDGHNLPSLVCVITKGGPLREYYSRLHKHFCH  LESRV*I\MTLDGHNLPSLVCVITKGGPLREYYSRLHKHFCH  AVTVYNKPASFFKETPLDLGHRCSGNSWVVLPFLRRTHRS  VELL'SLSRRI-SLEPTI*NGLUTGSRLSGPLRENGVFSCHESPLRVCVGVYEP  LKSINLPRPDMETLMDKLDHYNTVXSTLLLYQSPTTCLFPTKT  CGGQAKHGDSLVGVAGAAMALLYRR IDDDKGRTHELEHSAL  KCMGGLLYCYWRQADKVQOFKQDPRPTTCLHSVFNVHTGDELLS  YEEYGHLQINNSILYLLYMINGTSCLGLFFPTKJWMIDG  CV\ERVTRYPLDFG\VWINKEGSFY*ISTDLKKKKYGFKR  FERDSYRTSLEDPMRCYYRPAETKLEGGFPTFLYMIDG  VRGMPKOVGEYDOLLTPULHTTCTYVPKYYVPADPVYYY  KNNTOAALPCLISKTTOGQCSWSVI FVDLDAHMRNQTLCSLLPRESGR  PDPQRYVPLKOORDVSMFSPNQGPLENDLVWINALIAESGRLQV  PLNTYGLQTGTPQQVEPIOLWFQCGLVKAYLLGEDFYLKSKUR  DPVQRYPLKDQCSTRSYNGSSTPSAPGOPDNISKFKRPPILDMLAA  LKKGI IGGVKWHVDRQTLTLISGAVVEQDPVNISKFKRPPILDM	1	í	ì	GDTRALALDCEMVGVGPKGEESMAARVSIVNQYGKCVYDKYVKP
ILGLQVQQARICSIQDAQAMRILYYMVKKEMESMARDRRPLLTA   PDHCSDDA *GSCSPAAAAALQRCQDOSQGOITSPQSGNSGETFS   ESWQRGVAWCY		1		TEPVIDYRTAVSGIRPENLKQGEELEVVQKEVAEMLKGRILVGH
ILGLQVQQARICSIQDAQAMRILYYMVKKEMESMARDRRPLLTA   PDHCSDDA *GSCSPAAAAALQRCQDOSQGOITSPQSGNSGETFS   ESWQRGVAWCY	1			ALHNDLKVLFLDHPKKKIRDTQKYKPFKSQVKSGRPSLRLLSEK
PDHCSDDA*QSCPARAAPLQRQCDOSGGITSPQSGNSGETFS ESWQRYAMCY  LESROYTQNACY  AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSPEDPV TERSAFTERDAGSGUVTRLRERPALLVSSTSWTEDEDFSILLAA LESRY*T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHGKHFCH IQVCTPPLLEADPYLLIGSADLCHMTSSSGLDLPMKVVDMFG CCLPVCAVMFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNOFRKILRESQQLWEWSWOTVLPLWMDT  S869  2122  833  LTAGASHTQDASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR AVTVYDKPASFFKETPLDLQHRLFMKLGSSHSFFRARSPEDPV TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHGKHFCH IQVCTPMLEAEDPYLLLGSADLCHMTSSSGLDLPMKVVDMFG CCLPVCAVMFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNOFRKNLRESQQLRMDESWGTVLPLWMDT  S870  2122  833  LTAGASHTQDASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR AVTVYDKPASFFKETPLDLQHRLFMKLGSSHSFFRARSPEDPV TERSAFTERDAGSGUTTRLRERPALLVSSTSWTEDEDFSILLAA LESRV*T\MTLDGHNLPSLQCUTTGKGPLREYYSRLIHGKHFCH IQVCTPMLEAEDPYLLLGSADLGVHTSSSGLDLPMKVVDMFG CCLPVCAVMFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNOFRKNLRESQQLRMDESWGTUPLDMDT TERSAFTERDAGSGUTTRLRERPALLVSSTSWTEDEDFSILLAA LESRV*T\MTLDGHNLPSLGVCUTTGKGPLREYYSRLIHGKHFCH IQVCTPMLEAEDPYLLLGSADLGVHTSSSGLDLPMKVVDMFG CCLPVCAVMFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNOFRKNLRESQQLRHDSSWVLDFTKRTRS VLKLL*LSIRRI*LEPTI*NGLLT*CSRLSWFFFLKV\GSVYEP DRAGKLNOFRKNLRESQQLRHDSSWVTUPLDMDT  S871  3 3465  FFFCERPKLYSKTTDGRSAMAGAGLTAEVSWVLERRARTKRS VLKLL*LSIRRI*LEPTI*NGLLT*CSRLSWFFFLKV\GSVYEP LKSINLPRPDMETLUKKJDHYVXTSLLLVQSPTTGLFPTKT CGGDQKAKIQDSLYCAAGAWALALATRRIDDNKGRTHELEISAI KCMRGILKCYWRQADKVQFKQDPRFTTCLHSVFFNHTGDELLS YESYGHLQINAVSILLYLLVEMISSGLOIIYMTDEVSFIQNLVF CV\ERVYRVQDFGVWRENGKYY*\SSTELHSSSVGLGKRQ L*KORGINLGGNGCSSWSTYPUDLAHRNNGGTLCSLLPRESR SHNTDAALLPGISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLEDGYRTSLEDDNRCYYRABIKLFDGISCFFIFFLYMIDG VRGMPKGVGFYQDLTPVLHTTTEYPYVPKYYYVPADPVYEY KNNPGSQKRFSNCGGGSWSTPAGGLECFFIFFLYMIDG VRGMPKFGNGGGSWSTPAGGLECFFIFFLYMIDG PDVGRYVPLKDGNYSNFFSNGGDENGLVINGLALBSGRLQV FLNTGGIGTGFKYYRLGSTFFAGDEDFMKLOLBSGR PDRPIGCLGTSKIYRLIGKTVVCYPIITDLEDFFMSGDPFLLID DIKNALGFIKQYRKMHGRPLFIULVIREDNIRGSRRPIITDMLAA LKKGIIGGPVVNHUNGSSTFAGSPELGOOPDVNISSEKKKKKPPHETI	-		ł	ILGLQVQQAEHCSIQDAQAAMRLYVMVKKEWESMARDRRDILLTA
S868  2122  833  LTAGASHTODASOSTSAKYPAAAQNL/CVTNAWREDLADIWYTR AVTYYDKPASFFKETPLDLQHRLFMKLIGSHHSPFRARSRPEDPV TERSAFTERDAGSGLVTRLEERPALLVSSTWTEDEDPSILLAA LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHQKHFCH IQVCTPWLBAEDYPLLLGSADLGVCLHTSSGGLLDFKVVDMEG CCLPVCAVNFKCHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNOFKRNLRESQQLRWDESWVQTVLPLVMDT  S869  2122  833  LTAGASHTODASOSTSAKYPAAAQNL/CVTNAWREDLADIWYTR AVTYYDKPASFFKETPLDLQHRLFMKLGSMHSFFRARSRPEDPV TERSAFTERDAGSGLYTRLEERPALLVSSTSWTEDEDFSILLAA LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHQKHFQH IQVCTPWLBAEDYPLLLGSADLGVCLHTSSGLDLPMKVVDMFG CCLPVCAVWFKCHELVKHEENGLVFEDSEELAAQLQMLFSHFP DPAGKLNOFKKULRESQQLRWDESWQTVLPLVMDT  5870  2122  833  LTAGASHTODASGSTSAKYPAAAQNL/CVTNAWREDLADIWYTR AVTYYDKPASFFKETPLDLQHRLFMKLGSMHSFFRARSEPEDPV TERSAFTERDAGSGSTSAKYPAAAQNL/CVTNAWREDLADIWYTR AVTYYNKPASFFKETPLDLQHRLFMKLGSMHSFFRARSEPEDPV TERSAFTERDAGSGSTSAKYPAAAQNL/CVTNAWREDLADIWYTR LESRV*T\MTLDGHNLPSLVCVTTGKGPLREYYSRLHIQKHFQH IQVCTPWLBAEDYPLLLGSADLGVCHTSSGLDLPMKVVDMFG CCLPVCAVWFKCHLELVKHEENGLVFEDSEELAAQLQMLFSNFP TERSAFTERDAGSGLVTRLRERPALLVSSTSKTEDEDFSILLAA LESRV*T\MTLDGHNLPSKUVTTKGRPLREYSSRLHIQKHFQH IQVCTPWLBAEDYPLLLGSADLGVCHTSSGLDLPMKVVDMFG CCLPVCAVWFKCHLELVKHEENGLVFEDSEELAAQLGMLFSNFP TERSAFTERDAGSGLVTRLEERPATLVSSTSKTEDEDFSILLAA LESRV*T\MTLDGHNLPSKVVTTKGRPLREYSSLHIQKHFQH IQVCTPWLBAEDYPLLLGSADLGVCHTSSGLDLPMKVVDMFG CCLPVCAVWFKCHLELVKHEENAGLGLTAGGAGLTAEVSGRLVLFTGNFT LKGMTGNTATTSTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	ł	1	ļ	PDHCSDDA+QSCPAAAAAPLQRQCDQSQGQITSPOSGNSGETFS
AVTOYDRASFIRETPILLOGHRIFMKIGSHISPPRARSEPEDPU TERSAFTERDAGSGLUTRIKERRALLUSSTSWTEDEDEJLLAA LESRV="\m\TLOGHNIPSL\CQVITGKGPILEQYYSRLIHQXHPQH IQVCTPALEAEDYPLLIGSADLGVCLHTSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAGLQMLFSNFP DPAGKLNQPRKNLRESQLRMEDSWVOTVLPJVMDT  S869 2122 833 LTAGASHTODASGSTSAKYPAAAQNI,CVTNAMREDLADIWYIR AVTVYDKPASFFKETPLDLOGHFMKLGSMHSPFRARSEPEDPV TERSAFTERDAGSGLUTRIKERPALLVSTSWTEDEDFSILLAA LESRV=T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHQKHPQH IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLVFBJEBEELAAGLQMLFSNFP DPAGKLNQPRKNLRESQCLRWEDSWOTVLPJVMDT  5870 2122 833 LTAGASHTODASGSTSAKYPAAAQNI,CVTNAMREDLADIWYIR AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV TERSAFTERDAGSGLUTRIKERPALLVSTTSWTEDEDFSILLAA LESRV=T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHQKHPQH TERSAFTERDAGSGLVTRIKERPALLVSSTSWTEDEDFSILLAA LESRV=T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHQKHPQH TERSAFTERDAGSGLVTRIKERPALLVSSTSWTEDEDFSILLAA LESRV=T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHQKHPQH TERSAFTERDAGSGLVTRIKERPALLVSSTSTREDEDFSILLAA LESRV=T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHQKHPQH TERSAFTERDAGSGLVTRIKERPALLVSSTSTREDEDFSILLAA LESRV=T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHQKHPQH CCLPVCAVFKCHHEUVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQPRNALRESQQLRWDESWVQTVLPLVUDMFG CCLPVCAVFKCHHEUVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQPRNALRESQQLRWDESWVQTVLPLVUDMFG CCLPVCAVFKCHHEUVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQPRNALRESQQLRWDESWVQTVLPLVUDMFG CCLPVCAVFKCHHEUVKHEENGLVFEDSEELAAGLQMLFSNFP LKSINLPRPDNSTLNBKLDHYVINSTLLLVQSPTTGLPFTKT CGGDQKAKTQDSLYCAAGAMALALAYRRIDDDKGTHELEHSAI KCMGGILYCYMPQADKVQOFKQDPPTTCLHSVRNVHTGDELLS VEEYGHLQINAVSLVLLMUEVHISSGCJIVTNTEVSFJONLVF CV\ERVYRVP\DFG\VMGKREGKYY*/SGSTELHSSSVGLGKRQ VFGNPROVQEVQDLUTPVLHITTEGYPVVWKYYVPADPUYYE KNNPOSQKRFPSNCGRDGKLFLWGGALYIAKLLADELISPKDI DPVQRYVPLKDORNVSMFFSNGFLENDLVVVALLALESGREPDILDLNAA LKKGIGOTPGQVEYQOLLTPVLHTTEDLSDFYMSQDVFLLID DPVRYVPLKDORNVSMFSNGPLENDLVVVALLALESGREPDIDLNAA LKKGIGOTPGQVEYQOLLTRENLITERDNIRGSFRFPILDLNAA LKKGIGOTPGQVEYTOLLFGAPPULVIREDNIRGSFRFPILDLNAA LKKGIGOTPGQVEYTOLLFGAPPULVIREDNIRGSFRFPILDLNAA LKKGIGOTPGQVEYTOLLFGAPPULVIR				ESWQRGVAWCY
AVTYDKPASFFKETDLDCHRIFMKLGSMHSPFRARSEPEDPU TERSAFTERDAGSGLVTRLEERPRALLUSSTSWTEDEDPSILLAA LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHGKHFCH IQVCTPWLBAEDYPLLLGSADLGVCLHTSSGGLDLFKVVDMFG CCLPVCAVPKCLHELVKHEENGLVFEDSEELAAQLGMFSNPP DPAGKLNGPKRURESQQLKWDESWVQTVLPLWDDT  S869 2122 833 LTAGASHTODAGSTSAKYPAAQNIL/CVTNARREDLADIWYIR AVTYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV TERSAFTERDAGSGLTVRLREERPALLVSSTSWTEDEDFSILLAA LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHGKHFCH IQVCTPWLEAEDYPLLLGSADLGVCLHTSSGJDLPMKVVDMFG CCLPVCAVWFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFKRURESQQLRWDESWVQTVLPLVMDT  100000000000000000000000000000000000	2868	2122	833	LTAGASHTQDASQSTSAKYPAAAONL/CVTNAMPEDI.ADTWVTD
TERSAFTERDAGSGL/VTRLEREPALLVSSTSWITEDEDFSILLAA LESRV*T/MTLDGINLPSL/CVITAKGPLREYYSRLIHQKHFQH IQVCTPMLEABDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLDFEDSELAAQLQMLFSNFP DPAGKLMQFRKNLRESQQLRVDESWOTVUPLVMDT  S869 2122 833 LTAGASHTODASQSTSAKYPAAQNL/CVTNAMREDLADIWYIR AVTYDXRAPSFFKETPLDLQHRLFMKLGSMHSPFRARSPEEDPV TERSAFTERDAGSGL/VTRLRERPALLVSSTSWITEDEDFSILLAA LESRV*T/MTLDGHNLPSLVCVITGKGPLRBYYSRLIHQKHFQH IQVCTPWLEABDYPLLLGSADLGVCLHTSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVWDT  S870 2122 833 LTAGASHTODASQSTSAKYPAAQNL/CVTNAMREDLADIWYIR AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSPEEDPV TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA LESRV*T/MTLDGHNLPSLVCVITGKGPLREYYSRLIHQKHFQH IQVCTPWLEABDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA LESRV*T/MTLDGHNLPSLVCVITGKGPLREYYSRLIHQKHFQH IQVCTPWLEAEDYFPLLLGSADLGVCLHTSSGGLDPMKVVDMFG CCLPVCAVNFKCLHELVKHEGULVFEDSEELAAQLGMLFSNFP DPAGKLNQFFKNLRESQQLRWDESWVQTVLPLVWDT  S871 3 3465 FFFCRFLRYSKTTGDRSAMAGAAGITAEVSMKVLERRARTKGS VLKLL*LSLRRL*LEPTI*MGKLDHYYRIVKSTLLLYQSPTTGLFFTKT CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQDFKQDPRFTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV_ERVYRVP_DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KOFNGFNLFGNQGCSWSVIFVDLDAHNRNRGTLCSLLPRESR SHNTDAALLPCISYBAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRGGYRTLEDDNRCYYRRAEIKLFDGIECFEPIFFIXMIDG VFRGSPKGVQEXQDLLTPULHHTTEGYPVVPKYYYPADFVEYE KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLADELISPKDI DPVRYVPLKDQRNYSMRFSNGGPLENDLVVHWALLAESGRLQV FLNTYGIOTTOQOVEPIQIWPQGEUKAYLQDLFILBSCRRCP PDPPIGCLGTSKIYRILGKTVVCYPIIFDLSPYMSQDVFLLID DIKNALOFIKQYWKMHGRPLFLVLIREDNIRGSRNP ILDMLAA LKKGIIGGVKWHVDRLQTLISGAVVQDLDFLRISDTEELPEFKS FEELEPPHKISKVKRQSSTPSAPELGGOOPDVISEWKMFTHETI.	1	1		AVTVYDKPASFFKETPLDLOHRLFMKIGSMHSDEPARSEDEDDY
LESRY*T\MTLDGINLPSLVCUTTGKGPLREYYSRLIHGKHFCH IQVCTPMLEABDYPLILGSADIGVCLHTSSGOLDPMKVVDMRG CCLPVCAVNFKCHELVKHEENGLVFEDSELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRNDESWQTVLPLVMDT  LTAGASHTODASGSTSAKYPAAAQNL/CVTNAMREDLADIWYIR AVTVYDKPASFFKSTPLDLQGRLRMKLGSMISPFRARSEPEDPV TERSAFFERDAGSGLVTRERPALLVSTSWTEDEDFSILLAA LESRV*T\MTLDGHNLPSLVCVITGKGPLRBYYSRLIHQKHFQH IQVCTPMLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVNFKCHELVKHEENGLVFEDSELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRNDESWQTVLPLVMDT  LTAGASHTODASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR AVTVYDKPASFFKETPLDLQHRIFMKLGSMISPFRARSEPEDPV TERSAFTERDASGGLVTRLEERPALLVSSTSWTEDEDFSILLAA LESRV*T\MTLDGHNLPSLVCVITGKGPLRBYYSRLIHQKHFQH IQVCTPWLEAEDYPLLLGSADLGVCLHTSSGGLDPMKVVDMFG CCLPVCAVNFKCLHELVCVITGKGPLRFYYSRLIHQKHFQH IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDPMKVVDMFG CCLPVCAVNFKCLHELVRHERGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRNDESWVQTVLPLWDT  5871  3 3465 FFFCRFRLYSKTTGDRSAMGAAAGLTAEVSMKVLERRAFTKRS VLKLL*LSLRRL*LSEPTI*NGLLT*CSRLSVFFFLKV\GSVYEP LKSINLPRPDNETLWKLDHYYRIVSTLLLYQSPTTGLFPTKT CGGDCKAKTQDSLYCAAGAWALALAYRIDDDKGRTHELEHSAI KCMGGLYCYMRQADKVQGKOPPRTFCLISVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISGGLQIIYNTDEVSFIONLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KOFNGFNLFGNQGCSWSVIFVDLDAHNNRGTLCSLLPRESR SINTDAALLPCISYPAFALDDEVLFSQTLDKVVRKKKGKGFFKR FLRDGYRTSLEDDPNCYYKBAIKLFDGIECFFIFFITWMIDG VFRGPKGVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSQKRFFSNGCRGGKLFLNGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNYSMRFSNGGPLENDLVVHVALLAESGRLQV FLNTGGIOTOFQOVEPIQIWPQGELWKAYLQLGINEKLGLSGR PDRPIGCCGTSKIYRILLGHTVVCYPIIFDLDFYMSQDVFLLID DIKNALOFIKQYWRNHGRPLFFLVLIREDNIRGSRFNP ILDMLAA LKKGIIGGVKVHVDRLQTLISGAVVQCDFFLRISTSTEELPEFKS FEELEPPHKISKVKRGSSTFSAPELGGODPVNTSEMKERFHETI.	1	•		TERSAFTERDAGSGLVTRI.PEPPALLVCCTCUTEDEDBOTT T. A.
TQVCTPMLEADTYPLLIGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVMFKCLHELVKHEENGLVFEDSBELAAOLQMLFSMFP DPAGKLNQFRNLRESQQLRWDESWVOTVLPLVMDT  1 LTAGASHTQDASQTSAKYPAAAQNL/CVTNAMREDLADIWYIR AVTVYDKPASFFKETPLOLQRIFMKLGSMHSPFRARSEPBEDPV TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA LESRV*T\MTLDGHNLPSLVCVITGKGPLREFYSRLHQKHFQH IQVCTPMLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVMFKCLHELVKHEENGLVFEDSEELAAQLQMLPSNFP DPAGKLNQFKRNLRESQLRWDESWVOTVLPLVMDT GCLPVCAVMFKCLHELVKHEENGLVFEDSEELAAQLQMLPSNFP DPAGKLNQFKRNLRESQLRWDESWVOTVLPLVMDT TERSAFTERDAGSGLVTHLRERPALLVSSTSWTEDEDFSILLAA AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV TERSAFTERDAGSGLVTHLEREPALLVSSTSWTEDEDFSILLAA LESRV*T\MTLDGINLPSLVCVITGKGPLREYYSRLHQKHFQH IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVMFKCHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFFKNLRESQQLRWDESWVQTVLPLVMDT STENSAFTERDAGSGLVTHSSTSWTEDEDFSILLAA LESRV*T\MTLDGINLPSLVCVITGKGPLREYYSRLHQKHFQH IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVMFKCHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFFKNLRESQQLRWDESWVQTVLPLVMDT STENSAFTERDAGSGLVTYSTSSTSWTEFIKV\GSVYTEP LKSINLPRPDNETLWGHENGLVFTSGTLDKVVDMFG CCLPVCAVMFKCHELVKHEENGLVFEDSEELAAQLQMLFSNFP LKSINLPRPDNETLWGHLGHTYTUKSTLLLYQSPTTGLFPTKT CGGGDKAKIQDSLVCAAGAMALALAYRILDDKGRTHELEHSAI KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YBEYGHLQINAVSLYLLYLVBWINSGGLOIIYMTDEVSFTCNLVF CV\ERVYRVP\DFG\VMSKRGKYY*SGSTELHSSVGLGKRQ L*KOPNGFNLFGROGCSWSVIFVDLDAHNRNRQTLCSLLPRESR SHNTDAALLPGISYPAFALDDEVFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDDNRGVYKPAEIKLFDGIECFFFFTLYMMIG VPRGMPKQVQEYQDLTPVLHHTTGYPVVPKYYYPADPVEYE KNNPGSKRFPSNCGRGRGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVFLKDGRNVSMRFSNQGPLENDLVVHVALIAESQRLQQ FELNTGGIGTSKIYRILGKTVQCYPIIFDLSDFYNSQDVFLLID DIKNALQFIKKYNGKGRGRGKLFLWGQALYIIAKLLADELISPKDI DPVRYVFLKDGRNVSMRFSNQGPLENDLVVHVALIAESGRLQQ FELNTGGIGTSKIYRILGKTVQCYPIIFDLSDFYNSQDVFLLID DIKNALQFIKKYNGKSFTSAPELGQOPDVIISEKKDKDTHETII.				LESRY*T\MTLDGHNLPSLUCUTTCKCDLDEVYCDLTUCKYDD
CCLPVCAVNFKCLHELVKHEENGLYFDSEELAQLQMLFSNFP DPAGKLNGPFRINLRESQQLRWDESWVQTVLPLVMDT  AVTVYDKPASFFKETPLDLQHRIJFMKLGSMHSPFRARSEPEDPV TERSAFTERDAGSGLTAKTPAAQNL/CVTNAMREDLADIWYIR AVTVYDKPASFFKETPLDLQHRIJFMKLGSMHSPFRARSEPEDPV TERSAFTERDAGSGLVTKLRERPALLVSSTSWTEDEDFSILLAA LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLTHQKHFQH IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLPSNFP DPAGKLNGFRKNLRESQQLRWDESWVQTVLPLVMDT  833 LTAGASHTODASGSTSAKYPAAQNL/CVTNAMREDLADIWYIR AVTVYNKPASFFKETPLDLQHRIJFMKLGSMHSPFRARSEPEDDPV TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLTHQKHFQH IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT GCCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT SFFCRPLRLYSKTTGDFSAMAGAAGLTABVSMKVLBERRAFTKRS VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFFFLKV\GSVYEP LKSINLPRDNETLWDKLDHYYRIVKSTLLLYQSPTGLFPTKT CGGDQKAKLQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI KCMGGILYCYMRQADKVQQFXQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIONLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHESSVGLGKRQ L*KQFNGFNLFGNGGCSWSVI*FVDLDAHNRNNGTLCSLLPRESR SINNTDAALLDECTSYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFIXMMILG VPRGMPKQVQEYQDLTPVLHHTTEGYPVVPRYYYVPADFVEVE KNNPGSOKRFPSNCGRGKFLFWGGALVIIAKLLADELISPKDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESQRLQV FINTYGIGTOTPQQVEPIQIWPQGEVKATLQLGINEKLGLSGR PDRPIGGLGTSKIYRILGKTVVCYPIITGLBGSFFNQDVFLLID DIKNALQFIKKYGIFSKIYRILGKTVVCYPIITGLBGSFFNDIDLMLAA LKKGIIGGVKVHVDRLQTLISGSTPSAPELGQODPWILSEKKRDFTHETI.		j i		TOVCTPWI.PAEDVDI.I.I GENDI GUGI IMOGGGI DI DIVIZIONI
S869 2122 833 LTAGASHTODASGSTSAKYPAAQQNL/CVTNAMREDLADIWYIR AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEEDDPV TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA LESRV*T\MTLDGHNLPSLVCVITGKGPLRBYYSRLIHQKHFQH IQVCTPMLEABDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEBNGLVFEDSELAAQLQMLFSNFP DPAGKLNQFFRNLRESQQLKWDESWCOTVLPLVMDT TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA LESRV*T\MTLDGHNLPSLVCVITGKGPLRBYYSRLIHQKHFQH IQVCTPWLEABDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFFRNLRESQQLRWDESWVQTVLPLVMDT TERSAFTERDAGSGLVTRLRERPALLVSSTSGHTEDEDFSILLAA LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHQKHFQH IQVCTPWLEABDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRNLRESQQLRWDESWVQTVLPLVMDT TFFCRPLRLYSKTTGBRSAMAGAAGLTAEVSMKVLERRARTKRS VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVKFRLKV\GSVYEP LKSINLPRPDNETI*NDKLDHYYRIVKSTLLLYQSPTTGLFPTKT CGGDQKAKIQDSL*VCAAGAMALALAYRRIDDKGKTHELEHSAI KCMRGILYCYMQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQI'I INTDEVSTIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KOPNGFNLFGNGGCSMSVI FVDLDAHMRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKKKYGFKR FLRDSYRTSLEDDNRCYYKPAEIKLPDGIECEFPIFFLYMMILG VFRGPKGVQEYQDLLTPULHHTTEGYPVVPKYYYVPADFVEYE KNNPGSGKRPPSNGGDKLFTLWHTTEGYPVVPKYYYVPADFVEYE KNNPGSGKRPPSNGGDKLFTLWHTTEGYPVVPKYYYVPADFVEYE KNNPGSGKRPPSNGGDKLFTLWGQALYI IAKLLADELISPKDI DPVQRYVPLKDQRNVSMFFSNGGPLENDLVVHVALIAESGRLQV FILNTYGIGTGTFRQVERTIGKTVVCYPI IFDLSDFYMSQDVFILID DIKNALQFIKQYWKMHGRPLFLVLIREDNIRGSRFNFILDMLAA LKKGIIGGWKWHDRLQFLISGAVVEQLDFLRISDTEELPEFKS FEELEPPKHSKVKRQSSTPSAPELGGOPDVNIESEWKKEKPEFKS FEELEPPKHSKVKRQSSTPSAPELGGOPDVNIESEWKKEKERGERFRITII		1		CCLPACA AMERICA HEL TANDERS CONTROL SERVICE AND CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CON
LITAGASHTODASQSTSAKYPAAGNU/CUTNAMREDLADIWIR AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSPEDDPY TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA LESRV*T\MTLDGHLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAGLQMLFSNFP DPAGKLNQFFRNLRESQQLKMDESWYGTVLPLVMDT  LTAGASHTODASGSTSAKYPAAGNL/CUTNAMREDLADIWYIR AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSSPEDDPV TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHQKHFQH IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAGLQMLFSNFP 1QVCTPWLEAEDYPLLLGSADLGVCLHTSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAGLQMLFSNFP 1QVCTPWLEAEDYPLLLGSADLGVCLHTSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAGLQMLFSNFP DPAGKLNQFFRNLRESQGLRWDESWVQTVLPLVMDT  FFFCRPLRLYSKTTGDRSAMAGAGLTAEVSWKVLERRARTKRS VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFFFLKV\GSVYEP LKSINLPRPDNETLMDKLDHYYRIVKSTLLLVQSPTTGLFPTKT CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQQFKQDPFPTCLHSVFNVHTGDELLS YEEYGHLQINAVSILYLLVLUFMISSGLOIIYNTDEVSFIONLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KQFNGFNLFGNGCCSMSVIFVDLDAHNRNRQTLCSLLPRESR SHNTDAALLPGISVPAFALDDEVLFSQTLDKVMKLKGKYGFKR FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRONKOVGLYODLLTPULHHTTECYPVVVKYYVYADADFVEYE KNNPGSQKRPPSNCGRDGKLFILNGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESQRLQV FLNTYGIGTGTPQQVEFIGIMPQGELVKAYLQCGINEKLGLSGR PDRFIGCLGTSKTYRTLIGKTVVCYPIIFDLSDFWSQDVFLLID DIKNALQFIKQYWKMGRPLFLVLIREDNIRGSRFNPILDMLAA LKKGIIGGVKVHVDRLQTLLISGAVVEQDLPFLISDTELPEFKS FEELEPPKHSKVKRQSSTPSAPALGOOPDVNISEWKKKKFYHEII.	1 1	i i		DPACKL NOPPLYNI BESSOL BURDELINGER FEDSEELAAQLQMLFSNFP
AVTYTOKPASFKETPLDLOHRLPMKLGSMHSPFRARSEPEDDV TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA LESRV*T\MTLDGHRLPSLVCVITGKGPLREYYSRLIHQKHFQH IQVCTPWLEAEDYPLLIGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLPSNFP DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT AVTVYDKPASFFKETPLDLQHRLPMKLGSMHSPFRARSEPEDPV TERSAFTERDAGSGTSAKYPAAQONL/CVTNAMREDLADLWYIR AVTVYDKPASFFKETPLDLQHRLPMKLGSMHSPFRARSEPEDPV TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLHOKHFQH IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT  5871 3 3465 FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS VLKLL*LSLRL*LEPTI*NGLLT*CSRLSVFRFLKV\GSVYEP LKSINLPRPDNETLWKLDHYYHIVSTLLLYQSTTGLFPTKT CGGDQKAKIQDSLYCAACAWALALAYRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YSEYGHLQINAVSIJLLVLVEMISSGLQIINNTDSVSFTONLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KQFNGFNLFGNQGCSWSVIITDLDAHNRNQTLCSLLPRESR SINTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDDNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVQSYDLLTPVLHHTTEGYPVVPKYYYYPADFVEYE KNNPGSQKRFPSNCGRDGKLFINGQALYIITAKLADELISPKDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESQRLQV FLNTYGIOTTOPQOVEPIQIHPQGELVKAYLQLCINEKLGLGGR PDRFIGCLGTSKIYRILGKTVVCYPIITDLSDFMSQDVFLID DIKNALQFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA LKKGIIGGVKVHVDRLQTLISGAVVEQLDPLRISDTELPEFKS FEELEPPKHSKVKRQSSTPSAPELGGOPDVNISSBWKKDKPTHEII	5869	2122	933	LTAGA GUTTO DE CONTRESQUERWDESWVQTVLPLVMDT
TERSAFTERDAGSGLVTRLIRERPALLVSSTSWTEDEDFSILLAA LESRV*T\MTLDGHNLPSLVCVITGKGPLRBYYSRLHQRHFQH IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNOFRKNLESQQLRWDESWVQTVLPLVMDT  S870  2122  833  LTAGASHTODASGSTSAKYPAAAQNL/CVTNAMREDLADIWYIR AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLHQKHFQH IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRNLRESQQLRWDESWVQTVLPLVMDT  S871  3  3465  FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFRFLKV\GSVYEP LKSINLPRPDNETI*NDKLDHYRIVKSTLLLYQSPTTGLFPTKT CGGDQKAK\QDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQQFKQDPRPT*CLHSVFNVHTGDELLS YBEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIONLVF CV\ERVYRVP\DFG\VWGKREGKYY*\SGSTELHSSSVGLGKRQ L*KQFNGFNLFGNQGCSWSVIFVDLDAHNRNRGTLCSLLPRESR SHNTDAALLPGLISYPAFALDDEVLFSQTLDKVYRKLKGKYFFKR FLRDGYRTSLEDPNRCYYRPAEIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVPKYYYVPADFVEYE KNNPGSQKR*PFSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRVPLKDQRRVSMRFSNQGPLENDLVVHVALIAESQRLQV FLNTYGIQTQTPQQVEPIGIPWQQELVKAYLQLGINBKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSPFMSQDVFLLID DIKNALQFIKQYWRMHGRPLFLVLIREDNIRGSRFNPILDMLAA LKKGIIGGVKVHVDRLQTLIGGAVVEQLDFLRISDTEELPEFKS FEELEPPKHISKVKRKGSSTPSAPELGQODPVNISEWDKPTHEIL			633	DIAGASATQDASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR
LESRV*T/WILDGANLPSL/CVITGKGPLREYYSRLIHQKHFQH IQVCTPWLEAEDYPLLIGSADLGVCLHTSSGLDLPMKVVDMFG CCLPVCAVNFKCHELVKHEENGLVFEDSEELAAQLQMLPSNFP DPAGKLNQFRKNLRESQQLRWDESWVQTULPLVMDT LTAGASHTODASQSTSAKYPAAAQNL/CVTNANREDLADIWYIR AVTYDKPASFFETPLDLQHRLFMKLGSMHSPFRARSEPEDPV TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA LESRV*T/WILDGHNLPSLVCVTTGKGPLREYYSRLIHQKHFQH IQVCTPMLEAEDYPLLLGSADLGVCLHTSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLGMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLUMDT SFFCPLBLLYSKTGBRSAMAGAAGLTAEVSMKVLERRARTKRS VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFRFLKV\GSVYEP LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFPTKT CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YSEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KQFNFFNEGOGGSWSVIFDLDAHNRNRQTLCSLPPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDPNRCYYRPASIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVQBYQDLLTPVLHHTTEGYPVRKYYYVPADFVEYE KNNPGSQKRFFSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRXVPLKDQRNVSMRFSNGGPLENDLVVHVALLAESQRLQV FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLGGR PDRPIGCLGTSKIYRILGKTVVCYPTIFDLSDFYMSQDVFILID DIKNALQFIKQYWKHBGPPLFLVLIREDNIRGSRFNPILDMLAA LKKGIIGGVKVHVDRLQTLITSGAVEQLDFFRISTSTEELPEFKS	1 1	l		AVTVYDRPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV
1QVCTPMLEAEDTYELLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVMFKCLHELVKHEEMGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWQVTVLPLVMDT  LTAGASHTQDASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR AVTVYDKPASFFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV TERSAFTERDAGSGLVTHLRERPALLVSSTSWTEDEDFSILLAA LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLHIQKHFQH IQVCTPMLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVMFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWQVTVLPLVMDT  5871 3 3465 FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFFFLKV\GSVYEP LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFPTKT CGGDQKAKIQDSLYCAAGAWALALAYRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLVEMISSGLQIIYMTDEVSFIQNLVF CC\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KQFNGFNLFGNQGCSWSVIFVDLDAHMRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSGTLDKVVRKLKGKYGFKR FLRDGYRTSLEDDNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGMFKQVQEYQDLLTPVLHHTTEGYPVVRYYYVPADFVEYE KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNYSMFSNQGPLENDLVVHVALIAESQRLQV FLNTYGIOTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFILID DIKNALQFIKQYWKNHGRPLFLVLIREDNIRGSRRMPILDMLAA LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISTEELEPFKS	[			TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA
1QVCTPMLEAEDTYELLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVMFKCLHELVKHEEMGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWQVTVLPLVMDT  LTAGASHTQDASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR AVTVYDKPASFFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV TERSAFTERDAGSGLVTHLRERPALLVSSTSWTEDEDFSILLAA LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLHIQKHFQH IQVCTPMLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVMFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWQVTVLPLVMDT  5871 3 3465 FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFFFLKV\GSVYEP LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFPTKT CGGDQKAKIQDSLYCAAGAWALALAYRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLVEMISSGLQIIYMTDEVSFIQNLVF CC\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KQFNGFNLFGNQGCSWSVIFVDLDAHMRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSGTLDKVVRKLKGKYGFKR FLRDGYRTSLEDDNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGMFKQVQEYQDLLTPVLHHTTEGYPVVRYYYVPADFVEYE KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNYSMFSNQGPLENDLVVHVALIAESQRLQV FLNTYGIOTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFILID DIKNALQFIKQYWKNHGRPLFLVLIREDNIRGSRRMPILDMLAA LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISTEELEPFKS	1 1			LESRV+T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHOKHFOH
CCLPVCAVNFKCLHELVKHEENGLVFBDSELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT  AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA LESRV*T\MTLDGRNLPSLVCVITGKGPLREYYSRLIHQKHFQH IQVCTPWLEAEDYPLLLGSADLGVCLHTSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKULRESQQLRWDESWVQTVLPLVMDT  S871 3 3465 FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS VLKIL*SLRRL*LEPTI*NGLLT*CSRLSVFRFLKV\GSVYEP LKSINLPRPDNETLWGLDHYYRIVSTTLLYQSPTTGLFFTKT CGGDQKAKIQDSLYCAAGAWALALAYRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSIYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KQFNGFNLFENQGCSMSVIFVDLDAHNRNROTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECFFIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYVYPADFVEYE KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNVSMRFSNQGFLENDLVVHVALLAESQRLQV FLNTYGIQTOTPQQVEPTQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFILID DIKNALQFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTEELPEFKS	1 1			IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG
DPAGKLNOFRKNLRESQQLRWDESWVQTVLPLVMDT  LTAGASHTQDASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR AVTVYDKPASFFKETELDLQHRLFMKLGSMHSPFRARSEPEDPV TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHQKHFQH IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVMFKCLHELVKHEENGLVFEDSEELAAQLOMLFSNFP DPAGKLNOFRKNLRESQQLRWDESWVQTVLPLVMDT  5871  3 3465 FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS VLKIL*LSLRRL*LEPTI*NGLLT*CSRLSVFRFLKV\GSVYEP LKSINLPPPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFFTKT CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQOFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KOFNGFNLFGNGGCSWSVIFVDLDAHMRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDPNRCYYKPAEIKLFGGIECEFPIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESGRLQV FLNTYGIQTOTOPQOVEPIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLID DIKNALQFIKQVWKNHGRPLFLVLIREDNIRGSRFNPILDMLAA LKKGIIGGVKVHVDRLQTLIISGAVVEQLDFLRISDTEELPEFKS FEELEPPKHSKVKRQSSTPSAPELGOOPDVNISEWKDKFTHEIL	1	j		CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAOLOMLESNED
LTAGASHTODASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA LESRV+T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHQKHFQH IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVMFKCHHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT  3 3465 FFFCRPLRLYSKTTODRSAMAGAAGLTAEVSWKVLERRARTKRS VLKLL+LSLRRL+LEPTI+NGLLT+CSRLSVFRFLKV\GSVYEP LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFFTKT CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY+/SGSTELHSSSVGLGKRQ L*KQFNGFNLFGNGGCSWSVIFVDLDAHNRNRGTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDPNRCYYKPAEIKLFFGIECEFPIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSQKRFFSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALLAESQRLQV FLNTYGIQTOPQOVEPIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLID DIKNALQFIKQVWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTEELPEFKS FEELEPPKHSKVKRQSSTPSAPELGOOPDVNISEWKDKPTHEIL				DPAGKLNQFRKNLRESQOLRWDESWYOTVLPLVMDT
AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDDFSILLAA LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLHQKHFQH IQVCTPWLEAEDYPLLGSADLGVCLHTSSGGLDLPMKVVDMFG CCLPVCAVMFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT  3 3465 FFFCRPLRYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFRFLKV\GSVYEP LKSINLPRPPNETLWDKLDHYYRIVKSTLLLYQSPTTGLFPTKT CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQOFKQDPRPTTCLHSVFNVHTTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYMTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KQFNGFNLFGNGCSWSVIFVDLDAHNRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDPNCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSQKRFFSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESQRLQV FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLID DIKNALQFIKQYWKHMGRPLFTVLIREDNIRGSRFNFILDMLAA LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTEELPEFKS FEELEPPKHSKVKRQSSTPSAPELGOOPDVNISEWKDKPTHEIL	5870	2122	833	LTAGASHTODASOSTSAKYPAAAONI./CVTNAMPEDIADIWYTD
TERSAFTERDAGGLUTRLRERPALLVSSTSWTEDEDFSILLAA LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLHIQKHFQH IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT  5871 3 3465 FFFCRPLRYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFFFLKV\GSVYEP LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFFTKT CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KOFNGFFNLFGNQGCSWSVIFVDLDAHMRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVQEYQDLLTTVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNVSNRFSNQGPLENDLVVHVALLAESQRLQV FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLID DIKNALOFIKQYWKNHGRPLFLVLIREDNIRGSRNPILDMLAA LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTEELPEFKS FEELEPPKHSKVKRQSSTPSAPELGQOPDVNISEKKDKPTHEIL	] }			AVTVYDKPASFFKETPI.DI.OUPI.EMVI.GSMUCDEDABGEDEDA
LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHQKHFQH IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT  3 3465 FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS VLKKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFRFLKV\GSVYEP LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFPTKT CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KOFNGFNLFGNQGCSWSVIFVDLDAHMRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESQRLQV FLNTYGIQTOTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLID DIKNALQFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTEELPEFKS FEELEPPKHSKVKRQSSTPSAPELGOOPDWNISEWKDKPTHEII.	1			TERSAFTERDAGGGLATRI DERDAL LUGGROUMERRE DESCRIPTION
IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFFKNLRESQQLRWDESWVQTVLPLVMDT  FFFCRPLRLYSKTTGPRSAMAGAAGLTAEVSWKVLERRARTKRS VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFFFLKV\GSVYEP LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFPTKT CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQOFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KQFNGFNLFGNQGCSWSVIFVDLDAHNRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYVPADFVEYE KNNPGSQKRFFSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESQRLQV FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLID DIKNALQFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTEELPEFKS FEELEPPKHSKVKRQSSTPSAPELGQOPDVNISEWKDKPTHEII.	1 1	1		LESDVIT MILDOUNI DOLLAR TRANSPORTED TO THE TOTAL DESIGNATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY O
CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT  FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFFLKV\GSVYEP LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFPTKT CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KQFNGFNLFGNQGCSWSVIFVDLDAHNRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESQRLQV FLNTYGIQTQTPQQVEFIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFILID DIKNALQFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTEELPEFKS FEELEPPKHSKVKRQSSTPSAPELGQOPDVNISEWKDKPTHEII.	1 1	i		TOUCEDAL ENDRUGIA CONTRACTOR OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF
DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT  FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFRFLKV\GSVYEP LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFPTKT CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KQFNGFNLFGNQGCSWSVIFVDLDAHNRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESQRLQV FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKTYRILGKTVVCYPIIFDLSDFYMSQDVFLLID DIKNALQFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTEELPEFKS FEELEPPKHSKVKRQSSTPSAPELGQOPDVNISEWKDKPTHEII.		. 1		CCLDUCAIDIENCTIFFULGSADLGVCLHTSSSGLDLPMKVVDMFG
FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS  VLKILL*LSLRRL*LEPTI*NGLLT*CSRLSVFRFLKV\GSVYEP LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFPTKT CGGDQKAKIQDSLYCAAGAWALALAYRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KOFNGFNLFGNQGCSWSVIFVDLDAHNRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESQRLQV FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLID DIKNALQFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTEELPEFKS FEELEPPKHSKVKRQSSTPSAPELGQOPDVNISEWKDKPTHEII.	Į l	l		DENOVINGENELVKHEENGLVFEDSEELAAQLQMLFSNFP
VLKLL*LSLRRL*LEPTI*NGLT*CSRLSVFFLKV\GSVYEP LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFPTKT CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KQFNGFNLFGNQGCSWSVIFVDLDAHNRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESQRLQV FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLID DIKNALQFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTEELPEFKS FEELEPPKHSKVKRQSSTPSAPELGQOPDVNISEWKDKPTHEII.	5871			DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT
VLKIL*LSLRRL*LEPTI*NGLLT*CSRLSVFRFLKV\GSVYEP LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFPTKT CGGDQKAKIQDSLYCAAGAWALALAYRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KQFNGFNLFGNQGCSWSVIFVDLDAHNRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESQRLQV FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLID DIKNALQFIKQYWKMHGRPLFLVLIREDNIRGSRFNFILDMLAA LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTEELPEFKS FEELEPPKHSKVKRQSSTPSAPELGQOPDVNISEWKDKPTHEII.	1 20,7		3465	FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS
LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFPTKT CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLWEMISSGIQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KQFNGFNLFGNQGCSWSVIFVDLDAHNRNROTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVKKLKGKYGFKR FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESQRLQV FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFILID DIKNALQFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTEELPEFKS FEELEPPKHSKVKRQSSTPSAPELGQOPDVNISEKKDKPTHEII.		į		VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFRFLKV\GSVYEP
CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KQFNGFNLFGNQGCSWSVIFVDLDAHNRNROTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVKKLKGKYGFKR FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESQRLQV FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLID DIKNALQFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTEELPEFKS FEELEPPKHSKVKRQSSTPSAPELGQOPDVNISEKKDKPTHEII.	1	ţ		LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYOSPTTGLFPTKT
KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KQFNGFNLFGNQGCSWSVIFVDLDAHNRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESQRLQV FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFILID DIKNALQFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTEELPEFKS FEELEPPKHSKVKRQSSTPSAPELGQOPDVNISEWKDKPTHEII.	1 1	ł		CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGPTHELEDGAT
YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KQFNGFNLFGNQGCSWSVIFVDLDAHNRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESQRLQV FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLID DIKNALQFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTEELPEFKS FEELEPPKHSKVKRQSSTPSAPELGQOPDVNISEKKDKPTHEII.	1			KCMRGILYCYMROADKVOOFKODDDDDTTCI.ucvpmvumcont.
CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KQFNGFNLFGNQGCSWSVIFVDLDAHNRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESQRLQV FLNTYGIQTQTPQQVEFIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLID DIKNALQFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTEELPEFKS FEELEPPKHSKVKRQSSTPSAPELGQOPDVNISEKKDKPTHEII.	1	ļ		YEEYGHLOINAVSI, VI. VENTESCO OT TUMBOR OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF TH
L*KOFNGFNLFGNQGCSWSVIFVDLDAHNRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESQRLQV FLNTYGIQTQTPQQVEFIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLID DIKNALQFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTEELPEFKS FEELEPPKHSKVKRQSSTPSAPELGQOPDVNISEWKDKPTHEII				CV/ERVYRVD/DEG/VWGVBECKVV+/GGGGT
SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALLAESQRLQV FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLID DIKNALQFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA LKKGIIGGVKYHVDRLQTLISGAVVEQLDFLRISDTEELPEFKS FEELEPPKHSKVKRQSSTPSAPELGOOPDVNISEWKDKPTHEII	1		İ	LAKOFNOEMI FONOGGREGIET TOTAL
FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESQRLQV FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLID DIKNALQFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTEELPEFKS FEELEPPKHSKVKRQSSTPSAPELGOOPDVNISEWKDKPTHEII	1 1	l	ŀ	SINGS NOT NOT SUBSECT OF STREET
VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESQRLQV FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFMSQDVFLLID DIKNALQFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTEELPEFKS FEELEPPKHSKVKRQSSTPSAPELGQOPDVNISEWKDKPTHBII	1			STATE DARKED CISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR
VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESQRLQV FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLID DIKNALQFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTEELPEFKS FEELEPPKHSKVKRQSSTPSAPELGQOPDVNISEWKDKPTHEII	] [	į.	ļ	FLKLGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG
KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESQRLQV FLNTYGIQTQTPQQVEFIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLID DIKNALQFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTEELPEFKS FEELEPPKHSKVKRQSSTPSAPELGQOPDVNISEWKDKPTHEII	] ]	ĺ	į	VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE
DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESQRLQV FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLID DIKNALQFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTEELPEFKS FEELEPPKHSKVKRQSSTPSAPELGQOPDVNISEWKDKPTHEII	1 1		į	KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDT
FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLID DIKNALQFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTEELPEFKS FEELEPPKHSKVKRQSSTPSAPELGQOPDVNISEWKDKPTHEII	]	i	}	DPVQRYVPLKDORNVSMRFSNOGPLENDI.VVHVAT.TAFGORTOV
PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLID DIKNALQFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTEELPEFKS FEELEPPKHSKVKRQSSTPSAPELGOOPDVNISEWKDKPTHEII	; f	1		FLNTYGIOTOTPOOVEPTOIWPOOFINENT OF COMPUTER OF COM
DIKNALQFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTEELPEFKS FEELEPPKHSKVKRQSSTPSAPELGOOPDVNISEWKDKPTHEII	1 1	į.	ļ	PDRPIGCIGTSKIVETI GYMNICVETTEDY OF PROCESSES
LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTEELPEFKS FEELEPPKHSKVKRQSSTPSAPELGOOPDVNISEWKDKPTHEII	1 1	į		DIKNALOFIYOVHYMIGDDI HITE TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORRANDA TORR
FEELEPPKHSKVKRQSSTPSAPELGQOPDVNISEWKDKPTHEII.	] [	j		LAKELICEANIARDE ON TOOTEREDIESENPILDMINA
OKINDOSCIASON ILLOIT VERGONELEVICON INTERPRETATION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DEL CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION	į į	1		PERI PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDENCE OF THE PROVIDE
L LIKUNDCCCLACOATTICTII VDECOMETOVOCOMITONICO	1 1			PEDDEFFKHSKVKRQSSTPSAPELGQQPDVNISEWKDKPTHEIL
2 AND COCHASCATELEGIER REGION PITAL TRANSPORTER VYRR				QKLNDCSCLASQAILLGILLKREGPNFITKEGTVSDHIERVYRR

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide '	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
j	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
į	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
[	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
f	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence		Codon, /=possible nucleotide deletion,
		<del> </del>	\=possible nucleotide insertion)
		·	AGSQKLWSVVRRAASLLSKVVDSLAPSITNVLVQGKQVTLGAFG
			HEEEVISNPLSPRVIQNIIYYKCNTHDEREAVIQQELVIHIGWI
		l l	ISNNPELFSGTLKIRIGWIIHAMEYELQIRGGDKPALDLYQLSP
-		1	SEVKQLLLDILQPQQNGRCWLNRRQIDGSLNRTPTGFYDRVWQI
ļ			LERTPNGIIVAGKHLPQQPTLSDMTMYEMNFSLLVEDTLGNIDQ
1		Į	PQYRQIVVELLMVVSIVLERNPELEFQDKVDLDRLVKEAFNEFQ
L			KDQSRLKEIEKQDDMTSFYNTPPLGKRGTCSYLTKAVMNLLLEG EVKPNNDDPCLIS
5872	68	665	
1	i		VQGYMYRFVIKINSCYSEKTSICRHRCCPELPATQPWPTPTVFF
1			NIAIDSESLGCI\SFKLFADKV/PKRWKKNFVLLNTGEKVLGDK
	1	1	GPCFYRIIPG\LCQGGDFTHHNGTGGKSLYSKEFDDENFI/LKH
1	1	1	TAPGVLSTANAGPTTNGSQFFICTAKTEDG*QHVVFGKVKDGMS
5873	2240	506	IVEALERSGSRNGKTSKKITAANCGQL
}	ļ		RRPPEGGSGGGRRTRARMPLPWSLALPLLLSWVAGGFGNAASAR
1			HHGLLASARQPGVCHYGTKLACCYGWRRNSKGVCEATCEPGCKF
	i		GECVGPNKCRCFPGYTGKTCSQDVNECGMKPRPCQHRCVNTHGS
			YKCFCLSGHMLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCP
1		<b>4</b>	SSGLRLAPNGRDCLDIDECASGKVICPYNRRCVNTFGSYYCCH IGFELQYISGRYDCIDINECTMDSHTCSHHANCFNTQGSFKKC
			KQGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKKLLAHKNSMK
1			KKAKIKNVTPEPTRTPTPKVNLQPFNYEEIVSRGGNSHGG\KKG
			NEEKMKEGLEDEKREEKALKD*HRRERPFRG\DVFFPKVNEAGE
1			FGLIL\VQRKALTSKLEHKADLNISVDCSFNHG\ICDW\KQDR\
			EDDFDW\NPADR\DNAI\GFY\MAVPGLWQGHK\KDIGRLKLLL
	i		PDLQPQSNFCLLFDYRLAGDKVGKLRVFVKNSNNALAWEKTTSE
	i		DEKWKTGKIQLYQGTDATKSIIFEAERGKGKTGEIAVDGVLLVS
			GLCPDSLLSVDD
5874	2	3387	ACPRLARRRRRVRSLRRRRGWLRARWSRGQNNMAARRITQETFD
1			AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD
1 . 1			VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD
1	ľ	j	SYFRKECGRDLEFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW
1 1	ĺ	ſ	EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLEKE\
1			SRDYDVDHSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG
1 1	i	i	KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI
!!	i		QANTPSPDVTLGTNPGTEDIOFPIOKIPLGIDI, KNI.DI. DDD KMC
	i	1	FULLDRSDVFSRFGIEIIKWAGFHTIKDDIKFSOLFOTI FRI FT
1 1	j	i	ETCARMLASFKCSLKPEHRDFCFFTIKFIKHSALKTDDVDWEDT
1 1			NMULDIKGAVKTKNCFFEIIKPFDKYTMRI,ODDI.I.KGVTDI.I.MA.O
1 !			NAYELSVKMKTLSNPLDLALALETTNSLCRKSLALLCOTESLAC
]	i	i	STRUEKIL *AVGLODIAPSPAAFPNFEDSTI. ECDEVIDUI VAUT
1	ĺ		VSSGCPLQVKKAEPEPMREEEKMIPPTKPETOAKABGGIGDAUD
] [	1		QRADHRVVGTIDOLVKRVIEGSI,SPKEPTI, VEDDAVIET CDDA
1 1	1	1	SUBJECT YELKLAEMORMSENI.RGADOKPTSADCAMBAMI VCD 3-1
			RNLKKKLLP\WORRGLLRAOG\IRG\WKAPPA\TTCTOTII I EL D
			APGURHIGROAPGLS \OAKPSLPDRND\AAKD\CDLDBW\CDCD
	1	i	QUESCEASGESPREAGVDISEAPOTSSPCPSADTDMKDMCDTAR
		i	KLARFVAQVG\PEIEOF\SI\ENSTDNDDI.WEL\UDONEC\ADV
	İ		FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GGOEGRUDIAG
		ſ	GEALFEDEPPPREAELESPEVMPEEEDEDDEDGGERARA LOOPO
'		1	GPSDEGSTPADGLPGEA\AEDDI./AIGAPAI.FTGI.I.OUTGPDTG
i		ł	RGFSSKSLKVGMIPAPKRVCLIOEPKVHEPVRIAVDPDBCDDMC
i i			KARRENDEDFAQQKL\TDK\NLGFO\MLOKMGWKEGHGLGSLGV
1	i	[ '	GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWOL.
5875	296		1FVF
-3.3	470	1848	LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA
1		1 -	LEFSGSLFPHAICLGDVDNDTLNELVVGDTSGKVSVVVNDDCDD
		1.1	WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSAEGWEHI.EDI.TDAV
J	1	1 '	VLDASGHHETLIGEEORPVFKOHIPANTKVMI.TSDTDGDGGBBT
- 1		1.3	VVGYTDRVVRAFRWEELGEGPEHLTGOLVSIKKWMI.FGOVDET C
İ		1.7	VILGPLGLPELMVSQPGCAYAILLCTWKKDTGGDDAGRGDTDGG
			/SGDPSCPRRGAAPDIWPYPQQECLHSPNWQHQT\SHGTESSGS

Set	SEQ	Predicted	T personal and the	
NO: nucleotide corresponding to first amino acid cresidue of amino acid residue of amino acid sequence corresponding to first amino acid residue of amino acid sequence corresponding to first amino acid sequence corresponding to first amino acid sequence corresponding to first amino acid sequence corresponding to first corresponding to first corresponding to first amino acid sequence corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corr			Predicted end	Amino acid segment containing signal peptide
Costion   Corresponding   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst   Cofirst	1		1	M=Alanine, C=Cvsteine, D=Aspartic Acid p
corvesponding to first amino acid for the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control o	"""		i e	Grucamic Acid, F=Phenvialanine G-Glyging
to first amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid am				n=nistidine, I=Isoleucine K-Lycine
amino acid residue of sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequ	1			L=Leucine, M=Methionine, N-Asparagine
residue of amino acid sequence   Severine, TeThreonine, V-Valine, amino acid sequence   Severine, Y-Tyrosine, X-Unknown, *-Stop Codon, /-possible nucleotide deletion,	1		amino acid	P=Proline, Q=Glutamine, R=Arginine
### ### ### ### ### ### ### ### ### ##	İ	1	residue of	S=Serine, T=Threonine V=Valine
sequence    Appossible nucleotide deletion,   Appossible nucleotide deletion,   Appossible nucleotide insertion    GERECTLOGITALUMEREREADELLUSVOUDHOLFALEKLUDVTO   GERECTLOGITALUMEREREADELLUSVOUDHOLFALEKLUDVTO   GERECTLOGITALUMEREREADELUSVOUDHOLFALEKLUDVTO   GERECTLOGITALUMER   APPOSSIBLE   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APPOSTORY   APP	1	residue of	amino acid	W=Tryptophan Y=Tyroging V=U=1=
SPAN   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE	ľ	amino acid	sequence	Codon /=possible musl-stil
GLFALTIDGTIKLMEERIERALUMSVOUDHOLFALEKLDVYG MCHEEVYACARDOGTTILDGHRYVORROUDENIRARCAGUTYAN GHEEVYACARDOGTTILDGHRYVORROUDENIRARCAGUTYAN GHEEVYACARDOGTTILDGHRYVORROUDENIRARCAGUTYAN GHEEVYACARDOGTTILDGHRYVORROUDENIRARCAGUTYAN THEORY THE PROVINCE MERKET THE PROVINCE SERVICE AND STATE THEORY THE PROVINCE SERVICE AND STATE THE PROVINCE SERVICE AND STATE THE PROVINCE SERVICE AND STATE ANDICISULTE THE PROVINCE SERVICE AND STATE ANDICISULTE THE PROVINCE SERVICE SERVICE BEAGAGO ADRESVED TO STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STAT	į	sequence		\-possible nucleotide deletion,
S876  1122  224  HPJGDYSKVAGARDGOTY I IDHNETVUPFQVDENREAPCAGLYACK KERRISPCLUTYPROKITYVPROKITYVPTQVENULETERNSTIT TACCRSKAWILITEL LUDCTIKESTITOSHISULPOASHIPS TACCRSKAWILITEL LUDCTIKESTITOSHISULPOASHIPS TACCRSKAWILITEL LUDCTIKESTITOSHISULPOASHIPS TACCRSKAWILITEL LUDCTIKESTITOSHISULPOASHIPS TACCRSKAWILITEL LUDCTIKESTITOSHISULPOASHIPS TACCRSKAWILITEL LUDCTIKESTITOSHISULPOASHIPS TACCRSKAWILITEL LUDCTIKESTITOSHISULPOASHIPS TACCRSKAWILITEL LUDCTIKESTITOSHISULPOASHIPS TACCRSKAWILITEL LUDCTIKESTITOSHISULPOASHIPS TACCRSKAWILITEL LUDCTIKESTITOSHISULPOASHIPS TACCRSKAWILITEL LUDCTIKESTITOSHISULPOASHIPS TACCRSKAWILITEL LUDCTIKESTITOSHISULPOASHIPS TACCRSKAWILITEL LUDCTIKESTITOSHISULPOASHIPS TACCRSKAWILITEL LUDCKIKESTITOSHISULPOASHIPS TOTAL TACCRSKAWILITEL LUDCTIKESTITOSHISULPOASHIPS TACCRSKAWILITEL LUDCKIKESTITOSHISULPOASHIPS TACCRSKAWILITEL LUDCKIKESTITOSHISULPOASHIPS TOTAL LUDCKIKESTITOSHISULPOASHIPS TACCRSKAWILITEL LUDCTIKESTITOSHISULPOASHIPS TACCRSKAWILITEL LUDCTIKESTITOSHISULPOASHIPS TACCRSKAWILITEL LUDCTIKESTITOSHISULPOASHIPS TACCRSKAWILITEL LUDCTIKESTITOSHISULPOASHIPS TACCRSKAWILITEL LUDCTIKESTITOSHISULPOASHIPS TACCRSKAWILITEL LUDCTIKESTITOSHISULPOASHIPS TACCRSKAWILITEL LUDCTIKESTITOSHISULPOASHIPS TACCRSKAWILITEL LUDCTIKESTITOSHISULPOASHIPS TACCRSKAWILITEL LUDCTIKESTITOSHISULPOASHIPS TACCRSKAWILITEL LUDCTIKESTITOSHISULPOASHIPS TACCRSKAWILITEL LUDCTIKESTITOSHISULPOASHIPS TACCRSKAWILITEL LUDCTIKESTITOSHISULPOASHIPS TACCRSKAWILITEL LUDCTIKESTITOSHISULPOASHIPS TACCRSKAWILITEL LUDCTIKESTITOSHISULPOASHIPS TACCRSKAWILITEL LUDCTIKESTITOSHISULPOASHIPS TACCRSKAWILITEL LUDCTIKESTITOSHISULPOASHIPS TACCRSKAWILITEL LUDCTIKESTITOSHISULPOASHIPS TACCRSTAWILITEL LUDCTIKESTITOSHISULPOASHIPS TACCRSTAWILITEL LUDCTIKESTITOSHISULPATATATATATATATATATATATATATATATATATATAT			ļ	(-possible nucleotide insertion)
S876  1122  224  HIPJGYPSEXVGARAMEPTEL LIVEPCTRESTICTSHESULPOASHIPPS WTCLIAGGGFF*TPTTLPFKGVFGSKGARAGSITKQ  LIVEGVFSYSGARAMEPGERETQVARMIKIFGDHFISQYEV KERTTEILHHUSERNEVURANLSTGURFISQYEV KERTTEILHHUSERNEVURANLSTGURFISQYEV KERTTEILHHUSERNEVURANLSTGURFISQYEV KERTEILHHUSERNEVURANLSTGURFISQYEV KERLHSTEILHHUSERNEVURANLSTGURFISQAGGGL  LIMESVNFSSGARAMEPGERETQVARMIKIFGDHFISQYEV KERLHSTILHHUSERNEVURANLSTGURFISQAGGGL  KERLHSTEILHHUSERNEVURANLDTATLLECKJGEDV KERLHSTEILHHUSERNEVURANLDTATLLECKJGEDV KERLHSTEILHHUSERNEVURANLDTATLLECKJGEDV KERLHSTEILHHUSERNEVURANLDTATLLECKJGEDV KERLHSTEILHHUSERNEVURANLDTATLLECKJGEDV KERLHSTEILHHUSERNEVURANLDTATLLECKJGED  SARGQUARSVPTQSTVALITERNEVURANCHTERVS\MMEL LINGKHHEMQVLEKEVEKRSGIOGLGVAGGNSTERKLESALEDLEV LINGKHHEMQVLEKEVEKRSGIOGLGVAGGNSTERKLESALEDLEV LINGKHHEMQVLEKEVEKRSGIOGLGVAGGNSTERKLESALEDLEV LINGKHHEMQVLEKEVEKRSGIOGLGVAGGNSTERKLESALEDLEV LINGKHHEMQVLEKEVEKRSGIOGLGVAGGNSTERKLESALEDLEV LINGKHHEMQVLEKEVEKRSGIOGLGVAGGNSTERKLESALEDLEV LINGKHHEMQVLEKEVEKRSGIOGLGVAGGNSTERKLESALEDLEV LINGKHHEMQVLEKEVEKRSGIOGLGVAGGNSTERKLESALEDLEV LINGKHHEMQVLEKEVEKRSGIOGLGVAGGNSTERKLESALEDLEV LINGKHHEMQVLEKEVEKRSGIOGLGVAGGNSTERKLESALEDLEV LINGKHHEMQVLEKEVEKRSGIOGLGVAGGNSTERKLESALEDLEV LINGKHHEMQVLEKEVEKRSGIOGLGVAGGNSTERKLESALEDLEV LINGKHHEMQVLEKEVEKRSGIOGLGVAGGRSTERKHELSALEDLEV LINGKHHEMQVLEKEVEKRSGIOGLGVAGGRSTERKHELVE LINGKHHEMQVLEKEVEKRSGIOGLGVAGGRSTERKHELVE LINGKHHEMGVAGGRSTERVEKRSGIOTHANDERSELDITEGHTVAFIR EKKODDFTTMVLIGHARVYKKHKHINGERSELDITEGHTVAFIR ALAMPEYMEKGTHAGGGFAARGANEOUT ALAMPEYMEKGTHAGGGFAARGANEOUT ALAMPEYMEKGTHAGGGFAARGANEOUT ALAMPEYMEKGTHAGGGFAARGANEOUT ALAMPEYMEKGTHAGGGFAARGANEOUT ALAMPEYMEKGTHAGGGFAARGANEOUT ALAMPEYMEKGTHAGGGFAARGANEOUT ALAMPEYMEKGTHAGGGFAARGANEOUT ALAMPEYMEKGTHAGGGFAARGANEOUT ALAMPEYMEKGTHAGGGFAARGANEOUT ALAMPEYMEKGTHAGGGFAARGANEOUT ALAMPEYMEKGTHAGGGFAARGANEOUT ALAMPEYMEKGTHAGGGFAARGANEOUT ALAMPEYMEKGTHAGGGFAARGANEOUT ALAMPEYMEKGTHAGGGFAARGANEOUT ALAMPEYMEKGTHAGGGFAARGANEOUT ALAMPEYMEKGTHAGGGFAARGANEOUT ALAMPEYMEKGTHAGGGFAARGANEOUT ALAMPEYMEKGTHAGGGFAARGANEOUT ALAMPEYMEKGTHAGGGFA	1	1		GLFALCTLDGTLKLMEEMEEADKLLWSVQVDHQLFALEKLDVTG
S876  1122  224  HIPJGYPSEXVGARAMEPTEL LIVEPCTRESTICTSHESULPOASHIPPS WTCLIAGGGFF*TPTTLPFKGVFGSKGARAGSITKQ  LIVEGVFSYSGARAMEPGERETQVARMIKIFGDHFISQYEV KERTTEILHHUSERNEVURANLSTGURFISQYEV KERTTEILHHUSERNEVURANLSTGURFISQYEV KERTTEILHHUSERNEVURANLSTGURFISQYEV KERTEILHHUSERNEVURANLSTGURFISQYEV KERLHSTEILHHUSERNEVURANLSTGURFISQAGGGL  LIMESVNFSSGARAMEPGERETQVARMIKIFGDHFISQYEV KERLHSTILHHUSERNEVURANLSTGURFISQAGGGL  KERLHSTEILHHUSERNEVURANLDTATLLECKJGEDV KERLHSTEILHHUSERNEVURANLDTATLLECKJGEDV KERLHSTEILHHUSERNEVURANLDTATLLECKJGEDV KERLHSTEILHHUSERNEVURANLDTATLLECKJGEDV KERLHSTEILHHUSERNEVURANLDTATLLECKJGEDV KERLHSTEILHHUSERNEVURANLDTATLLECKJGED  SARGQUARSVPTQSTVALITERNEVURANCHTERVS\MMEL LINGKHHEMQVLEKEVEKRSGIOGLGVAGGNSTERKLESALEDLEV LINGKHHEMQVLEKEVEKRSGIOGLGVAGGNSTERKLESALEDLEV LINGKHHEMQVLEKEVEKRSGIOGLGVAGGNSTERKLESALEDLEV LINGKHHEMQVLEKEVEKRSGIOGLGVAGGNSTERKLESALEDLEV LINGKHHEMQVLEKEVEKRSGIOGLGVAGGNSTERKLESALEDLEV LINGKHHEMQVLEKEVEKRSGIOGLGVAGGNSTERKLESALEDLEV LINGKHHEMQVLEKEVEKRSGIOGLGVAGGNSTERKLESALEDLEV LINGKHHEMQVLEKEVEKRSGIOGLGVAGGNSTERKLESALEDLEV LINGKHHEMQVLEKEVEKRSGIOGLGVAGGNSTERKLESALEDLEV LINGKHHEMQVLEKEVEKRSGIOGLGVAGGNSTERKLESALEDLEV LINGKHHEMQVLEKEVEKRSGIOGLGVAGGNSTERKLESALEDLEV LINGKHHEMQVLEKEVEKRSGIOGLGVAGGNSTERKLESALEDLEV LINGKHHEMQVLEKEVEKRSGIOGLGVAGGRSTERKHELSALEDLEV LINGKHHEMQVLEKEVEKRSGIOGLGVAGGRSTERKHELVE LINGKHHEMQVLEKEVEKRSGIOGLGVAGGRSTERKHELVE LINGKHHEMGVAGGRSTERVEKRSGIOTHANDERSELDITEGHTVAFIR EKKODDFTTMVLIGHARVYKKHKHINGERSELDITEGHTVAFIR ALAMPEYMEKGTHAGGGFAARGANEOUT ALAMPEYMEKGTHAGGGFAARGANEOUT ALAMPEYMEKGTHAGGGFAARGANEOUT ALAMPEYMEKGTHAGGGFAARGANEOUT ALAMPEYMEKGTHAGGGFAARGANEOUT ALAMPEYMEKGTHAGGGFAARGANEOUT ALAMPEYMEKGTHAGGGFAARGANEOUT ALAMPEYMEKGTHAGGGFAARGANEOUT ALAMPEYMEKGTHAGGGFAARGANEOUT ALAMPEYMEKGTHAGGGFAARGANEOUT ALAMPEYMEKGTHAGGGFAARGANEOUT ALAMPEYMEKGTHAGGGFAARGANEOUT ALAMPEYMEKGTHAGGGFAARGANEOUT ALAMPEYMEKGTHAGGGFAARGANEOUT ALAMPEYMEKGTHAGGGFAARGANEOUT ALAMPEYMEKGTHAGGGFAARGANEOUT ALAMPEYMEKGTHAGGGFAARGANEOUT ALAMPEYMEKGTHAGGGFAARGANEOUT ALAMPEYMEKGTHAGGGFAARGANEOUT ALAMPEYMEKGTHAGGGFA	İ	1	I	NGHEEVVACAWDGOTYTTDHNRTVVRFOVDFNTDAECACT VACU
S876   1122   224   HIPLIGYPSKVAGAAAMERQEERETQVAAMUKKIFGUHT 190EV   FORTTEIJENIELERENEVENDEVISCHAANUKKIFGUHT 190EV   FORTTEIJENIELERENEVENDEVIVIJEIDKAASEYSERAKVIQ DILIMESVYNSPANIJOSAVALEKTOTISLISTIP   AVROLITSDIPETKSKSEEIKEKLEKLEKLEKLEKLEKSLESTIP 190EV   KRAELILISTER \AKUDRRQNM\DFI.KAKSEEFRIGJAGEQL   SARGQ\DARSTYOSIVALILIBRINDPILKQTIPLIK\KKLESVID   KRAELILISTER \AKUDRRQNM\DFI.KAKSEEFRIGJAGEQL   SARGQ\DARSTYOSIVALILIBRINDPILKQTIPLIK\KKLESVID   MP\NPSHCSK*RIEEREKKERLEKLEKEKLEKLIKKKESLESTIP 1906   KRAELILISTER \AKUDRRQNM\DFI.KAKSEEFRIGJAGEQL   SARGQ\DARSTYOSIVALILIBRINDPILKQTIPLIK\KKLESVID   MP\NPSHCSK*RIEEREKK\RELA\SITEAKURALISTER \AKUBRITARVIY\RELA\BERTARVIA\RELA\BERTARVIA\RELA\BERTARVIA\RELA\BERTARVIA\RELA\BERTARVIA\RELA\BERTARVIA\RELA\BERTARVIA\RELA\BERTARVIA\RELA\BERTARVIA\RELA\BERTARVIA\RELA\BERTARVIA\RELA\BERTARVIA\BERTARVIA\RELA\BERTARVIA\RELA\BERTARVIA\RELA\BERTARVIA\RELA\BERTARVIA\BERTARVIA\RELA\BERTARVIA\RELA\BERTARVIA\RELA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVIA\BERTARVI		İ		BGRNSPCLVYVTFNOKIYVYWEVOLERMESTNIAVKI LETYPA COL
S876   1122   224   HIPGGYPSEVAGAAAGSITKQ   PRITEILHHUSERNEVUREPETOVAMUKITGEHEJOYEV   RERTEILHHUSERNEVURDITUTIELKKIKTGEHEJOYEV   RERTEILHHUSERNEVURDITUTIELKGYTEJASTIS   RERTEILHHUSERNEVURDITUTIELKGYTEJASTIS   RERTEILHHUSERNEVURDITUTIELKGYTEJASTIS   RAVIDINGRASEVESERKYLQ   DLUMESVINESPANLSTIGSRYLMALUSBAVALLETKOTSLASTIJ   RAVIDINGRAMASESBETKICAJEDEV   KKARLHLISTER   KARUNINGRAMI DEILKKESTURDITUTIELKEVIA   RAVIDINGRAM   DEILKKESTURDITUTIELKEVIA   RAVIDINGRAM   DEILKKESTURDITUTIELKEVIA   REREILEKURSTALBULEV   LERGILEMURT   SARGQLORENOVIELLI   RAVIDINGRAM   REREILEMURT   SIRGKLUGAGERNOVIELLI   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDINGRAM   RAVIDI	ł		1	TACCESWAWILTTSL*LVPCFTKRSTIOTSHHSVT.DOX CDIDDC
HIPLIGYPSKYAGAAAMEPGEERETTOVAMILKKI FEGHET JOYEN RERTETLIHLISERRENVENDENVILVITEIOLKSYESEAKIVAL DLIMESVINFSPANLSSIGSRYLINALUDSAVALETKOTIASF 1P ANNOLTISLIP PRIKKSKESE IK KLEKLKEKHILJKEKLGENDEN KKAELHSTER \ARVONRROMM\DFI.KAKSSEERRETGIOAAGEOL SARGO\DAFVICISVALITEIBENPEPLKOGTICK\KKLESYLD LMP\UNPSHCSIV-RIEBEK\RELA\SILERMORPER\GOTICK\KKLESYLD LMP\UNPSHCSIV-RIEBEK\RELA\SILERMORPER\GOTICK\KKLESYLD LMP\UNPSHCSIV-RIEBEK\RELA\SILERMORPER\GOTICK\KKLESYLD LMP\UNPSHCSIV-RIEBEK\RELA\SILERMORPER\GOTICK\KKLESYLD LSRELIEMIAISRIOKILOAGEBIOQUICK\KKLESYLD LSRELIEMIAISRIOKILOAGEBIOQUICLIHROGENQEIMILA LNOGKIHHEMOVILEKEVEKRISDIOQUICK\UNDSULIATAVVO AKEKLISIEKARKGAISSEETI IKYAHIRISASINAVCAPLITAVPOD PREPYPTOLEMENSILOAGONIPSTINOVIGHIPATOP AKEKLISIEKARKGAISSEETI IKYAHIRISASINAVCAPLITAVPOD PREPYPTOLEMENSILOAGONIPSTINOVIGHIRIOLAY AKEKLISIEKARKGAISSEETI IKYAHIRISASINAVCAPLITAVPOD PREPYPTOLEMENSILOAGONIPSTINOVIGHIRIOLAY AKEKLISIEKARKGAISSEETI IKYAHIRISASINAVCAPLITAVPOD PREPYPTOLEMENSILOAGONIPSTINOVIGHIRIOLAY ROMARSILOSOONIPSTINOVIGHIRIOLAY ROMARSILOSOONIPSTINOVIGHIRIOLAY ROMARSILOSOONIPSTINOVIGHIRIOLAY ROMARSILOSOONIPSTINOVIGHIRIOLAY ROMARSILOSOONIPSTINOVIGHIRIOLAY ROMARSILOSOONIPSTINOVIGHIRIOLAY ROMARSILOSOONIPSTINOVIGHIRIOLAY ROMARSILOSOONIPSTINOVIGHIRIOLAY ROMARSILOSOONIPSTINOVIGHIRIOLAY ROMARSILOSOONIPSTINOVIGHIRIOLAY ROMARSILOSOONIPSTINOVIGHIRIOLAY ROMARSILOSOONIPSTINOVIGHIRIOLAY ROMARSILOSOONIPSTINOVIGHIRIOLAY ROMARSILOSOONIPSTINOVIGHIRIOLAY ROMARSILOSOONIPSTINOVIGHIRIOLAY ROMARSILOSOONIPSTINOVIGHIRIOLAY ROMARSILOSOONIPSTINOVIGHIRIOLAY ROMARSILOSOONIPSTINOVIGHIRIOLAY ROMARSILOSOONIPSTINOVIGHIRIOLAY ROMARSILOSOONIPSTINOVIGHIRIOLAY ROMARSILOSOONIPSTINOVIGHIRIOLAY ROMARSILOSOONIPSTINOVIGHIRIOLAY ROMARSILOSOONIPSTINOVIGHIRIOLAY ROMARSILOSOONIPSTINOVIGHIRIOLAY ROMARSILOSOONIPSTINOVIGHIRIOLAY ROMARSILOSOONIPSTINOVIGHIRIOLAY ROMARSILOSOONIPSTINOVIGHIRIOLAY ROMARSILOSOONIPSTINOVIGHIRIOLAY ROMARSILOSOONIPSTINOVIGHIRIOLAY ROMARSILOSOONIPSTINOVIGHIRIOLAY ROMARSILOSOONIPSTINOVIGHIRIOLAY ROMARSILOSOONIPSTINOVIGHIRIOLAY ROMARSILOSOONIPSTINOVIGHIRIOLAY	<b></b> _		<u> </u>	WICLIAGEGFF*TPTLPPKGVFGSHCAAAGSTTVO
DILHESWISSPANLSSTGSRYLNALVDSAVALETEDISLSSIP  DILHESWISSPANLSSTGSRYLNALVDSAVALETEDISLSSIP  AVHOLTSULFRYKSKSELKIELEKLEKNITATIJULEKICGEDV  KKASIHLISTER AKVONRONN\DELKKICKTOSTAGSGOL  SARGO(DAFSVPIGSLVALIRENMPRIKQGTIPLK\KKLESYLD  BYNPSHEKR AKVONRONN\DELKKICKTOSTOV  SARGO(DAFSVPIGSLVALIRENMPRIKQGTIPLK\KKLESYLD  SARGO(DAFSVPIGSLVALIRENMPRIKQGTIPLK\KKLESYLD  GTLGKMAASSSGEKKERLGGGLGVAGGNSTERILISALEDLEV  AKRELKSIELKERALSTROKLLOGGENOVLEHRIGGEPGHMKLA  LNGGKHHHBMOVLEKEVEKROSDIQOLOKOLKEAGOILATAUVQ  AKRELKSIELKARKGATISSELIKVARHISROVLAPGIURGILATAUVQ  AKRELKSIELKARKGATISSELIKVARHISROVLAPGIURGILATAUVQ  AKRELKSIELKARGATISSELITYAHISROVLAPGIURGILATAUVQ  AKRELKSIELKARGATISSELITYAHISROVLAPGIURGILATAUVQ  AKRELKSIELKARGATISSANUAGYEHVAVAFGURGIOHTP  FELOSIHLIELEDDILYCISANUAGYEHVAVAFGURGIOHTP  ISIKNARVSQHYKASLITATFILIFPEAKFAVVLEEDLIJATDFTS  FELOSIHLIELEDDILYCISANUAGYEHVAVLEGDLIJATDFTS  KKRAYEVEWHELLSEAEVLDISKNPCEDSFLDDTEGHTVVAFIL  GWALRSLIYKEELBFWBFTPEKLSDDDWMMMEMBEQREGRECTI  PDVSRSYHGFIVOLANCHIN HOLDURGNHEMPERKRIPTVOLVELMING  KKRAYEVEWHELLSEAEVLDISKNPCEDSFLDDTEGHTVVAFIL  MEKDDDFTTWOLAKCHIN HOLDURGNHEMPERKNHFLVV  GVPASPYSVKPPSVYFITILEPPKSGAPGAPDFOV  GVPASPYSVKPPSVYFITILEPPKSGAPGAPDFOV  GVPASPYSVKPPSVYFITILEPPKSGAPGAPDFOV  ALMWENTENGARSSTAGMANGSFPTTLLFTSTAMLTFYDLAMTAGULVL  ALMWENTENGARSHETVOLAKCHIN HOLDURGNHEMPERKNHFLVV  GVPASPYSVKPRSVYFITILEPPKSTOMTHVFLORESVULFLVARTVY  FITRYSFFTFSLLDHLPYFINANTHFITILITAASTPLIPPOL  YFHMINGRRYKSTOKTOKTVANTYTYDLAMTAGULVL  ALMWENTENGARSHETVOLAKCHIN SLOTTARFTRANGTULTURGHTV  ALMWENTENGARSHETVOLAKCHIN SLOTTARFTRANGTULTURGHTV  ALMWENTENGARSHADEN SLOTTARFTRANGTULTURGHTV  FITRYSFTFSLLDHLPYFINANTHFITILITAASTPLIPPOL  YFHMINGRRYKSTOKTOKTVANTYTYDLAMTAGULVL  ALMWENTENGARSHADEN SLOTTARFTRANGTULTURGHTV  ALMWENTENGARSHADEN  SENCULAGOSTAMATAGULTARFTRANGTYSALTACSA  SVISKASSGMPBSAASDRDSPVFLRPGROCHLERGHTANGULTURGHTV  ALMWENTENGARSHADEN  SARGURGHESSTAMATAGULTARFTRANGERMINGERMING  ARGENTAAGADVAWARGALARFTRANGTYSHANGERMING  ARGENTAAGADVAWARGALARFTRANGTYSHANGERMINGERMING  ARGENTAAGADVAWARGALARFTRANGTYSHANGERMING  ARGENTAAGADVAWARGAL	5876	1122	224	HLPLGVPSKVAGAAAMEPOEERETOVAAWIKKIECOVAL
### PROPRESS OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PROPERTY OF PR	1	i	1	NPRTTETI-HHLSEPNPVPDPDVVLVITEDI YOMA COMPT DOYEV
S877   2030   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907   1907	ì		i	DILMESIMES DAM COTTONY NATIONAL ASEYES EAKYLO
S877 2030 1907 GTLGKNAKONNOPLKAKSEEFREGJAGGEOL LMP, WPSHCSK*RIEBAK (REIA) SIEAELTRRVS) NMEL  GTLGKWARSSGEKEKERIGGGLGVAGGENELMELAS LEAELTRRVS (LMP, WPSHCSK*RIEBAK (REIA) SIEAELTRRVS) NMEL  GTLGKWARSSGEKEKERIGGGLGVAGGERIGHLATAVYO  AKEKLISIEKARKGAISSEEI KYAHRISASKAVCAPLTWEGD  PRRYYPTDLEMRSGLLGGOMNPSTRIGHGEABGOLLATAVYO  AKEKLISIEKARKGAISSEEI KYAHRISASKAVCAPLTWEGD  PRRYYPTDLEMRSGLLGGOMNPSTRIGHGEABGOLLATAVYO  AKEKLISIEKARKGAISSEEI KYAHRISASKAVCAPLTWEGD  PRRYYPTDLEMRSGLLGGOMNPSTRIGHGEABGOLLATAVYO  AKEKLISIEKARKGAISSEEI KYAHRISASKAVCAPLTWEGD  PRRYYPTDLEMRSGLLGGOMNPSTRIGHGEADALARKITAR  GUMKCMCLOGPHTERVOP PYPTROGGEOV VPFAVLAGENRYNLY  GUMKCMCLOGPHTERVOP PYPTROGGEOV VPFAVLAGENRYNLY  RHARSLLSAGOVSPOMITYFIDGY YEEPMOVVALFGLRGIOHTP  LISINARAVSOMYRASLITAPTLEP PEAKFAVVLEEDLIAVDFTS  FLSOSIHLLEEDDSLYCISANNBOQ TEHALDRALIKTRETHOP  LGWALRESLYKELEPENBYRHOGVEHANDOWNMEMEERGRGECII  SINNANGVYRASLITAPTLEP PEAKFAVVLEEDLIAVDFTS  KEKADDDFTTPTOLAKCHINAMOY FIEAT KKIMPTVOGVCIRNDOSL  KKRASTEVERHLLSEERSYNTELDISKIPCEDSFEDPTEEMTVOFTIS  MEKODDFTTPTOLAKCHINAMOY FIEAT KKIMPTVOGVCIRNDOSL  KKRASTEVERHLLSEERSYNTELTETTIVOGVCIRNTDSLITATATIVOGVCIRNTDSLITATATIVOGVCIRNTDSLITATATIVOGVCIRNTDSLITATATIVOGVCIRNTDSLITATATIVOGVCIRNTDSLITATATIVOGVCIRNTDSLITATATIVOGVCIRNTDSLITATATIVOGVCIRNTDSLITATATIVOGVCIRNTDSLITATATIVOGVCIRNTDSLITATATIVOGVCIRNTDSLITATATIVOGVCIRNTDSLITATATIVOGVCIRNTDSLITATATIVOGVCIRNTDSLITATATIVOGVCIRNTDSLITATATIVOGVCIRNTDSPS  NINNNOLCEISMIVWELMI  SANCLINAGGIGLEFSKONPLORAGILAXPREARGTESALITACSA  SVISKASSSGMPSAASDROSPVPLRPGGVOLPSGTGWVLSD  *KKKRGRCSS'NISGOOMERKEKVVLLIRSKARGERARAASDVL  CRSLANDTHOLRTITATATIMCCHILAKCLDERGHAQRAVGEROP  ASSOVENDARASSON MAS PADEREKEVVLLERKENDELMENDTACSA  SVISKASSGMPSAASDROSPVPLRPGGVOLPSGTGWVLSD  *KKKRGRCSS'NISGOOMERKEKVVLLERKANDEPSGTGWVLSD  *ARKOBLABARTARDAALERYOMLEGOLLANDOMERGARGAGGGOLQCH  ASSOVENDARASSON MAS PADERSKEVVLLERKENDELMENDTACSA  ADALELMYEGGVFROTTSGOOPEP PABGGHPGAACAGGGOLQCH  AGGRIFSFETEARGRUCHERGENTALKETSRDTAVOVLERG  MCQARTOSPROMERGENTALKETTATATICGSCANTHAVOOLOGGG  SEVKKRGGRCSS'NISGOOMERKERVLLERKENDELTANDOMERGANDERG		İ	ł	AVNOLTED PRINCIPALISION AND TERMINAL VOSAVALETROTSLASFIP
SARKON LARSY IGSLVALIREMYPILKQQTIPIK KIKLESYLD	1		i	AVNOLISHERTKSKSEEIKIELEKLEKNLTATLVLEKCLQEDV
SARKON LARSY IGSLVALIREMYPILKQQTIPIK KIKLESYLD		i	}	KKAELHLSTER\AKVDNRRQNM\DFLKAKSEEFRFGIQAAGEOL
1907 TICKMARASSGEREKELGGIGUNGSTREELISALEDLEV LSRELIEMLAISRNOKLLQAGENQUIELLHERGEPGELMKLA LNOGKIHEMPOULEEKEVEKGSGIGUNGKEREGILATAVYO AKEKLKSIEKARKGAISSEEIIKYAHRISANAVCAPLTWYPGD PREPYPTDILEMSGILLGOMINDESTNOKULEAGOILATAVYO AKEKLKSIEKARKGAISSEEIIKYAHRISANAVCAPLTWYPGD PREPYPTDILEMSGILLGOMINDESTNOKULEAGOILATAVYO AKEKLKSIEKARKGAISSEEIIKYAHRISANAVCAPLTWYPGD PREPYPTDILEMSGILLGOMINDESTNOKULEAGOILATAVYO AKEKLKSIEKARKGAISSEEIIKYAHRISANAVCAPLTWYPGD PREPYPTDILEMSGILLGOMINDESTNOKULEAGOILATAVYO AKEKLKSIEKARKGAISSEEIIKYAHRISANAVCAPLTWYPGD PREPYPTDILEMSGILLGOMINDESTNOKULEAGOILATAVYOH COLOTIVA MILLEDDOILYOSANDOGYPETMORUHAGOILATAVETHOP LGWILKRSIYKEELEPKWPTPEELUMDMMMRIMBEGRGRGECII PDVSRSYHEGIVGIMMGYPHEAYKKINTUPGOURDISL KKEAYEVEVHELLSEABVLDHSKNPCEDSIJPDTEGHTYVAPIR MEKODDFTTWYOLAKCLHIMLDUNGHIMMINEMBEGRGRGECII POVASSYSKKRSVESYVENDESTPIPLEPPPRECAPRAPEOT  S879 3 981 RIFEAAAAGSSRAAGASSPPILLEPSTPECATHASSDED GTINGASSAGEBRAPGKRRIGGILATAWLTFYDIAMTAGULU ALAMVEFWHEKOTHERILYSSIOKTLIMALETYPOLAMTOV EITYSPYTYPSILLDHLPYFIKARANNFIILIYPOUAGELLITI ALAMVEFWHEKOTHERILYSSIOKTLIMASSTPYPOLAMTUT EITYSPYTYPSILLDHLPYFIKARANNFIILIYPOVAGELLITI AALHVKKTGMFSIRLDHINNYNSPYYYFILITMASYTIPPOL YFHMLRORRKVLHE\G-V-KRRIK*SLOTROFFORNODYLSBSS NNINKOLGELIWI WPLIK  SINGKUVAGGIGLGFSSONPLORAGILARPREARGTFSALTACSA SVITSKGSSSGMPSASRDDSPYPLEDEROHOPROVEDEP DOSENTIDHTSVOSVIEKLOEENILLKOKYTHYEDIAKKOR NI ASRDEYVEGILHAUNGLAPTAHMOCHLAGLEENINDC ASVKORLAASTARDAALERVOMLEOQILAYRODMSERADER AOSRIGELEEVASLUHRUSAGOS ESVKKROGLAASTARDAALERVOMLEOQILAYRODMSERADER AOSRIGELEEVASLUHRUSAGOS SSVKKPGASVMVSCYVSGYTITKLSMINWVOAPCKGLE*MGPED LOPUTITYPKOFGGRUNTETSTETTO/AYLELSSLRSEDTAV HICATOTY HICATOTY HICATOTY HICATOTY HICATOTY HICATOTY HICATOTY HICATOTY HICATOTY HICATOTY HICATOTY HICATOTY HICATOTY SCHOOL PROGREGIOPLOGEED ITSDEPTLDEVOG\VDLR HYSKOVELELGOILEGNSINTALBIOITACDAVLER REQWILGAFGSDLSSISSEIRTLOGOSGANIRIRRROAVERGE ELVDSILVERSLEVARENTETSTETO/AYKARSHTENDOWACHLI		I		SARGQ \DAFS VPIQSLVALIRENWPRIKOOTIDIK \ KKT. PCVT D
S878 950 2113 GILGMANASSSGKEKERLGGGGGVAGGNSTREELLSALEDLEV ARELIKES IEKAIKGAI SEEDI INYAHEANDAYOLEKEVEKKIDI QOLGKOLKEAEGI LATAVYO AKELIKES IEKAIKGAI SEEDI INYAHEANNAVOHIPTAVPGD PRRYYTDLEMBIGLIGGMINDSTNOWOHLPGDALA/RRKIAR CPCSTVS/NGSMTCRT INTILILIQAESANAVCHIPTAVPGD PRRYYTDLEMBIGLIGGMINDSTNOWOHLPGDALA/RRKIAR CPCSTVS/NGSMTCRT INTILILIQAESANAVCHIPTAVPGD PRRYYTDLEMBIGLIGGMINDSTNOWOHLPGDALA/RRKIAR CPCSTVS/NGSMTCRT INTILILIQAESANAVCHIPTAVPGD PRRYYTDLEMBIGLIGGMINDSTNOWOHLPGDALA/RRKIAR THE SEEDING THE SEEDING TO SEEDING TO SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEEDING THE SEED				LMP \NPSHCSK*RIEEAK\RELA\STEARLTDDUC\MMDT
LINGKIHEMQVLEKVERKENDIQLQKQLKEREJELIATAVVQ AKKELKISIEKARKGAISSEETIKYAHRISASNAVCAPITWUPGD PRRYPYPDLEMRSGLIGOMNIPSTRIGVINGHQDDALA/RKKIAR CPCSTVS/NOSQMTCR*INILLIQKSVCEL  5878  950  2113  GLIKKOMGLOGPHIRHWQP-PPERGOGPQ\VPVAVALGORRPNYLY RMLRSLLSAQGVSPQMITVFIDGYYEEPMDVVALEGLRGIGHTP- ISIKNAVSGHYKASLTATPRLFFEARFAVULEEDLDIAVDFFS FLSOSIHLLEEDDSLYCISANNDG PHATEDPALLYNVETMPG LGWVLRSIJKRELEPKMPTPEKLMDMDMMMMPEQRRGRECII PDVSRSYHRGIVGIRMNOYPHEAYFKKHKRNYPGVOLGRNVDSI. KKKRAYSVEVHRILISEABVLDHSKMPCEDSFIDTEGHTYVAFIR MEKDDPSTTWTQLAKACHIMDLDVGRHRGLWRLPRKIMPLVV GVPASPYSVKKPPSVTDIFLEPPPKEESAPGAPEOT  RIHEAAAAGSGFRAGAMAGSPFTLEPPTSCHATMASSDED GTNGGASEAGEBREAPGKRRRLGFLATAMITTYDIAMTAGKUVL ALMVYFMEKGTHRGIYKSIGNKTHEFTPTPLAMTAGKUVL ALMVHKKTGMPSIRLHPYFIKMARYNFFTLIPTVAMTAGKUVL ALMVHKKTGMPSIRLHPYFIKMARYNFFTLIPTVAMTAGKUVL ALMVHKKTGMPSIRLHPYFIKMARYNFFTLIPTVAMTAGKUVL ALMVHKKTGMPSIRLHPYFIKMARYNFFTLIPTVAMTAGKUVL ALMVHKKTGMPSIRLHPYFIKMARYNFFTLIPTVAMTAGKUVL ALMPHYKKTGMPSIRLHPYFIKMARYNFFTLIPTVAMTAGKUVL ALMPHKKTGMPSIRLHPYFIKMARYNFFTLIPTVAMTAGKUVL ALMPHKKTGMPSIRLHPYFIKMARYNFFTLIPTVAMTAGKUVL ALMPHKKTGMPSIRLHPYFIKMARYNFFTLIPTVAMTAGKUVL ALMPHKKTGMPSIRLHPYFIKMARYNFTLIPTVAMTAGKUVL ALMPHYKKTGMPSIRLHPYFIKMARYNFTLIPTVAMTAGKUVL ALMPHKKTGMPSIRLHPYFIKMARYNFTLIPTVAMTAGKUVL ALMPHYKKTGMPSIRLHPYFIKMARYNFTLIPTVAMTAGKUVL ALMPHKKTGMPSIRLHPYFIKMARYNFTLIPTVAMTAGKUVL ALMPHKKTGMPSIRLHPYFIKMARYNFTLIPTVAMTAGKUVL ALMPHKKTGMPSIRLHPYFIKMARYNFTLIPTVAMTAGANARYNFTLIPTVAMTAGANAGANAGANAGANAGANAGANAGANAGANAGANAGA	30//	2030	1907	GTLGKMAASSSGEKEKERLGGGLGVAGGNSTRERLLGALEDI EU
AKERIKKSIEGARGADISSEIIIVANISANAVAPITAWYOO PRRYYPTDLEMRSGLIGOMNIPSTINGWIGHLEGOMLA/RRKIAR CPCSTUS/MSGMTCR*NIILILILUGSUCEL  5878  950  2113  GLWKCMQLQOPHTHRVQD*PTFRQQGPQ\VPVAVIAGNRPNYLY RNLRSLSAQGUSPQMITVFILOTYYEEPMDVVALFGLRGIGHTP. ISIKNAVSOHYKASLTATFRLIFPEAKFAVVLEEDLIAVDFFS FLSOSIHLEBDDSIYCISAANDQGYBHTAGVVLEEDLIAVDFFS FLSOSIHLEBDDSIYCISAANDQGYBHTAGVVLEEDLIAVDFFS FLSOSIHLEBDDSIYCISAANDQGYBHTAGVVLEEDLIAVDFYSFPLSOSIHLEBDSIYCISAANDQGYBHTAGVVLEEDLIAVDFYSFPLSOSIHLEBDSIYCISAANDQGYBHTAGVVLEEDLIAVDFYSFPLSOSIHLEBDSIYYAFIR KKRAYSEVHRILISEABVJDBIKSMPTDFSFRGATHAGSDED GVRASFYSKKPBSYVSYPSYTTIFLEPPSCBSFLDPTSFRGATWASDED GVRASFYSKKPBSYTVIFIFLEPPSCBSFLDPTSFRCAATWASDED GYDASFYSKKPBSYTVIFIFLEPPSGRAGAPBCT GYBASAAAGSGFAAGMAGSPFTLIPLSFTSPRCAATWASDED GTNGGASAGGDERBAPGKRRLIGFIATMITTFYIAWTAGKIVL ALAMVSFYMEKOTHGIYKSIQKTLKFFGTPALLEIVHCLIGIV PTSVIVTVQVQVSSRIFMWILITHSIRPIONESSVLETIVAMTUT EITRYSFYTFSLIDHLEFYFIKWAFFFILIPPVGAGELLTY AALDHVKKTGMFSIRLDFYFIKWAFFILIPPGAUGGELLTY AALDHVKKTGMFSIRLDFYFIKWAFFILIPPGAUGGELLTY AALDHVKKTGMFSIRLDFYFIKWAFFILIPPGAUGGELLTY AALDHVKKTGMFSIRLDFYFIKWAFFILIPPGAUGGELTY AALDHVKKTGMFSIRLDFYFIKWAFFILIPPGAUGGELTY AALDHVKKTGMFSIRLDFYFIKWAFFILIPPGAUGGELTY AALDHVKKTGMFSIRLDFYFIKWAFFILIPPGAUGGELTY AALDHVKKTGMFSIRLDFYFIKWAFFILIPPGAUGGELTY AALDHVKKTGMFSIRLDFYFIKWAFFILIPPGAUGGELTY AALDHVKKTGMFSIRLDFYFIKWAFFILIPPGAUGGELTY AALDHVKKTGMFSIRLDFYFIKWAFFILIPPGAUGGELTY AALDHVKKTGMFSIRLDFYFIKWAFFILIPPGAUGGELTY ASHLOVAGGGGGGAAGAAGAAAGAAAAAAAAAAAAAAAAAAAA		i		LSRELIEMLAISRNOKLLOAGEENOVIELLTUBBORDEN
AREBUS 1 EKARKGAT ISSELT I KYAHRI SASANACAPIT WUPGD PRRYPTDLEMRSGILGOMNNPSTNGVNGILGEDALA/RKKIAR CPCSTUS/NSGMTCR*INIILIQKSUCUL  GUMKOMOLQGPHTHWOP PTPROQGPO/VPVAVIAGNRPNYLY RMLRSLLSAQGUSPOMITVFIDGYTEEPMDVVALEGLEGICHTP- ISIKNARVSQHYKASLTATFALFFEAKFAVUEEDLDIAUDFFS PLSGSIHLLEEDDSLYCISAANDG YEHTAEDPALLYAVETMPGE LGWUKRSLIYKEELEPKUPTEKLUDDUMMMMPBEQRGRECII PDUNSRYHGIVGIMMONOYPHEAY FKCHKENTYPDEVOLRNYDSL KKERYEVEHRILSEAEVLUBISKNPCEDSELDTECHTYVAPIR MEKDDDFTTWTGLAKCHIMDLDVGNHRGLWRLPRKKNHFLVV GVPASPYSVKKPPSVTPIFLEPPPKEEGAPGAPEGT  S879  3 981 RLFARAAGSGSRAAGWAGSPPTLLFLSFTSRCAATMASSDED GTNGGASEAGEDREAPGKRRILGFLATHJITTSTRCAATMASSDED GTNGGASEAGEDREAPGKRRILGFLATHJITTSTRCAATMASSDED GTNGGASEAGEDREAPGKRRILGFLATHJITTYDIAWTACKLUL ALAMVKFYMEKGTHRGLYKSIOKTLKKFFGTPALLEIVHCLIGIV PTSVIVTGQVUSSRIFMWILITISHIONESVULFLAWATUT EITRYSFYTFSLLDHLPYFIKWARYMFFILLYPQUAGELLTIY AALPHWKNIGMFSIELBENKYNVSPHYJFLITMASYTPFPQL YFMLRQRRKVLHGG-G-L-KRMIK*SLQTRCFFONNQDYLSPSP NNINKOLCELISWIUMPIKI  SLWCLVAGGLGLGFSSONFLQRAGILAREREARGTFSALTACSA SVISKOKSSSOMWESAASDRDSPVILPRPGTQLPGSTGWVLSD *KKKRGCSS/MLSGPOHREKEKVULLRSNAECERRAASDUL CRSLANETHOLRRTLTATAHMCCHLAKCLDERGRAQRNVGERSP DOSENTIDHTSVOSVYIKLGCENRIKLOKVTHVEDLNAKNQRYN ASRDEYVRGLHAOLRGLQI PHEPELMRKEISRINNGLEEKINDC CRSLANETHOLRRTLTATATHMCCHLAKCLDERGRAQRNVGENP ADABELWPGGWRPGTGSQOPEPPAEGGHPAAQCRGGGLQCPH CLOCTSDEGGEELLINHVABCCQ ASVKOBLASERTARDAALERVOMLEGQILAVTGHARGHAVOLLOGG SVKKPGSAWWSCYVGSTLTKLKLAKVDFMSERABRER AQSRIQELEEKVASLLHOVSMRODSREPDAGRHAKGLEKINDC SVKKPGSAWWSCYVGSTLTKLKLAMHAVRQAPGKGLE*MGPFD LODVETIYPOKPGGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HICATDTV HICATDTV SCHORMYSHSLEYNPEWISVOSAVAPAQLALNSDGDL*LHSGE RTRRD*CLPSEOGGEELLRAKALHLARGLERKINGCAULCH MEQMLGAFOSDLSSISSEIRTLOGGSGMMIRLRNQAVRGKLG RTRRD*CLPSEOGGEELLRAFERIALERDVTCAAULER MEQMLGAFOSDLSSISSEIRTLOGGSGMMIRLRNQAVRGKLG ELVDGLUVPSALVTAILEAPVTEPFILEQULDARAAAVREQE ARGTAACADVRGVLDRAKKOTHENSTLENDITTSLHNOTTACAULER MEQMLGAFOSDLSSISSEIRTLOGGSGMMIRLRNQAVRGKLG ELVDGLUVPSALVTAILEAPVTEPFILEQULDARAAAVREQE ARGTAACADVRGVLDRAHAKVAPTLAKTEFILLKYRTLSKIYLLSYYR SYLCHEMKWOYEEVARKDLMOKYDTLAKKFFSKESL	1	1		LNOGKIHHEMOVI.EKRVEKEDEGITOOLOVOLVOLVOLVOLVOLVOLVOLVOLVOLVOLVOLVOL
5878  950  2113  GLMKCMGLQGPHTHRVGP*PTFRQGEP\PVPAVIAGNEPNILY RMLRSLLSAGGVSPGMTVFTGGYFVPAVIAGNEPNILY RMLRSLLSAGGVSPGMTVFTGGYFVPAVIAGNEPNILY IS IKNARVSGNTYKASLTATFPLFPEAKFAVVLEEGLDIAVDFFS FLSGSTHLEEDDSLYCISANNDGYSHTAEDPALLYRVETMPG LGWVLRRSLYKELLEPRWPTEKLUDWDMMMEMPEGRGRECTI PDVSRSYHRGTUGLAMNGYFHEAYFKHKHNTYGVQLRNVDSL KKRAYSEVEWHRLLSEABVLDHSKMPCBGSPLDTTEGHTYVAFIR MEKDDPFTTWTQLAKCLHIMDLDVRGHRGLURLFRKKNHFLVV GVPASFYSKKPBSTVTFIFLEPPSRCAATMASSDED GTNGGSSEAGEDREAPGRRFRLGFATAMLTFYTDIAMTAGWLU ALAMVSFYMEKGTHRGLYKSTGKTLKFFGTFALLEIUHCLIGITV PTSVIVTUGVUSSRIFMVWLITHSIRPIONESVVLETVAMTUT EITRYSFYTFSLLDHLEYFIKMARYNFFILLYPGVVGELLTIY AALDHVKKTGMFSIRLDHLKYNVSFDYYYFLLITMASVIPLFPGL YFHMLEGRKVLHG\G+1*KRMIK-GUTGRCFFGNNQDYLSPSF NNKNKGLCEISWIWWFLKI SLMCLVAGGGLGIGFSCNPLORAGILARFREARGFFSALTACSA SVTSKGKSSSGWIPSAASDRDSVPLR.PPGDVQLPSGTGWVLSD *KKKRGCSS/MLSGOPHEREKSVLRUFMKDLMAKKORYN ASRDSYVRGLAGARTARDAALBRVOMLEGGILARFREARGFFSALTACSA SVTSKGKSSSGWIPSAASDRDSVPLR.PPGDVQLPSGTGWVLSD *KKKRGCSS/MLSGOPHEREKSVLRUFMKDLMAKKORYN ASRDSYVRGLAGARTARDAALBRVOMLEGGILARKTDFMSERADRER AGSRIGELEEKVASLLHOVSNKQDSREPDAGRHAGKTAKYLA ADALELMYPGGWRFGTGSQOPEPPAEGHPAAQRGGGDLQCPH CLQCFSDGGEELIRHVABCCQ CLQCFSDGGEELIRHVABCCQ CLQCFSDGGEELIRHVABCCQ SSVKKPASSWWRGTSGOPEPPAEGHPAAQRGGGDLQCPH CLQCFSDGGGELIRHVABCCQ CLQCFSDGGGELIRHVABCCQ SSVKKPASSWWRGTSGOPEPPAEGHPAAQRGGGDLQCPH CLQCFSDGGGELIRHVABCCQ CLQCFSDGGGELIRHVABCCQ SSVKKPASSWWRGTSGSTTTV/AYLELSSLRSEDTAV HRCATDTV HRCATDTV SGCVEMIYSISLEYNPEWISVQSAVAPAQLALMSDGDL-LINGGE RTRRD*QLPSAGGPGLOGPLQLGGLDTSDEFTLDEVDG\VDLR HYSKQVLSLEQQJEGKSIDDYTGSGELDAKAAAVERGQE ELVDCLVVPSALVTAILEAPVTERFFLEQUEGLAKAAAVERGQE ELVDCLVVPSALVTAILEAPVTERFFLEQUEGLAKAAAVERGQE ARGTAACADVRGVLDDRLRKKADTKLREFILGKTYSFRKMTNYQ IPOTALLKYRFYQFILGNERATAKERIDKYTLSKYTYLBYYR SYLORIKMKVOYEEVASKDDLMGVERDTLAKKFFSKPILKRUNDYN IPOTALLKYRFYQFILGNERATAKERIDKYTLSKYTLYDYYR SYLORIKMKVOYEEVASKDDLMGVERDTLAKKFFSKPILSKRTIF TLGTRGSVISPTELBAPILVPHTAQRGRGRPTLAKHTRUNDLANDLANDLANDLANDLANDLANDLANDLANDLANDLA		1		AKEKI KSTEKABKCA TCCHETTAKA MENGUKEAEQILATAVYO
5878  950  2113  GLMKCMQLQQPHTRVOPP *PTPRQQGPQ \ VPYAVITAGNRPNYLY RMLRSLLSAQGVSPQMITVFIDGYYEEPROVALFGLRGIQHTP IS INNAVSQHYKASITAFTHE PRAKFAVVLEEDLIADIFFS FLSQSIHLLEEDDSLYCISAWNDQGYEHTAEDPALLYRVETMPG LGWVLRSLYKEELEPKRWFTPEKLDWWMEMMEQRRGECII PDVSRSYHGIVGLKKLHTWIGHTAYFKKHKPHTVPOVQLRNVDSL KKRAYEVEVHRLLSEABULDHSKNPCDSTLPDTEGHTYVAFIR MEKDDFTTWTQLAKCLHTWIDLDVRSNIRGLWRIFRKWHFPTVAFIR MEKDDFTTWTQLAKCLHTWIDLDVRSNIRGLWRIFRKWHFPTVAFIR MEKDDFTTWTQLAKCHTWIDLDVRSNIRGLWRIFRKWHFPTVAFIR MEKDDFTTWTQLAKCHTWIDLDVRSNIRGLWRIFRKWHFPTVAFIR MEKDDFTTWTQLAKCHTWIDLDVRSNIRGLWRIFRKWHFPTVAFIR THE ALAMVRYMEKGTHRGLYKSIQKTLKFFCTFALLEIVHCLIGIV FISVAFYTSLLDHLPYFIKAARNIFFTILATMJTFYDIAMTAGWLVL ALAMVRYMEKGTHRGLYKSIQKTLKFFCTFALLEIVHCLIGIV FISVAFYTSLLDHLPYFIKAARNIFFILLYPYGVAGELLTIY EITRYSFYTFSLLDHLPYFIKAARNIFFILLYPYGVAGELLTIY FALAPHVKKTGMSIFLENWKYLWSPYYYFLLITMASYTDLFPQL YFFMLEQRKVLHGQG*L*KRMIK*SLQTRCFFQNNQDYLSPSF NNNKQLCELSHIVWFLKI  5880  1138  1324  SLECLVAGGIGGFSSONPLQRAGILARFREARGTFSALTACSA SVISKGKSSSCMWFSAASDRDS PVPLRPPGFQVQLPSGTGWVLSD YKKKRGRCS/MLSQCHCEREVVLLRSMARGEFRRAASDVL CRSLANETHQLRRTLTATAHMCQHLAKCLDERGHAQRNVGERSP DOSEHTDGHTSVQSVIELQEBLIKKOKVTHEDLINAKMQRYN ASRDEYVRGLHAQLRGLQIPPEBLMKRETSRLNRQLEEKINDC CRSLANETHQLRRTLTATAHMCQHLAKCLDERGHAQRNVGERSP DOSEHTDGHTSVQSVIELQEBLIKKOKVTHEDLINAKMQRYN ASRDEYVRGLHAQLRGLQIPPEBLMKRETSRLNRQLEEKINDC ASVKGRASSTARDALERVOMLEQQILAYKDDFMSERADRER AQSRIGELEKVASLLHOVSWRQDSREPDAGRHAGSKTAKVLA ADALELWYPGGWRFGTGSQOPEPPAEGGHPGAQRAGGGGLQCPH LQCFSDEGGERGARAFACSTAKVLA ADALELWYPGGWRFGTGSQOPEPPAEGGHPGAQRAGGGGLQCPH LCQCFSDEGGERGARAFACSTAKVLA ADALELWYPGGWRFGTGTSQOPEPPAEGGHPGAQRAGGGGLQCPH LCQCFSDEGGERGARAFACSTAKVLA ADALELWYPGGWRFGTGTSGOPEPPAEGGHPGAQRAGGGGLQCPH LCQCFSDEGGERGAFAGSTATACSTROWLDGGGGRAFACSTATACSTROWLDGGGGAMNILRRINGAVRCKLG RTRRD*QCFGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1	1		PPP PVPTDI EMPSCI'I COMPANY CAPLTWVPGD
GLMKCMGLQGPHTHRVOFP PTFRQGGFOV VFVAVTAGRRENYLY  RMLRSLLSAGGVSPOMITVFIDGYTERMOVVALFGLRGIGHTP  IS IKNAZVSGHYKASLTATFNLFFEAKFAVVLEEDLDIAVDFFS  FLSQSIHLLEEDDSLYCISAMNDQGYEHTAEDPALLYRVETMPG  LGWVLRRSLYKEELEFKWFTPEEKLUBDWMWWEMPEQRRGERCII  PDVSRSYHRGIVGLNNNGYFHBAYFKKHRMTVPGVGLRNVDSL  KKERYZEVEVHRLISEAEVLJHBAYPFENDFILPTGGHTVVAFIR  MEKDDDFTTWTQLAKCLHIWDLDVRGNHRGLWRLFRKKNHFLVV  GVPASFYSVKKPSVSVTPILEFEPPRECAATMASSDED  GTNGGASEAGEDREAPGKRRRIGFLATAWLFYPIAMTAGWLVL  AIAMVSFYMEKGTHRGLYKSIGKHFFOTFALLEIVHCLIGIV  PTSVIVTGVQVSSRIFMWWLITHSIKPTOTFALLEIVHCLIGIV  PTSVIVTGVQVSSRIFMWWLITHSIKPTOTFALLEIVHCLIGIV  PTSVIVTGVQVSSRIFMWWLITHSIKPTOTFALEIVHCLIGIV  PTSVIVTGVQVSSRIFMWWLITHSIKPTOTFALEIVHCLIGIV  PTSVIVTGVQVSSRIFMWWLTHSIKPTOTFALEIVHCLIGIV  PTSVIVTGVQVSSRIFMWWLITHSIKPTOTFALEIVHCLIGIV  PTSVIVTGVQVSSRIFMWWLITHSIKPTOTFALEIVHCLIGIV  PTSVIVTGVQVSSRIFMWWLITHSIKPTOTFALEIVHCLIGIV  PTSVIVTGVQVSSRIFMWWLITHSIKPTOTFALEIVHCLIGIV  PTSVIVTGVQVSSRIFMWWLITHSIKPTOTFALEIVHCLIGIV  PTSVIVTGVQVSSRIFMKNNSFDYYYFLLITMASVIDEPPOL  AALPHVKKTGMSSILDHPYKNNSPDYYYFLLITMASVIDEPPOL  VPHMLQRRKVLHG\G*L*RMIK*SLUCHCLPGHAGRNVGENSP  NNKNKQLECISHIVWFLKI  SLMCLVAGGIGLGFSSONPLQRAGILARFREARGTFSALTACSA  SVISKKASSGSWWSPAADREDSPVLRPREARGTFSALTACSA  SVISKKASSGSWWSPAADREDSPVLRPREARGTFSALTACSA  *KKKRGRCSS/MLSQPQHEREKEVVLLRRSMAEGERARASVVL  CRSLAMFHQLRFTLTATAHMCQHLAKCLDERGHAGRNVGERSP  DQSEHTDGHTSVQSVIEKLQESHNLLKQKVTHVEDLNAKUNGENSP  ASRUCELEBKVASLLHQVSHRODSREPDAGRIHAGSKTAKYLA  AALBLMYPGGWRFGTGSQCPEPPAEGGHPGAAGRGCOLQCPH  CLQCFSDEOGEELLRHVAECCQ  GGHBFFFTEAFRAGHLTMDCTWRIFINAAAATGHAQVQLLQSG  SEVKKPGASVMVSCVYSGYTLTKISMMVVQAPGKGLB*MGPFD  LQDVETTYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV  HHCATDTV  SGCVEMLYSHSLEYQPEWISVQSAVAPAQLALNSGGDL*LHSGE  RTRRD*QLPPSAGGPGLQEPLQLEGLDITSDFFILDEVGGVDLER  MEQMLGAFQSDLSSISSEIRTLQGSSRNNILRNRQAVRGKLG  MEQMLGAFQSDLSSISSEIRTLQGSSRNNILRNRQAVRGKLG  BLVDCLVVPSALVTATLEAPVTEDFFILGOLGELDITSDFTILDEVGGVDLE  MEQMLGAFQSDLSSISSEIRTLQGSSRNNILRNRQAVRGKLG  BLVDCLVVPSALVTATLEAPVTEDFFILGOLGELDITSKYLTSKIYLYSYYR  SYLERMMVQYEEVARKDDLMGVCGOTAKGFFSKLFRNTTIF  TLGTRGSVISPTLEAPILVPHTAGRGGVFFFE	1	1	i	CROSSING (NICE CONTROLLED AND AND AND AND AND AND AND AND AND AN
SUNCELLEGIST UNDER STATEMENT OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STRE	5878	950	2112	CPCSTVS/NGSQMTCR*INIILILQKSVCEL
ISINGARGOSPENDITION TO THE PROPAGE IGNTE  ISINGARVSCHYRASITATHINE PERKEAVALUEDLDIAND FES FLOGSIHLLEEDBILYCISAMNDOGYEHTAEDPALLYRVETMPG LGWYLRRSILYKELEPKWPTPEKLWDDMWMEMPEGRBECII AGNURRSILYKELEPKWPTPEKLWDDMWMEMPEGRBECII BDVSRSYHFGIVGLNMNGYFHEAYFKKHKPHTVPGVQLRNVDSI KKRAYEVEVHRLLSEAEVLDHSKNPCEDSFLPDTEGHTYVAFIR MEKDDFTTWTGLAKCHH WILDVRGNIRGLWRIFRKWNFPKNHFLVV GVPASPYSVKKPPSVTPI FLEPPPKEGAPGAPEOT  SARYEVEVHRLLSEAEVLDHSKNPCEDSFLPDTEGHTYVAFIR MEKDDFTTWTGLAKCHH WILDVRGNIRGLWRIFPKKNHFLVV GVPASPYSVKKPPSVTPI FLEPPPKEGAPGAPEOT  ALAPHANAGSGERAAGWAGSPPTLLFJSFTSFRCAATMASDED GTNGGASEAGEDREAPGKRRRLGFLATAWLTFYDIANTAGWLVL ALAWNEFYMEKGTHRGLYKSIQKTLKFFOTFALLEIVHCLIGIV PTSVIVTGQVQSST FMWULITHSKPIQNETVLEIVHATVT EITRYSFYTFSLLDHLPYFIKKARNNFFILLYPVGVAGELLTIY AALPHVKKTGMPSIRIPWKNVSPPTYYFLLITMASYIPLFPQL YFHMLRQRRKVLHGG*L*KMMIK*SLQTRCFFONNODYLSPSF NNENKQLCEISHIVWFIKKARNNFFILLYPVGVAGELLTIY AALPHVKKTGMPSIRIPWKNVSPPTYYFLLITMASYIPLFPQL YFHMLRQRRKVLHGG*L*KMMIK*SLQTRCFFONNODYLSPSF NNENKQLCEISHIVWFIKARNAFGERARAASDVL CRSLANETHQLRRTLTATAHACQHLAKCLDERQHAQRNVGERSP DOSEHTDGHTSVQSVIERLOEENELKQKVTHVEDLNAKWQRYN ARREDEYVAGLHAQURGLQIPHACHACHACKLDERQHAQRNVGERSP DOSEHTDGHTSVQSVIERLOEENELKQKVTHVEDLNAKWQRYN AARDEYVAGLHAQURGLQIPHACHACHACKLDERQHAQROGGDLQCPH CLQCFSDEQGEFLRHVAECCO SCHWALYSHALVRACCO GGHPSPTEAPRAGHTMDCTWRTLFILVAAATGTHAQVQLLOGG SEVKKPGASWWSCYVSGYTLTKLSMMVVRQAPGKGLE*MGFFD LQDVETIYPQKFQGRVSMTEETSTETTO/AYLESSLRSEDTAV HCATDTV  SCVEMLYSHSLEVNPEWISVOSAVAPAQLAINSDGDL*LHSGE RTRD-OLPSAGGGGLQEPLQLGELDITSDEFFILDEVDG/VDLR MEQMLGAFGSDLSSISSEIRTLQEGSSNIALINGITACDAVLER MEQMLGAFGSDLSSISSEIRTLQEGSSNIALINGITACDAVLER MEQMLGAFGSDLSSISSEIRTLQEGSSNIALINGITACDAVLER MEQMLGAFGSDLSSISSEIRTLQEGSSNIALINGITACDAVLER MEQMLGAFGSDLSSISSEIRTLQEGSSNIALINGITACDAVLER MEQMLGAFGSDLSSISSEIRTLQEGSRANIRLRNROAVRGKLG BLUDELVYPSALVTATLEPPVTEPRIEQLOGELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVYKIREFILQKTYSFRKPMINYQ IPQTALLKYRFFYQFLLGHERATAKEIRDEVYETLSKIYLSYYR SYLGRLMKVQYEEVARKDDLMGCVCTAKKGFFKSFSLRSNTTIF TLGTRGSVISPTELEAPILVPHTAGRGGRYFFEALFRSCHYAL LDNSCREPFVUSGRAADLLAMADETT AMRTI LUDGY	1		2113	GLWKCMQLQGPHTHRVQP + PTPRQQGPQ\VPVAVIAGNRPNYLY
SINANAVQHYKASITATENIFEEAKFAVVLEEDLDIAVDFFS   FLSGSTHLLEEDDSLYCISAMNDOGYEHTAEDPALLXRYSTMPG    LGWVLRRSLYKEELEPFKLMDHDMWMRMEQREGRECII     PDVSRSYHFGIVGLMNMGYFBAYFKKHKPNTVPGVQLRKVVDSI     KKEAYEVEVURLLSEAEVLDHSKOPCEDSTLPDTEGHTYVDSI     KKEAYEVEVURLLSEAEVLDHSKOPCEDSTLPDTEGHTYVDFIK     KKEAYEVEVURLLSEAEVLDHSKOPCEDSTLPDTEGHTYVDFIK     KKEAYEVEVURLHDLDVRGHRGLMKLIFRKKNHFLVV     GVPASPYSVKKPPSVTPIFLEPPFKESAPADEOT     RLTEAAAAGSGSRAAGGAGSPTLLFLSPTSPECAATMASSDED     GTNGGASEAGEDREAPGKRAGFJATAWLTFYDIAMTAGWLUT     ALAMVEFYMEKGTHRGLYKSIQKTLKFFOTPALLEIVHCLIGIV     PTSVIVTGVQVSSRIPMVMLITHSIRFIQREESVULFLVAMTVT     ALAMVEFYMEKGTHRGLYKSIQKTLKFFOTPALLEIVHCLIGIV     PTSVIVTGVQVSSRIPMVMLITHSIRFIQREESVULFLVAMTVT     ALAPHVKKTGMFSIRLPNKYNVSFDYYFFLLITMASYIPLFPQL     FTRULAGRAGGASPTLOFT     ALAPHVKKTGMFSIRLPNKYNVSFDYYFFLLITMASYIPLFPQL     FTRULAGRAGGASPTLOFT     ALAPHVKKTGMFSIRLPNKYNVSFDYYFFLLITMASYIPLFPQL     FTRULAGRAGGASPTLOFT     ALAPHVKKTGMFSIRLPNKYNVSFDYYFFLLITMASYIPLFPQL     FTRULAGRAGGASPTLOFT     ALAPHVKKTGMFSIRLPNKYNVSFDYYFFLLITMASYIPLFPQL     FTRULAGRAGGASPTLOFT     ALAPHVKKTGMFSIRLPNKYNVSFDYYFFLLITMASYIPLFPQL     SLWCLVAGGIGGFSSONFLORAGILARPREARGTFSALTACSA     SLWCLVAGGIGGFSSONFLORAGILARPREARGTFSALTACSA     SLWCLVAGGIGGFSSONFLORAGILARPREARGTFSALTACSA     SLWCLVAGGIGGFSSONFLORAGILARPREARGTFSALTACSA     SLWCLVAGGIGGFSSONFLORAGILARPREARGTFSALTACSA     SLWCLVAGGIGGFSSONFLORAGILARPREARGTFSALTACSA     SVISKKASSGNMFSAASNDSDFVPLRPPEDPUQLPSGTUWULSD     AKKARGRCSS/MLSOPOHERKEVVLLLRSMAGGERARAASDVL     ASDBETYGGLHAALAGLQIPHPEPEBAGGHPGAAQRGGGDLQCPH     CRILANETOLIKARRYLLA     ASDBETYGGLHAALAGLQIPHPEPEBAGGHPGAAQRGGGDLQCPH     CLQCFSBEOGEELLRHVABCCQ     GGHPSPTEADAGRAGGAGGAGGAGGAGGAGGAGGAGGAGGAGAGAGAG	1	i i		AMLKSULSAQGVSPOMITVFIDGYYEEPMDVALEGIDGTOVER
GWYLRSIYKEELEPKMPTPEKLWDWDMWRPDERREGCII	1			1 ISTANARVSQHYKASLTATFNLFPEAKFAVVI.FFDI.DTAUDERG
LGWURRSLYKEELEPKMPTDEKLUDWDMWMMPEQRRGRECII   PDUSRSYHFGIVGLUMNUSTHERAYFKKHKPNTYDGUCLNRVDSL   KKRAYEVEVHRILGEABULDHSKNPCEDSFLDDTECHTVVAFIR   MEKDDDFTTWTQLAKCHIWDLDVRRNHRGLWRIFRKKHHFLVV   GVPASPYSVKKPPSVTDIFLEPPKEGAPGAPGOT   GVPASPYSVKKPPSVTDIFLEPPKEGAPGAPGOT   GTNGASEAGGEDREAPGKRRRIGIFLATAWLTFYDIAMTAGWLUL   ALAWVRFYMEKGTHRGLYKSIQKTLKFFQTPALLEIVHCLIGIV   PTSVIVTGVQVSSRIFMVWLITHSIKPIQNESSVULFLVAWTUT   EIRYSFYTFSLLDHLBYFILLPVGVAGGELTTY   AALPHVKKTGMFSIRLPNKYNVSPDYYYFLLITMASYIPLFPQL   YFHMLRQRRKVLHG\G*L*KRMIK*SLQTRCFFGNNODYLSPSF   NNCNKQLCEISWIVWFLKI   SLWCLVAGGLGLGFSSONPLQRAGILARPREARGTFSALTACSA   SVTSKKKSSSSGMPSAASNESVPLRPPGPVQLPPSGTGWVLSD   KKKRGRCSS/WLSQPQHEREKEVVLURRSMAEGERARASDVL   CRSLANETHQLRTLTAHMCQHLAKCLDERQHAQRNVGERSP   DQSEHTDGHTSVQSVIEKLGGENRLKKGVTHVEDLANKKNQRYN   ASRDBYVRGLHAQLRGLQIHAYKDDFMSERADRER   AQSRIQELEEKVASLLHQVSWRODSREPDAGRHAGKLEKINDC   CLCFSDEQGEELLRHVAGVGNPGBREPDAGRHAGKSKTAYLA   ADALELMVPGGRPFGTGSQQPEPPAEGGHPGAAQRGQGDLQCPH   CLCFSDEQGEELLRHVAGVGNPGBREPADRER   AQSRIQELEKVASLHQVSWRODSREPDAGRHAGKSKTAYLA   ADALELMVPGGRPFGTGSQQPEPPAEGGHPGAAQRGQGDLQCPH   CLCFSDEQGEELLRHVAGVSWRODSREPDAGRHAGKSKTAYLA   ADALELMVPGGRPFGTGSQQPEPPAEGGHPGAAQRGQGDLQCPH   CLCFSDEQGEELLRHVAGVSWRODSREPDAGRHAGKTAYLA   ADALELMVPGGRPFGTGSQQPEPPAEGGHPGAAQRGGGDLQCPH   CLCFSDEQGEELLRHVAGVSWRODSREPDAGRHAGKERAYLA   ADALELMVPGGRPFGTGSQQPEPPAEGGHPGAAQRGGGDLQCPH   CLCFSDEQGEELLRHVAGVSWRODSREPDAGRHAGKERAYLA   ADALELMVPGGRPFGTGSQQPEPPAEGGHPGAAQRGGGLE*MOPPFD   LQDUETIYPPKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV   HHCATDTV   SGCVEMLYSHSLEYNPEWISVQSAVAFQQLALNSDGDL*LHSGE   RTRRD*QLPFAGGGPGLQPFLQGELDITSDEFILDEVGQVDLR   HYSKQUELELQQIEQKSIRDYIQGSGAMIRLRNRQAVEGKLG   ELVDGLVVPSALVTAILEAPTPRFLEQCJELDKTARAVRCQE   ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMINYQ   IPQTALKKYRFFYQFLLGMPRATAKEIRDEVVETISKIYLSYYR   SYLGRLMKVQYEVARKDDLMGVPTCNSTLYRLDSVYTLL LLDSV	[			FLSQSIHLLEEDDSLYCISAWNDOGYEHTAEDDALLVRUSTMDG
FUNSKYHFGIVGINMNOYFHEAYFKHKRYTYPGVOLRNVDSL KKRAYEVEVHILLSEAEVLÜHSKNPCEDSFLOTEGHTYVAPIR MEKDDDFTTWTQLAKCLHIWDLDVRGNHRGLWRLFRKKNHFLVV GVPASPYSVKKPPSVTPIFLEPFPKEGAPGAPEOT  RLTEAAAAGSGSRAAGMAGSPPTLIFLSFTSPRCAATMASSDED GTNGGASEAGEDREAPGKRRILGFLATAMLTFYDIAMTAGWLVL AIAMVRFYMEKGTHRGLYKSIOKTKLKFPOTPALLEIVHCLIGIV PTSVIVTGVQVSSRIFMVWLITHSIKPIQNEESVVLFLVAWTVT EITRYSFYTFSLIDHLFYFIKMARKNFFIILYPVGVAGELLTIY AALPHVKKTGMFSIRLENKVASPYYYFLLITMASYTPLFPQL YFHMLRQRRKVLHG\G*L*KMMIK*SLQTRCFFQNNQDYLSPSP NNKNKOLCEISWIVWPLKI  SUTSKKKSSSGMWPSAASDRDSPVPLRPPGGPVOLPSGTGWVLSD *KKKRGRCSS\MLSQPGHERKEVVLLRRSMAGERFARAASDVL CRSLANETHOLRETLTATAMMCQHLAKCLDERQHAQRNVGERSP DOSEHTDGHTSVQSVIEKLQENRILKGKVTHVEDLNAKKQRYN ASRDEYVRGLHAQLRGLQI PHEPELMRKEISRINRQLERKINDC ASVKOBLAASRTARDAALERVQMLBQQILAYKDDFMSERADRER AQSRIQELEEKVASLLHOVSRQDSREPDAGRIHAGSKTAKYLA ADALELMVPGGRPGTGSQQPEPPAEGGHPGAAQRGGDLQCPH LODVETIYPQKFQGRVSMTEETSTETTQ\AYLELSSLRSEDTAV HCATDTV  5881  26  441 GGIHPSPTEAPRAQHLIMDCTWRILFLVAAATGTHAQVQLLQSG SEVKKPGASVMVSCYVSGYTLTKLSMMVRQAPGKGLE*MGPFD LODVETIYPQKFQGRVSMTEETSTETTQ\AYLELSSLRSEDTAV HCATDTV  5682  2407 2216 SGCVEMLYSHSLEYNPEWISVQSAVAPAQLAINSDGDL*LHSGE RTRRD*QLPZAGGGOLQCDLICLEDLITSDEFILDEVDG\VDLR HYSKQVELELQQIEQKSIRDYIQESENIASLINQITACDAVLER MEQMLGAFQSDLSSISSEITRILQEOGAMNIRLRNRQAVEGKLG ELVDGLVVPSALVTAILEAPUTEPRFLEGLOELDLANARVEGC ARGTAACADVRGVLDRLRVKAVTKIREFILOKIYSPRKPMINYQ IPQTALKKYRFFYOFLLGNERATAKEIRDSYVETLSKIYLSYYR SYLGRLMKVOYEEVAEKDDLMGVEOTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTBLEAPILVPHTAGRGEGRYPFEALFRSCHYAL LDNSCREYLFICTEFFVVSROPDTTAKGFFSKPSLRSRNTIF TLGTRGSVISPTBLEAPILVPHTAGRGEGRYPFEALFRSCHYAL LDNSCREYLFICTEFFVVSROPDTTAKGFFSKPSLRSRNTIT	1 1			LGWVLRRSLYKEELEPKWPTPEKI.WDWDMWMPMDEOPDCDBCT
S879  3 981  REKRODDFTTWQLAKCH.BULDURGRINEGURELPREKRHFLVV GVPASPYSVKKPPSGTPIFLEPPPKEGGAPGAPEGT  RITEAAAAGSGSRAAGMAGSPFTLTLPLSFTSFRCAATMASSDED GTNGGASEAGEDREAPGRRRIGGFLATAMITFYDLAMTAGWLUL AIAMVRFYMEKGTHRGLYKSIQKTLKFFGTPALLEIVHCLIGIV PTSVIVTGVQUSSRIFMVWLITHSIKKPIQNEEGUVLFLVAMTVT EITRYSFYTFSLLDHLFYIKMARVNFFIILYPVGVAGELLTIY AALPHVKKTGMFSIRLPNKYMVSPDYYVFLLITMASYIPLFPQL YFFMLRQRRKVLHG\G^4L*KRMIK*SLQTRCFFGNNQDYLSPSF NNKNKQLCEISWIVWFLKI  SLWCLVAGGIGLGFSSGNPLQRAGILARPREARGTFSALTACSA SVTSKGKSSSGMMPSAASDRDSPVPLRPPGPVQLPSGTGWVLSD *KKKKRGCSS/MLSQPQHEREKEVVLLRRSMAEGERARASDVL CRSLANETHQLRRTLTATAHMCQLAKCLDERQHAQRNVGERSP DQSEHTDGHTSVQSVIEKLQEENRLLKGKVHVSDLNAKKQRYN ASRDEYVRGLHAQIRGLQIPHEPBLMRKEISRLNRQLEEKINDC AZVKGBLAASRTARDAALERVQMLEQQILAYKDDFMSERADRER AQSRIQELEEKVASLHUVSWRQDSREPDAGRIHAGSKTAKYLA ADALELMYPGGWRPGTGSQQPEPPAEGHPGAAQRGQGDLQCPH CLQCFSDEGGEELLRHVAGECQ  5881  26  441  GGIHFSPTEAPRAQHLTMDCTWRILFLVAAATGTHAQVQLLQSG SEVKKPGASVMVSCVYSGTTLTKLSMMVVRQAPGKGLE*MSPFD LQDVETIYPQKFQGRVSMTCETSTETTQ/AYLELSSLRSEDTAV HCATDTV  5882  2407  2216  SGCVEMLYSHSLEYNPEWISVQSAVAPAQLALNSDGDL*LHSGE RTRRD*QLPEAGGPGLQEPLQGELDITSDEFILDEVGLYUER MEQMLGAFQSDLSSISSEIRTLQQSGAMNIRLRNRQAVERKLG ELVDGLVVPSALVTAILEAPVTEPRELEQQEGAMNIRLRNRQAVERKLG ELVDGLVVPSALVTAILEAPVTEPRELEQQEILARRNRQAVERKLG ARGTAACADVRGVLDRLKVKAVTKIREFILQKIYSFRKPMINYQ IPQTALKKYRFFYOFLLGNERATAKEIRDEVYETLSKIYLSYYR SYLGRLMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISFTELEAPILVPHTAQRGGRYPFEALFRSCHYAL LDNSCRFYLFICTEFFVVSBADADLFHAUMGPTLSKTITHUNDEY	1			PDVSRSYHFGIVGLMMNGVENEAVERVENDAMINENEEQRRGRECTI
S879 3 981 RLTEAAAAGSGSRAAGWAGSPPTLIPERPRESEDED  RLTEAAAAGSGSRAAGWAGSPPTLIPERPTSPRCAATMASSDED GTMGGASEAGEDREAPGKRRILGFLATAWLITYDIAMTAGWLUL ALAMVRFYWREGTHREJYKSIOKTLKFQTFALLEIVHCLIGIV PTSVIVTGUQVSSRIFMVWLITHSIKPIQNESSVVLFLVAWTVT EITRYSPYTFSLLDHLPYFIKWARYNFFIILYPVGVAGELLTIY AALPHVKKTGMFSIRLDHKYNVSFDYYYFLLITMASYTPLFPQL YFFMLRQRRKVLHGG-*L** KRMIK*SLQTRCFFQNNDDYLSPSF NNKNKQLCEISWIVWFLKI  SLWCLVAGGGGLGFSGNDFLQRAGILARPREARGTFSALTACSA SVTSKGKSSGMWPSAASDRDSPVPLRPPGPVQLPSGTGWVLSD *KKKRGRCSS/WLSQPQHEREKEVVLLRRSMABGERRRAASDVL CRSLANETHQLRRTLTATAHMCQHLAKCLDEQHAQRNVGERSP DQSEHTDGHTSVQSVIEKLQEENRLLKQKVTHVEDLNAKWQRYN ASRDEVVRGLHAQLRGLQIPHEPELMRKEISRLNRQLEEKINDC AEVKQELAASRTARDAALERVQMLEQQILAYKDDFMSERADRER AQSRIQELEEKVASLLHQVSWRQDSREPDAGRHAGSKTAKYLA ADALELMVPSGWRPGTGSQQPPPPAEGGHPGAAQRGQGDLQCPH CLQCFSDEQGEELLRHVAECCQ  SGVKKPGASWWSCVYSVTITKLSMHWVRQAPGKGLE*WGPFD LQDVETIYPQKPQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HHCATDTV SEVKKPGASSWWSCVYSVTITKLSMHWVRQAPGKGLE*WGPFD LQDVETIYPQKPQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HHCATDTV  SGVVKMYSHSLEYNPEWISVOSAVAPAQLALNSDGDL*LHSGE RTRRD*QLPEAGGPGLQEPLQGELDITSDEFILDEVDG\VDLR HYSKQVELELQQIEQKSIRDYIQGSENTASLINQITACDAVLER MEQMIGAPGSDLSSISSIFITLQEGSGAMNIRLRNRQAVRGKLG ELVDGLVVPSALVTAILEAPVTEPFFLEQCGDLAKAAAVREGE ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMTNYQ IPQTALLKKYRFYYQFLLGRENTATAEIR BLEYVETLSKIYLSYYR SYLGRLMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLKSRNTIF TLGTRGSVISPTELEAPILVPHTAQRGEQRYPFEALFRSQHYAL LDNSCREVIFTCEFFFVSGGAAHDLFHAWGDTI-GWTX-KH DEV	ł I	1		KKEAVEVEUHDI I CEARUI DUGUNGUNGUNGUNGUNGUNGUNGUNGUNGUNGUNGUNGUN
S879  3 981  RITERARAGSGRARAGSPTLLPLSPTSPRCAATMASSDED GTNGGASEAGEDREAPGKRRLGFLATAWLTYTPLAMTAGWLVL ALAMVRYMEKGTHEGLYKSIGNTLKFFQTPALLEIVEKCLIGIV PTSVIVTGVQUSSRIFMWLITHSIKPIQNESSVULFLVAWTUT EITRYSFYTFSLLDHLPYFIKWARYNFFILLYPVGVAGELLTIY AALPHVKKTGMFSIRLPNKYNVSFDYYYFLLITMASYIPLFPQL YFHMLRQRRVLHOG*L**KRMIK*SLQTRCFFQNNQDYLSPSF NNKNKQLCEISWIWFLKI SLWCLVAGGGLGFPSONPLQRAGILARPREARGTFSALTACSA SVTSKGKSSGMWPSAASDRDSPVPLRPPGPVQLPSCTGWVLSD *KKKRGRCSS/MLSQPQCHEREKEVVLLRRSMABGERARAASDVL CRSLANETHGLARTLATAHMCQHLAKCHDRQHAQRNVGERSP DQSEHTDGHTSVQSVIEKLQEENRLLKQKVTHVEDLNAKWQRYN ASRDEYVRGLHAAGRTARDAALRCVMLEGQILAYKDDFMSERADRER AQSRIQELEEKVASLLHQVSWRQDSREPDAGRIHAGSKTAKYLA ADALELMVPGGKRPGTGSQQPEPPAEGGHPGAAQRGQDLQCPH CLQCFSDEGGEELLRHVAECCQ  5881  26  441  GGIHPSPTEAPRACHITMDCTWRILFLVAAATGTHAQVQLLQSG SEVKKPGASVMVSCYVSGYTLTKLSMHWVRQAPGKGLE**MSPFD LQDVETIYPQKRPGGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HHCATDTV  SGCVEMLYSHSLEYNPEWISVQSAVAPAQLALNSDGDL*LHSGE RTRRD*QDPBAGGGLQEPLQGELDITSDEFILDEVDG\VDLR HYSKQVELELQQIEQKSIRDYIQESENTASLINQITACDAVLER MEQMLGAPGSDLSSISSEIRTLQESGAMNIRLRNRQAVRGKLG ELVDGLVVPSALVTAILEAPVTEPFFLEQLOELDAKAAAVREGE ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMTNYQ IPOTALLKKRFFYQFLLGREPATAKEIRDFUTLSKIYLSYYR SYLGRLMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISTTELEEAPILVPHTAQRGRGRRYPFEALFRSQHYAL LDNSCRFEIFTGEFFVSGFAABHDLFPHAMGFILGKTIKHLBEV		i		MEKADA ETTEMOT AKOT WITTEN AND CEDSFLADTEGHTYVAFIR
RLTEAAAAGSGERAGEWAGSPPTLDFLSPTSPRCAATMASSDED GTNGGASEAGEDREAPGKRRKGFLATAWLTYDIAMTAGWLVL AIAMVRFYMEKGTHRGLYKSIQKTLKFFGTPALLEIVHCLIGIV PTSVIVTGVQVSSRIFMVWLITHSIKPIQNEGSVVLFLVAWTVT EITRYSFYTFSLLDHLPYFIKWARVNFFIIYPVGVAGELLTIY AALPHVKKTGMFSIRLPNKYNVSFDYYYFLLITMASVTPLFPQL YPHMLRQRRKVLHG\G*L*KRMIK*SLQTRCFFQNNQDYLSPSF NNENKQLCEISWIVWFLKY SUTSKGKSSGSMWPSAASDRDSPVPLRPPGPVQLPSGTGWVLSD *KKKRGRCSS/WLSQDQHEREKEVVLLRRSMAEGERARAASDVL CRSLANETHQLRRTLTATAHMCQHLAKCLDERQHAQRNVGERSP DQSEHTDGHTSVQSVIEKLQEENRLLKQKVTHVEDLNAKWQRYN ASRDEYVRGLHAQINGLQIPHEPEIMREISRLNRQLEEKINDC AZVKQBLAASRTARDAALERVQMLEQQILAYKDDFMSERADRER AQSRIQELEEKVASLLHQVSWRQDSREPDAGRIHAGSKTAKYLA ADALELMVPGGWRPSTGSQQPEPPAEGGHPGAAQRGQGDLQCPH CLQCFSDEGGEELLRHVAECCQ  5881 26 441 GGIHPSPTEAPRAQHLTMDCTMSILFIVVAAATGTHAQVQLLQSG SVKKRGASVMVSCYVSGYTLTKLSMINVRQAPGKGLE*MGPFD LQDVETIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HHCATDTV HCATDTV HCATDTV HCATDTV HCATDTV SGCVEMLYSHSLEYNPEWISVQSAVAPAQLALNSDGDL*LHSGE RTRRD*QLPBAGGPGLQESIRDYLQESENIASLHNQITACDAVLER MEQMLGAFGSDLSSISSEIRTLQEQSGAMNIRLRNRQAVRGLG ELVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAAVRRQE ARGTAACADVRGVLDRLRVKAVTKIREFILQKIVSFRRMTNYQ IPQTALLKYRFFYQFLLGNERATAKEIRDEYVETLSKIYLSYYR SYLGRLMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLKSRNTIF TLGTRGSVISPTBLEAPILVPHTAQRGGRYPFBALFRSQHYAL LDNSCREVILFICEFFVVSGPAAHDLEHAWGRYIF, SMTLKUL DEV	i l	ì		CVPACAVCHARDELT TO THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF
GTNGGASEAGEDREAPGKRRLGFLATAMLTYDIAMTAGWLVL ALAMVRFYMEKGTHRGLYKSIQKTLKFFQTPALLEIVHCLIGIV PTSVIVTGVQVSSRIFMVMULTHSIKPIQNEESVVLFLVAMTVT EITRYSFYTFSLLDHLPYFIKWARVMFFILIPYDGVAGELLTIY AALPHVKKTGHFSIRLPNKYNVSPDYYYFLLITMASYIPLFPQL YFHMLRQRRKVLHG\G-*L**KMIK**SLQTRCFFQNNQDYLSPSF NNKNKQLCEISWIVWFLKI  5880  1138  1324  SLWCLVAGGLGLGFSSONPLQRAGILARFREARGTFSALTACSA SVISKGKSSGMWPSAASDRDFVPLRPPGPVQLPSGTGWVLSD *KKKRGRCSS/WLSQDQHEREKEVVLLRRSMAGEGRARAASDVL CRSLANETHQLRRTLTATAHMCQHLAKCLDERQHAQRNVGERSP DQSEHTDGHTSVQSVIEKLQEENRLLKQKVTHVEDLNAKWQRYN ASRDEYVRGLHAQLRGLQIPHPEPIMKEISRLNRQLEEKINDC AEVKQBLAASRTARDAALERVQMLEQQILAYKDDFMSERADRER AQSRIQELEEKVASLLHQVSWRQDSREPDAGRIHAGSKTAKYLA ADALELMVPGGWRPSTGSQQPEPPAEGGHPGAAQRGQGDLQCPH CLQCFSDEGGEELLRHVABCCQ GGHPSPTEAPFAQHLTMDCTWRILFLVAAATGTHAQVQLLQSG SEVKKPGASWWSCTVSGYTLTKLSMHWVRQAPGKGLE**MGPPD LQDVETIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HHCATDTV HCATDTV HCATDTV HCATDTV SGCVEMLYSHSLEYNPEWISVQSAVAPAQLALNSDGDL**LHSGE RTRRD*QLPEAGGPGLQEPLQLGELDITSDEFILDEVDG\VDLR HYSKQVELELQOIEQKSIRDYLQESENIASLHNQITACDAVLER MEQMLGAFGSDLSSISSEIRTLQEGSGAMNIRLRNRQAVRGLG ELVDSLVVPSALVTAILEAPVTEPRFLEQLGELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVTKIREFILQKIVSFRRMTNYQ IPQTALLKYRFFYOFLLGNERATAKEIRDEXVETLSKIYLSYYR SYLGRLMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLKSRNTIF TLGTRGSVISPTELEAPILVPHTAQRGGGRYPFPEAFFSQHYAL LDNSCREVILFICEFFVVSGPAAHDLFHAWMGPTI.SMTLKULRU	5879	3	001	GVPASPISVKKPPSVTPIFLEPPPKEEGAPGAPEQT
ALMAVER PYMEKGTHEGLYKSIOKTLKFPQTPALLEIVHCLIGIV PTSVIVTGVQVSSRIFMVWLITHSIKPIQNESSVULFLVAWTVT EITRYSFYTFSLLDHLPYFIKWARVNFFIILYPVGVAGELLTIY AALPHVKKTGMPSISLDHKYNIVSPDYYYFLLITMASYIPLFPQL YFHMLRQRRKVLHG\G*L*KRWISPDYYYFLLITMASYIPLFPQL YFHMLRQRRKVLHG\G*L*KRWISPDYYYFLLITMASYIPLFPQL YFHMLRQRRKVLHG\G*L*KRWISPDYYYFLLITMASYIPLFPQL YFHMLRQRRKVLHG\G*L*KRWISPDYYYFLLITMASYIPLFPQL YFHMLRQRRKVLHG\G*L*KRWISPDKYNYSPSF NNKNKQLCEISWIVWFLKI  SUNCLVAGGIGLGFSSONPLQRAGILARPREARGTFSALTACSA SVTSKGKSSSGMWPSAASDRDSPVPLRPPGPVQLPSGTGWVLSD *KKKRGRCSS\WLSQPQHEREKEVVLLRRSMAEGERARASDVL CRSLANETHQLRRTLTATAHMCQHLAKCLDERQHAQRNVGERSP DQSEHTDGHTSVQSVIEKLQEENRLLKQKVTHVEDLNAKWGRYN ASRDEVVRGLHAQLRGLQIPHEPELMRKEISRLNRQLEEKINDC ASVKQELAASRTARDAALERVQMLEQQILAYKDDFMSERADRER AQSRIQELEEKVASLLHQVSWRQDSEPDAGRHAGSKTAKYLA ADALELMVPGGWRPGTGSQQPEPPAEGGHPGAAQRGQGDLQCPH CLQCFSDEQGEELLRHVAECCQ SEVKKPGASVMVSCYVSGYTLTKLSMHWVRQAPGKGLE*MGPFD LQDVETIYPQKFQGRVSMTEETSTETTQ\AYLELSSLRSEDTAV HHCANDTV  5882 2407 2216 SGCVEMLYSHSLEYNPEWISVQSAVAPAQLALNSDGDL*LHSGE RTRRD*QLPEAGGGPGLQEPLQIGELDITSDFFILDEVDG\VDLR HYSKQVELBLQQIEQKSIRDYIQESENIASLHNQITACDAVLER MEQMLGAPGSDLSSISSEIRTLQEGQSGAMMIRLRNRQAVREKLG ELVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRRMTNYQ IPQTALLKYRFFYQFLLGNERATAKEIRDEYVETISKIYLSYYR SYLGRLMKVQYEEVAEKDDLMGVEDTAKKGFFSKFSLRSRNTIF TLGTRGSVISPTELEAPILUPHTAQRGERYPFEALFRSQHYAL LDMSCREYLFICEFFYVSGPAAHDLFHAWMCPIT,SMTLKUR PV	1 1	I	961	RLTEAAAAGSGSRAAGWAGSPPTLLPLSPTSPRCAATMASSDED
ALAMVRY YMEKTHRIGLYKSIQKTLKFFQTPALLEIUHCLIGIV PTSVIVTGUQUSSRI FMWWLITHSI KPIQNEESVULFLVAWTVT EITRYSFYTFSLLDHLPYFI KWARYNFFI ILYPVGVAGELLTIY AALPHVKKTGMFSIRLENKYNVSFDYYYFLLITMASVIPLFPQL YFHMLRQRRKVLING-61-k KRMIK*SLQTRCFFQNNODYLSPSF NNKNKQLCEISWIVWFLKI  5880  1138  1324  SLWCLVAGGLGLGFSSONPLORAGILARPREARGTFSALTACSA SVTSKGKSSSGMWPSAASDROSPYLRPPGPGVQLPSGTGWVLSD *KKKRGRCSS/WLSQPQHEREKEVVLLRRSMAEGERARAASDVL CRSLANETHQLRRTLTATAHMCQHLAKCLDERQHAQRNVGERSP DQSHTTDGHTSVQSVIEKLQEENRLLKQKVTHVEDLNAKQRYN ASRDEYVRGLHAQLRGLQIPHEPELMKEISRLNRQLEEKINDC AEVKQELAASATARDAALERVQMLEQQILAYKDDPMSERADRER AQSRIGELEEKVASLLHQVSWRQDSREPDAGRIHAGSKTAKYLA ADALELMVPGGWRPGTGSQQPEPPAEGGHPGAAQRGGDLQCPH CLQCFSDEGGEELLRHVAECCQ GGHPSPTEAPRAQHLTMDCTWRILFLVAAATGTHAQVQLLQSG SEVKKPGASVMVSCTVSGYTLTKLSMHWVRQAPGKGLE*MGPFD LQDVETIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HHCATOTV  5882  2407  2216  SGCVEMLYSHSLEYNPEWISVQSAVAPAQLALNSDGDL*LHSGE RTRRD*QLPEAGGPGLQEPLQIEGLDITSDEFILDEVDG\VDLR HYSKQVELELQQIEQKSIRDYIGESENIASLHNQITACDAVLER MEQMLGAFGSDLSSISSEIRTLQSQSGANNIRLRNRQAVRGKLG ELVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAAVREQE ARGTAACADVRGVLDRLRKKAVTKIREFILQKTYSFRYPMINYQ 1PQTALLKYRFFYGFLLGNERATAKEIRDEYVETLSKIYLSYYR SYLGRLMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLKSRNTIF TLGTRGSVISPTELEAPILLVPHTAQRGEGRYPFEALFRSQHYAL LDDNSCREVLFICEFFVVSGPAABLEHPAUMDTISMTLUNDRY	1 1	1		GINGGASEAGEDREAPGKRRRLGFLATAWLTFYDIAMTACHI VI
FISTITUGUQUSSRIFMULITHSIKPIQNEESUVLFLVAMTUT EITRYSFYTFSLLDHLPYFIKWARYNFFIILYPUGVAGELLTIY AALPHVKKTGMFSIRLPNKYNVSFDYYYFLLITMASYIPLFPQL YFHMLRQRRKVLHG\G*L*KRMIK*SLQTRCFFQNNQDYLSPSF NKNKKQLCEISEN UFFLKI NKNKKQLCEISEN UFFLKI SLWCLVAGGLGLGFSSONPLQRAGILARPREARGTFSALTACSA SVTSKGKSSGMWPSASDRDSPVPLRPPGPVQLPSCTGWVLSD *KKKRGRCSS/WLSQAGDEREKEVVLLRRSMAEGERARAASDVL CRSLANETHQLRRTLTATAHMCOHLAKCLDERQHAQRNVGERSP DQSEHTDGHTSVQSVIEKLQEENRLLKQKVTHVEDLNAKMQRYN ASRDEYVRGLHAQLRGLQIPHEPELMRKEISRINRQLEEKINDC ASVKQBLAASHTARDAALERVQMLEQQILAYKDDFMSERADRER AQSRIQELEEKVASLLHQVSWRQDSREFDAGRIHAGSKTAKYLA ADALELMVPGGWRPGTTCSQOPEPPAEGGHPGAAQRGQGDLQCPH CLQCFSDEQGEELLRHVAECQQ CLQCFSDEQGEELLRHVAECQQ SEVKKFGASVMVSCYVSGYTLTKLSMHWVRQAPGKGLE*MGPFD LQDVETIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HHCATDTV  SGCVEMLYSHSLEYNPEWISVQSAVAPAQLAINSDGDL*LHSGE RTRRD*QLPSAGGPGLQEPLQLGELDITSDEFILDEVDG\VDLR HYSKQUFLELQQIEQKSIRDYIQESENIASLHNQITACDAVLER MEQMLGAFQSDLSSISSEIRTLQEGSGAMNIRLRNRQAVRGKLG ELVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMTNYQ IPQTALLKYRFFYQFLLGNERATAKEIRGEVYETLSKIYLSYYR SYLGRIMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTELEAPILUPHTAGRGQRYFFFELFFSCHYAL LDNSCREYLFICEFFVVSGFAAHDLFHAVMGPTLSMTLHN DGV	i i	i		A LAMVE YMEKGTHRGLYKSIOKTLKFFOTPALLETURGLICTU
ETRYSFYTFSLIDHLSPTIKWARYNFFILLYPVGVAGELLTIY AAAPHVKKTGMFSIRLPNKYNVSPDYYYFLLITMASYIPLPPQL YFHMLRQRRKVLHG\G*L*KRMIK*SLQTRCFFQNNQDYLSPSF NNKNKQLCEISWIVWFLKI  SLWCLVAGGLGLGFSSONPLQRAGILARPREARGTFSALTACSA STYSKGKSSSGMWSAASDRDSPVPLRPPGPVQLPSGTGWVLSD *KKKRGRCSS/WLSQPQHEREKEVVLLRRSMAEGERARASDVL CRSLANETHQLRRTLTATAHMCCHLAKCLDERQHAQRNVGERSP DOSEHTDGHTSVQSVIEKLQEENRLLKQKVTHVEDLINAKWQRYN ASRDEYVRGLIAQLRGLQIPHEPELMRKEISRLNRQLEEKINDC ABVKQBLAASRTARDAALERVQMLEQQILAYKDDFMSERADRER AQSRIQELEEKVASLLHQVSWRQDSREPDAGRIHAGSKTAKYLA ADALELMVPGGWRPGTGSQQPEPPAEGGHPGAAQRGQGDLQCPH CLQCFSDEQGEELLRHVAECCQ GGIHFSPTEAPRAQHITMDCTWRILFLVAAATGTHAQVQLLQSG SEVKKPGASVMVSCYVSGYTLTKLSMHWVRQAPGKGLE*MGPFD LQDVETIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HHCATDTV  5882 2407 2216 SGCVEMLYSHSLEYNPEWISVQSAVAPAQLALNSDGDL*LHSGE RTRRPQLPPAGGPGLQEPLQLGGLDITSDETILDEVDG\VDLR HYSKQVELELQQIEQKSIRDVIQESENIASLINQITACDAVLER MEQMLGAFQSDLSSISSEIRTLQEQSGAMNIRLRNRQAVRGKLG ELVDGLVVPSALVTAILEAPVTEPRFLEQLOELDAKAAAVREQE ARGTAACADVRGVUPSALVTAILEAPVTEPRFLEQLOELDAKAAAVREQE ARGTAACADVRGVUPSALVTAILEAPVTETSRIYGHYSPKRPMINYQ IPQTALLKYRFFYQFLLGMBRATAKEIRDEYVETLSKIYLSYYR SYLGRIMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTELEAPILVPHTAGRGQRYFFELFFRSCHYAL LDMSCREYLFICEFFVVSGPAAHDLFHAVMGPTLSWTLKHDGV	1	ļ		PTSV1VTGVQVSSR1FMVWLITHS1KPIONERGING BY MANUFACTURE
AALPHVKRTGMFSIRLPNKYNVSFDYYYFLLITMASYIPLFPQL YPHMLRQRRKVLHG\G*L*KRMIK*SLQTRCFFQNNQDYLSPSF NNKNKQLCEISWIWFLKI  SLMCLVAGGIGLGFSSONPLQRAGILARFREARGTFSALTACSA SVTSKGKSSSGMWPSAASDRDSPVPLRPPGPVQLPSGTGWVLSD *KKKRGRCSS/WLSQPQHEREKEVVLLRRSMAEGERARAASDVL CRSLANETHQLRRTLTATAHMCQHLAKCLDERQHAQRNVGERSP DQSEHTDGHTSVQSVIEKLQEENRLLKQKVTHVEDLNAKWQRYN ASRDEYVRGLHAQLRGLQIPHEPELMRKEISRLNRQLEEKINDC AEVKQBLAASRTARDAALERVQMLEQQILAYXDDFMSERADRER AQSRIQELEEKVASLLHQVSWRQDSREPDAGRIHAGSKTAKYLA ADALELMVPGGWRPGTGSQQPEPPAEGGHPGAAQRGQGDLQCPH CLQCFSDEQGEELLRHVAECCQ  GGIHPSPTEAPRAQHLTMDCTWRILFLVAAATGTHAQVQLLQSG SEVKKPGASVMVSCYVSGYTLTKLSMHWVRQAPGKGLE*MGPFD LQDVETIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HCATDTV  SGCVEMLYSHSLEYNPEWISVQSAVAPAQLAINSDGDL*LHSGE RTRRD*QLP=AGGPGGLQEPLQLGELDITSDEFILDEVDG\VDLR HYSKQVELELQQIEQKSIRDYIQESENIASLHNQITACDAVLER MEQMLGAFQSDLSSISSEIRTLQEQSGAMIRLRNRQAVRGKLG ELVDGLVVPSALVTAILEAPVTEPFFLEQLQELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVTKIREFILQELYSTYYR SYLGRLMKVQYEEVABKDDLMGVEDTAKKGFFSKPSLRSNTIF TLGTRGSVISPTBLEAPJILVPHTAQRGEGRYPFEALFRSGHYAL LDNSCREYLFICEFFVVSGPAAHDLFHAWGPTILKHTLYBLDEV				EITRYSFYTFSLLDHLPYFIKWARYNFFTTI.VDVGVAGELLETV
THIMLEGURKVULHG (% L*KRMIK*SLQTRCFFQNNQDYLSPSF NNKNKOLCEISWIVWFLKI  SLWCLVAGGLGLGFSSONPLQRAGILARPREARGTFSALTACSA SVTSKGKSSSGMWPSAASDRDSPVPLRPPGPVQLPSGTGWVLSD *KKKRGRCSS/WLSQPQHEEKEVVLLRRSMAGGERARAASDVL CRSLANETHQLRTLTATAHMCQHLAKCLDERQHAQRNVGERSP DQSEHTDGHTSVQSVIEKLQEENRLLKQKVTHVEDLINAKWQRYN ASRDEYVRGLHAQLRGLQIPHEPELMRKEISRLNRQLEEKINDC AEVKQBLAASRTARDAALERVQMLEQQILAYXDDFMSERADRER AQSRIQELEEKVASLLHQVSWRQDSREPDAGRIHAGSKTAKYLA ADALELMVPGGWRPGTGSQQPEPPAEGGHPGAAQRGQGDLQCPH CLQCFSDEQGEELLRHVAECCQ GGIHPSPTEAPRAQHLTMDCTWRILFLVAAAATGTHAQVQLLQSG SEVKKPGASVMVSCYVSGYTLTKLSMHWVRQAPGKGLE*MGPFD LQDVETIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HHCATDTV  SGCVEMLYSHSLEYNPEWISVQSAVAPAQLAINSDGDL*LHSGE RTRRD*QLPEAGGPGLQEPLQLGELDITSDEFILDEVDG\VDLR HYSKQVELELQQIEQKSIRDYIQESENIASLHNQITACDAVLER MEQMLGAFQSDLSSISSEIRTLQEQSGAMNIRLRNRQAVRGKLG ELVDGLVVPSALVTAILEAPVTEPFFFLEQLQELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMINYQ IPQTALLKYRFFYQFLLGNERATAKEIRDEYVETLSKIYLSYYR SYLGRIMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTELEEAPLLVPHTAQRGEGRYPFEALFRSQHYAL LDNSCREYLFICEFFVVSGPAAHDLFHAWGPTLSMTLKHUPGY		Į.		AALPHVKKTGMFSIRLPNKYNVSFDVVVETLITMACVTDLIDGE
SHOULVAGGIGIGPSSONPLQRAGILARPREARGTFSALTACSA  SUNCLVAGGIGIGPSSONPLQRAGILARPREARGTFSALTACSA SVTSKGKSSSGMWPSAASDRDSPVPLRPPGPVQLPSGTGWVLSD *KKKRGRCSS/WLSQPQHEREKEVVLLRRSMAEGERARAASDVL CRSLANETHQLRRTITATAHMCQHLAKCLDERQHAQRNVGERSP DQSEHTDGHTSVQSVIEKLQEENRLLKQKVTHVEDLNAKWQRYN ASRDEYVRGLHAQLRGLQIPHEPELMRKEISRLNRQLEEKINDC AEVKQBLAASRTARDAALERVQMLEQQILAYKDDFMSERADRER AQSRIQBLEEKVASLLHQVSWRQDSREPDAGRIHAGSKTAKYLA ADALELMVPGGWPGTGSQQPEPPAEGGHPGAAQRGQGDLQCPH CLQCFSDEQGEELLRHVAECCQ  GGIHPSPTEAPRAQHLTMDCTWRILFLVAAATGTHAQVQLLQSG SEVKKPGASVMVSCYVSGYTLTKLSMHWVRQAPGKGLE*MGPFD LQDVETIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HCATDTV  SGCVEMLYSHSLEYNPEWISVQSAVAPAQLALNSDGDL*LHSGE RTRRD*QLPEAGGPGLQEPLQLGELDITSDEFILDEVDG\VDLR HYSKQUELELQQIEQKSIRDYIQESENIASLHNQITACDAVLER MEQMLGAFQSDLSSISSEIRTLQEQSGAMNIRLRNRQAVRGKLG ELVDGLVVPSAUVTAILEAPVTEPRFLEQLQELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMINYQ IPQTALLKYRFFYQFLLGNERATAKEIRDEYUETLSKIYLSYYR SYLGRIMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTELEAPILVPHTAQRGEQRYPFEALFRSQHYAL LDDNSCREYLFICEFFVVSGPAAHDLFHAVMGEPILSMTLWIDEY		i		YFHMLRORRKVING\G*I.*KPMIK*CLOTEGEPONEDULA
1138  1324  SLWCLVAGGIGLGFSSONPLQRAGILARPREARGTFSALTACSA SVTSKGKSSSGWMPSAASDRDSPVPLRPPGPVQLPSGTGWVLSD *KKKRGRCSS/WLSQPQHEREKEVVLLRRSMAEGRARAASDVL CRSLANETHQLRRTLTATAHMCQHLAKCLDERQHAQRNVGERSP DQSEHTDGHTSVQSVIEKLQEENRLLKQKVTHVEDLNAKWQRYN ASRDEYVRGLHAQLRGIQIPHEPELMRKEISRLNRQLEEKINDC AEVKQELAASRTARDAALERVQMLEQQILAYKDDFMSERADRER AQSRIQELEEKVASLLHQVSWRQDSREPDAGRIHAGSKTAKYLA ADALELMVPGGWRPGTGSQQPEPPAEGGHPGAAQRGQGDLQCPH CLQCFSDEQGEELLRHVAECCQ  SGIHPSPTEAPPAQHLTMDCTWRILFLVAAATGTHAQVQLLQSG SEVKKPGASVMVSCTVSGYTLTKLSMHWVRQAPGKGLE*MGPFD LQDVETIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HCATDTV  SGCVEMLYSHSLEYNPEWISVQSAVAPAQLAINSDGDL*LHSGE RTRRD*QLPEAGGPGLQEPLOLGELDITSDEFILDEVDG\VDLR HYSKQVELELQQIEQKSIRDYIQESENIASLHNQITACDAVLER MEQMLGAFQSDLSSISSEIRTLQEQSGAMNIRLRNRQAVRGKLG ELVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMINYQ IPQTALLKYRFFYQFLLGNERATAKEIRDEYVETLSKIYLSYYR SYLGRIMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTELEAPILVPHTAQRGGRYPFEALFRSQHYAL LDMSCREYLFICEFFVVSGPAHDLFHAWRGTLSMTLKH DEV		1		NUKNKUI CEISMINNEI NI
SVTSKGKSSSGWPSAASDRDSPVPLRPPGPVQLPSGTGWVLSD *KKKRGRCSS/WLSQPQHEREKEVVLLRRSMAEGERARASDVL CRSLANETHQLRRTLTATAHMCQHLAKCLDERQHAQRNVGERSP DQSEHTDGHTSVQSVIEKLQEENRLLKQKVTHVEDLNAKWQRYN ASRDEYVRGLHAQLRGLQIPHEPELMRKEISRLNRQLEEKINDC AEVKQELAASRTARDAALERVQMLEQQILAYKDDFMSERADRER AQSRIQELEEKVASLLHQVSWRQDSREPDAGRIHAGSKTAKYLA ADALELMYPGGWRPGTGSQQPEPPAEGGHPGAAQRGQGDLQCPH CLQCFSDEQGEELLRHVAECCQ  SGVKKPGASVMVSCYVSGYTLTKLSMHWVRQAPGKGLE*MGPFD LQDVETIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HHCATDTV  5882  2407  2216  SGCVEMLYSHSLEYNPEWISVQSAVAPAQLAINSDGDL*LHSGE RTRRD*QLPEAGGPGLQEPLQLGELDITSDEFILDEVDG\VDLR HYSKQVELELQQIEQKSIRDYIQESENTASLHNQITACDAVLER MEQMLGAFQSDLSSISSEIRTLQEQSGAMNIRLRNRQAVRGKLG ELVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMTNYQ IPQTALLKYRFFYQFLLGNERATAKEIRDEYVETLSKIYLSYYR SYLGRLMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTBLEAPILVPHTAQRGEQRYPFEALFRSQHYAL LDNSCREYLFICEFFVVSGPAAHDLFHAVMGPTI.GMTLKHLDEV	5880	1138	1324	SIWCLVACCICICECCOVO
*KKKRGRCSS/WLSQPQHEREKEVVLLRRSMAEGERARAASDVL CRSLANETHQLRRTLTATAHMCQHLAKCLDERQHAQRNVGERSP DQSEHTDGHTSVQSVIEKLQEENRLKQKVTHVEDLNAKWQRYN ASRDEYVRGLHAQLRGLQIPHEPELMRKEISRLNRQLEEKINDC AEVKQELAASRTARDAALERVQMLEQQILAYKDDFMSERADRER AQSRIQELEEKVASLLHQVSWRQDSREPDAGRIHAGSKTAKYLA ADALELMVYEGWRPGTGSQQPEPPAEGGHPGAAQRGQGDLQCPH CLQCFSDEQGEELLRHVAECCQ GGHPSPTEAPRAQHLTMDCTWRILFLVAAATGTHAQVQLLQSG SEVKKPGASVMVSCYVSGYTLTKLSMHWVRQAPGKGLE*MGPFD LQDVETIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HHCATDTV  5882 2407 2216 SGCVEMLYSHSLEYNPEWISVQSAVAPAQLALNSDGDL*LHSGE RTRRD*QLPEAGGPGLQEPLQLGELDITSDEFILDEVDG\VDLR HYSKQVELELQQIEQKSIRDYIQESENIASLHNQITACDAVLER MEQMLGAFQSDLSSISSEIRTLQEQSGAMNIRLRNRQAVRGKLG ELVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMTNYQ IPQTALLKYRFFYQFLLGMERATAKEIRDEYVETLSKIYLSYYR SYLGRIMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTELEAPILVPHTAQRGEQRYPFEALFRSQHYAL LDNSCREYLFICEFFVVSGPAAHDLFHAVMGPTLSMTLHUDGV	Ì	1	<b>_</b>	CUTEVERGECOMORDA CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTRO
DOSEHTDCHTSVQSVIEKLQEENRLLKQKVTHVEDLNAKWQRYN ASRDEYVRGLHAQLRGLQIPHEPELMRKEISRLNRQLEEKINDC AEVKQELAASRTARDAALERVQMLEQQILAYKDDFMSERADRER AQSRIQELEEKVASLLHQVSWRQDSREPDAGRIHAGSKTAKYLA ADALELMVPGGWRPGTGSQQPEPPAEGGHPGAAQRGQGDLQCPH CLQCFSDEQGEELLRHVAECCQ  5881 26 441 GGHPSPTEAPRAQHLTMDCTWRILFLVAAATGTHAQVQLLQSG SEVKKPGASYMVSCYVSGYTLTKLSMHWVRQAPGKGLE*MGPFD LQDVETIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HHCATDTV  5882 2407 2216 SGCVEMLYSHSLEYNPEWISVQSAVAPAQLALNSDGDL*LHSGE RTRRD*QLP=BAGGPGLQEPLQLGELDITSDEFILDEVDG\VDLR HYSKQVELELQQIEQKSIRDYIQESENIASLHNQITACDAVLER MEQMICAFQSDLSSISSEIRTLQEQSGAMIRLRNRQAVRGKLG ELVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMTNYQ IPQTALLKYRFFYQFLLGNERATAKEIRDEYVETLSKIYLSYYR SYLGRLMKVQYEEVAEKDDLMGVEDTTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTELEAPILVPHTAQRGEQRYPFEALFRSQHYAL LDNSCREYLFICEFFVVSGPAAHDLFHAVMGPTLSMTLKHLDGV		ł		5VISKGKSSSGMWPSAASDRDSPVPLRPPGPVQLPSGTGWVLSD
DOSEHTDCHTSVQSVIEKLQEENRLLKQKVTHVEDLNAKWQRYN ASRDEYVRGLHAQLRGLQIPHEPELMRKEISRLNRQLEEKINDC AEVKQELAASRTARDAALERVQMLEQQILAYKDDFMSERADRER AQSRIQELEEKVASLLHQVSWRQDSREPDAGRIHAGSKTAKYLA ADALELMVPGGWRPGTGSQQPEPPAEGGHPGAAQRGQGDLQCPH CLQCFSDEQGEELLRHVAECCQ  5881 26 441 GGHPSPTEAPRAQHLTMDCTWRILFLVAAATGTHAQVQLLQSG SEVKKPGASYMVSCYVSGYTLTKLSMHWVRQAPGKGLE*MGPFD LQDVETIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HHCATDTV  5882 2407 2216 SGCVEMLYSHSLEYNPEWISVQSAVAPAQLALNSDGDL*LHSGE RTRRD*QLP=BAGGPGLQEPLQLGELDITSDEFILDEVDG\VDLR HYSKQVELELQQIEQKSIRDYIQESENIASLHNQITACDAVLER MEQMICAFQSDLSSISSEIRTLQEQSGAMIRLRNRQAVRGKLG ELVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMTNYQ IPQTALLKYRFFYQFLLGNERATAKEIRDEYVETLSKIYLSYYR SYLGRLMKVQYEEVAEKDDLMGVEDTTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTELEAPILVPHTAQRGEQRYPFEALFRSQHYAL LDNSCREYLFICEFFVVSGPAAHDLFHAVMGPTLSMTLKHLDGV		1		*KKKKGKCSS/WLSQPQHEREKEVVLLRRSMAEGERARAASDVL
ASSENTIGHTS VQSVIEKLQEERRLLKQKVTHVEDLNAKWQRYN ASRDEYVRGLHAQLRGLQIPHEPELMRKEISRLNRQLEEKINDC AEVKQELAASRTARDAALERVQMLEQQILAYKDDFMSERADRER AQSRIQELEEKVASLLHQVSWRQDSREPDAGRIHAGSKTAKYLA ADALELMVPGGWRPGTGSQQPEPPAEGGHPGAAQRGQGDLQCPH CLQCFSDEQGEELLRHVAECCQ GGIHPSPTEAPRAQHLTMDCTWRILFLVAAATGTHAQVQLLQSG SEVKKPGASVMVSCYVSGYTLTKLSMHWVRQAPGKGLE*MGPFD LQDVETIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HHCATDTV SGCVEMLYSHSLEYNPEWISVQSAVAPAQLALNSDGDL*LHSGE RTRRD*QLPEAGGPGLQEPLQLGELDITSDEFILDEVDG\VDLR HYSKQVELELQQIEQKSIRDYIQESENIASLHNQITACDAVLER MEQMLGAFQSDLSSISSEIRTLQEQSGAMNIRLRNRQAVRGKLG ELVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMTNYQ IPQTALLKYRFFYQFLLGNERATAKEIRDEYVETLSKIYLSYYR SYLGRLMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTELEAPILVPHTAQRGEQRYPFEALFRSQHYAL LDNSCREYLFICEFFVVSGPAAHDLFHAVMGPTLSMTLKHLDSV	1	İ		CRSLANETHQLRRTLTATAHMCOHLAKCLDEBOHAODMICEBCD
ASKLEYVRGLHAQIRGLQIPHEPELMRKEISRLNRQLEEKINDC AEVKQELAASRTARDAALERVQMLEQQILAYKDDFMSERADRER AQSRIQELEEKVASLLHQVSWRQDSREPDAGRIHAGSKTAKYLA ADALELMVPGGVRPGTGSQQPEPPAEGGHPGAAQRGQGDLQCPH CLQCFSDEQGEELLRHVAECCQ GGIHPSPTEAPRAQHLTMDCTWRILFLVAAATGTHAQVQLLQSG SEVKKPGASVMVSCYVSGYTLTKLSMHWVRQAPGKGLE*MGPFD LQDVETIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HHCATDTV SGCVEMLYSHSLEYNPEWISVQSAVAPAQLALNSDGDL*LHSGE RTRRD*QLPEAGGPGLQEPLQLGELDITSDEFILDEVDG\VDLR HYSKQVELELQQIEQKSIRDYIQESENIASLHNQITACDAVLER MEQMLGAFQSDLSSISSEIRTLQEQSGANNIRLRNRQAVRGKLG ELVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMTNYQ IPQTALLKYRFFYQFLLGNERATAKEIRDEYVETLSKIYLSYYR SYLGRLMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTELEAPILVPHTAQRGEQRYPFEALFRSQHYAL LDNSCREYLFICEFFVVSGPAAHDLFHAVMGPTLSMTLKHLDSV	1	1	j	DUSERTUGHTSVOSVIEKLOFFNRI.I.KOKUTUREDI MAVMODIDI
AQSRIQELEEKVASLLHQVSWRQDSREPDAGRIHAGSKTAKYLA AQSRIQELEEKVASLLHQVSWRQDSREPDAGRIHAGSKTAKYLA ADALELMVPGGKRPGTGSQQPEPPAEGGHPGAQQRGQGDLQCPH CLQCFSDEQGEELLRHVAECCQ GGIHPSPTEAPRAQHLTMDCTWRILFLVAAATGTHAQVQLLQSG SEVKKPGASVMVSCYVSGYTLTKLSMHWVRQAPGKGLE*MGPFD LQDVETIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HHCATDTV SGCVEMLYSHSLEYNPEWISVQSAVAPAQLALNSDGDL*LHSGE RTRRD*QLPFAGGPGLQEPLQLGELDITSDEFILDEVDG\VDLR HYSKQVELELQQIEQKSIRDYIQESENIASLHNQITACDAVLER MEQMLGAFQSDLSSISSEIRTLQEQSGANNIRLRNRQAVRGKLG ELVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMTNYQ IPQTALLKYRFFYQFLLGNERATAKEIRDEYVETLSKIYLSYYR SYLGRLMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTGSVISPTELEAPILVPHTAQRGEQRYPFEALFRSQHYAL LDNSCREYLFICEFFVVSGPAAHDLFHAVMGPTLSMTLKHLDGV	1	į.		ASKDEYVRGLHAQLRGLOIPHEPELMRKETSRINDOLFERINDO
AQSKIQELEKVASILHQVSWRQDSREPDAGRIHAGSKTAKYLA ADALELMVPGGWRPGTGSQQPEPPAEGGHPGAAQRGQGDLQCPH CLQCFSDEQGEELLRHVAECCQ  SGIHPSPTEAPRAQHLTMDCTWRILFLVAAATGTHAQVQLLQSG SEVKKPGASVMVSCYVSGYTLTKLSMHWVRQAPGKGLE*MGPFD LQDVETIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HHCATDTV  SGCVEMLYSHSLEYNPEWISVQSAVAPAQLAINSDGDL*LHSGE RTRRD*QLPEAGGPGLQEPLQLGELDITSDEFILDEVDG\VDLR HYSKQVELELQQIEQKSIRDYIQESENIASLHNQITACDAVLER MEQMLGAFQSDLSSISSEIRTLQEQSGAMNIRLRNRQAVRGKLG ELVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMTNYQ IPQTALLKYRFYQFLLGNERATAKEIRDEYVETLSKIYLSYYR SYLGRLMKVQYEEVAEKDDLMGVEDTTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTELEAPILVPHTAQRGEQRYPFEALFRSQHYAL LDNSCREYLFICEFFVVSGPAAHDLFHAVMGPTLSMTLKHLDGV	J	i		AZVKQELAASRTARDAALERVOMI FOOTI AVVDDEMCEDADA
ADALELMY GGWRPGTGSQQPEPPAEGGHPGAAQRGQGDLQCPH CLQCFSDEQGEELLRHVAECCQ GGHPSPTEAPRAQHLTMDCTWRILFLVAAATGTHAQVQLLQSG SEVKKPGASVMVSCYVSGYTLTKLSMHWVRQAPGKGLE*MGPFD LQDVETIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HHCATDTV  SGCVEMLYSHSLEYNPEWISVQSAVAPAQLAINSDGDL*LHSGE RTRRD*QLPEAGGPGLQEPLQLGELDITSDEFILDEVDG\VDLR HYSKQVELELQQIEQKSIRDYIQESENIASLHNQITACDAVLER MEQMLGAFQSDLSSISSEIRTLQEQSGAMNIRLRNRQAVRGKLG ELVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMTNYQ IPQTALLKYRFFYQFLLGNERATAKEIRDEYVETLSKIYLSYYR SYLGRLMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTELEAPILVPHTAQRGEQRYPFEALFRSQHYAL LDNSCREYLFICEFFVVSGPAAHDLFHAVMGPTLSMTLKHLDGY		j		AQSRIQELEEKVASLIHOVSWPODSPEDDAGATTADDFFISERADRER
5881  26  441  GGIHFSPTEAPRAQHLTMDCTWRILFLVAAATGTHAQVQLLQSG SEVKKPGASVMVSCYVSGYTLTKLSMHWVRQAPGKGLE*MGPFD LQDVETIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HHCATDTV  5882  2407  2216  SGCVEMLYSHSLEYNPEWISVQSAVAPAQLAINSDGDL*LHSGE RTRRD*QLPEAGGPGLQEPLQLGELDITSDEFILDEVDG\VDLR HYSKQVELELQQIEQKSIRDYIQESENIASLHNQITACDAVLER MEQMLGAFQSDLSSISSEIRTLQEQSGAMNIRLRNRQAVRGKLG ELVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMTNYQ IPQTALLKYRFFYQFLLGNERATAKEIRDEYVETLSKIYLSYYR SYLGRIMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTELEAPILVPHTAQRGEQRYPFEALFRSQHYAL LDNSCREYLFICEFFVVSGPAAHDLFHAVMGPTLSMTLKHLDGV	ŀ	I		ADALELMVPGGWRPGTGSOOREDDAGGGGGGGAAKTAKYLA
GGIHPSPTEAPRAQHLTMDCTWRILFLVAAATGTHAQVQLLQSG SEVKKPGASVMVSCYVSGYTLTKLSMHWVRQAPGKGLE*MGPFD LQDVETIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HHCATDTV  SGCVEMLYSHSLEYNPEWISVQSAVAPAQLALNSDGDL*LHSGE RTRRD*QLPEAGGPGLQEPLQLGELDITSDEFILDEVDG\VDLR HYSKQVELELQQIEQKSIRDYIQESENIASLHNQITACDAVLER MEQMLGAFQSDLSSISSEIRTLQEQSGANNIRLRNRQAVRGKLG ELVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMTNYQ IPQTALLKYRFFYQFLLGNERATAKEIRDEYVETLSKIYLSYYR SYLGRLMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTELEAPILVPHTAQRGEQRYPFEALFRSQHYAL LDNSCREYLFICEFFVVSGPAAHDLFHAVMGPTLSMTLKHLDGV		j		CLOCESDEGGEELI PHUNECCO
SEVKKPGASVMVSCYVSGYTLTKLSMHWVRQAPGKGLE*MGPFD LQDVETIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HHCATDTV  SGCVEMLYSHSLEYNPEWISVQSAVAPAQLAINSDGDL*LHSGE RTRRD*QLPEAGGPGLQEPLQLGELDITSDEFILDEVDG\VDLR HYSKQVELELQQIEQKSIRDYIQESENIASLHNQITACDAVLER MEQMLGAFQSDLSSISSEIRTLQEQSGAMNIRLRNRQAVRGKLG ELVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMTNYQ IPQTALLKYRFFYQFLLGNERATAKEIRDEYVETLSKIYLSYYR SYLGRLMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTELEAPILVPHTAQRGEQRYPFEALFRSQHYAL LDNSCREYLFICEFFVVSGPAAHDLFHAVMGPTLSMTLKHLDGV	5881	26	441	CCTUDEDTEADDAON TOWNS COLUMN
LQDVETIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HHCATDTV  SGCVEMLYSHSLEYNPEWISVQSAVAPAQLALNSDGDL*LHSGE RTRRD*QLPPAGGPGLQEPLQLGELDITSDEFILDEVDG\VDLR HYSKQVELELQQIEQKSIRDYIQESENIASLHNQITACDAVLER MEQMLGAFQSDLSSISSEIRTLQEQSGANNIRLRNRQAVRGKLG ELVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMTNYQ IPQTALLKYRFFYQFLLGNERATAKEIRDEYVETLSKIYLSYYR SYLGRLMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTELEAPILVPHTAQRGEQRYPFEALFRSQHYAL LDNSCREYLFICEFFVVSGPAAHDLFHAVMGPTLSMTLKHLDGV	}		***	GRINGER CHAPKAQHLTMDCTWRILFLVAAATGTHAQVQLLQSG
LQDVETIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HHCATDTV  SGCVEMLYSHSLEYNPEWISVQSAVAPAQLALNSDGDL*LHSGE RTRRD*QLPEAGGPGLQEPLQLGELDITSDEFILDEVDG\VDLR HYSKQVELELQQIEQKSIRDYIQESENIASLHNQITACDAVLER MEQMLGAFQSDLSSISSEIRTLQEQSGAMNIRLRNRQAVRGKLG ELVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMTNYQ IPQTALLKYRFFYQFLLGNERATAKEIRDEYVETLSKIYLSYYR SYLGRLMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTELEAPILVPHTAQRGEQRYPFEALFRSQHYAL LDNSCREYLFICEFFVVSGPAAHDLFHAVMGPTLSMTLKUDGV	1	ľ	l	SEVERPGASVMVSCYVSGYTLTKLSMHWVRQAPGKGLE*MGPFD
5882 2407 2216 SGCVEMLYSHSLEYNPEWISVQSAVAPAQLALNSDGDL*LHSGE RTRRD*QLPEAGGPGLQEPLQLGELDITSDEFILDEVDG\VDLR HYSKQVELELQQIEQKSIRDYIQESENIASLHNQITACDAVLER MEQMLGAFQSDLSSISSEIRTLQEQSGAMNIRLRNRQAVRGKLG ELVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMTNYQ IPQTALLKYRFFYQFLLGNERATAKEIRDEYVETLSKIYLSYYR SYLGRLMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTELEAPILVPHTAQRGEQRYPFEALFRSQHYAL LDNSCREYLFICEFFVVSGPAAHDLFHAVMGPTLSMTLKUDGV	i	1	į	LQDVETIYPQKFQGRVSMTEETSTETTO/AYLELSSLRSEDTAV
SGCVEMTYSHSLEYNPEWISVQSAVAPAQLAINSDGDL*LHSGE RTRRD*QLPEAGGPGLQEPLQLGELDITSDEFILDEVDG\VDLR HYSKQVELELQQIEQKSIRDYIQESENIASLHNQITACDAVLER MEQMICAFQSDLSSISSEIRTLQEQSGAMNIRLRNRQAVRGKLG ELVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMTNYQ IPQTALLKYRFFYQFLLGNERATAKEIRDEYVETLSKIYLSYYR SYLGRLMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTELEAPILVPHTAQRGEQRYPFEALFRSQNYAL LDNSCREYLFICEFFVVSGPAAHDLFHAVMGPTLSMTLKHLDGY	5000			HCATOTV
RTRRPQDPEAGGPGLQEPLQLGELDITSDEFILDEVDG\VDLR HYSKQVELELQQIEQKSIRDYIQESENIASLHNQITACDAVLER MEQMLGAFQSDLSSISSEIRTLQEQSGAMNIRLRNRQAVRGKLG ELVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMTNYQ IPQTALLKYRFFYQFLLGNERATAKEIRDEYVETLSKIYLSYYR SYLGRLMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTELEAPILVPHTAQRGEQRYPFEALFRSQHYAL LDNSCREYLFICEFFVVSGPAAHDLFHAVMGPTLSMTLKHIDGY	2002	2407	2216	SGCVEMLYSHSLEYNPEWISVOSAVAPAOLATMEDODI TITTE
HYSKQVELELQQIEQKSIRDYIQESENIASLHNQITACDAVLER MEQMLGAFQSDLSSISSEIRTLQEQSGAMNIRLRNRQAVRGKLG ELVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMTNYQ IPQTALLKYRFFYQFLLGNERATAKEIRDEYVETLSKIYLSYYR SYLGRLMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTELEAPILVPHTAQRGEQRYPFEALFRSQHYAL LDNSCREYLFICEFFVVSGPAAHDLFHAVMGPTLSMTLKHIDGY	[			RTRRD*OLPEAGGPGLORDLOLGELDTERDEDT********************************
MEQMICGAFQSDLSSISSEIRTLQEQSGAMNIRLRNRQAVRGKLG ELVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMTNYQ IPQTALLKYRFFYQFLLGNERATAKEIRDEYVETLSKIYLSYYR SYLGRLMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTELEAPILVPHTAQRGEQRYPFEALFRSQHYAL LDNSCREYLFICEFFVVSGPAAHDLFHAVMGPTLSMTLKUDGSV	ſ	ľ		HYSKOVELELOOTEOVETEDATOREDIT : SUEETLDEVUG/VDLR
ELVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMTNYQ IPQTALLKYRFFYQFLLGNERATAKEIRDEYVETLSKIYLSYYR SYLGRLMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTELEAPILVPHTAQRGEQRYPFEALFRSQHYAL LDNSCREYLFICEFFVVSGPAAHDLFHAVMGPTLSMTLKHLDGY	ľ	ĺ		MEONI CLEOCOL COLORD LOCAL TOUR LANGITACDAVLER
ELVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMTNYQ IPQTALLKYRFFYQFLLGNERATAKEIRDEYVETLSKIYLSYYR SYLGRLMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTELEAPILVPHTAQRGEQRYPFEALFRSQHYAL LDNSCREYLFICEFFVVSGPAAHDLFHAVMGPTLSMTLKHLDGY	1			MEQMLGAFQSDLSSISSEIRTLOEOSGAMNIRI.RNROAVDCKI.C
ARGIAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMTNYQ IPQTALLKYRFYQFLLGNERATAKEIRDEYVETLSKIYLSYYR SYLGRLMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTELEAPILVPHTAQRGEQRYPFEALFRSQHYAL LDNSCREYLFICEFFVVSGPAAHDLFHAVMGPTLSMTLKHLDGY	j	I	İ	ELVDGLVVPSALVTAILEAPVTEPRFLEOLOEI.DAKAAAVDEOR
1PQIALLKYRFFYQFLLGNERATAKEIRDEYVETLSKIYLSYYR SYLGRLMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTGSVISPTELEAPILVPHTAQRGEQRYPFEALFRSQHYAL LDNSCREYLFICEFFVVSGPAAHDLFHAVMGPTLSMTLKULDGY	1	ļ		ARGTAACADVRGVLDRLRVKAVTKIREFILOKTYSFRKPMTNYO
SYLGRLMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTELEAPILVPHTAQRGEQRYPFEALFRSQHYAL LDNSCREYLFICEFFVVSGPAAHDLFHAVMGPTLSMTLKULDGV	1			IPQTALLKYRFFYOFLLGNERATAKETPDEVIETI CKTV
TLGTRGSVISPTELEAPILVPHTAQRGEQRYPFEALFRSQHYAL LDNSCREYLFICEFFVVSGPAAHDLFHAVMGPTLSMTLKULDSV	J	Į.		SYLGRIMKVOYEEVAEKDDIMGVEDTAVVGGGGGGGGGG
LDNSCREYLFICEFFVVSGPAAHDLFHAVMGPTI.SMTI.KUI.DGV	1			TIGTEGGVIGETELEADILUDINGVEDIARAGFFSKPSLRSRNTIF
LADCYDAIAVFLCIHIVLRFRNIAAKRDVPALDDVWFQW AT I W	J	ł	}	L DNCCBEYL ELGERTHICAGE AND
LADCYDAIAVFLCIHIVLRFRNIAAKRDVDAI, DDVWDOUT AT TW	1	I	1	HDMSCKEILFICEFFVVSGPAAHDLFHAVMGRTLSMTLKHLDSY
THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET THE TABLET			<del></del>	TADCYDATAVFLCIHIVLRFRNIAAKRDVPALDRYWEQVLALLW

SEC	) Decdie		
ID	1	Predicted end	Amino acid segment containing
NO:	beginning	nucleotide	Amino acid segment containing signal peptide
140	1 0 - 1 - 1 - 1	location	
	location	corresponding	
	corresponding	to first	
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	
1	residue of	amino acid	1 D-Detile, 1=Inreonine V-V-1:
ì	amino acid	sequence	In-12 ypcopnan. Y=Twrosing v r-1
	sequence	aedneuce	
			1 /-Egggrafe HRCIGOLIDE incertion/
			FREELILEMN VOSVRSTDPOPLCCLDTPDUVTTPD
l l			T TO THE TEXT TO THE CONTROL OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT O
		Į	NNYDMMLGVLM\E*ERAADDSKEVESFQQLLNARTQEFIEELLS
	{	1	PPFGGLVAFVKEAEALIERGQAERLRGEEARVTQLIRGFGSSWK
1		1	SSVESLSODVMRSETNERNGTGTTGGTTGGTGTGGTGSSWK
5883		<u> </u>	SSVESLSQDVMRSFTNFRNGTSIIQGALTQLIQ\LYHRFHRV\L SQPQLRALPARAELINIHHLMVELKKHKPNF
3683	2	1374	EFPGREEDAYMENCHCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA
ľ			EFPGRRFRAVMEAGAGAGAGAGWSCPGPGPTVTTLGSYEASEG CERKKGOPVGSLERBOMONIO
1	1	i	1 VIIIIVOVIVIGODERRIGINI (AMERICENTE DAT UNESSESSESSESSESSESSESSESSESSESSESSESSESS
- i	1	1	I A . A . COCO A CO PRONINCIO CI LA CALLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DEL LA COLLA DEL LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE L
- 1	ĺ		
	l	ļ	
	J		
- 1	i		THE STATE OF THE PROPERTY AND THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF
- 1	Ĭ		
1	1		
- 1	- [		T = Z Z Z Z Z Z Z
5884	1355		LVVISALLWCWWAETSS (SFSHPEPPIPPSSPCLL*A
2004	4251	2522	GVLARASARLRVPLTGVRACAEPEVGAEPAKVAGAAEPDEDGGR SRLEDCGDVTDSEPLGDVGAEPAKVAGAAEPDEDGGR
	ļ	•	SRLRDCGDYTPSERLGPKGAMLWFQGAIPAAIATAKRSGAVFVV
1	1		FVAGDDEOSTOMAR SWEDDOWNERS CONTRACTOR OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PARTACLE OF THE PA
- 1	ļ.		FVAGDDEQSTQMAASWEDDKVTEASSNSFVAIKIDTKSEACLQF
F			
	1 1		
	[		1
- 1	1		
	]		
	1		
- (	1 1		
1	1 1		The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
	1 1		
1	1		I TO THE TAKEN THE ARGULF K KEGKT VP I. PTO DOCUMENTS
5885	900		
	] 300 ]	467	AAGGGRRSRLSRSWPTGPSKSPSGVRCCG\RR\AWEDKDEFLDV
ĺ	1 1		
			YLQIDEEEYGGTWELTKEGFMTSFA/IVHGHLDHLLHCHPL*LM
5886			VYSSQVLPIQSKGPS TVHGHDDHLLHCHPL*LM
2000	86	1341	PFRGRALTI-KKOPPPGVAPPGV CMCVV
	1	Í	PFRGRALTLKKQPRPGVAPPSLGTCHKSDPGRPAAQSQPPSPGS GTFGLLSFRMIPTKTHTLKWITHOUTH
į	1 }		GTFGLLSFRMVRTKTWTLKKHFVGYPTNSDFELKTSELPPLKNG EVLLFALFLTVDPVMRVANNOL
	1	ŀ	EVLLEALFLTVDPYMRVAAKRLKEGDTMMGQQVAKVVESKNVAL
	1	- 1	PKGTIVLASPGWTTHSISDGKDLEKLLTEWPDTIPLSLALGTVG
ł		l.	
1		j	
1	į į	Ì	
	1	J	
L .	l j	j	
5887	1937		THE TABLE TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF T
1 1	-	104	APGCRGCRATRCPCRGPRWDSLGDEAARSPAAPGGAPGLLGLRE
1 1	i		
1	Į.		
1 1			
1 1	j		***
1	ł	1,	VSFTTKLDIPTAAKYEYGVPLQTSDSFLRFPSSLTSSLCTDNNP
1 1	ļ	1 :	AAFLVNQAVKCTRKINLEGGERIERI GARRESSLTSSLCTDNNP
	I	13	AAFLVNQAVKCTRKINLEQCEEIEALSMAFYSSPEILRVPDSRK
1 1	ł		
1 1	ł		
]	<b>!</b>		
1 1	i		
	Į .	1 -	TO SOLUTION OF CONSUME OF A DISTRICT OF A SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLU
	ſ		
	ľ	; -	ONDRITHIS TAVIF VOVSAPAEAGERADDA TNADI DENTURBE
<u> </u>		V	A STANDAL MARKEDE

SEO	1 5 - 3/ - 5		
ID	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	,	nucleotide	(A=Alanine, C=Cysteine, D=Asparric Acid E-
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine
	location	corresponding	H=H1Stldine, I=Isoleucine, K=Lysine
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
- !	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
ŀ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown *-Ston
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
· <u>L</u>	sequence	1	\=possible nucleotide insertion)
5888	375	2302	LLCRTPGVAMQRADSEQPSKRPRCDDSPRTPSNTPSAEADWSPG
- [			LELHPDYKTWGPEQVCSFLRRGGFEEPVLLKNIRENEITGALLP
1	Į.	1	CLDESRFENLGVSSLGERKKLLSYIQRLVQIHVDTMKVINDPIH
1			GHIELHPLLVRIIDTPQFQRLRYIKQLGGGYYVFPGASHNRFEH
ĺ		1	SLGVGYLAGCLVHALGEKQPELQISERDVLCVQIAGLCHDLGHG
1		1	PFSHMFDGRFIPLARPEVKWTHEQGSVMMFEHLINSNGIKPVME
1	1		QYGLIPEEDICFIKEQIVGPLESPVEDSLWPYKGRPENKSFLYE
i	)		IVSNKRNGIDVDKWDYFARDCHHLGIQNNFDYKRFIKFARVCEV
	1	į .	DNELDICARDEFECAL ADMINISTRAÇÃO SE SE SE SE SE SE SE SE SE SE SE SE SE
1	}	]	DNELRICARDKEVGNLYDMFHTRNSLHRRAYQHKVGNIIDTMIT
İ			DAFLKADDYIEITGAGGKKYRISTAIDDMEAYTKLTDNIFLEIL
}			YSTDPKLKDAREILKQIEYRNLFKYVGETQPTGQIKIKREDYES
	ŀ		LPKEVASAKPKVLLDVKLKAEDFIVDVINMDYGMQEKNPIDHVS
Į.			FYCKTAPNRAIRITKNQVSQLLP\EKFAEQ\LIRVYCKKVDRKS
			LYA\ARQYFVQW\CADR\NFT\KPQDGRCY*PPTP*HPQKKGW\
5889	1831	731	NDSTFSPKIPTRLPRRLPKSRV\QLFKDDPM
	1	731	LPAACGRPVTARPRQAPEGRSGRPRDLDPYPPQVFPPRPDRVAI
			VTGGTDGIGYSTAKHLARLGMHVIIAGNNDSKAKQVVSKIKEET
1			LNDKET*VLLCCPGWLCLWNSSDPPTSASRGAGTTGVHHHFLLK
1			FGIFIL\DLASMTSIRQFVQKFKMKKIPLHVLINNAGVMMVPQR
<b>1</b> i			KTRDGFEEHFGLNYLGHFLLTNLLLDTLKESGSPGHSARVVTVS
			SATHYVAELNMDDLQSSACYSPHAAYAQSKLALVLFTYHLQRLL
1 1			AAEGSHVTANVVDPGVVNTDLYKHVFWATRLAKKLLGWLLFKTP
			DEGAWTSIYAAVTPELEGVGGRYLYNKKETKSLHVTYNQKLQQQ LWSKSCEMTGVLDVTL
5890	1322	200	
		200	FRRGWSAAGRAVPVAFCSRISASSPRRPRGAVRLQSGTEAACRS
1			GRPDPRPASAAGGHAGERMSQRDTLVHLFAGGCGGTVGAILTCP
			LEVVKTRLQSSSVTLYISEVQLNTMAGASVNRVVSPGPLHCLKV
			ILEKEGPRSLFRGLGPNLVGVAPSRAIYFAAYSNCKEKLNDVFD
			PDSTQVHMISAAMAGFTAITATNPIWLIKTRLQL*/SQGTAGKR
	]		RMGAFECVRKVYQTDGLKGFYRGMSASYAGISETVIHFVIYESI
	i		KQKLLEYKTASTMENDEESVKEASDFVGMMLAAATSK\LVATTI
			AYPHEVVRTRLREEGTKYRSFFQTLSLLVQEEGYGSLYRGLTTH
5891	1322	200	LVRQIP\NTAIMMATYELVVYLLNG
		200	FRRGWSAAGRAVPVAFCSRISASSPRRPRGAVRLQSGTEAACRS
			GRPDPRPASAAGGHAGERMSQRDTLVHLFAGGCGGTVGAILTCP
1			LEVVKTRLQSSSVTLYISEVQLNTMAGASVNRVVSPGPLHCLKV
1	i		ILEKEGPRSLFRGLGPNLVGVAPSRAIYFAAYSNCKEKLNDVFD
1	į.		PDSTQVHMISAAMAGFTAITATNPIWLIKTRLQL*/SQGTAGKR
1 1			RMGAFECVRKVYQTDGLKGFYRGMSASYAGISETVIHFVIYESI
1	į.		KQKLLEYKTASTMENDEESVKEASDFVGMMLAAATSK\LVATTI
1			AYPHEVVRTRLREEGTKYRSFFQTLSLLVQEEGYGSLYRGLTTH
5892	1764	379	LVRQIP\NTAIMMATYELVVYLLNG
		379	VVLRVCGRLSVNSAVSSRTGGWSAGLTCAMQRLQVVLGHLRGPA
1	Í		DSGWMPQAAPCLSGAPHASAADVVVVHGRRTAICRAGRGGFKDT
1	J		TPDELLSAVMTAVLKDVNLRPEQLGDICVGNVLQPGAGAIMARI
1			AQFLSDIPETVPLSTVNRQCSSGLQAVASIAGGIRNGSYDIGMA
1 1	1		CGVESMSLADRGNPGNITSRLMEKEKARDCLIPMGITSENVAER
] [	i		FGISREKQDTFALASQQKAARAQSKGCFQAEIVPVTTTVHDDKG
l i			TKRSITVTQDEGIRPSTTMEGLAKLKPAFKKDGSTTAGNSSQVS
[	1	ì	DGAAAILLARRSKAEELGLPILGVLRSYAVVGVPPDIMGIGPAY
		İ	AIPVALQKAGLTVSDVDIFEINE\AFASQAAYCVEKLRLPP*EG
		l	*TPLGGASGP*GHPLGLHWGHVQVITLAQ*S*SARGKRAYRSGC
5893	3		PCAIGSWNGSPLPVFEYPWGT
	٠	1653	ILSKRRCQKAKTKELMAKKVAVIGAGVSGLISLKCCVDEGLEPT
į l		. [	CFERTEDIGGVWRFKENVEDGRASIYQSVVTNTSKEMSCFSDFP
]		j	MPEDFPNFLHNSKLLEYFRIFAKKFDLLKYIQFQTTVLSVRKCP
		1	DFSSSGQWKVVTQSNGKEQSAVFDAVMVCSGHHILPHIPLKSFP
) <i>i</i>			GMERFKGQYFHSRQYKHPDGFEGKRILVIGMGNLGSDIAVELSK
		į	NAAQVFISTRHGTWVMSRISEDGYPWDSVFHTRFRSMLRNVLPR
			TAVKWMIEQQMNRWFNHENYGLEPQNKYIMKEPVLNDDVPSRLL
<u> </u>			CGAIKVKSTVKELTETSAIFEDGTVEENIDVIIFATGYSFSFPF

S	Q Predicted	Predicted end	
	D beginning	nucleotide	
No		location	\nentalling, C=CVsteine, D=Achartic Acta =
	location		Giucamic Acid, F=Phenvialaning C-Class
i	corresponding	corresponding	n=nistidine, i=1soleucine K-Tagine
	to first	,	L=Leucine, M=Methionine, N=Asparagine
- 1	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine
1	residue of	residue of	S=Serine, T=Threonine, V=Valine
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine Y-Inknown + at
Į.		sequence	codon, /=possible nucleotide deletion
	sequence		\=Possible nucleotide insertion)
	•		LEDSLVKVENNMVSLYKYIFPAHLDKSTLACIGLIQPLGSIFPT
		1	AELQARWVTRVFKGLCSLPSERTMMMDIIKRNEKRIDLFGESQS
ĺ	1	[	QTLQTNYVDYLDELALEIGAKPDFCSLLFKDPKLAVRLYFGPCN
			SY*YRLVGPGQWEGARNAIFTQKQRILKPLKTRALKDSSNFSVS
		1	FLLKILGLLAVVVAFF\CQLQWS
589	174	1673	BASBKKALOMKECCA KA CANADA MA
			RYSPKKVLQNKESSLKLGMATALVSAHSLAPLNLKKEGLRVVRE
	]		DHYSTWEQGFKLQGNSKGLGQEPLCKQFRQLRYEETTGPREALS
			RLRELCQQWLQPETHTKEHILELLVLEQFLIILPKELQARVQEH
	•		RESERVANALEDLOLDLGETGOOVDDDOOKKOKII VERMARI
1	Í	•	AGVQEQQVRHECEVTKPEKEKGEETRTENGKLTIMTEGGERING
1	ĺ	ļ	SGRISEPMEAHNEGSNLERHOAKPKEKTEVKCGEPPOPELOUID
	ł	1	I DIEMASTHIGKKLUESDVCOSSSIJTGHKKVI.9*FPKVIAC\ HOLL
1		1	LGCAT QKSSHLVRHQKIHLGEKPYOCNECGKVESONAGI I BUT D
		Ì	I THIGE REFILCING KNFRRSSHLNRHOR I HSOEEDCRCKE COVE
1	1	1	FSQALLTHHQRIHSHSKSHOCNECGKAFSI.TSDI.TPHUBTUTG
		i	EKPFKCNICQKAFRLNSHLAQHVRIHNEEKPYQCSECGEAFRQR
-500		_ <b>i</b>	SGLFQHQRYHHKDKLA
589	5 2967	86	HPSLLGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE
İ		1	MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT
		ľ	RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW
			EATELOPTLSAALYYL\VVQGKKG\EDVLGSVRTLTHIDHSLS
İ	ľ	1	RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW
		1	FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA
		1	EGKGLSPIEDEZERI ATI CERRIAMANTANA
1	ĺ	1	EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ
1	i	1	NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS
		1	RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA
1.	ĺ	1	DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD
1		ľ	1 TOURCEMEARY LADREVEGVCPFCGVREAPGDOCDWGGTG -
	1		MAYEDARPOCKVCRSCPVVOSSOHI,FI,DI,PKI,FKPI,FPWI,GPWI
	ĺ		FGSDWIENAUFITEFFGFREWPSKPRWO*TPDLK/WGWDGD+D
1	1	J .	GEEDK (VFYVWFDATIGYLSITANYTDOWERUM) KNDROWDLYG
ŀ	ł	1	FM (ARDNVPFHSLVFPSSALGAEDNVTI.) VQUI.TATEVT NVEDE
	i i	1	A\FSASKGVGVFRDM\AHDTGTDDDTGDEVt\tVTDDEGV\DGS
1			FOW I DILLIANNS (ELLNNLGNFINDA) CMEVERECO ( 1777 D. C.
	1	[	DIFDOURLEA HOTLELOHYHO LILEKVOTODALDOTI DIR
1		! !	GNQ11 \QVNEPW\KRIKGSEADRORAGTVTGIAVNTAATT CIMT
1	i	i	VEINETVOATIUAULULPPPACSTILTNET.CTI.DAGUOTCONTOR
	1		DEVALENDULESLRORFGGGOAKTSPKPAMMRTVTTAKDOOLGA
i	1		LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG
			KPPEAPKGKKKK
5896	2967	86	HPSLLGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE
1	Į i	1	MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT
1	1	[	RPKVPVLOLDSGNVLESTOR TODARD TO STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE
	į l	l l	RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW
		!	EATELOPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS
ŀ	Į l	i	RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW
1	j	İ	FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA
l		ľ	BONGLSPIEPEEEELATLSEEEIAMAVTAWEKGI.FCI.DDI.DDOO
1	1 1	j	MEVIEVAGERNVLITSALPYVNNVPHI.GNTTGCVI.GADVEADVG
1	1	i	KLKQWNTLYLCGTDEYGTATETKAI.\ FEGI TEOFT CDIGGTT TOO
]	] [	1	DII \KWFNISFDIFGRTTTPOO\TKIT\ODIFOOLI VPCRIT OF
[	1		TVEQUACERCARY\LADREVEGVCPFCGVEEARGDOCDVCCVI +
	1	ı	NAVELXXPQCKVCRSCPVVOSSOHI.FI.DI.DKI.FKDI.FFWI.CDMT
1	1		PGSDWTPNAQFITPFFGFREWPSKPRWO*TPDLK\WGNDCTD+F
	1	l	GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYO
	1	į	FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG
	Į į		K/FSKSRGVGVFDDM/ANDWGTDDD77077.
	1		K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA
	.	<b>↓</b> :	FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV
	· ·		ALERIA OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STAT
		1 .	LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH
			GNQII \QVNEPW\KRIKGSEADRORAGTVTGI.AVNITAATI GIRKI
			GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP LFQKLENDQIESLRQRFGGGQQKTSPKPAVVETVTTAKPQQIQA

	SEQ	Predicted	Predicted end	Amino and
	ΙĎ	beginning	nucleotide	Amino acid segment containing signal peptide
	NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
		location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
- 1		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ı		amino acid	residue of	S=Serine, T=Threonine, V=Valine,
		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ		sequence		\=possible nucleotide insertion)
- 1				QKAPEEFELLSKSAI\KHEYIEDVGECHQPHDWDWAQS*ISTHG
- 1				/YKELYLIRYNNYDRAVINTVPYDVVHRWYTAHRTLTIELRRPE
- 1				NEFWVKLKPGRVLFIDNWRVLHGRECFTGYRQLCGCYLTRDDVL
ŀ	5901			NIARLEGLQA
- 1	2901	1	2121	VAIEQTSLKMMQAVGGAPARPTGEYICNQCGAKYTSLDSFQTHL
- 1		j	1	ATHEOTY LPKLTCPQCNKEFPNOESLLKHVTTHEMITSTVVICE
- 1		·		SCDRQFTSVDDLQKHLLDMHTFVFFRCTLCOEVFDSKVSTOLHI
- 1				\AVKHSNEKKVYRCTSCNWDFRNETDLOLHVKHNHLENDGVALV
-			ļ	CIFCGESFGTEVELQCHITTHSKKYNCKFCSKAFHATILLERUI
				REARCVESTRIPNCGINGASEOVOKEEVELOTI. TUSOFCHNOW
- [				DGSEEDVDTSEPMYGCDICGAAYTMETLIONHOLDDUNIBDGES
- 1		Í		ALVKKKAELIKGNYKCNVCSRTFFSENGLREHMOTHLGDUVENM
-				CPICGERFPSLLTLTEHKVTHSKSLDTGNCRICKMPLQSEEEFL
				EHCQMHPDLRNSLTGFRCVVCMQTVTSTLELKIHGTFHMQKTGN
				GSAVQTTGRGQHVQKLYKCASCLKEFRSKQDLVKLDINGLPYGL
				CAGCVNLSKSASPGINVPPGTNRPGLGQNENLSAIEGKGKVGGL
				KTRCS*LATFKF*VLKVELPEPHPKPFHRGVSRPDSNSTQLKTP QVSPMPRISPSQSDEKKTYQCIKCQMVFYNEWDIQVHVANHMID
-	- 1			EGLNHECKLCSQTFDSPAKLQCHLIEHSFEGMGGTFKCPVCFTV
	i			FVQANKLQQHIFSAHGQEDKIYDCTQCPQKFFFQTELQNHTMTQ
F	5000			HSS
1	5902	712	209	LKNRRRSRPSIRQSIGSTSVSRWLTSLFTYLDHTADVQ*V*REF
1	ì			1 PLAPKU*ED*MFQSWLHAWGDTLEEAFEOCAMAMEGYMTDTCT
-	ļ			VEPLQTVEVETQGDDLOSLLFHFLDEWLVKFSADEREID\CMCF
H	5903	2106	735	BFSDSKHPQGTEVKAITYSAMOVYNEENPEVEVIIDI
		2200	735	DTPGPSLPSTTAPFSLRSLSFPSRPSYLLPGDPQPLQGRGLPTT
i				PALFALSAVPGGAASPMPPSGLRLLPLLPLLWLLVLTPGRPAA
				GLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGEVPPGP
1	· 1	1		LPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVET HNEIYDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRI
1	ĺ			KLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEWLSFDVTGVV
1		1		ROWLSRGGETEGFRLSAHCSCDSRDNTT.OVDINGETTCD\ DCDt
	l			ATTHGMNRPFLLLMATPLERACHTOG/ CDUBOAT / DOWNS GROOD
1				HOGENCERC/VHC*HLIFRKDI.\GW\KWT\UE\DECVUANEC\+
	,			GPCPYIWSLDTOYSKVLALYNO\HKPG\ AGAAD\ CCUDOAT HD\
	5904	3	1126	TELVII VGRKEKVEOLSNMIVRSCKCS
1	İ			MMEEIENAINTFKEEQRLIYEELIKEEKTTNNELSAISRKIDTW
1		1		ALGNSETEKAFRAISSKVPVDKVTPSTLPEEVLDFEKFLQQTGG RQGAWDDYDHQNFVKVRNKHKGKPTFMEEVLEHLPGKTQDEVQQ
	I			HEKWYQKFLALEERKKESIQIWKTKKQQKREEIFKLKEKADNTP
				VUERNAQEDNOKOKEEORKKOKI.AVEAWKKOVCTEMONKOA CO.
1	1	İ		KEEEEKEKKHQKERQROFKLKI LLESYTOOKKEOEEEIDI PURT
ł		į		REMARKANAADE ISRFOERDLHKI.FI.KII.DROAKEDEKSO
l				AQRRLAKLKEKVENNVSRDPSRLY/NTHORLGRTNOKDPTNPLW
┝	5905	287		ALSTYPT*GYSNLETRNTEKSMR
l		207	2912	MASFPPRVNEKEIVRLRTIGELLAPAAPFDKKCGRENWTVAFAP
l	1		j.	DGS 1 FAWSQGHRTVKLVPWSOCLONFI, LHGTKNVTNGGGLDI OD
				QNSDGGQKNKPREHIIDCGDIVWSLAFGSSVPEKQSRCVNIEWH
ŀ	i			RFRFGQDQLLLATGLNSGRIKIWDVYTGKLLLNLVDHTGVVRDL
ŀ				TFAPDGSLILVSASRDKTLRVWDLRDDGN\MMKVLRGHQNWVY\
	- 1		ľ	SCAFSPDSSMLCSVGASKAVVAAILV*LRLCWHHSHTGATMVLS
		1		WAERVASLATGLGATFTIG*SNLAFVLQGVLYVHRCWSMSTFCF
	İ		1	SFFLFFFFKVISPTVKYH*LLSKLIFQFYGIGSLTSETNLM*SI WLSNGFSVLFFGILSDSRDILRL*PNLKFVLIFF*K*CIVSVQK
	J	ļ		KKKPKRIALLQEERLS*DKPPSSHLI*QTEVNIRILFRAILHS*
	1	ĺ		LLIFRI*NCI*TYS*IIDPFYIQMTYDRG*FGKNKMVKF*FIEM
	}			*LYYFHKIAFSFCNVV*HPCCLPKKFHLAVNTI.FACSTCFSS+A
		İ	Ι,	QVGDPSLL*TSDYLKGRCOWSNNLLTLRFLSVYFFKNIANGGER
	}	}	1.	REGGL*YLTLFISVYFS*LVFGINGFOYSFVVKIHCLVEMEDIT
			1.3	FKLTFNRNI*NRICMSALINLKTDFNLTMTLSIFFKLLTTVMA*
				YNLN*I*QF*YKMCHFVLCMSE*SYNICLFIAGF\LWNMDKYTM

Deginning   noutbottde   location   corresponding   corresponding   corresponding   corresponding   cofirst   amino acid   cofirst   amino acid   corresponding   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   cofirst   co	SEQ	Predicted	Predicted end	Desire
NO: nucleotide corresponding to first amino acid corresponding to first amino acid residue of amino acid sequence corresponding to first amino acid sequence corresponding to first amino acid sequence corresponding to first amino acid sequence corresponding to first amino acid sequence corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first correspondin	4	1		Amino acid segment containing signal peptide
Cocation   Corresponding   Coffree   Contragonding   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   Coffree   C	t .		1	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
corresponding to first amino acid to first amino acid cresidue of amino acid cresidue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence se			l e	W-Wishidden T. Tank
to first amino acid residue of amino acid residue of amino acid sequence    P-Prolime, Y-Tyrcosine, X-Unknown, *=Stop   Codon, /=possible muclectide daletion	1			La Louisian M. Mahlainaine, Kabysine,
amino acid residue of amino acid sequence  S-Sertine, T-Threonine, Medicine, Medicine, Sequence  amino acid sequence  Sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence  FIRESHIP - Not acid sequence			ľ	Balance, Mamethionine, NaAsparagine,
xesidus of amino acid sequence		-		Partoline, QaGiutamine, RaArginine,
sequence  Codon, '-possible mucleotide insertion'  - possible mucleotide insertion'  FREESHINDWORDFSPERALLATASYPTRY/IRPERINDLY  FREESHINDWORDFSPERALLATASYPTRY/IRPERINDLY  FREESHINDWORDFSPERALLATASYPTRY/IRPERINDLY  FREESHINDWORDFSPERALLATASYPTRY/IRPERINDLY  FREESHINDWORDFSPERALLATASYPTRY/IRPERINDLY  FREESHINDWORDFSPERALLATASYPTRY/IRPERINDLY  FREESHINDWORDFSPERALLATASYPTRY/IRPERINDLY  FREESHINDWORDFSPERALLATASYPTRY/IRPERINDLY  FREESHINDWORDFSPERALLATASYPTRY/IRPERINDLY  FREESHINDWORDFSPERALLATASYPTRY/IRPERINDLY  FREESHINDWORDFSPERALLATASYPTRY/IRPERINDLY  FREESHINDWORDFSPERALLATASYPTRY/IRPERINDLY  FREESHINDWORDFSPERALLATASYPTRY/IRPERINDLY  FREESHINDWORDFSPERALLATASYPTRY/IRPERINDLY  FREESHINDWORDFSPERALLATASYPTRY/IRPERINDLY  FREESHINDWORDFSPERALLATASYPTRY/IRPERINDWORDFSPERALLATASYPTRY  FREESHINDWORDFSPERALLATASYPTRY/IRPERINDWORDFSPERALLATASYPTRY  FREESHINDWORDFSPERALLATASYPTRY/IRPERINDWORDFSPERALLATASYPTRY  FREESHINDWORDFSPERALLATASYPTRY/IRPERINDWORDFSPERALLATASYPTRY  FREESHINDWORDFSPERALLATASYPTRY/IRPERINDWORDFSPERALLATASYPTRY  FREESHINDWORDFSPERALLATASYPTRY/IRPERINDWORDFSPERALLATASYPTRY/IRPERINDWORDFSPERALLATASYPTRY/IRPERINDWORDFSPERALLATASYPTRY/IRPERINDWORDFSPERALLATASYPTRY/IRPERINDWORDFSPERALLATASYPTRY/IRPERINDWORDFSPERALLATASYPTRY/IRPERINDWORDFSPERALLATASYPTRY/IRPERINDWORDFSPERALLATASYPTRY/IRPERINDWORDFSPERALLATASYPTRY/IRPERINDWORDFSPERALLATASYPTRY/IRPERINDWORDFSPERALLATASYPTRY/IRPERINDWORDFSPERALLATASYPTRY/IRPERINDWORDFSPERALLATASYPTRY/IRPERINDWORDFSPERALLATASYPTRY/IRPERINDWORDFSPERALLATASYPTRY/IRPERINDWORDFSPERALLATASYPTRY/IRPERINDWORDFSPERALLATASYPTRY/IRPERINDWORDFSPERALLATASYPTRY/IRPERINDWORDFSPERALLATASYPTRY/IRPERINDWORDFSPERALLATASYPTRY/IRPERINDWORDFSPERALLATASYPTRY/IRPERINDWORDFSPERALLATASYPTRY/IRPERINDWORDFSPERALLATASYPTRY/IRPERINDWORDFSPERALLATASYPTRY/IRPERINDWORDFSPERALLATASYPTRY/IRPERINDWORDFSPERALLATASYPTRY/IRPERINDWORDFSPERALLATASYPTRY/IRPERINDWORDFSPERALLATASYPTRY/IRPERINDWORDFSPERALLATASYPTRY/IRPERINDWORDFSPERALLATASYPTRY/IRPERINDWORDFSPERALLATASYPTRY/IRPERINDWORDFSPERALLATASYPTRY/IRPERINDWORDFSP	1	,		Seserine, TeThreonine, Vevaline,
Sequence    A-possible mociacide timeset solescon.	1	•		w=1ryptopnan, Y=Tyrosine, X=Unknown, *=Stop
FRILEGHIRDWINCDFSDEGILLATRESYDTENT (INDPINIBILITIES FIGHLEPPIPT I FAGGANDHUNGUS BIBLIGHT ALDDOWNAY FOR IDED PUVOVAPLSINGLICA, PETOS SUBJECT ALDDOWNAY FOR IDED PUVOVAPLSINGLICA, PETOS SUBJECT ALDDOWNAY FOR IDED PUVOVAPLSINGLICA, PETOS SUBJECT ALDDOWNAY FOR IDED PUVOVAPLSINGLICA, PETOS SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT AND SUBJECT A	}		sequence	Codon, /=possible nucleotide deletion,
FEGILLEP PTET FRAGANDRWINGSYSFINDS/LAAGFILDS/VYFWAT FRIEDRYPYQUAPLS.GNICLOR/STICOS/LAAGFILDS/VYFWAT FROM TREDRYPYQUAPLS.GNICLOR/STICOS/LAAGFILDS/VYFWAT FROM TREDRYPYQUAPLS.GNICLOR/STICOS/LAAGFILDS/VYFWAT FROM TREDRYPYQUAPLS.GNICLOR/STICOS/LAAGFILDS/VYFWAT FROM THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE	<del></del>	Doqueinee	<u> </u>	\=possible nucleotide insertion)
FRR IDED PYCYPALSANGLCAFSTDOS YLAGGHUGS VYPME FROM PYCHALLAGA THROW YOU SIGNATURE TREMPTOSCUELP IP SKILEFLEY FIT FROM PAGE TO THE TREMPTOSCUELP IP SKILEFLEY FIT FROM THE TREMPTOSCUELP IP SKILEFLEY FIT FROM THE TREMPTOSCUELP IP SKILEFLEY FIT FROM THE TREMPTOSCUELP IP SKILEFLEY FIT FROM THE TREMPTOSCUELP IP SKILEFLEY FOR THE TREMPTOSCUELP IP SKILEFLEY FOR THE TREMPTOSCUELP FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFLEY FOR THE TREMPT SKILEFL		1		TRKLEGHHHDVVACDFSPDGALLATASYDTRVYIWDPHNGDILM
5906  146  2036  REAGASGRASA AVAPYETE IN EXPENDING PRICE WESTAGES FOR STITUTE AND AVERHER DEVEKTION RETURN REPORT OF THE PROPERTY EXPENSION RECYTEMENTS OF THE PROPERTY EXPENSION RECYTEMENTS OF THE PROPERTY EXPENSION RECYTEMENT OF THE PROPERTY EXPENSION RECYTEMENT OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE	1			EFGHLFPPPTP1FAGGANDRWVRSVSFSHDGLHVASLADDKMVR
### ### ### ### ### ### ### ### ### ##				FWRIDEDYPVQVAPLSNGLCCAFSTDGSVLAAGTHDGSVYFWAT
PORISONARISM IN TIGHT STUDY GUNGGENERY KERSAGS I PORISONARITY PSIQIANY YGRGKVAITYK NOPYKPHEN DIVGKOCED (SYYEAF GCE NEP LIF FQN LIGHCYKKEVGE ALITALIPPUV SSIP YDRAPATAELEVCKVINKOGSVOG BEI PILLORW GOKOD I EVREY LINDWERKE I FEGODVHRQVAIVE ROMA, TTALPPVV SSIP YDRAPATAELEVCKVINKOGSVOG BEI PILLORW GOKOD I EVREY LINDWERKE I FEGODVHRQVAIVE TPPYCKAITEPVTV KYOLER SDGEVYEKEPHLIFSHDAVYRBMP TUVS GABSTYPE FOR I GEGEVER FRUDDELES SHESVAIPPTE SORTINELSS FSTETLES NSQSI I PPELET PVGNDLMARAGINN ADDIVOMEAS SHESHASMAD I PSSS SASSVAIPPTE SORTINELSS FSTETLES NSQSI I PPELET PVGNDLMARAGINN ADDIVOMEAS SHESPESCAINS HIESEGPSSTANSHYVPUDSOV SORTINELSS FSTETLES NSQSI I PPELET PVGNDLMARAGINN ADDIVOMEAS SHOPS CAINS HIESEGPSSTANSHYVPUDSOV SORTINELSS FSTETLES NSQSI I PPELET PVGNDLMARAGINN ADDIVOMEAS SHOPS CAINS HIESEGPSSTANSHYPVQUDSOV SORTINELSS FSTETLES NSQSI I PPELET PVGNDLMARAGINN ADDIVOMEAS SHOPS CAINS HIESEGPSSTANSHYPVQUDSOV SORTINELSS FSTETLES NSQSI I PPELET PVGNDLMARAGINN ADDIVOMEAS SHOPS TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP TO SHOP	5906	146	2020	PROVPSLQHLCRMSIRRVMPTQEVQELPIPSKLLEFLSYRI
DLVGKNCER)-GYYEAFGGE RRPLLFRON LGIRCVEKKEVE A LITR\IRAGINEPDY-PKGNDTED CHANCE A CHANGE CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE A CHANGE	1 2200	1 30	2038	REGAGSGRMASGA\YNPYIEIIEQPRQRGMRFRYKCEGRSAGSI
A LITRITATION FOR PROLIBORIDATION AND THE CONSTRUCTION OF THE PROLIBORING TO STANDAM THE PROLIBORATION OF THE PROLIBORING TO STANDAM THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORIST OF THE PROLIBORI		1		PGEHSTDNNRTYPSIQIMNYYGKGKV\RITLVTK\NDPYKPHPH
HGNN_TTALPPV\VSSFITUNRARNTAELRYCRVNKYGSVEGG DEIPLICORVQKODIEVERVLMOMAGIG ZADVHROVAIVFK TPPYCKAITEPVTVKMQLRRFSDGEVSESMDFRYLPDEKDTTGM AKKGKTTLFCKLCOPHETGFRHVDGELLTSGDEPPTLAS GSAGITVNFPERFRFGLLSSIGEGRYFKKEPMLFSIDAVVREMP TOVSSQASSYTPSDGIFFFRENGSISPMSVANPPPR SONTNPLSSFSTRTLPSNSGIFFPLRIPVGMDLMASNACIVNN ADDIVGMERSSMFSADLYGISDPMSMTTSSSSMSSANPPPR SONTNPLSSFSTRTLPSNSGIFFPLRIPVGMDLMASNACIVNN ADDIVGMERSSMFSADLYGISDPMSMTTSSSSMSGANSHTT VPVSGSDAFEGSDFSCADMSMINESGFSNSTYMPSHVPVQUSGY SIGSMGMRGUSDSFYTEFFQU  SIGSMGMRGUSDSFYTEFFQU  **TILLSSMSS**INLDFTKESQWX/PKEMPKLTSMSYPQDAKQMGK** KATSKVESAPHFVUPNDHAMREAELKKKWVEMPREKQOAAREGE ROKEPTIESYCQDULRRGGEFBHKEEVLQELMMFPGDEAVRAGGNK KATSKVESAPHFVUPNDHAMREAELKKKWVEMPREKQOAAREGE ROKEPTIESYCQDULRRGGEFBHKEEVLQELMMFPGDEAVRAGGNK KILVLVINALDLIPPEVVEKWILDVLRMELDTVAFKAFGGWYNDK NECSVPUQDASBSLLKSKACGGANIMATUGNYCRGGEVFTHIR VCVVGLPPWGMSSLINSLKERRACSWGAVPGITKFGGEVFTHIR VCVVGLPWGMSSLINSLKERRACSWGAVPGITKFGGEVFTHIR VCVVGLPWGMSSLINSLKERRACSWGAVPGITKFGGEVTHIR VCVVGLPWGMSSLINSLKERRACSWGAVPGITKFGGEVTHIR VCVVGLPWGMSSLINSLKERRACSWGAVPGITKFGGEVTHER VCVVGLPWGMSSLINSLKERRACSWGAVPGITKFGGEVTHER VCVVGLPWGMSSLINSLKERRACSWGAVPGITKFGGEVTHER VCVVGLPWGMSSLINSLKERRACSWGAVPGITKFGGEVTHER VCVVGLPWGMSSLINSLKERRACSWGAVPGITKFGGEVTHER VCVVGLPWGMSSLINSLKERRACSWGAVPGITKFGGEVTHER VCVVGLPWGMSSLINSLKERRACSWGAVPGITKFGGEVTHER VCVVGLPWGMSSCSTYPTHTLTPTHLSENFMTLADAT ENTITYKTGLDTGTGTTMCVVGWGTHEAVLGNYCKGGEVTHERIT VCXWGAVSTARAGCGTTREFLTAVARRACKGGLYSGEQAAA AVLADAWVSKISTSTYLPDGAGAAALKKKKKMGKRADKIASKI SUMMSALDJSGANDGOVGU VSUGRESGGSSSGFGGGGGGGGAAALKKKKKMGKRADKIASKI  **SOMMSALDJSGANDGOVGU VKSCSCFFGQVAGTTRARPSCVDASIVKKKKMGKRADKIASKI ULDRKGMSCSSGNKVKTRTTH.PPHSHSTHERIGABPTVLKKATAGCCMMSKTPLDTUTSDGS STLMARSSYVSIGHSGDLIVKTGGGGGAAALAGCGARAPP VKSCSFFGQUAGTTRARPSCVDASIVERGCGGASKLILISFSLS DFQAMGLKKGMFRNDPVLKTSTOPGGASRLILISFSLS DFQAMGLKKGMFRNDPVLKTSTOPGGASRLILISFSLS DFQAMGLKKGMFRNDPVLKTSTOPGGASRLILISFSLS DFQAMGLKKGMFRNDPVLKTSTOPGGASRLILISFSLS DFQAMGLKKGMFRNDPVLKTSTOPGGASRLILISFSLS SSISHAPEGUAGGGSAAALEE GERLGLAFSVVKNSKRPCLEVSLLETVIASACCDETTRTHYTT INTLHEMPSGAGGSAAA				DLVGKDCRD\GYYEAEFGQE\RRP\LFPQN\LGIRCVKKKEVKE
DEITLICDRVQKDDIEVREVUNDURGGIFSGADVHRQVAIUPK TFPYCKAITEPVTUKMGLREPSDGEVESGMPTLEPEKDTYGN KAKKQKTTLIFOKLOCOHVETGFRUDGGLELITGDPTLAS GSGAGITVNP PERPREJGLISGEGRYFKEDDIANSANGLYRM TOVSSQASSYPSDGISGLISGERYFKEDDIANSANGLYRM ADDIVOMEASSMPSADLYGISDPMLSNGSWAWATTSDBWGET DNFRLISMILENPSCNSVLDPPDILGAUDIANSANGLYNN ADDIVOMEASSMPSADLYGISDPMLSNGSWAWATTSDBWGET DNFRLISMILENPSCNSVLDPPDILGAUDIANSANGLYNN ADDIVOMEASSMPSADLYGISDPMLSNGSWAWATTSDBWGET DNFRLISMILENPSCNSVLDPPDILGAUDIANSANGLYNN ADDIVOMEASSMPSADLYGISDPMLSNGSWAWATTSDBWGET DNFRLISMILENPSCNSVLDPPDILGAUDIANSANGLYNN ADDIVOMEASSMPSADLYGISDPMLSONGSWAWATTSDBWGET DNFRLISMILENPSCNSVLDPPDILGAUDIANSANGLYNN ADDIVOMEASSMPSADLYGISDPMLSONGSWAWATTSDBWGET DNFRLISMILENPSCNSVLDPPDIV VEVSGSDAFERDEVICLEDPDILGAUDIANSANGLYBOORG KATSKUPSAPVUPKIPHUHANNERGLKKKWERMERKOANSKOR KATSKUPSAPVUPKIPHUHANNERGREHKKKWERMERKOANSKOR KUPLVINKINLUTYREVERMIDURINELETIMPFOLIDBATRK AYKEFRKVURYSDVILEVLDARDPIGCRCPQMEBAVLBAQOMK KUPLVINKINLUTYREVERMIDURINELEKKKKKGULSGURATHA AYKADROVASSLINSLKERSRACSWADHARASTATOVANA KUPLVINKINLUTYREVERMIDURINGURTHANGEVERHENPOLIDBATRK KUPLVINKINGUNGSSLINSLKERSRACSWADHARASTATOVANA VALADAVSAKISFYIPPATHTILTAHRILKKKKKGGLYSGCOAAA AVLADAVSAKISFYIPPATHTILLHITAHRILKKKKKGGLYSGCOAAA AVLADAVSAKISFYIPPATHTILLHITAHRILKKKKKGGLYSGCOAAA AVLADAVSAKISFYIPPATHTILLHISMITAHDA ENKTYTYKIGDLTSYCTYRINRHOMGAKRNVOHAPKSISMIDVU SVORRSVLGRATHATYCTYRINRHOMGAKRNVOHAPKSISMIDVU SVORRSVLGRATHATYCTYRINRHOMGAKRNVOHAPKISMIDVU SVORRSVLGRATHATYCTYRINRHOMGAKRNVOHAPKISMIDVU SVORRSVLGRATHATYCTYRINRHOMGAKRNVOHAPKISMIDVU SVORRSVLGRATHATYCTYRINRHOMGAKRNVOHAPKISMIDVU SVORRSVLGRATHATYCTYRINRHOMGAKRNVOHAPKISMIDVU SVORRSVLGRATHATYCTYRINRHOMGAKRNVOHAPKISMIDVU SVORRSVLGRATHATYCTYRINRHOMGAKRNVOHAPKISMIDVU SVORRSVLGRATHATYCTYRINRHOMGAKRNVOHAPKISMIDVU SVORRSVLGRATHATYCTYRINRHOMGAKRNVOHAPKISMIDVU SVORRSVLGRATHATYCTYRINRHOMGAKRNVOHAPKISMIDVU SVORRSVLGRATHATYCTYRINRHOMGAKRNVOHAPKISMIDVU SVORRSVLGRATHATYCTYRINRHOMGAKRNVOHAPKISMITAH HTTILBATITARPPHSHSTIRGGAGGARAFALVATARACH UTUMPKISMIDANATATARATATARATATARATATARATATARATATARATATARATATARATATARATATARATATARATATARA	<u> </u>	ļ.	1	A/11TR/1KAGINPFDVP*KQLNDIEDCDLDVVRLWFRVFLPDG
TFPYCKAITEPUTVKMOLERESDOEVSESMDERTLEPEKUTYGEN KAKKOKTLIFCKLCOUNFUTFERHUNDELLITSCOPPTLAS QSAGITVNPPEREPRGLLSSICSEGRYFKKEPRLSSIGNVTREPT TOVSSQASSYTYSDEOTISGLSHEAMSAPLEPSSWSSVANPTPR SONTNDLSSFSTRTLPSNSQLIPPTLRIVGENDLANGACIYNN ADDIVOMEASSYMSADLYGISDPMISGNSCVMMTTSSDSMGET DNPRLISMHLENBSCNSVLDPRDLRQLHOMSSSSMSAGANSHTV VFVSQSDAFESGSDSSCANDSMINESGSSNSTWHSHVYQDSQY SGIGSMONDLSDSFYTEFFQV SGISSMONDLSDSFYTEFFQV SGISSMONDLSDSFYTEFFQV SGISSMONDLSDSFYTEFFQV SGISSMONDLSDSFYTEFFQV SGISSMONDLSDSFYTEFFQV SGISSMONDLSDSFYTEFFQV SGISSMONDLSDSFYTEFFQV SGISSMONDLSDSFYTEFFQV SGISSMONDLSDSFYTEFFQV SGISSMONDLSDSFYTEFFQV SGISSMONDLSDSFYTEFFQV SGISSMONDLSDSFYTEFFQV SGISSMONDLSDSFYTEFFQV SGISSMONDLSDSFYTEFFQV SGISSMONDLSDSFYTEFFQV SGISSMONDLSDSFYTEFFQV SGISSMONDLSDSFYTEFFQV SGISSMONDLSDSFYTEFFQV SGISSMONDLSDSFYTEFFQV SGISSMONDLSDSFYTEFFQV SGISSMONDLSDSFYTEFFQV SGISSMONDLSDSFYTEFFQV SGISSMONDLSDSFYTEFFQV SGISSMONDLSDSFYTEFFQV SGISSMONDLSDSFYTEFFQV SGISSMONDLSDSFYTEFFQV SGISSMONDLSSSSSSTAGSGOLGCOTPEPSLSSEGFTLIGGV SGISSMONDLSGSSDSFLLGDTDPLEMERIKLHSPMTKLDADI SGISSMONDLSGSSDSFLLGDTDPLEMERIKLHSPMTKLDADI SGISSMONDLSGSSDSFYTEFFQV SGISSMONDLSGSSDSFYTEFFQV SGISSMONDLSGSSDSFYTEFFQV SGISSMONDLSGSSDSFYTEFFQV SGISSMONDLSGSSDSFYTEFFQV SGISSMONDLSGSSDSFYTEFFQV SGISSMONDLSGSSDSFYTEFFQV SGISSMONDLSGSSDSFYTEFFQV SGISSMONDLSGSSDSFYTEFFQV SGISSMONDLSGSSDSFYTEFFQV SGISSMONDLSGSSDSFYTEFFQV SGISSMONDLSGSSDSFYTEFFQV SGISSMONDLSGSSDSFYTEFFQV SGISSMONDLSGSSDSFYTEFFQV SGISSMONDLSGSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	1	1		HGNL\TTALPPV\VSSPIYDNRAPNTAELRVCRVNKNCGSVRGG
KAKKOKTTLIFOKICODHUETGFRHUDQDGLELLTSGDPPTLAS  SASAITUNP PERRPREJALSGIGSGEVERPENJENDAVREMP TUVSSQAESYYPSOPISSGISHASMAPLESSSWSSVAHPPER SONTNILSSFSTRTLPENSOGIPPH_PORONIASSASSMSACAINSTT UPVSQSDAFEGSDFSCADNSMINESGPSNSTNPNSHVFVQUSQY SGIGSMGNNGLSDSSPYSFPTOV  TULISSKSS**ALDPKTRSQVV/RKGRKKISMPYPQPAKONGK KATSVVPSAPHFVHPNDHANREAELKKKWVERMFREKQOAAREQE ROKRRTIESYCQDULRRQEBFBHKEVYLQEINMFPGLIDDEATRK AYYKEFRKVVEYSDVILEVLDARDPLGCKCORGRAVLAGGNK KULVLINKLDLVPKEVVEKHLDYLKRHEVTVARKASTOHVOKNIL NRCSVPVQASESLLKSKACFGABNIMSVLGNYCRIGEVTHIK VGVVGLPNNGKSSLINSLKSRACSGABNIMSVLGNYCRIGEVTHIK VGVVGLPNNGKSSLINSLKSRACSGABNIMSVLGNYCRIGEVTHIK VGVVGLPNNGKSSLINSLKSRACSGABNIMSVLGNYCRIGEVTHIK VGVVGLPNNGKSSLINSLKKSRACSGABNIMSVLGNYCRIGEVTHIK VGVVGLPNNGKSSLINSLKKSRACTSGABNIMSVLGNYCRIGEVTHIK VGVVGLPNNGKSSLINSLKKSRACTSGABNIMSVLGNYCRIGEVTHIK VGVVGLPNGKSSLINSLKKSRACTSGABNIMSVLGNYCRIGEVTHIK VGVVGLPNGKSSLINSLKKSRACTSGABNIMSVLGNYCRIGEVTHIK VGVVGLPNGKSSLINSLKKSRACTSGABNIMSVLGNYCRIGEVTHIK VGVVGLPNGKSSLINSLKKSRACTSGABNIMSVLGNYCRIGEVTHICK NLEEISNYYGVGSGOYTEHPLTAVARHCKKKGGLYSGOQAAA AVLADWVSGKISTYIPPPATHTIPHLSAEIVKKKGGLYSGOQAA AVLADWVSGKISTYIPPPATHTIPHLSAEIVKKKGGLYSGOQAA AVLADWVSGKISTYTORPRINGMGMAKRNUDHRYKSNSMYDVC SURRSVLORIMETELATORSDELIGUTDPLEMELLLHSPMYKIADAI ENKTTYVKIGDLTGYCTNPNRINGMGMAKRNUDHRYKSNSMYDVC SURRSVLORIMETELATORPRINGMGMAKRNUDHRYKSNSMYDVC SURRSVLORIMETELATORPRINGMGMAKRNUDHRYKSNSMYDVC SURRSVLORIMETELATORPRINGMGMAKRNUDHRYKSNSMYDVC SURRSVLORIMETELATORPRINGMGMAKRNUDHRYKSNSMYDVC SURRSVLORIMETELATORPRINGMGMAKRNUDHRYKSNSMYDVC SURRSVLORIMETELATORPRINGMGMAKRNUDHRYKSNSMYDVC SURRSVLORIMETELATORPRINGMGMAKRNUDHRYKSNSMYDVC SURRSVLORIMETELATORPRINGMGMAKRNUDHRYKSNSMYDVC SURRSVLORIMETELATORPRINGMGMAKRNUDHRYKSNSMYDVC SURRSVLORIMETELATORPRINGMGMAKRNUDHRYKSNSMYDVC SURRSVLORIMETELATORPRINGMGMAKRNUDHRYKSNSMYDVC SURRSVLORIMETELATORPRINGMGMAKRNUDHRYKSNSMYDVC SURRSVLORIMETELATORPRINGMGMAKRNUDHRYKSNSMYDVC SURRSVLORIMETELATORPRINGMGMAKRNUDHRYKSNSMYDDAF HTGTLERGATORPRINGMGMAKRNUDHRYKSNSMYDVC SURRSVLORIMETELATORPRINGMGMAKRNUDHRYKSNSMYDDAF HTGTLERGATORPRINGMGMAKRNUDHRYKSMYDDAF SURRSV		İ	1	DEIFLLCDKVQKDDIEVRFVLNDWEAKGIFSQADVHRQVAIVFK
OSAGITUNPPERREGLIGSIGERYPKKERNLESIBLAVVERPER TOVSGOAGS YYPSGOF ISSGLSHHADLESISMSVAHPPER SGNTNPLSSFSTRTLPSNSGGI PPFLRI PVGNDLNASNACIYNN ADDIVGMEASSMFSALDYGISDPNASOWMMTTSSPSMGET DNPRLLSMLERPSCNSVLDPTRLRQLIGMSSSSMSAGANSNT VPGSGSBAFEGSDFSCADNSMINESGOPSNSTNPNSHVEVQDSQY SGIGSMONEQLESSFPYEFFOV  \$1873  \$1873  \$1873  \$1874  \$1875  \$1874  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875  \$1875			1	TPPYCKAITEPVTVKMQLRRPSDQEVSESMDFRYLPDEKDTYGN
TOVSQAESYTYSEGPISSGISHASMAPLESSWSSVAHPTPR SOMTNULSSFSTRTLPSNSQIIPPINGSIONACIYM ADDIVGMEASSWSABUJGISDPMM_SINCSVMMTTSSDSMGET DNPALLSMMLENPSCNSVLDPRDLKGWSSSSMSAGANSHTT VFVSQSDAFEGSDFSCADNSHINESGPSNSTNPNSVFVQUSQY SGIGSMONEQLSDSFYPSFTQV  5907  99 1873  TILLSSWSS**BLDTKTKSQVV/REGHEKISWYPPPARKQQAAREQE KATSKVPSAPHFVHPNDHANREBLKKKWVERMEKQQAAREQE ROKERTIESYCQDVLRRQEBFEKLEVLQELNHFPQLIDEATRK AYYKEFRKVVEYSOVILEVLDARDDLGCRCCQMERAVLRAGGNK KLVLVLNKLDLVPKEVVVEKNLDYLRAUPPLAKASTOMYOKNL NRCSVPVQQAESSLLKSKACFGABNLMSVLGNYCRIGEVETHIK VGVVGLPNGKSSLINSLKSRACFGABNLMSVLGNYCRIGEVETHIK VGVVGLPNGKSSLINSLKSRACFGABNLMSVLGNYCRIGEVETHIL VGVVGLPNGKSSLINSLKSRACFGABNLMSVLGNYCRIGEVETHIL VGVVGLPNGKSSLINSLKSRACFGABNLMSVLGNYCRIGEVETHIL VGVVGLPNGKSSLINSLKSRACFGABNLMSVLGNYCRIGEVETHIL VGVVGLPNGKSSLINSLKSRACFGABNLMSVLGNYCRIGEVETHIL VGVVGLPNGKSSLINSLKSRACFGABNLMSVLGNYCRIGEVETHIL VGVVGLPNGKSSLINSLKSRACFGABNLMSVLGNYCRIGEVETHIL VGVVGLPNGKSSLINSLKSRACFGABNLMSVLGNYCRIGEVETHIL ROTTERFECTION OF STATE OF STATE OF STATE OF STATE OF STATE ROTTERFECTION OF STATE OF STATE OF STATE OF STATE ROTTERFECTION OF STATE OF STATE OF STATE ROTTERFECTION OF STATE OF STATE ROTTERFECTION OF STATE OF STATE ROTTERFECTION OF STATE OF STATE ROTTERFECTION OF STATE ROTTERFECTION OF STATE ROTTERFECTION OF STATE ROTTERFECTION OF STATE ROTTERFECTION OF STATE ROTTERFECTION OF STATE ROTTERFECTION OF STATE ROTTERFECTION OF STATE ROTTERFECTION OF STATE ROTTERFECTION OF STATE ROTTERFECTION OF STATE ROTTERFECTION OF STATE ROTTERFECTION OF STATE ROTTERFECTION OF STATE ROTTERFECTION OF STATE ROTTERFECTION OF STATE ROTTERFECTION OF STATE ROTTERFECTION OF STATE ROTTERFECTION OF STATE ROTTERFECTION OF STATE ROTTERFECTION OF STATE ROTTERFECTION OF STATE ROTTERFECTION OF STATE ROTTERFECTION OF STATE ROTTERFECTION OF STATE ROTTERFECTION OF STATE ROTTERFECTION OF STATE ROTTERFECTION OF STATE ROTTERFECTION OF STATE ROTTERFECTION OF STATE ROTTERFECTION OF STATE ROTTERFECTION OF STATE ROTTERFECTION OF STATE ROTTERFECTION OF STATE ROTTERFECTION OF STATE ROTTERFECTION OF STATE ROTTERFECTION OF STATE ROTTERFEC	1			KAKKQKTTLLFQKLCQDHVETGFRHVDQDGLELLTSGDPPTLAS
SSMYNDLSSFSTRTLPSNSGG1PFFRIPVONDLASNACTYMN ADDIVGMEASSWEADLUGISDPMLSOWMMITISSSMGET DNPRLISMNLENPSCNSVLDPTDLRQLIQMSSSSMSAGANSNTT VPAGSBAPEGSDFSCADNSMINESSNTNPNSHVPVQUSQY SGLGSMGNEQLSDSPYEFFQV  SGLGSMGNEQLSDSPYEFFQV  TILLSSWSS-*NLDPK-KRSQVKV/RKGHKKISWPYPQPAKQNGK KATSKVPSAPHTVHPNDHAMREAELKKKWWEEMPERQQAAREQE RQKRTIESYCQDULRRQESFEHKEEVIQELNMFFGLDDEATRK AYKEFRKVUE'SDVILEVLDARDPLGCRCTQMEEAVLRAGGNK KLULVLNKIDLVPKEVVEKHLDVLENLEPTVAFKASTOHQVKNI, NRGSVPVODASBELLKSKACFGABRHUGHTCHGKVERGHVLDK IRLIDAPGIVPERVVEKHLDVLENLEPTVAFKASTOHQVKNI, NRGSVPVODASBELLKSKACFGABRHUGHTVAFKASTOHQVKNI, RUSDYGDASSLINSLKSSRACSVGAVPGITKFMQEVYLDKF IRLIDAPGIVPERVEKVEKHLDVTPUTTILORC NLEEISNYYGVSGFGTTEHFLITAVAHRLGKKKKGLYSOEQAAK AVLADUVSKKISFTIPPDPATHTPHLAGHVKKKKGLYSOEQAAK AVLADUVSKKISFTIPPDPATHTPHLAGHVKKKKGLYSOEQAAK AVLADUVSKKISFTIPPDPATHTPHLAGHVKKKKKGLYSOEQAAK AVLADUVSKKISFTIPPDPATHTPHLAGHVKKKKKGLYSOEQAAK AVLADUVSKKISFTIPPDATHTTPHLAGHVKKKKKKMQKRADKTAKKL SUBMMSALDLSGNADDOVOD BORNEVICUSTAPHHGUNGAKKIFTSNDWRPKSNSMVDVC SVDRSVLQRIMETDPLQQGOALASALKNKKKMQKRADKTAKL SUBMMSALDLSGNADDOVOD SVDRSVLQRIMETDPLQQGOALASALKNKKKMQKRADKTAKL SUBMSALDLSGNADDOVOD  ***GCSPFGQOVAGTTRAAPSCVDASIVGMCMMGPCLEGECK VLEDRKGNSCSSGKKVKTTRVTH UTLMGKVVSSANHHKAHHVKTGTCVVALHRCCNNKKEERSGT VLEDRKGNSCSSGKKVKTTRVTH VTMGKVVSSANHHKAHHVKTGTLAAMAPSRNSGSLRR CKEPIRSYSTNDOPHMUDLRGGPHGAVMCHMGPCLEGECK VLEDRKGNSCSSGKKVKTTRVTH  ***SSINLADRSMTCAQARRGNILYHNRFLGLAAMAPSRNSGSLRR CKEPIRSYSTNDOPHMUDLRGGPHGATTLGFKYYHOV SGALRATTPSVTVINSAAPIFKSGADETVQCOSRRLISFSLS DFQAMGLKKMFRPNPDYJKKIS 10PGKHSIFPALHHGOERRSK ILGNITVNINGARGSFSVSIJETOLLETVSRFABLHGGGRRSK ILGNITVNINGARGSFSVSIJETOLLETVSRFABLHGGGRRSK ILGNITVNINGARGSFSVSIJETOLLETVSRFABLHGGGGRSFSLLE GKLSMPVQRLERRAIGDRVVSYTLGRRLPTHVSGQLQFRFEI TSSIHPDDEEILSSTFPSAQIODSFRABLILE GKLSMPVQRLERRAIGDRVVSYTLGRRLPTHVSGQLOFFFEI TSSIHPDDEEILSSTFPSAQIODSFRABCHDLGEERSALLLE DGSAPASTKEEPLEEATTOGRAGREEBKEGEEPGOVSTLOG GEGLGLAAVKRISRPCSLPVSLETTVTARAGCOPMOETALDGE GGRLGLAAVKRISRPCSLPVSLETTVTARAGCOPMOETALDGE GGRLGLAAVKRISRPCSLPVSLETTVTARGFGGGFTFTTTVTR IHTLLHSMPSAQGGSAAEEEDGREESTLKDSSENGLESTVFSSQOD		ľ		QSAGITVNFPERPRPGLLGSIGEGRYFKKEPNLFSHDAVVREMP
ADDTYGNEASSMESADLYGISDPMLSNCSYMMTTSSDSNGET DNPELLSMNLENGESCNSTUNDROLOGHGNSSSMAGAMSNTT VFVSQSDAFEGSDFSCADNSHNESGESNSTNPNSHVFVQUSQY SGIGSMONEQLSDSFYEFFOW  TYLLSSGSS**NLDTKIKSGDKV/RKGHKKISMPYPQPAKONGK KATSKVESAPHFVHPNDHANRAELKKKWUSMPYPQPAKONGK KATSKVESAPHFVHPNDHANRAELKKKWUSMPYPQPAKONGK KATSKVESAPHFVHPNDHANRAELKKKWUSMPYPQPAKONGK KATSKVESAPHFVHPNDHANRAELKKKWUSMPYPQPAKONGK KATSKVESAPHFVHPNDHANRAELKKKWUSMPYPQPAKONGK KATSKVESAPHVHPNDHANRAELKKKUSMPYPQPAKONGK KATSKVESAPHVHPNDHANRAELKKKUSMPYPQPAKONGK KULVLIKILDLAPGTVPUSASSLLKSKASCGBARNLMRVLGBYCHLGEVRTHIR VGVVGLPNVGKSSLIKNSKASRCSAVPGTIKKROEVYLDKK IRLIDAPGTVPGPNSEVGTILRNCVHVQKLADPVTPVETILOGC NESISNYGVSGFOTTHHFITAVGAVPGCLESVETHIR VGVVGLPNVGKSSLIKNSKASRCSAVPGTIKKROEVYLDKK IRLIDAPGTVPGPNSEVGTILRNCVHVQKLADPVTPVETILOGC NLESISNYGVSGFOTTHHFITAVHKIKKKKGGLS(SOEQAA AVLADWSGK1SFYTPPPATHTLETHLSABIVKEMTEVPDIEDT EQAMEDTMECLATGSGDELLGDTDELMEIKLKKKKGGLS(SOEQAA AVLADWSGK1SFYTPPPATHTLETHLSABIVKEMTEVPDIEDT EQAMEDTMECLATGSGDELLGDTDLEMEIKLKHSPMTKITADAI ENKTTVYKIGDLTGYCTTPNHHQMGAKRNVDHARKSNSMTDVC SVERREVLQRIMETDPLQQGGALASALKNKKKMQKRADKTASKI SDEMMSALDLSGNADDGVGD HCCIKKREGSGSFSPASGGFOLGCOI PEPSLPSEEETHPHTRA HTTILEARTITRRPPHSHSTRIRFPMPLDGDGGLASWKYPMEE* GWRPAKAAGASLGVAATGKGCMSKRVLQXATGKGLLIIIFI VTLKGKVVSSAMHHKAHNVTGTCEVALHECCNKNKTERGT VKCSCFPGQVAGTTRAAPSCVDASIVEQXWCHMQPCLEGGECK VLPDRINGNSCSSGNKVTTRVTH  5909  1 5002 PAIFGSTIIWAPGSHSAARADGHGSISPSQSQAFGALCGARAPP SSNLRADRSMICAGARAGKNIVHNRICLGLAWAPFPSRNSQSLER CKEPIRSYNPQCHMDLRGGPHDCVTIPRSTSDTLVTSDSS STLMGRSSYYSIGHSQDLVHWDLKGEPDAQUTGMYLIDEVLS ENLDVKNRGVMGSHROGIIWKLNGHSIPPALPHHQGRGSK IGNTVNPIWGAQOFSRVSLTGGDIFWTSTLVHNSGPLOGGRRESK IGNTVNPIWGAQOFSRVSLTGGGIIWKLDASSYPVEPETKICFKYHOV SGALRATTPSVVVNNSAAPIFKSIGADETVOQGGSRLLISFSLS DFQAMLKKGMFFRPIDPVLIKISIGPSMNNLMESGGSPRSEAPE SSSSWKPRQLGEGSVPDRPCNOSIELSPARAEAVITEAGDOOM VSGDEGAGELLAAVGKORGCGIFKTLADASSFKOGLSEVDTV AADPSALEDREEPEGFTGTAPFGSVDGSKNISESTVVSSCSTSTCYS SSCYSASCYSPSCYNGNFASHTRFSSVDSAKISESTVVSSGDD EEEEMSAGESEVDORGSPELDEESTUAGSCFOGLSAALEL DGGAPASTKEBPLEEFETTGSGFPHQGOLDLGEGAALLE DGGAPASTKEBPLEEFETTGSGFPHQLARAAQDGCS		r		TGVSSQAESYYPSPGPISSGLSHHASMAPLPSSSWSSVAHPTPR
DNPRLISMALENPSCASUAPPILIZGENSTATMENSHYEVQUSQY SGIGSMONEGLISDSFYEFFOV  11LSSASS-**NEDTRIKTSÖVEV/PKGHKKISMPYPQPAKONGK KATSKVPSAPHFVHPNDHANREAELKKKWVESMPEKQQAAREOG RQKRETIES-YCQDVLRRGSFEHKEFVLGELMMFPCLDDEATRK AYYKEFFKVVEYSDVILEVLDARPGCRFGPMESPAURAGGNK KLVLVLNKLDLVPKEVVEKMLDYLRNELPTVAFKASTOHQVKNL NGCSVPUQASBELLKSKACRGARDLMRVLGRYCHLGEVRTHIK VGVVGLPNVGKSSLINSLKRSRACSVQAVPGITKFMQEVYLDKP LIRLIDAGGIVPGPNSEVGTLINGLVGKKKKGLYSQEQAK AVLADWVSGKISFYIPPAHTLPTHLSAEIVKENTEVFDIEDT EQANEDTMECLATGESDELLGDTDPLEMEIKLLHSPMTKLDAC SVRRSVLGRINGTPTLQGGGLASLKNKKKMGKRAKTASKL SDSMMSALDLSGNADDGVGD  1247  975  HCGIKKNEGSGGSFSPASGGFOLGCIPEVSLPSEFETHPITRA HTRILATLITRPPPSHSTRLRFPMPLDGCGLASWK/PMRER* GWRPAKAAGASLGVAATGKRGCRMSKRILGATKGKLLIITI VTLWGKVVSSANHIKAHHVKTGTGEVVALHRCCKNKKLERSGT VKCSCFFGGVAGTTRAAPSCVDASIVEQXWCHMQPCLEGEECK VLDDRRGMSCSSGNKVKTTRVTH SSILRADSSYSSICHSGNSTARLAGARGAPFASSYSSICHSSSYSSICHSGNSTARLAGARGAPFASTYLVKNSAPIFKSIGDATGVQGGSRRLISFSLS SSILRADSSYYSIGHSQDLVHMDIKEEVDAGGSRLISFSLS DFQAMGLAKGMFFRPDFYLLISTGADTSVOGGSRRLISFSLS DFQAMGLKKGMFFRPDFYLLISTGADTSVOGGSRRLISFSLS DFQAMGLKKGMFFRPDFYLLISTGADETVOGGSRRLISFSLS DFQAMGLKKGMFFRPDFYLLISTGADETVOGGSRRLISFSLS DFQAMGLKKGMFFRPDFYLLISTGADETVOGGSRRLISFSLS DFQAMGLKKGMFFRPDFYLLISTGADETVORGSRRLISFSLS DFQAMGLKKGMFFRPDFYLLISTGADETVOGGSRRLISFSLS DFQAMGLKKGMFFRPDFYLLISTGADETVOGGSRRLISFSLS DFQAMGLKKGMFFRPDFYLLISTGADETVORGSRRLISFSLS DFQAMGLKKGMFFRPDFYLLISTGADETVORGSRRLISFSLS DFQAMGLKKGMFFRPDFYLLISTGAREDELGDTGMTLDEAUS SSENKPPQLGEGSVPDPVGNSIELSFRPAERAVITEAGDOGM VSUGGEGAGELLAQVOKDIOPAPSELAECHLOLGESSALLLE DGGAPASTKEEPLEEATTGSRGREEBERAVITEAGDOGM VSUGGEGAGELLAQVOKDIOPAPSELAECHLOLGERSALLLE DGGAPASTKEEPLEEATTGSRGREEBERAGLDEGGERSALLLE DGGAPASTKEEPLEEATTGSRGREEBERAGLDEGGFTSTLFCG SSCXSSCYSPSCYSPSCYSSCYSTSCYS SSCYSASCYSPSCYNONGRARGSFFFTHFTFTWORTHTHAAAPGDOKM AAPPSALEERAEEPEGETATTCTARFTGAPPTHVTGAPTDHTAAAPGDOKM SSCCSSSSCYSPSCYSPSCYSSCYSTSCYS SSCYSASCYSPSCYNONGRARGSFFTLHDSSPFORGERPEHHTPT IHTLIHAMPSAGGSAABEEBEGATFCTARPGGPFPGLANAAADGGT HFSTGSESDSS PROGGDHSCEGCDASCCSPSCYSSSCYSTSCYS SSCYSASCYSPSCYNONGRARGTTTTAGAGPPOOLATH			Į.	SGNTNPLSSFSTRTLPSNSQGIPPFLRIPVGNDLNASNACIYNN
SGIGSMOREGLISTS PIEFFUY  5907 99 1873 TILLSSWSS'**NLDTKIKSOVKVJRKGHKKISSPYRGPAKONGK KATSKVVESAPHVYHDDIANNEALKKKWUSEMREKOQAAREGE ROKRRTIESYCOVLRRQBEPEHKEEVLQELMMFPQLAKOKOK KATSKVVESAPHVYHDDIANNEALKKKWUSEMREKOQAAREGE ROKRRTIESYCOVLRRQBEPEHKEEVLQELMMFPQLDLGATRK AYYKEFKVVEYSDVILEVLDARDPILGCRCFOMEBAVLRAQGIN KULVLINKIDLUPKEVVEKUDILMENELPTVAFKASTOHOVKNI. NRCSVPVDQASBELLKSRACFGARINLMVLGBYCRLGEVRTHIR VGVVGUPHOVASSELLKSRACFGARINLMVLGBYCLGEVRTHIR VGVVGUPHOVASSELLKSRACFGARINLMVLGBYCLGEVRTHIR VGVVGUPHOVASSELLKSRACFGARINLMVLGBYCLGEVRTHIR ROKETYTVSGTOTTHEHITAVHICKKKKGGLSYOGQAAK AVLADWUSGKISFY1DPPATHTLPTHLSAEIVKEMTEVPDIEDT EQAMEDTMECLATESBELLGIDTOLEHIKLLKSPMFKLADAI ENKTTYVKIGDLTGVCTMPRHQMGWAKRNVDHRPKSNSWDVC SVDERSVLQRIMETDPLQOGOALASALKNKKKMOKRADKIASKL ENKTTYVKIGDLTGVCTMPRHQMGWAKRNVDHRPKSNSWDVC SVDERSVLQRIMETDPLQOGOALASALKNKKKMOKRADKIASKL SDMMSALDLSGNADDGWGD HCCIKKRGEGSGSFSPASGGFOLGCIPPSPSEETHPHTRA HTRILBATLITRPPWSHSTRLRFPMPLDGDGGLASWK/PWREF* GWRFPAKAAGASLGVAATGKGCCMSKYLQATKGKLLIIIFI VTLKGKVVSSAMHKKHHVKTGTCAVAHRCCNKNKLEERSGT VKCSCFPGGVAGTTRAAPSCVDASIVEQKWCHMQPCLEGEECK VLPDRRGWSCSGMKVXTTRVTH  5909 1 5002 PAIFGSTIIWAPGSHSAARADGRHGSLPSQSQAFGALCGARAPP SSHLRADRSMICAGARAGKHLYHNRFLGLAAAAFPSSNSGSLER CKSPIRYSYNPQC/HMDLKGGPHDVVTIPRSTSDTDLVTSDSR STLMGRSSYYSIGHSQDLVJHWDIKSEVDAGDGIGMTLIDEVLS ENILDVKNIRGVMGSHMDLKGGPHDVVTIPRSTSDTDLVTSDSR STLMGRSSYYSIGHSQDLVJHWDIKSEVDAGDGTGMTLIDEVLS ENILDVKNIRGVMGSHMDLKGGPLOVTIPRSTSDTDLVTSDSR STLMGRSSYYSIGHSQDLVJHWDLKSEVDAGGSRRLISFSLS DFQAMELKKGMFFRPDPYLLISIGDPGVTGASFSLS DFQAMELKKGMFFRPDPYLLISIGDPGKMSIFPALPHHOGGRRKK LIGNTVNPIWGAGOPSPVSLDFDVLLIEVKDKFAKSRPIIKRFL GKLSPVQRCLERHAIGDRVVSYTLGRRLPTHVSGQLGFRFFII TSSHPDDEEILSTPPESAQIODSFMNILMESGSGPSREAPE SSESMKPRQLGEGSVPDRCHONGSIELSPRAEAVTTEAGDOOM VSGCPGGAGELLAQVKKOPCSLPPDFRTHYTR IHTLLHISMPSAGGSAABEEBGREGEGBFSALLE DGGAPASTKEEPLEEATTGGRAFREEERSQLDLSERSALLE DGGAPASTKEEPLEEATTGGRAFREGLEVSLAGCDDFTPRTHYTR IHTLLHISMPSAGGSAABEEBGRAFGGHPSLANGARDCOTT HPSTGSESDSSPRQGGDHSCEGCDASCCS PSCYSSSCYSSCYS SSCYSASCYSPSCYNGNRFASHTRFSSVDSAKISESTVPSGDD EEEEMARESEVDDOMGSPELDEESTNAGGFWQDELAARAPG	1	1		ADDIVGMEASSMPSADLYGISDPNMLSNCSVNMMTTSSDSMGET
5907  99  1873  TILLSSMSS'*NDDTKIKSCVV/RKGHKKISWPYPQPAKONGK KATSKVPSAPHFVHPNDHANREAELKKKAVPEMREKQQAAREQE ROKERTIESVCQDULRRQEFEHKEVLQELMMFPGLDEATRK AYYKEFRKVVEYSDVILEVLDARDPLGCRCYMEEAVLRAQGNK KLVLVLNKIDLVPKEVVEKKLDYLRNELPTVAFKASTOHOVKNIL NGCSVPVDQASESLLKSKACTGRAMINEVLGNYCRGLGEVRTHIR VGVVGLPNVGKSSLINSLKRSRACSVGAVPGITKFMGEVVILDKE IRLLDAPGIVPGPNSEVGTILENCVHVQKLADPVTPVETILORC NLEEISNYYGVSGFQTTEHFLTAVAHRILGKKKKGGLVSQEQAAK AVLADAWSGKISTYIPPATHTHAAHRILGKKKKGGLVSQEQAAK AVLADAWSGKISTYIPPATHTHAAHRILGKKKKGGLVSQEQAAK AVLADAWSGKISTYIPPATHTHAAHRILGKKKKGGLVSQEQAAK AVLADAWSGKISTYIPPATHTHAABRILGKKKKGGLVSQEQAAK AVLADAWSGKISTYIPPATHTHAABRILGKKKKGGLVSQEQAAK AVLADAWSGKISTYIPPATHTHAABRILGKKKKGGLVSQEQAAK AVLADAWSGKISTYIPPATHTHAABALIKKKKKGGLVSQEQAAK AVLADAWSGKISTYIPPATHTHAABALIKKKKKGGLVSQEQAAK AVLADAWSGKISTYIPPATHTAABALIKKKKKGGLVSQEQAAK AVLADAWSGKISTYIPPATHTAABALIKKKKKGGLVSQEQAAK AVLADAWSGKISTYIPPATHTAABALIKKKKKGGLVSQEQAAK AVLADAWSGKISTYIPPATHTAABALIKKKKKGGLVSGEGAKAP ENKTTVYKIGDLTGYCTTNNRRQMGMARRNVDHAPKSSNIVDVC SVDRRSVLGRINSTTRAPSTYLKARFPMPLDGGGLASMK/PMRER HTTLRATLITRRPPRSHSTRLFPMPLDGGGLASMK/PMRERS GWRRPAKAAGASIGVAATKKGRCNKKYTTYVH  TULKGKVVSSANHKAHHVKTGTCEVVALHRCCKKKNLIEERGGT VKCSCFPGQVAGTTRAAPSCVDASIVEKWCHMQPCLEGEECK VLEPRKMSCSSGNKKYTTRYTH  THALBALIKARJASMICAQARAGKNILYHRRFLGLAAMAPPSKNSQSLER CKSPIRYSNIPDQFHNMDLRGGPHDGVTIPPSTSDTDLVTSDSS STILMGRSSYYSIGHGQARAGKNILYHRRFLGLAAMAPPSKNSQSLER CKSPIRYSNIPDQFHNMDLRGGPHDGVTIPPSTSDTDLVTSDSS STILMGRSSYYSIGHGSQDLVHNRFLGLAAMAPPSKNSQSLER CKSPIRYSNIPDQFHNMDLRGGPHDGVTIPPSTSDTDLVTSDSS STILMGRSSYYSIGHGSQDLVHNRFLGLAAMAPPSKNSGLIFE BFGDARANTKRSPDPYLKISTGRADETVGGGGSRRLISFSLS DFQAMCLKKGMFRDPPYLKISTGRADETVGGGGSRRLISFSLS DFQAMCLKKGMFRDPYLKISTGRRLPTDHVSGGLQFRFSI TSSIHDDBEGISLSTEPSSAQIQOSPMNIMESGGGPRSEAPE SSSMKPEGLGGGSVDDRRGNGSIELDSFARAANTTEAGDQGM VSVGPEGAGELLAQVKGNIQPASAEELBERGGEFEGDVTVT AADPSALEDREFSTGGFFFSTAGAGREBERGGEEGDVSTLEQG GEGLOLRASVKKRSRPCSLEVSETVASAKSODETTFRTHYIR IHTLLHSMPSAQGGSAAEEEGGAEESTILKDSSKNGLSEVDTV AADPSALEDREFSTGGGFFFSTAAATTSSCKSSGDD DEEENSAFESVPOSMGSSELDPSTTMAATGDGGMCPTTAMATPOGAR SSCYSASCYSPSCY				DNPRLLSMNLENPSCNSVLDPRDLRQLHQMSSSSMSAGANSNTT
1873 TILLSSKSS**NLDTKIKSOKV/REGHEKKISØPPPDEAKONGE KATSKVESAHPHYPHDHAMRAELKKKWEEMREKQOAAREGE ROKERTIESYCQDVLRRQEEFEHKEVLQELMMFFQLDEATRK AYYKEFAKVUEYSDVILEVLDARDPLGCRCFQMEEAVLRAQGNK KLVLVLKILLVEVEVVEKKUDYLRNELPTVAFKASTOHOVKNI. NRCSVPVDQASESLLKSKACFGABNIMRVLGNYCRLGEVRTHIK VGVVGLPNGKSKSLINSLKKSRACSVGAPPGITKFMGEVYLDKE IRLIDAPGIVPGPNSEVGTILRNCVHVQKLADPVTPVETILQRC NLEELSMYGVSVGOTTEHFLTAVAHPLICKKKGGLYSQCAAK AVLADWVSGKISFYIPPPATHTLPTHLSAEIVKEMTEVFDIEDT EQANEDTMECLATGESDBLLGDTDPLEMEHKLLHSPPMTKIADAI ENKTYVKIGDLTGVCTNPRNIMGMWARKNVDHAPKSNSWYDVC SVDRRSVLQRIMETDFLQGQAALASALKNKKKMQKRADKIASKL SDSMMSADLDLSGNADDGVGD  5908 247 975 HCGIKKRGGGSSPSPASGGFQLGCQIPSPLSFSEEFTHPHTRA HTRILRATIITRRPPRSHSTRIRFPMPLDGDGLASMK/PMRER* GWRRPAKAAGASLGVAATCKRCGNKRYLQKARKGKLLIIII VTLMGKVVSSANHHKAHHVKTGTCEVVAJHRCCKNKNIEBESGT VKCSCFPGQVAGTTRAPSCVDASIVECKWMCHMQPCLEGEECK VLPDRKGNSCSSGNKVKTRVTH  5909 1 5002 PAIFGSTIWAPGSHSARADGRHGSLPSQSQAFGALCGARAPP SSNLRADRSMICAQARAGKNILYHNRFLGLAAMAPPSRNSGSLRR CKEPIRYSVNPDQFHIMMLRGCPHEDVTIRRSTDTDLVTSDSR SSLRADRSMICAQARAGKNILYHNRFLGLAAMAPPSRNSGSLRR CKEPIRYSVNPDQFHIMMLRGSPHEDVTIRRSTDTDLVTSDSR STIMMESSYYSIGHSQDLVIHNDIKERVDAGDMIGWYLIDEVLS ENFLDVKNRGVNGSIRGQIIWKIDASSYFVEPETKICFKYYHOV SGALRTTPSVTVKNSAAPIRKGLAGDATVOQGGSRRLISFSLS DFQAMGLKKGMFFNPDPYLKISIQPGHISTFPALPHHGGERRSK IGNTVNIPIQAEGYSFVSLFTDVLEIEVKKFAKSRPIIKRFL GKLSMFVQRLLEERHAIGGRVVSYTLGRRLPTDHVSGQLQFREFI TSSIHPDDEEISLSTEPESAQIQOSPNNINMESGSGEPRSEAPE SSESMKPEQLEGESVPDPROGNSTLEGRPAEFAAVTEGADOGM VSVGPBGAGELLAQVOKDIQPAPSAEELAEQLDLGEBGADGM VSVGPBGAGELLAQVOKDIQPAPSAEELAEQLDLGEBGADGM VSVGPBGAGELLAQVOKDIQPAPSAEELAEQLDLGEBGADGM HPSTGSESDSSPQGGSAABEEDGASEESTLKDSSEKNGLSEVDTV AADPSALEEDREEPSEPGATPGTAHGHSGGHPSLANGADQDGDT HPSTGSESDSSPGGGSAABEEDGASCSSPCVSSSCYSTSCYS SSCYSASCYSPSCYNGNFRASHTRFSSVDSAKISESTYPSSQDD EEEMSAFESVPDSMGSPELDPESTNAAGPWGDELAAPSGHVER SPGLESSVAGGSNAREGCCILINNSQPVSQLPSLRPEHHYPT IDEPLIPPMWEARIDSHGVFVVDNNTTTWORPTAATPPGMR	1			VFVSQSDAFEGSDFSCADNSMINESGPSNSTNPNSHVFVQDSQY
THISSYS "NILITATISQUKV/KKKISWPYPOPAKONGK RATSKVPSAPHFVPPNDHANEALEKKKUVEMMEKQQAAREQE RQKRRTIESY CQDVLRRQEFPHKEEVLZEIMMFPGLDBATRK AYYKEFKKVVEYSBVULLEVLADADPLGCRCPOMERAVLRAGGINK KLVLINKIDLVPKEVVEKHLDYLRNELDTVAFKASTOHQVKNL NRCSVPVDQASESLLKSKACFGAENLINEVCHCKLGEVRTHIK VGVVGLPNVGKSSLINSLKRSRACSGAPVGITKFMQEVYLDKF IRLIDAPGIVPGPNSEVGTILENCCHVQKLADPVTPVETILQRC NLEELSNYYGVSGFQTTHEFLTAVAHRLGKKKKGLYSQEQAAK AVLADWYSGKISFYIPPDATHTLPTHLSAGTVKEMTSVPIEDT EQANEDTMECLAGESDELLGPLEMEIKLLHSPMTKLADAI ENKTTYYKIGDLTGYCTNPNRHQMGMARNNVDHAPKSNSNVDVC SVBRRSVLQRIMETDPLQGQAALSALKNKKMQKRADKTASKL SDEMMSALDLSGNADDGVGD  HCGIKKRGGSGSFSFSAGGFGLGCGIFPUSLSPSEETHDHTRA HTRILARATURRPYPRSHSTRLAFPMPLDGDGGLASWK/PMEER- GWRPAKAAGASLGVAATGKRGCRNSKRYLQKATKGKLLIIFI VTLNGKVVSSANHHKAHHVKTGTEVVALHRCCNKNKLEERSGT VKCSCFPGQVAGTTRAABSCVDASTVCKWNCHMQPCLEGEECK VLPDRKGNSCSSGNKVKTTRVTH  5909  1 5002  PAIFGSTIWAPGSHSAARAGGRGSDSGSQAPGALCGARAPP SSNLRADRSMICAQARAGKNLYHNRFLGLAMMFPSRNSQSLRR CKEPIRYSYNPDQFHNWDLKGEVDAGDWIGWYLIDEVLS ENFLDYKNIGVNGSRINGGIIWKIDASSYFVEPETKICFKYYHGV SGALRATTPSVTVKNSAAPIFKSTGADFTVGGOSGRRLISFSLS DFQAMGLKKGMFFNDDYLKISIGDFTVERTSTDTDLVTSDSR SGALRATTPSVTVKNSAAPIFKSTGADFTVGGOSGRRLISFSLS DFQAMGLKKGMFFNDDYLKISIGDFTVERVSGGLGRRESS IIGNTVNPIWQAEQPSFVSLPTDVLEIEVKNFAKSRPIIKRFL GKLSMFVGRLEERHAIGGRVVSYTLGRRLPTDHVSQGLQFREFI TSSIHDDGETSLSTEPPSAGIQDSPHNNIMESGSGEPRSEAPE SSSSWFEQLGESSYDPSCHOOLSIELSTPAEEBAVTEAGDGM VSVGPBGAGELLAQVOKDIQPAPSAEELAPOLDLGEBASALLE DGGAPASTKEEPLEEBATTQSRAGREEBEKEQEEGGUYTLOG EGRLQLRASVKRKSRPCSLEVSELETVIASACDPETFRTHYIR IHTLLHSMPSAQGSAAEEDGABEESTLKDSSEKGGLBEVDTV AADPSALEEDREESGSPOPSCHORGSGEPSTSSCYSSCYSTSCYS SSCYSSCYSSCYSSCYSTSCYS SSCYSSCYSPSCYNGNRFASHTFSSVDSAKISESTVFSSQDD HESENSAFESVDDSMGSFELDPESTNGAGPWQDELAAPSGHVER SPEGLESPVAGPSNRREGCCILINSQPVQDELAAPSGHVER SPEGLESPVAGPSNRREGCCILINSQPVQDFLAAPSGHVER SPEGLESPVAGPSNRREGCCILINSQPVSQLELRPEHHHYPT IDEPLIPPHWEARITGBIGRVYFVVORNTTTWORPTAATPPOGMR	5907	96		SGIGSMQNEQLSDSFPYEFFQV
ROKERTIESYQDULRRQEEPEHREUJGELNMFPQLDDEATRK AYYKEFAKUVEYSDULEVYSDULEVUGNEEAULRAGGINK KLVLVLAKIDLVPKEVVEKWLDYLRRELPTVAFKASTQHQVKNL NRCSSPVUQASESLLKSKACFGAERLLMRVLGNYCRGEVERTHIK VGVVGLPNVGKSSLINSLKKRACFGAERLLMRVLGNYCRGEVERTHIK VGVVGLPNVGKSSLINSLKKRACFGAERLLMRVLGNYCRGEVERTHIK VGVVGLPNVGKSSLINSLKKRACFGAENLMRVLGNYCRGEVARTHIK VGVVGLPNVGKSSLINSLKKRACFGAENLADDVTDVETILQRC NLEEISNYYCVGGFQTTEHFLTAVAHRLIGKKKGGLYSQCAAK AVLADWVSGKISFYIPPARHTLPTHLSAEIVKEMTEVPDIEDT EQANEDTMECLATGESDELLGTDPLEMEIKLLHSPMTKIADAI ENKTYVKIGDLTGYCTNPNRHQMGWAKKNOKRADKIASKL SDEMMSALDLSGANDDOWD SVERSVLQRIMETDELQGGALASALKNKKKMQKRADKIASKL SDEMMSALDLSGANDDOWD SVERSVLQRIMETDELQGGALASALKNKKKMQKRADKIASKL SDEMMSALDLSGANDDOWD SVERSVLQRIMETTELQGGALASALKNKKKMQKRADKIASKL SDEMMSALDLSGANDDOWD VKCSCFPGQVAGTTRAPSCTUASIVEKWLMACKMOKRADKIASKL HTTLATLITRIPPRSHSTARFDRPDLOGGGLASMK/PMRER* GWRPAKAAGASLGVAATGKRGCTMSKRYLQKATKGKLLIIIFI VTLMGKVVSSANHKKAHVKTGTCEVVALHRCCNKMKIEERSGT VKCSCFPGQVAGTTRAPSCVDASIVEQKWMCMPQCLGEECK VLPDRKGWSCSSGNKVKTTRVTH  PAIFGSTIIMPAGSHSAARADGRHGSLPSGSQAPGALCGARAPP SSNLRADRSMICAQARGKNLYHNRFLGLAAMAFPSNNSQSLRR CKEPIRYSYNPDQFHNMDLRGGPHDCVTIPRSTSDTDLVTSDSR SSLRADRSMICAQARGKNLYHNPIKEUDAGDWIGMYLLDEVLS ENFLDYKNRGVNGSHRGQIIWKIDASFYPEBTRICFKYYHGV SGALRATTPSVTYKNSAAPIFKSIGADETVQGGSRRLIFSFLS DFQAMGLKKGMFFNPDPYLKISIOPGKHSIFPALPHHGQERRSK IIGNTVNPIWQAEQFSFVSLPTDVLEIEVXDKFAKSRPIIKRFL GKLSMPVGRLLERHAIGDRVVSVTLGRRLPTDVSGQLGFREII TSSIHPDDEISLSTFPESAQIQDSFMNIMBESGGEPRSEAPE SSESMPEGLGESVPDRPRONGSIELSFRAEERAVITERAGDGM VSVGPBGAGELLAQVKDIQPAPSAEELAEOLDLGEEASALLLE DGEAPASTKEEPLEEATTQSRAREEBEKQEEBEGVSTELQG EGRLQLRASVKRNSRPCSLPVSSELETVIASACGDPETPRTHYIR IHTLHHSMPSAQGGSAAEEDGAEESTIKDSSEKDGISEVDTV AADPSALEEDREEPGGATFGTHYGHGSGHFPSLANGADQDGT HPSTGSEBDSSPRQGGDHSCEGCDASCCSPSCYSSSCYSTSCYS SSCYSASCYSPSCYNGNRFASHTTPSSVDSAKISESTVFSSQDD EEEEMSAFESVPDSNGFELDPESTNGAGPWQDELAAPSGHVER SPEGLESPVAGPSNRREGECPILHNSQPVSQLPSLERPHHHYPT IDEPLPFWMERAHDGBIGHKYPVONNTTTWGORTPAAATPDGMR	1 330,	99	1873	TYLLSSWSS**NLDTKIKSQVKV/RKGHKKISWPYPQPAKQNGK
AYYKEFAKVUSYSDUILEVLDARDPLGGRCFOMEBAULRAQGINK KLVULNKIDLVPKEVVEKMULRADENTUAFKASTOHOVKINL NRCSVPUQASESILKSKACFGABNIMRVLGNYCRLGEVRTHIR VGVVGLPNVGKSSIJNSLKRSRACSVGAVPGITKFMGEVYLDKF IRLIDAPGIVPGRNSEVGTITLRNCVHVQKLADPVTPVETILORC NLBEISNYYGVGGFOTTEHFILTAVAHHIGKKKGGLISQEQAAK AVLADWVGGKISFYIPPPATHTLPTHLSABIVKEMTSEVPIEDT EQANEDTMECLATGESDELIGDTDPLEMEIKLIHSPMTKIADAI ENKTTVYKIGDLTGYCTNPRRHDMGMAKRVUDHFPKSNSHVDVC SVDRRSVLQRIMETDELQQGQALASALKNKKKMQKRADKIASKL SDSMMSALDLSGNADDGVGD  5908 247 975 HCGIKKRGEGGSGFSPASGGFOLGCOIPEPSLPSEFETHPHTRA HTRTLRATLTRRPPRSHSTRLRFPMPLDGDGSLASKK/PMRER* GWRRPAKAAGASLGVAATGKRGCCMSKRYLQKATKGKLIIIFI VTLWGKVVSSANHKAHHVSTCEVVALIKECNNKKIEBERGT VKCSCFFGQVAGTTRAAPSCVDASIVECKWKCHKGLLIIIFI SSULRADRSMICAQARAGKNILYNNRFLGLAAMAFPSRNSGSLRR CKEPIRYSNYDDFHNMDLRGGPHDGVTIFRSTDTDLVTSDSR STLMGRSSYYSIGHSQDLVIHWDIKBEVDAGDWIGMYLIDEVLS ENFLDVKNRGVNGSHRQQIIWKIDASSYFVEPETKICFKYYHGV SGALRATTPSVTVKNSAAPIFKSIGADETVQQGGSRALISFSLSS DFQAMGLKKGMFFNPDPYLKISIOPGKHSIFPALPHHGGERRSK IIGNTVNPIWAGAPGFSFUSHTPVLEIEVKMFAKSRPIKRFL GKLSMPVQRLLERHAIGDRVVSYTLGRLPTDHVSGQLQFRFEI TSSIHPDDEEISLSTEPESAQIQDSPMNNIMBSGSGERSEAPE GKLSMPVQRLLERHAIGDRVVSYTLGRLPTDHVSGQLQFRFEI TSSIHPDDEEISLSTEPESAQIQDSPMNNIMBSGSGERSEAPE SSESMKPQLGEGSVPDRRCNGSIELSRPAERAAVITERGDOM VSVGPBGAGELLAQVKDIQPAPSAEELABGLDLGEGEASALLLE DGEAPASTKEEPLEEBATTGSRREBEBEKGEBEGDVSTLEQG EGGLLQLRASVKRKSRPCSLPVSELETVIASACGDPETRTHYIR IHTLLHSMPSAQGGSAAEEDGAEEESTLKDSSEKDGLSEVDTV AADPSALEEDREEPEGATTESTLADSCEDESCUSTLOGG EGGLDLRASVKRKSRPCSLPVSELETVIASACGDPETRTHYIR HTSTGSESDSSPRQGGDHSCECCDASCCSPSCYSSSCYSTSCYS SSCYSASCYSPSCYNONRPASTTRFSSVDSAKISESTVFSSQDD EEEENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSGHVER SPEGLESVVAGPSNRREGECTILHNSQPVSQLPSLERPHHHYPT IDEPLPFWMEARIDSIIGKYPTQDVANNTTTWGORPTAAATPDGMR		ļ		KATSKVPSAPHFVHPNDHANREAELKKKWVBEMREKQQAAREQE
KLVL/LNKIDL/PYESVYEKULDYLRNELPTVAFKASTOHOVKNIL NRCSVPVDQASESLLKSK-GGARNLMRVLGNYCRLGEVRTHIR VGVVGLPNVGKSSLINSLKRSRACSVGAVPGITKFNQEVYLDKF IRLLDAFGIVEGPMSEVGTILENCVHQKLADPVTPVETILQRC NLEEISNYYGVSGFGTTERHITAVAHRLGKKKGGGLYKSQEQAK AVLADWVSGKISFYIPPPATHILPTHLSAEIVKEMTGEVPDIEDT EGANEDTMECLATGESDELLGDTDPLEMEIKLLHSPMTKIADAI ENKTTVYKIGDLTGYCTHPNRHQMGWAKRNVDHRPKSNSMVDVC SVDRRSVLQRIMETDPLQQGQALASALKNKKKMQKRADKIASKL SDSMMSALDLSGNADDGVG SVDRRSVLQRIMETDPLQQGQALASALKNKKKMQKRADKIASKL SDSMMSALDLSGNADDGVG HCTIKKRGEGSGSPSPASGGFQLGCQIPSPSLPSEESTHPHTRA HTRTLRATLIRRPPRSHSTRLFFNPHDLOGGGLASWK/PMRER* GWRRPAKAAGASLGVAATGKCCMSKRYLQATKGKLLIIFI VTLWGKVVSSANHHKAHHVKTGTCEVVALHRCCNKNKLEERSQT VKCSCFPGQVAGTTRAAPSCVDASIVEQKWCHMQPCLEGEBCK VLPDRKGWSCSSGNKVKTTRVTH  5909  1 5002 PAIPGSTILWAPGSHSAARADGRHGSLPSQSQAFGALCGARAPP SSNLADRSMICQAGRAGKLYHNDRILGLAMMAFPSHNSQSLER CKEPIRYSYMPDQ*HNMDLRGGPHDGVTIPRSTSDTDLVTSDSR SILRADRSMICQAGRAGKLYHNDRILGLAMMAFPSHNSQSLER CKEPIRYSYMPDQ*HNMDLRGGPHDGVTIPRSTSDTDLVTSDSR STLMGRSSYYSIGHSQDLVHMDLKEBVDAGDWIGMYLIDEVLS ENFLDYKNRGVNGSHRGQIIWKIDASSYVPSEPTTLCFKYHGV SGALRATTPSVTVKNSAAPIFKSIGADETVQGQGSRRLISFSLS DFQAMGLKKGMFFNPDPYLKSIQDFSHNSHLMSFGSGERFSEAPE SGALRATTPSVTVKNSAAPIFKSIGADETVQGQGSRRLISFSLS DFQAMGLKKGMFFNPDPYLKSIQDFSHNSHLMSGGSGFRSEAPE SSSSWKPQLLERHAIGDRVVSYTJGRRLPFDHVGGQLQFRPEI TSSIHPDDEEISLSTEPESAQIODSPMNINLMESGGSGFRSEAPE SSSSWKPQLLERHAIGDRVVSYTJGRRLPFDHVGGQLQFFRPEI TSSIHPDDEEISLSTEPESAQIODSPMNINLMESGGSGFRSEAPE SSSSWKPQLGGGSVPDRPGNQSIELSRPAEEAAVITEAGDQGM VSVGPEGAGELLAQVOKDIQPAPSABELAEQLDLGEEASALLLE DGEAPASTKEPLEEEATTTGSRAGREEBEKQEEGBVSTLEQG EGRLQLRASVKRKSRPGSLPVSELETVIASACGDPETFRTHYIR HTLLHISMPSAQGGSAAEEEDGAEESTLKDSSEKGGLSEVDTV AADPSALEEDREEPEGATFOTAHHGHSGGHFPSLANGAQDQDGT HBSTGSESDSSPRQGGGHSCEGCDASCCSPSCYSSSCYSTSCYS SSCYSASCYSPSCYNSPSGVDD SSCYSASCYSPSCYNSRFSSHTPSSQDD EEEENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSGHVER SPEGLEEPVAGPSVPDSMQSPELDPESTNGAGPWQELAAPSGHVER SPEGLEEPVAGPSVPDSMQSPELDPESTNGAGPWQELAAPSGHVER SPEGLEEPVAGPSVPDSMQSPELDPSTNGAGPWQELAAPSGHVER SPEGLEEPVAGPSVPJVDHVNNETTTWGRFTAAATPDGMR		1		RQKRRTIESYCQDVLRRQEEFEHKEEVLQELNMFPQLDDEATRK
NRCSVPUDQASESLLKSKACFGABINIMRVIGHYCRLGEVRITHIR VGVVGLPNVGKSSLINSLKRSRACSVGAVPGITKFMQEVYLDKI IRLIDAPGIVPGPNSEVGTILRNCVHVQKLADPVTPVETILQRC NLBEISNYYGVSGGTTEHFLTAVAHRLGKKKKGGLYSQEQAAK AVLADWVSGKISFYIPPPATHTLPHLISAEIVKEMFWEVPIETT EQANEDTMECLATGESDBLLGDTDPLEMBIKLLHSPMTKIADAI ENKTYVKIGDLTGVCTPMRIQMGWAKRNVDHRPKSNSMVDVC SVDRRSVLQRIMETDPLQQGQALASALKNKKMQKRADKIASKL SDSMMSALDLSGNADDGVGD  1 SOOS HCCIKKRGEGGSPSPASGGFGLGCQIPSPSLPSEEETHPHTRA HTRTLRATLTRRPPPRSHSTRRFPMPLDGDCGLASWK/PMRER* GWRRPAKAAGASLGVAAFGCCMSKKRYLQKATKGKLLIIFI VTLWGKVVSSANHHKAHVKTGTCEVVALHRCCNNKKIEERSQT VKCSCFPGQVAGTTRAAPSCVDASIVEQKWWCHMQPCLEGEECK VLPDRKGWSCSGKNVXTRVTH  SSNLRADRSMICQGARAGKNLYHNRFLGLAAWAFPSRNSQSLRR CKEPIRYSTMPDGPHNMURFLGLAAWAFPSRNSQSLRR CKEPIRYSTMPDGPHNMURFLGLAAWAFPSRNSQSLRR CKEPIRYSTMPDGPHNMURFLGLAAWAFPSRNSQSLRR CKEPIRYSTMPDGPHNMUREPUDAGBHIGMYLIDEVLS STLMGRSSYYSIGHSQDLVIHWDLKEVDAGBWIGMYLIDEVLS ENFLDVKNRGWNGSHGGGIIWKIDASSYPVEPETKICFKYYHGV SGALRATTPSVTVKNSAAPIFKSIGADETVQGQSRRLISFSLS DPQAMGLKKGMFRNPDPYLKISIGPGHENVITENGDFRAFFIIKFFI GKLSMPVQRLLERHAIGDRVVSYTLGRLPPDHVSGQLOFRREI TSSIHDDEETSLSTEPESAQIQDSPMNNLMESGSGPRSEAPE SSESWKPEQLGEGSVDRPCNQSIELSRPAEEAAVITEAGDQGM VSVGPBGAGELLAQVQKDIQDSPMNNLMESGSGPRSEAPE SSESWKPEQLGEGSVDRPCNQSIELSRPAEEAAVITEAGDQGM VSVGPBGAGELLAQVQKDIQDSPANNLMESGSGPRSEAPE SSESWKPEQLGEGSVDRPCNQSIELSRPAEEAAVITEAGDQGM VSVGPBGAGELLAQVQKDIQDSPANNLMESGSGPRSEAPE GEGLDLRASVKRKSRPCSLPVSELETVIASACGDPETPRTHYIR IHTLLHSMPSAQGGSAAEEEDGAEESTLKDSSEKDGLSEVDTV AADPSALEEDDREEPEGATPTAHHGHSGGHFPSLANGAQDGDT HPSTGSESDSSPRQGGHSCEGCDASCSPSCYSSSCYSTSCYS SSCYSASCYSPSCYNSCTSPSSACYSSSCYSTSCYS SSCYSASCYSPSCYNSCTSPSCYSSACYSTSCYS SSCYSASCYSPSCYNSCTSPSCYSSACYSTSCYS SSCYSASCYSPSCYNSCTSPSCYSSACYSTSCYS SSCYSASCYSPSCYNSCTSPSCYSSACYSTSCYS SSCYSASCYSPSCYNSCTSPSCYSSACYSTSCYS SSCYSASCYSPSCYNSCTSPSCYSSACYSTSCYS SSCYSASCYSPSCYNSCTSPSCYSSACYSTSCYS SSCYSASCYSPSCYNSCTSTVTWORPTAAATPPOMR	i			AYYKEFRKVVEYSDVILEVLDARDPLGCRCFQMEEAVLRAQGNK
VGVVGLPNVGKSSLINSLKRSRAGSVGAUPGITKFMQEVYLDKF IRLIDAPGIVPGPNSEVGTILENCYHVQKLADPVTPVETILQRC NLEEISNYYGVSGFQTTEHFLTAVAHRLGKKKKGGLYSGEQAAK AVLADWVSGKISFYIPPPATHTLPHLSAEIVKEMTEVPDIEDT EQANEDTMECLATGESDBILGDTDFLEMEIKLLHSPMTKIADAI ENKTTVKKIGDLTGYCTHPNRHQMGWAKRNVDHRPKSNSMVDVC SVDRRSVLQRIMETDPLQQGQALSAALKNKKKMQKRADKIASKL SDMMSALDLSGNADDGVGD  5908  247  975  HCGIKKRGEGGSFSPRASGGFQLGQIPSPSEEETHPHTRA HTRTLRATLTRHPPKSHSTRLFPMPLDGDCGLASWK/PMRER* GWRRPAKAAGASLGVAATGKRGCRMSKRYLQKATKKKLLIIIFI VTLWGKVVSSANHHKAHHVKTGTCEVVALHRCCNKNKLEERSGT VKCSCFFGQVAGTTRAAPSCVDASIVEQKWWCHMQPCLEGEECK VLPDRKGWSCSSGMKVKTTRVTH  5909  1 5002  PAIFGSTIIWAPGSYBSAARADGRHGSLPSQSQAPGALCGARAPP SSNLRADRSMICAQARAGKNLYHNFFLGLAAMAPSPSRNSGSLRR CKEPIRYSYMPDGPHNMDLRGGPHBGVTIPRSTSDTDLVTSBG STLWGRSSYVSIGHSQDLVIHWDIKEEVDAGDWIGMYLIDEVLS ENFLDYKNRGVNGSHRGQIIWKIDASSTFVEPETTLCFKYYHGV SGALRATTPSVTVKNSAAPIFKSIGADETVQGQGSRRLISFSLS DFGAMGLKKGMFNNDPDYLKISIOPGKHSIFPALPHGHGGRRSK IIGNTVNPIWQAEQFSFVSLPTDVLEIEVKNKFAKSRPIIKRFL GKLSMPVQRLLERHAIGDRVVSYTIGRRLPPDHVSGQLQFFREI TSSIHPDDESISSTEPESAQIQDSPMNINESGSGEFRSEAPE SSESWKPEQLGEGSVPDRPGNGSIELSRPAFEAAVITEAGDQGM VSVGPEGAGELLAQVQKDIQPAPSAELARQLDLGEEASALLLE DGEAPASTKEEPLEEEATTTGSRAGREEBEKRQEEEGBVSTLEGG EGRLQLRASVKRKSRPCSLPVSELETVIASACGPETTRTHYIR IHTLHISMPSAQGGSAABEEEDGAEESTLKDSSEKDGLSEVDTV AADPSALEEDREEPEGATFGTAHFGHSGGHFPSLANGAAQDGDT HFSTGSESDSSPRQGGDHSCEGCDASCSPSCYSSSCYSTSCYS SSCYSASCYSPSCYNSCYSPSCYNSTSTSSQDD SEEENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSGHVER SPEGLESPVAGPSNREGECPILINSQPVSQLFSLREHHHYPT IDEPLPPNWEARRIDSIGNVFVYDHVNRTTTWGRFTAAATPSOMR				KLVLVLNKIDLVPKEVVEKWLDYLRNELPTVAFKASTQHQVKNL
IRLIDAPGIVEOPNSEVGTILRNCHYUÇKLADPUTPUETILQRC NLEEISNYYGVSGGTOTTEHFLTAVAHRLGKKKKGLYSQEQAAK AVLADWVSGKISFYIPPPATHTLPTHLSAEIVKEMTEVPDIEDT EQAMEDTMECLATGESDELLGDTDPLEMEIKLHSPMTKIADAI ENKTIVYKIGDLTGYCTNPRNHOMGWAKRNUDHR KSNSMYDVC SUDRRSVLQRIMETDPLQQGQALASALKNKKKMGKRADKIASKL SDSMMSALDLSGNADDGVGD  FREGIKKRGEGGSSFSPSAGGFOLGCQIPEVSLPSEEETHPHTRA HTRTLRATLTRRPPRSHSTRLRFPMPLDGDGGLASWK/PMRER* GWRRPAKAAGASLGVAATGKRGCMSKRYLQKATKGKLLIIFI VTLWGKVVSSANHHKAHHVKTGTCEVVALHRCCKNKKIEERSOT VKCSCFPGOVAGTTRAAPSCVDASIVEQKWWCHMQPCLEGEECK VLPDRKGMSCSSGNKVKTTRVTH  5909  1 5002 PAIPGSTIIWAPGSHSAARADGRHGSLPSOSOAPGALCGARAPP SSNLRADRSMICAQARAGKNLYHNRFLGLAAMAFPSRNSQSLRR CKEFIRYSYNPDQFHNMDLRGPHDGVTIPRSTSDTDLVTSDSR STLMGRSSYYSIGHSQDLVIHMDIKEVDAGDWIGMYLIDEVLS ENFLDYKNRGVNGSHRGQIIWKIDASSYFVEPETKLCFKYYHGV SGALRATTPSVTVKNSAAPIFKSIGADETVQGQGSRRLISFSLS DFQAMGLKKGMFNPDPVLKISIQPEKWSYLGRKYHGV SGALRATTPSVTVKNSAAPIFKSIGADETVQGQGSRRLISFSLS DFQAMGLKKGMFPNDPDPVLKISIQPETVAGGOLFRFEI TSSIHPDDEEISLSTEPESAQIQDSPMNNIMESGSGBPRSEAPE SSESWKPEQLEGEGSVPDREPGNSIELSFRAEEAAVITEAGDOGM VSVGPEGAGELLAQVOKDLAPSABELABCOLDGEBSALLLE DGEAPASTKEEPLEEEATTQSRAREEBEKEQEEEGDVSTLEQG EGRLQLRASVKRSPCSLPVSLETVIASACCDPETPRTHYIR IHTLLHSMPSAQGGSAABEEDGAEEESTLKDSSEKDGLSEVDTV AADPSALEEDREEPEGATPGTAHPGHSGGHFPSLANGAQDGDT HPSTGSESDSSPRGGDHSCEGCDASCCSPSCYSSSCYSTSCYS SSCYSASCYSPSCYNGRNFASHTRFSSVDSAKISESTVFSSQDD EEEEMSAFESVPDOMQSPELDPESTNGAGPWQDELAAPSGHVER SPEGLESPVAGPSNRREGECTILHNSQEVGJESLRPEHHHYPT IDEPLPPNWEARIDSHIGRFFYVDHVNRTTTWORPTAAATPDGMR		1		NRCSVPVDQASESLLKSKACFGABNLMRVLGNYCRLGEVRTHIR
NLEBISNYYGVSGFQTTEHFLITAVAHRLIGKKKGGLYSGEQAAK AVLADWVSGKISFYIP DPATHTLEHTLSAEIVKEMTEVPDIEDT EQANEDTMECLATGESDELLGDTDPLEMEIKLLHSPMTKIADAI ENKTTVYKIGDLTGYCTNPNRHMGWAKRNVDHRPKSNSMYDVC SVDRRSVLQRIMETDPLQGGQALASALKNKKKMQKRADKIASKL SDSMMSALDLSGNADDGVGD  1001 1002 1003 1003 1003 1003 1003 100	İ			VGVVGLPNVGKSSLINSLKRSRACSVGAVPGITKFMQEVYLDKF
AVLADWYSKISFYIPPBATHILPTHLSAEIVKEMTEVPDIEDT EQANEDTMECLATGESDELLGDTDPLEMEIKLLHSPMTKIADAI ENKTTVYKIGDLTGYCTNPNRHQMGWAKRNVDHRPKSNSMYDVC SVDRRSVLQRIMETDPLQQGQALASALKNKKKMQKRADKIASKL SDSMMSALDLSGNADLOVGD  1 HCGIKKRGEGSGSPSPASGGFQLGCQIPEPSLPSEEETHPHTRA HTRTLRATLITRPPRSHSTRLFPMPLDGGGLASWK/PMRER* GWRPPAKAAGASLGVAATGKEGCTMSKRYLVAKAKGKLLIIIFI VTLWGKVVSSANHHKAHHVKTGTCEVVALHRCCNKNKIEERSQT VKCSCFPGQVAGTTRAPBSCVDASIVEQKWWCHMQPCLEGEECK VLEPRKGWGCSSGNKVKTTRVTH  SSNLRADRSMICAQARAGKNLYHNRFLGLAAMAFPSRNSQSLRR CKEPIRTSYNPPQFHMMDLRGGPHEVTIPRETSDTDLVTSDSR STLWGRSSYYSIGHSQDLVIHWDIKEEVDAGWIGMYLIDEVLS ENFLDYKNRGVNGSHRGQIIWKIDASSYFVEPETKICFKYYHGV SGALRATTPSVTVKNSAPIFKSIGADETVQGQGSRRLISFSLS DFQAMGLKKGMFFNPDPYLKISIQPGKHSIFPLPHHGQERRSK IIGNTVNPIWQAEQPSFVSLPTDVLEIEVKDKFAKSRPIIKRFL GKLSMPVQRLLERHAIGDRVVSYTIGRRLPTDHVSGQLQFFFEI TSSIHPDDEEISLSTEPESAQIQDSPMNNLMESGSGEPRSEAPE SSESWKPQLGEGGSVPDRPCNQSIELSRPAEEAAVITEAGDQGM VSVGPBEGAGELLAQVQKDIQPAPSAEELAGOLDGEBASALLLE DGEAPASTKEEPLEEEATTQSRAGREEBEKQEEEGDVSTLEQG EGRLQLRASVKRKSRPCSLPVSBLETVIASACGDPETFRTHYIR IITLLHSMPSAQGGSAAEEEBGABEESTIKDSSEKDGLSSVDTV AADPSALEEDREEPEGATPGTAHPGHSGGHFPSLANGAQDGDT HPSTGSESDSSPRGGGBHSCEGCDASCCSPSCYSSSCYSTSCYS SSCYSASCYSPSCYMGNRFRASHTYFSSVDSAKISESTVFSSQDD EEEENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSGHVER SPEGLESPVAGPSWARREGECDLHNSQPVQLPSLAAPSGHVER SPEGLESPVAGPSWARREGECTLHINSQPVQLPSLAAPSGHVER SPEGLESPVAGPSWARREGECTHINSQPVQLPSLAAPSGHVER SPEGLESPVAGPSWARREGECTHINSQPVAGTAAATPDGMR		1		IRLLDAPGIVPGPNSEVGTILRNCVHVQKLADPVTPVETILQRC
EGANEDTMECLATGESDELLEGITDPLEMETKLLHSPMTKIADAI ENKTYVKIGDLTGYCTNPNRHQMGMAKRNVDHRPKSNSMVDVC SVDRRSVLQRIMETDPLQQGALASALKNKKKMQKRADKIASKL SDSMMSALDLSGNADDGVGD  1 HCGIKKRGEGSGSPSPASGGFQLGCQIPEPSLPSEEETHPHTRA HTRILRATLITRPPRSHSTRLRFPMPLDGDGGLASMK/PMER* GWRRPAKAAGASLGVAATGKRGCRMSKRYLQKATKGKLLIIIFI VTLWGKVVSSANHHKAHHVKTGTCEVVALHRCCNKNKIEERSQT VKCSCFPGQVAGTTRAPSCVDASIVEQKWWCHMQPCLEGEECK VLPDRKGMSCSSGNKVKTTRVTH  5002 PAIPGSTIIWAPGSHSAARADGRHGSLPSQSQAPGALCGARAPP SSNLRADRSMICAQARAGKNLYHNRFLGLAAMAFPSRNSQSLRR CKEPIRYSYNPDQFHNMDLRGGPHDGVTIPRSTSDTDLVTSDR STLWGRSSYSIGHSQDLVHMDIKEEVDAGDWIGMYLIDEVLS ENFLDYKNRGVNGSIRGQIIWKIDASSYPVEPSTKICFKYYHGV SGALRATTPSVTVKNSAAPIFKSIGADETVQQQGSRRLISFSLS DFQAMGLKKGMFFNPDPYLKISIQPGKHSIFPALPHHGQERRSK IIGNTVUPHIWQAEQFSFVSLPTDVLEIEVKDKFAKSPIIKRFL GKLSMPVQRLLERHAIGDRVVSYTLGRRLPTDHVSGGLQFFFEI TSSIHPDDESISLSTEPESAQIQDSPMNNIMESGSGEPRSEAPE SSESWKPEQLGEGGSVPREPORGAGEEEKEQBEEGDVSTLEQG EGRLQLRASVKRKSRPCSLPVSELETVIASACGDPETPRTHYIR IHTLLHSMPSAQGGSAAEEEDGAEESTLKDSSEKDGLSSVDTV AADPSALEEDREEPFGATTGTAHFGHSGGHFPSLANGAAQDGDT HPSTGSESDSPRQGGDHSCEGCDASCCSPSCYSSCYSTSCYS SSCYSASCYSPSCYNGNRFASHTTFSSVDSAKISESTVFSSQDD EEEENSAFESVPDSMQS PELDPESTNGAGPWQDELAAPSGHVER SPEGLESPVAGNRFRASHTTFSSVDSAKISESTVFSSQDD EEEENSAFESVPDSMQS PELDPESTNGAGPWQDELAAPSGHVER SPEGLESPVAGSNRREGECPILHNSQVSLPSLRPEHHHYPT IDEPLPPNWBARIDSIGRVFYVDHVNNTTTWQRPTAAATPGGM				NLEEISNYYGVSGFQTTEHFLTAVAHRLGKKKKGGLYSQEQAAK
ENKTTVYKIGDLTGYCTTPPRHOMGWAKRNVDHRPKSNSMYDVC SUPERSVLQRIMETDPLQQGQALASALKNKKKMQKRADKIASKL SDSMMSALDLSGNADDGVGD  1 HCGIKKRGEGGSFSPASGGFQLGCQIPEPSLPSEEETHPHTRA HTRTLRATLTRRPPSHSTRRFFPMPLDGDGGLASWK/PMRER* GWRRPAKAAGASLGVAATGKRGCRMSKRYLQKATKGKILIIIFI VTLWGKVVSSANHHKAHHVKTGTCEVVALHRCCNKWKIEERSQT VKSCFPGQVAGTTRAAPSCVDASIVEQKWCHMQPCLEGEECK VLPDRKGWSCSSGNKVKTTRVTH  5909  1 5002 PAIFGSTIIWAPGSHSAARADGRHGSLPSQSQAPGALCGARAPP SSNLRADRSMICAQARAGKNLYHNRFLGLAAMAFPSRNSQSLRR CKEPIRYSYNPDQFHNMDLRGGPHDGVTIPRSTSDTDLVTSDSR STLMGRSSYYSIGHSQDLVIHWDIKEEVDAGDWIGMYLIDEVLS ENFLDYKNRGVNGSHRGQIIWKIDASSYFVEPETKICFKYYHGV SGALRATTPSVTVKNSAAPIFKSIGADETVQGQGSRRLISFSLS DFQAMGLKKGMFFNPDPYLKISIQPGKHSIFPALPHHGQERRSK IIGNTVNPIWQAQEGFSVSLTDVLEIEVKDKFAKSRPIIKRFL GKLSMPVQRLLERHAIGDRVVSYTLGRRLPFDHVSGQLQFRFEI TSSIHPDDEEISLSTEPESAQIQDSPMNNLMESGSGEPRSEAPE SSESWKPQQLGGSVVPDRPGNQSIELSRPAEEAAVITEAGDQGM VSVGPEGAGELLAQVQKDIQPAPSAEELAEQLDLGEEASALLLE DGGAPASTKEBFLEEEATTGSRAGREEBEKEQEEEGDVSTLEQG EGRLQLRASVKRKSRPCSLPVSELETVIASACGDPETPRTHYIR IHTLLHISMPSAQGGSAAEEEDGAEEESTLKDSSEENDGLEPUTV AADPSALEEDREEPEGATPGTAHPGHSGGHPSLANGAAQDGDT HPSTGSESDSSPRQGGDHSCEGCDASCCSPSCYSSSCYSTSCYS SSCYSASCYSPSCYNONRFASHTRFSSVDESKGIESEVTFSSQDD EEEENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSGHVER SPEGLESPVAGPSNRREGECPILHNSQPVSQLFSLRPEHHHYPT IDEPLPPNWEARIDSIIGRVFYVDHVNRTTIWRQFTAAAATPDGKR	1	1 1		AVLADWVSGKISFYIPPPATHTLPTHLSAEIVKEMTEVFDIEDT
SVDRRSVLQRIMETDPLQQGQALASALKNKKKMQKRADKIASKL SDSMMSALDLSGNADDGVGD  1 CGIKKRGEGSGSPSPASGGFQLGCQIPEPSLPSEEETHPHTRA HTRTLRATLTRRPPRSHSTRLRFPMPLDGDCGLASWK/PMRER* GWRRPAKAAGASLGVAATGKRGCRMSKRYLQKATKGKLLIIIFI VILWGKVVSSANHHKAHHVKTGTCEVVALHRCCNKNKIEERSQT VKCSCFPGQVAGTTRAAPSCVDASIVEQKWWCHMQPCLEGEECK VLPDRKGWSCSSGNKVKTTRVTH  5002 PAIFGSTIIWPGSHSAARADGRHGSLPSQSQAPGALCGARAPP SSNLRADRSMICAQARAGKNLYHNRFLGLAAMAFPSRNSQSLRR CKEPIRTSYNPQOFHNDLRGGPHDGVTIPRSTSDTDLVTSDSR STLMCRSSYYSIGHODLVIHWDIKEEVDAGDWIGMYLIDEVLS ENFLDYKNRGVNGSHRGQIIWKIDASSYFVEPETKLCFKYYHGV SGALRATTPSVTVKNSAAPIFKSIGADETVQQGGSRLISFSLS DFQAMGLKKGMFFNPDPYLKISIQPGKHSIFPALPHHGQERRSK IIGNTVNPIWQARQFSFVSLPTDVLEIEVKDKFAKSRPIIKRFL GKLSMPVQRLLERHAIGDRVWSYTLGRLPTDHVSGQLQFFFEI TSSIHPDDEEISLSTEPESAQIQDSFMNNIMESGGEPRSEAPE SSESWKPEQLGEGSVPDRPGRQSIELSRPAREAAVITEAGDQGM VSVGPEGAGELLAQVQKDIQPAPSAEELAEQLDLGEEASALLLE DGEAPASTKEEPLEEATTGSRAGREEBEKRQEEEGDVSTLEQQ EGRLQLRASVKRKSRPCSLPVSELETVIASACGDPETPRTHYIR IHTLLHSMPSAQGGSAAEEEDGAEESTLKDSSEKDGLSEVDTV AADPSALEEDREEPEGATPGTAHPGHSGGHPSLANGAQDGDT HPSTGSSDSSPRQGGDHSCCSCDSCCSPSCYSSSCYSTSCYS SSCYSASCYSBSCYMONRFASHTRFSSVDSAKIEESTVFSSQDD EEEENSAFESVPDSMGSPELDPESTNGAGPWQDELAAPSGHVER SPEGLESPVAGPSNRREGECPILHNSQPVSQLPSLRPEHHHYPT IDEPLPPNWEARIDSIIGRVFYVDHVNRTTTWORPTAAATPDGMR	1	1		EQANEDTMECLATGESDELLGDTDPLEMEIKLLHSPMTKIADAI
SDEMMSALDLSGNADDGVGD  HCGIKKRGEGGSSPSPAGGFQLGCQIPEPSLPSEEETHPHTRA HTRTLRATLITRRPPRSHSTRLRFPMPLDGDGGLASWK/PMRER* GWRPAKAAGASLGVAATGKRGCRMSKRYLQKATKGKLLIIIFI VTLWGKVVSSANHHKAHHVKTGTCEVVALHRCCNKNKIEERSOT VKCSCFPGQVAGTTRAAPSCVDASIVEQKWWCHMQPCLEGEECK VLPDRKGWSCSSGNKVKTTRVTH  5002 PAIFGSTIIWAPGSHSAARADGRHGSLPSQSQAPGALCGARAPP SSNLRADRSMICAQARAGKNLYHNRFLGLAAMAFPSNRSQSLRR CKEPIRYSYNPDQFHNMDLRGGPHBGVTIPRSTSDTDLVTSDSR STLMGRSSYYSIGHSQDLVIHWDIKEEVDAGDWIGMYLIDEVLS ENFLDYKNRGVNGSHRGQIIWKIDASSYFVEPETKICFKYYHGV SGALRATTPSVTVKNSAAPIFKSIGADETVQGQGSRRLISFSLS DFQAMGLKKGMFFNPDPYLKISIQPGKHSIFPALPHHGGERRSK IIGNTVNPIWQARQFSFVSLPTDVLEIEVKDKFAKSRPIIKRFL GKLSMPVQRLLERHAIGDRVVSYTLGRRLPTDHVSQQLQFRFEI TSSIHPDDEEISLSTEPESAQIODSPMNNIMESGGEPRSEAPE SSESWKPEQLGEGSVPDRPGNQSIELSRPAEEAAVITEAGDQCM VSVGPEGAGELLAQVQKDIQPAPSAEELAROLDLGEEASALLLE DGGAPASTKEEPLEEATTQSRAGREEBEKEQEEEGDVSTLEQG EGRLQLRASVKRKSRPCSLPVSRLETVIASACGDPETPRTHYIR IHTLLHSMPSAQGGSAAEEEDGAEEESTLKDSSEKDGLSEVDTV AADPSALEEDREEPEGATTGTAHPGHSGGHFPSLANGAAQDGDT HPSTGSESDSSPRQGGHSCEGCDASCCSPSCYSSCYSTSCYS SSCYSASCYSPSCYNGNRFASHTRFSSVDSAKISESTVFSSQDD EEEENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSGHVER SPEGLESPVAGPSNRREGECPILHNSQPVSQLPSLRPEHHHYPT IDEPLPPNWEARIDSIGRVFYVDHVNRTTTWORPTAAATTPDGKR	1	į		ENKTTVYKIGDLTGYCTNPNRHQMGWAKRNVDHRPKSNSMVDVC
HCGIKKRGEGSGSPSPASGGTQLGCQIPEPSLPSEEETHPHTRA HTRTLRATLITRRPPRSHSTRLFPMPLDGDGGLASWK/PMER* GWRRPAKAAGASLGVAATGKRGCRMSKRYLQKATKGKLLIIFI VTLWGKVVSSANHKKAHHVKTGTCEVVALIRCCNKNKIEERSQT VKCSCFPGQVAGTTRAAPSCVDASIVEQKWCHMQPCLEGEECK VLEDRKGMSCSSGNKVKTTRVTH  5002 PAIPGSTIIWAPGSHSAARADGRHGSLPSQSQAPGALCGARAPP SSNLRADRSMICAQARAGKNLYHMRFLGLAAMAFPSRNSQSLRR CKEPIRYSYNPDQFHNMDLRGGPHDGVTIPRSTSDTDLVTSDSR STLWGRSSYYSIGHSQDLVIHWDIKEEVDAGDWIGMYLIDEVLS ENFLDYKNRGVNSHRGQIIWKIDASSYFVEPETKICFKYYHGV SGALRATTPSVTVKNSAAPIFKSIGADETVQGQGSRRLISFSLS DFQAMGLKKGMFRNPDPYLKISIOPGKHSIFPALPHHGQERRSK IIGNTVNPIWQAEQFSFVSLPTDVLEIEVKDKFAKSRPIIKRFL GKLSMPVQRLLERHAIGDRVVSYTIGRRLPFDHVSGQLQFRFEI TSSIHPDDEEISLSTEPESAQIQDSPMNNIMESGSGEPRSEAPE SSESWKPEQLGEGSVPDRPGNQSIELSRPAEEAAVITEAGDQGM VSVGPEGAGELLAQVQKDIQPAPSAELAEQLDLGEEASALLLE DGEAPASTKEEPLEEEATTQSRAGREEBEKEQEEEGDVSTLEQG EGRLQLRASVKRKSRPCSLPVSELETVIASACGDPETPRTHYIR IHTLLHSMPSAQGGSAABEEDGABEESTLKDSSEKDGLSEVDTV AADPSALEEDREEPEGATPGTAHPGHSGHFPSLANGAAQDGDT HSTGSESDSSPRQGGHSCEGCDASCCSPSCYSSCYSTSCYS SSCYSASCYSPSCYNGNFASHTRFSSVDSAKISESTVFSQDD EEEENSAFESVPDSMQSPELDPESTNGAGPWODELAAPSGHVER SPEGLESPVAGPSNRREGECPILHNSQPVSQLPSLRPEHHHYPT IDEPLPPNWEARIDSIGRVFYVDHVNRTTTWORPTAAATPDGKR	1	1		SVDRRSVLQRIMETDPLQQGQALASALKNKKKMQKRADKIASKL
HTRTLRATLITRIPPRSHSTRLRFPMPLDGDGGLASWK/PMRER* GWRRPAKAAGASLGVAATGKRGCRMSKRYLQKATKGKLLIIIFI VTLWGKVVSSANHHKAHHVKTGTCEVVALHRCCNKNKIEERSQT VKCSCFFGQVAGTTRAAPSCVDASIVEQKWWCHMQPCLEGEECK VLPDRKGWSCSSGNKVKTTRVTH  5002 PAIFGSTIIWAPGSHSAARADGRHGSLPSQSQAPGALCGARAPP SSNLRADRSMICAQARAGKNLYHNRFLGLAAMAFPSRNSQSLRR CKEPIRYSTNPDQFHNMDLRGGPHDGVTIPRSTSDTDLVTSDSR STLMGRSSYYSIGHSQDLVIHWDIKEEVDAGDWIGMYLIDEVLS ENFLDYKNRGVNGSHRGQIIWKIDASSYFVEPSTKICFKYYHGV SGALRATTPSSVYXNISAAPIFKSIGADETVQQQSRRLISFSLS DFQAMGLKKGMFFNPDPYLKTSIQADETVQGQGSRRLISFSLS DFQAMGLKKGMFFNPDPYLKTSIQADETVQGQGSRRLISFSLS GKLSMPVQRLLERHAIGDRVVSYTLGRRLPTDHVSGQLQFRFEI TSSIHPDDEEISLSTEPESAQIQDSFMNNIMESGGEPRSEAPE SSESWKPEQLGEGSVPDRPGNQSIELSRPAEEAAVITEAGDQCM VSVGPEGAGELLAQVQKDIQPAPSAEELAEQLDLGEEASALLLE DGEAPASTKEEPLEEEAATTQSRAGREEBEKEQEEEGDVSTLEQG EGRLQLRASVKRKSRPCSLPVSELETVIASACGDPETRTHYIR IHTLLHSMPSAQGGSAAEEEDGAEESTLKDSSEKDGLSEVDTV AADPSALEEDREEPGATPGTAHPGHSGGHFPSLANGAAQDGDT HPSTGSSEDSSPRGGGDHSCEGCDASCCSPSCYSSCYSTSCYS SSCYSASCYSPSCYNGNRFASHTRFSSVDSKKISESTVFSSQDD EEEENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSGHVER SPEGLESPVAGPSNRREGECPILHNSQPVSQLPSLRPEHHHYPT IDEPLPPNWEARIDSIGRVFYVDHVNRTTTTMQRPTAAATPDGMR	5908	242		
GWRPPAKAAGASLGVAATGKRGCRMSKRYLQKATKGKLLIIIFI VTLWGKVVSSANHHKAHHVKTGTCEVVALHRCCNKNKTEERSQT VKCSCFPGQVAGTTRAAPSCVDASIVEQKWCHMQPCLEGEECK VLPDRKGWSCSSGNKVKTTRVTH  PATPGSTIIWAPGSHSAARADGRHGSLPSQSQAPGALCGARAPP SSNLRADRSMICAQARAGKNLYHNRFLGLAAMAFPSRNSQSLRR CKEPIRYSYNPDQFHNMDLRGGPHDGVTIPRSTSDTDLVTSDSR STLWGRSSYYSIGHSQDLVIHWDLKEEVDAGDWIGMYLIDEVLS ENFLDYKNRGVNGSHRGQIIWKIDASSYFVEPETKICFKYYHGV SGALRATTPSVTVKNSAAPIFKSIGADETVQQQGSRRLISFSLS DFQAMGLKKGMFFNPDPYLKISIQPGKHSIFPALPHHGQERRSK IIGNTVNPIWQAEQFSFVSLPTDVLEIEVKDKFAKSRPIIKRFL GKLSMPVQRLLERHAIGDRVVSYTLGRRLPTDHVSGQLQFRFEI TSSIHPDDEEISLSTEPESAQIQDSPMNNLMESGSGEPRSEAPE SSESWKPEQLGEGSVPDRPGNQSIELSRPAEEAAVITEAGDQGM VSVGPEGAGELLAQVQKDIQPAPSAEELAEQLDLGBEASALLLE DGEAPASTKEEPLEEEATTQSRAGREEBEERQEEEGDVSTLEQG EGRLQLRASVKRKSRPCSLPVSELETVIASACGDPETPRTHYIR IHTLLHSMPSAQGGSAAEEBDGAEESTLKDSSEKDGLSEVDTV AADPSALEEDREEPEGATPGTAHPGHSGGHFPSLANGAAQDGDT HPSTGSESDSSPRQGDHSCEGCDASCCSPSCYSSSCYSTSCYS SSCYSASCYSPSCYNGNRFASHTRFSSVDSAKISESTVFSSQDD HPSTGSESDSSPRQGGDHSCEGCDASCCSPSCYSSSCYSTSCYS SSCYSASCYSPSCYNGNRFASHTRFSSVDSAKISESTVFSSQDD EEEENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSGHVER SPEGLESPVAGPSNRREGECPILHNSQPVSQLPSLRPEHHHYPT IDEPLPPNWEARIDSIIGRVFYYDHVNRTTTWQRPTAAATPDCMR	1 3300	24/	975	HCGIKKRGEGSGSPSPASGGFQLGCQIPEPSLPSEEETHPHTRA
VTLWGKVVSSANHHKAHHVKTGTCEVVALHRCCNKNKIEERSQT VKCSCFPGQVAGTTRAAPSCVDASIVEQKWWCHMQPCLEGEECK VLPDRKGWSCSSGNKVKTTRVTH  5002  PAIPGSTIIWAPGSHSAARADGRHGSLPSQSQAPGALCGARAPP SSNLRADRSMICAQARAGKNLYHNRFLGLAAMAFPSRNSQSLRR CKEPIRYSYNPDQFHNMDLRGGPHDGVTIPRSTSDTDLVTSDSR STLMGRSSYYSIGHSQDLVIHWDLKEEVDAGDWIGMYLIDEVLS ENFLDYKNRGVNGSHRGQIIWKIDASSYPVEPETKICFKYYHGV SGALRATTPSVTVKNSAAPIFKSIGADETVQGQGSRRLISFSLS DFQAMGLKKGMFNPDPYLKISIQPGKHSIFPALPHHGQERRSK IIGNTVNPIWQAEQFSFVSLPTDVLEIEVKDKFAKSRPIIKRFL GKLSMPVQRLLERHAIGDRVVSYTLGRRLPTDHVSGQLQFFFEI TSSIHPDDEEISLSTEPESAQIQDSPMNNLMESGSGEPRSEAPE SSESWKPEQLGEGSVPDRPGNQSIELSRPAEEAAVITEAGDQGM VSVGPEGAGELLAQVQKDIQPAPSAEELAEQLDLGEASALLLE DGEAPASTKEEPLEEEATTQSRAGREEBEKEQEEEGDVSTLEQG EGRLQLRASVKRKSRPCSLPVSELETVIASACGDPETPRTHYIR IHTLLHSMPSAQGGSAAEEEDGAEEESTLKDSSEKDGLSEVDTV AADPSALEEDREEPEGATPGTAHPGHSGGHFPSLANGAQDGDT HPSTGSESDSSPRQGGHSCEGCDASCCSPSCYSSCYSTSCYS SSCYSASCYSPSCYNGNRFASHTRFSSVDSAKISESTVFSSQDD EEEENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSGHVER SPEGLESPVAGPSNRREGECPILHNSQPVSQLPSLRPEHHHYPT IDEPLPPNWEARIDSIGRVFYVDHVNRTTTWORPTAAATPDCMR		í l		HTRTLRATLTRRPPRSHSTRLRFPMPLDGDGGLASWK/PMRER*
VKCSCFPGQVAGTTRAAPSCVDASIVEQKWWCHMQPCLEGEECK VLPDRKGWSCSSGNKVKTTRVTH  PAIPGSTIIWAPGSHSAARADGRHGSLPSQSQAPGALCGARAPP SSNLRADRSMICAQARAGKNLYHNRFLGLAAMAFPSRNSQSLRR CKEPIRYSYNPDQFHNMDLRGGPHDGVTIPRSTSDTDLVTSDSR STLWGRSSYYSIGHSQDLVIHWDIKEEVDAGDWIGMYLIDEVLS ENFLDYKNRGVNGSHRGQIIWKIDASSYFVEEPTKICFKYYHGV SGALRATTPSVTVKNSAAPIFKSIGADETVQGQGSRRLISFSLS DFQAMGLKKGMFFNPDPYLKISIQPGKHSIFPALPHHGQERRSK IIGNTVNPIWQAEQFSFVSLPTDVLEIEVKDKFAKSRPIIKRFL GKLSMPVQRLLERHAIGDRVVSYTLGRRLPTDHVSGQLQFRFEI TSSIHPDDEEISLSTEPESAQIQDSPMNNLMESGSGEPRSEAPE SSESWKPEQLGEGSVPDRPGNQSIELSRPAEEAAVITEAGDQGM VSVGPEGAGELLAQVQKDIQPAPSAEELAEQLDLGEEASALLLE DGEAPASTKEEPLEEEATTQSRAGREEEEKEQEEEGDVSTLEQG EGRLQLRASVKRKSRPCSLPVSELETVIASACGDPETPRTHYIR IHTLLHSMPSAQGGSAAEEEDGAEEESTLKDSSEKDGLSEVDTV AADPSALEEDREEPEGATPGTAHPGHSGGHFPSLANGAAQDGDT HPSTGSESDSSPRQGGDHSCEGCDASCCSPSCYSSSCYSTSCYS SSCYSASCYSPSCYNGNRFASHTRFSSVDSAKISESTVFSSQDD EEEENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSGHVER SPEGLESPVAGPSNRREGECPILHNSQPVSQLPFLRPEHHYPT IDEPLPPNWEARIDSHGRVFVVDHVNRTTTWQRPTAAATPDGMR	1			GWRRPAKAAGASLGVAATGKRGCRMSKRYLQKATKGKLLIIIFI
VLPDRKGWSCSSGNKVKTTRVTH  5909  1 5002  PAIPGSTIIWAPGSHSAARADGRHGSLPSQSQAPGALCGARAPP SSNLRADRSMICAQARAGKNLYHNRFLGLAAMAFPSRNSQSLRR CKEPIRYSYNPDQFHNMDLRGGPHDGVTIPRSTSDTDLVTSDSR STLMGRSSYYSIGHSQDLVIHWDIKEEVDAGDWIGMYLIDEVLS ENFLDYKNRGVNGSHRGQIIWKIDASSYFVEPETKICFKYYHGV SGALRATTPSVTVKNSAAPIFKSIGADETVQQQGSRRLISFSLS DFQAMGLKKGMFFNPDPYLKISIQPGKHSIFPALPHHGQERRSK IIGNTVNPIWQAEQFSFVSLPTDVLEIEVKDKFAKSRPIIKRFL GKLSMPVQRLLERHAIGDRVVSYTLGRRLPTDHVSGQLQFRFEI TSSIHPDDEEISLSTEPESAQIQDSPMNNLMESGSGEPRSEAPE SSESWKPEQLGEGSVPDRPGNQSIELSRPAEEAAVITEAGDQCM VSVGPEGAGELLAQVQKDIQPAPSAEELAEQLDLGEEASALLLE DGEAPASTKEEPLEEEATTQSRAGREEBEKEQEEEGDVSTLEQG ECRLQLRASVKRKSRPCSLPVSELETVIASACGDPETPRTHYIR IHTLLHSMPSAQGGSAAEEEDGAEEESTLKDSSEKDGLSEVDTV AADPSALEEDREEPEGATPGTAHPGHSGGHFPSLANGAAQDGDT HPSTGSESDSSPRQGGDHSCEGCDASCCSPSCYSSSCYSTSCYS SSCYSASCYSPSCYNGNRFASHTRFSSVDSAKISESTVFSSQDD EEEENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSCHVER SPEGLESPVAGPSNRREGECPILHNSQPVSQLPSLRPEHHHYPT IDEPLPPNWEARIDSIGRVFYVDHVNRTTTWQRPTAAATPDGMR	i			VILWGKVVSSANHKAHHVKTGTCEVVALHRCCNKNKIEERSQT
PAIPGSTIIWAPGSHSAARADGRHGSLPSQSQAPGALCGARAPP SSNLRADRSMICAQARAGKNLYHNRFLGLAAMAFPSRNSQSLRR CKEPIRYSYNPDQFHNMDLRGGPHDGVTIPRSTSDTDLVTSDSR STLMGRSSYYSIGHSQDLVIHWDIKEEVDAGDWIGMYLIDEVLS ENFLDYKNRGVNGSHRGQIIWKIDASSYFVEPETKICFKYYHGV SGALRATTPSVTVKNSAAPIFKSIGADETVQGQGSRRLISFSLS DFQAMGLKKGMFFNPDPYLKISIQPGKHSIFPALPHHGQERRSK IIGNTVNPIWQAEQFSFVSLPTDVLEIEVKDKFAKSRPIIKRFL GKLSMPVQRLLERHAIGDRVVSYTLGRRLPTDHVSGQLQFRFEI TSSIHPDDEEISLSTEPESAQIQDSPMNNLMESGSGEPRSEAPE SSESWKPEQLGEGSVPDRPGNQSIELSRPAEEAAVITEAGDQGM VSVGPEGAGELLAQVQKDIQPAPSAEELAEQLDLGEEASALLLE DGEAPASTKEEPLEEEATTQSRAGREEBEKQEEEGDVSTLEQG EGRLQLRASVKRKSRPCSLPVSELETVIASACGDPETPRTHYIR IHTLLHSMPSAQGGSAAEEEDGAEEESTLKDSSEKDGLSEVDTV AADPSALEEDREEPEGATPGTAHPGHSGGHFPSLANGAAQDGDT HPSTGSESDSSPRQGGDHSCEGCDASCCSPSCYSSSCYSTSCYS SSCYSASCYSPSCYNGNRFASHTRFSSVDSAKISESTVPSSQDD EEEENNAFESVPDSMQSPELDPESTNGAGPWQDELAAPSGHVER SPEGLESPVAGPSNRREGECPILHNSQPVSQLPSLRPEHHHYPT IDEPLPPNWEARIDSIGRVFYVDHVNRTTTWQRPTAAATPDGMR	1	]		VKCSCFPGQVAGTTRAAPSCVDASIVEQKWWCHMQPCLEGEECK
SSNIRADRSMICAQARAGKNLYHNRFLGLAAMAFPSRNSQSLRR CKEPIRYSYNPDQFHNMDLRGGPHDGVTIPRSTSDTDLVTSDSR STLMGRSSYYSIGHSQDLVIHWDIKEEVDAGDWIGMYLIDEVLS ENFLDYKNRGVNGSHRGQIIWKIDASSYFVEPETKICFKYYHGV SGALRATTPSVTVKNSAAPIFKSIGADETVQGQGSRRLISFSLS DFQAMGLKKGMFFNPDPYLKISIQPGKHSIFPALPHHGQBRRSK IIGNTVNPIWQAEQFSFVSLPTDVLEIEVKDKFAKSRPIIKRFL GKLSMPVQRLLERHAIGDRVVSYTLGRRLPTDHVSGQLQFRFEI TSSIHPDDEEISLSTEPESAQIQDSPMNNLMESGSGEPRSEAPE SSESWKPEQLGEGSVPDRPGNQSIELSRPAEEAAVITEAGDQGM VSVGPEGAGELLAQVQKDIQPAPSAEELAEQLDLGBEASALLLE DGEAPASTKEEPLEEEATTQSRAGREEEEKEQEEEGDVSTLEQG EGRLQLRASVKRKSRPCSLPVSELETVIASACGDPETPRTHYIR IHTLLHSMPSAQGGSAAEEEDGAEEESTLKDSSEKDGLSEVDTV AADPSALEEDREEPEGATPGTAHPGHSGGHFPSLANGAAQDGDT HPSTGSESDSSPRQGGDHSCEGCDASCCSPSCYSSSCYSTSCYS SSCYSASCYSPSCYNGNRFASHTRFSSVDSAKISESTVFSSQDD EEEENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSGHVER SPEGLESPVAGPSNRREGECPILHNSQPVSQLPSLRPEHHHYPT IDEPLPPNWEARIDSIGRVFYVDHVNRTTTWQRFTAAATPDGMR	5909	<del></del>	5000	VLPDRKGWSCSSGNKVKTTRVTH
CKEPIRYSYNPDQFHNMDLRGGPHDGVTIPRSTSDTDLVTSDSR STLMGRSSYYSIGHSQDLVIHWDIKEEVDAGDWIGMYLIDEVLS ENFLDYKNRGVNGSHRGQIIWKIDASSYFVEPETKICFKYYHGV SGALRATTPSVTVKNSAAPIFKSIGADETVQGQGSRRLISFSLS DFQAMGLKKGMFFNPDPYLKISIQPGKHSIFPALPHHGQERRSK IIGNTVNPIWQAEQFSFVSLPTDVLEIEVKDKFAKSRPIIKRFL GKLSMPVQRLLERHAIGDRVVSYTLGRRLPTDHVSGQLQFRFEI TSSIHPDDEEISLSTEPESAQIQDSPMNNLMESGSGEPRSEAPE SSESWKPEQLGEGSVPDRPGNQSIELSRPAEEBAVITEAGDQGM VSVGPEGAGELLAQVQKDIQPAPSAEELAEQLDLGEEASALLLE DGEAPASTKEEPLEEEATTQSRAGREEBEKEQEEEGDVSTLEQG EGRLQLRASVKRKSRPCSLPVSELETVIASACGDPETPRTHYIR IHTLLHSMPSAQGGSAAEEEDGAEEESTLKDSSEKDGLSEVDTV AADPSALEEDREEPEGATPGTAHPGHSGGHFPSLANGAAQDGDT HPSTGSESDSSPRQGGDHSCEGCDASCCSPSCYSSSCYSTSCYS SSCYSASCYSPSCYNGNRFASHTRFSSVDSAKISESTVFSSQDD EEEENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSGHVER SPEGLESPVAGPSNRREGECPILHNSQPVSQLPSLRPEHHHYPT IDEPLPPNWEARIDSIGRVFYVDHVNRTTTWQRPTAAATPDGMR	1 -505	·	5002	PATPGSTI IWAPGSHSAARADGRHGSLPSQSQAPGALCGARAPP
STLMGRSSYYSIGHSQDLVIHWDIKEEVDAGDWIGMYLIDEVLS ENFLDYKNRGVNGSHRGQIIWKIDASSYFVEPETKICFKYYHGV SGALRATTPSVTVKNSAAPIFKSIGADETVQGQGSRRLISFSLS DFQAMGLKKGMFFNPDPYLKISIQPGKHSIFPALPHHGQERRSK IIGNTVNPIWQAEQFSFVSLPTDVLEIEVKDKFAKSRPIIKRFL GKLSMPVQRLLERHAIGDRVVSYTLGRRLPTDHVSGQLQFRFEI TSSIHPDDEEISLSTEPESAQIQDSPMNNLMESGSGEPRSEAPE SSESWKPEQLGEGSVPDRPGNQSIELSRPAEEAAVITEAGDQGM VSVGPEGAGELLAQVQKDIQPAPSAEELAEQLDLGEEASALLLE DGEAPASTKEEPLEEEATTQSRAGREEBEKEQEEEGDVSTLEQG EGRLQLRASVKRKSRPCSLPVSELETVIASACGDPETPRTHYIR IHTLLHSMPSAQGGSAAEEEDGAEEESTLKDSSEKDGLSEVDTV AADPSALEEDREEPEGATPGTAHPGHSGGHFPSLANGAAQDGDT HPSTGSESDSSPRQGGDHSCEGCDASCCSPSCYSSSCYSTSCYS SSCYSASCYSPSCYNGNRFASHTRFSSVDSAKISESTVFSSQDD EEEENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSGHVER SPEGLESPVAGPSNRREGECPILHNSQPVSQLPSLRPEHHHYPT IDEPLPPNWEARIDSIGRVFYVDHVNRTTTWQRPTAAATPDGMR	1			SSNLKADRSMICAQARAGKNLYHNRFLGLAAMAFPSRNSQSLRR
ENFLDYKNRGVNGSHRGQIIWKIDASSYFVEPETKICFKYYHGV SGALRATTPSVTVKNSAAPIFKSIGADETVQGQGSRRLISFSLS DFQAMGLKKGMFFNPDPYLKISIQPGKHSIFPALPHHGQERRSK IIGNTVNPIWQAEQFSFVSLPTDVLEIEVKDKFAKSRPIIKRFL GKLSMPVQRLLERHAIGDRVVSYTLGRRLPTDHVSGQLQFRFEI TSSIHPDDEEISLSTEPESAQIQDSPMNNLMESGSGEPRSEAPE SSESWKPEQLGEGSVPDRPGNQSIELSRPAEEAAVITEAGDQGM VSVGPEGAGELLAQVQKDIQPAPSAEELAEQLDLGEEASALLLE DGEAPASTKEEPLEEEATTQSRAGREEBEKEQEEEGDVSTLEQG EGRLQLRASVKRKSRPCSLPVSELETVIASACGDPETPRTHYIR IHTLLHSMPSAQGGSAAEEEDGAEEESTLKDSSEKDGLSEVDTV AADPSALEEDREEPEGATPGTAHPGHSGGHFPSLANGAAQDGDT HPSTGSESDSSPRQGGDHSCEGCDASCCSPSCYSSSCYSTSCYS SSCYSASCYSPSCYNGNRFASHTRFSSVDSAKISESTVFSSQDD EEEENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSGHVER SPEGLESPVAGPSNRREGECPILHNSQPVSQLPSLRPEHHHYPT IDEPLPPNWEARIDSHGRVFYVDHVNRTTTWQRPTAAATPDGMR	1			CKEPIKYSYNPDQFHNMDLRGGPHDGVTIPRSTSDTDLVTSDSR
SGALRATTPSVTVKNSAAPIFKSIGADETVQGQGSRRLISFSLS DFQAMGLKKGMFFNPDPYLKISIQPGKHSIFPALPHHGQERRSK IIGNTVNPIWQAEQFSFVSLPTDVLEIEVKDKFAKSRPIIKRFL GKLSMPVQRLLERHAIGDRVVSYTLGRRLPTDHVSGQLQFRFEI TSSIHPDDEEISLSTEPESAQIQDSPMNNLMESGSGEPRSEAPE SSESWKPEQLGEGSVPDRPGNQSIELSRPAEEAAVITEAGDQGM VSVGPEGAGELLAQVQKDIQPAPSAEELAEQLDLGEEASALLLE DGEAPASTKEEPLEEEATTQSRAGREEBEKEQEEEGDVSTLEQG EGRLQLRASVKRKSRPCSLPVSELETVIASACGDPETPRTHYIR IHTLLHSMPSAQGGSAAEEEDGAEEESTLKDSSEKDGLSEVDTV AADPSALEEDREEPEGATPGTAHPGHSGGHFPSLANGAAQDGDT HPSTGSESDSSPRQGGDHSCEGCDASCCSPSCYSSSCYSTSCYS SSCYSASCYSPSCYNGNRFASHTRFSSVDSAKISESTVFSSQDD EEEENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSGHVER SPEGLESPVAGPSNRREGECPILHNSQPVSQLPSLRPEHHHYPT IDEPLPPNWEARIDSHGRVFYVDHVNRTTTWQRPTAAATPDGMR	1	[		STEWGRSSYYSIGHSQDLVIHWDIKEEVDAGDWIGMYLIDEVLS
DFQAMGLKKGMFFNPDPYLKISIQPGKHSIFPALPHHGQERRSK IIGNTVNPIWQAEQFSFVSLPTDVLEIEVKDKFAKSRPIIKRFL GKLSMPVQRLLERHAIGDRVVSYTLGRRLPTDHVSGQLQFRFEI TSSIHPDDEEISLSTEPESAQIQDSPMNNLMESGSGEPRSEAPE SSESWKPEQLGEGSVPDRPGNQSIELSRPAEEAAVITEAGDQGM VSVGPEGAGELLAQVQKDIQPAPSAEELAEQLDLGEEASALLLE DGEAPASTKEEPLEEEATTQSRAGREEBEKEQEEEGDVSTLEQG EGRLQLRASVKRKSRPCSLPVSELETVIASACGDPETPRTHYIR IHTLLHSMPSAQGGSAAEEEDGAEEESTLKDSSEKDGLSEVDTV AADPSALEEDREEPEGATPGTAHPGHSGGHFPSLANGAAQDGDT HPSTGSESDSSPRQGGDHSCEGCDASCCSPSCYSSCYSTSCYS SSCYSASCYSPSCYNGNRFASHTRFSSVDSAKISESTVFSSQDD EEEENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSGHVER SPEGLESPVAGPSNRREGECPILHNSQPVSQLPSLRPEHHHYPT IDEPLPPNWEARIDSHGRVFYVDHVNRTTTWQRPTAAATPDGMR	1		ĺ	ENFLDYKNRGVNGSHRGQIIWKIDASSYFVEPETKICFKYYHGV
IIGNTVNPIWQAEQFSFVSLPTDVLEIEVKDKFAKSRPIIKRFL GKLSMPVQRLLERHAIGDRVVSYTLGRRLPTDHVSGQLQFRFEI TSSIHPDGEISLSTEPESAQIQDSPMNILMESGSGEPRSEAPE SSESWKPEQLGEGSVPDRPGNQSIELSRPAEEAAVITEAGDQGM VSVGPEGAGELLAQVQKDIQPAPSAEELAEQLDLGEEASALLLE DGEAPASTKEEPLEEEATTQSRAGREEBEKEQEEEGDVSTLEQG EGRLQLRASVKRKSRPCSLPVSELETVIASACGDPETPRTHYIR IHTLLHSMPSAQGGSAAEEEDGAEEESTLKDSSEKDGLSEVDTV AADPSALEEDREEPEGATPGTAHPGHSGGHFPSLANGAAQDGDT HPSTGSESDSSPRQGGDHSCEGCDASCCSPSCYSSSCYSTSCYS SSCYSASCYSPSCYNGNRFASHTRFSSVDSAKISESTVFSSQDD EEEENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSGHVER SPEGLESPVAGPSNRREGECPILHNSQPVSQLPSLRPEHHHYPT IDEPLPPNWEARIDSIGRVFYVDHVNRTTTWQRPTAAATPDGMR				SGALKATTPSVTVKNSAAPIFKSIGADETVQGQGSRRLISFSLS
GKLSMPVQRLLERHAIGDRVVSYTLGRRLPTDHVSGQLQFRFEI TSSIHPDDEEISLSTEPESAQIQDSPMNNLMESGSGEPRSEAPE SSESWKPEQLGEGSVPDRPGNQSIELSRPAEEAAVITEAGDQGM VSVGPEGAGELLAQVQKDIQPAPSAEELAEQLDLGEEASALLLE DGEAPASTKEEPLEEEATTQSRAGREEBEKEQEEEGDVSTLEQG EGRLQLRASVKRKSPCSLPVSELETVIASACGDPETPRTHYIR IHTLLHSMPSAQGGSAAEEEDGAEEESTLKDSSEKDGLSEVDTV AADPSALEEDREEPEGATPGTAHPGHSGGHFPSLANGAAQDGDT HPSTGSESDSSPRQGGDHSCEGCDASCCSPSCYSSSCYSTSCYS SSCYSASCYSPSCYNGNRFASHTRFSSVDSAKISESTVFSSQDD EEENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSGHVER SPEGLESPVAGPSNRREGECPILHNSQPVSQLPSLRPEHHHYPT IDEPLPPNWEARIDSHGRVFYVDHVNRTTTWQRPTAAATPDGMR	1	1		DECAMGLEKKGMFFNPDPYLKISIQPGKHSIFPALPHHGQERRSK
TSSIHPDDEEISLSTEPESAQIQDSPMNNIMESGSGEPRSEAPE SSESWKPEQLGEGSVPDRPGNQSIELSRPAEEAAVITEAGDQGM VSVGPEGAGELLAQVQKDIQPAPSAEELAEQLDLGEEASALLLE DGEAPASTKEEPLEEEATTQSRAGREEBEKEQEEEGDVSTLEQG EGRLQLRASVKRKSRPCSLPVSELETVIASACGDPETPRTHYIR IHTLLHSMPSAQGGSAAEEEDGAEEESTLKDSSEKDGLSEVDTV AADPSALEEDREEPEGATPGTAHPGHSGGHFPSLANGAAQDGDT HPSTGSESDSSPRQGGDHSCEGCDASCCSPSCYSSSCYSTSCYS SSCYSASCYSPSCYVNGNRFASHTRFSSVDSAKISESTVFSSQDD EEEENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSGHVER SPEGLESPVAGPSNREGECPILHNSQPVSQLPSLRPEHHHYPT IDEPLPPNWEARIDSIGRVFYVDHVNRTTTWQRPTAAATPDGMR	į l			TIGHT VNPIWQAEQFSFVSLPTDVLEIEVKDKFAKSRPIIKRFL
SSESWKPEQLGEGSVPDRPGNQSIELSRPAEEAAVITEAGDQGM VSVGPEGAGELLAQVQKDIQPAPSAEELAEQLDLGEEASALLLE DGEAPASTKEEPLEEEATTQSRAGREEBEKEQEEEGDVSTLEQG EGRLQLRASVKRKSRPCSLPVSELETVIASACGDPETPRTHYIR IHTLLHSMPSAQGGSAAEEEDGAEEESTLKDSSEKDGLSEVDTV AADPSALEEDREEPEGATPGTAHPGHSGGHFPSLANGAAQDGDT HPSTGSESDSSPRQGGDHSCEGCDASCCSPSCYSSSCYSTSCYS SSCYSASCYSPSCYNGNRFASHTRFSSVDSAKISESTVFSSQDD EEEENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSGHVER SPEGLESPVAGPSNRREGECPILHNSQPVSQLPSLRPEHHHYPT IDEPLPPNWEARIDSHGRVFYVDHVNRTTTWQRPTAAATPDGMR	Į.			GKLSMPVQKLLERHAIGDRVVSYTLGRRLPTDHVSGQLQFRFEI
VSVGPEGAGELLAQVQKDIQPAPSAEELAEQLDLGEEASALLLE DGEAPASTKEEPLEEEATTQSRAGREEBEKEQEEEGDVSTLEQG EGRLQLRASVKRKSRPCSLPVSELETVIASACGDPETPRTHYIR IHTLLHSMPSAQGGSAAEEEDGAEEESTLKDSSEKDGLSEVDTV AADPSALEEDREEPEGATPGTAHPGHSGGHFPSLANGAAQDGDT HPSTGSESDSSPRQGGDHSCEGCDASCCSPSCYSSSCYSTSCYS SSCYSASCYSPSCYNGNRFASHTRFSSVDSAKISESTVFSSQDD EEEENSAFESVPDSMQSPELDPESTNGAGFWQDELAAPSGHVER SPEGLESPVAGPSNRREGECPILHNSQPVSQLPSLRPEHHHYPT IDEPLPPNWEARIDSHGRVFYVDHVNRTTTWQRPTAAATPDGMR	. 1	ı		TSSIHPDDEEISLSTEPESAQIQDSPMNNLMESGSGEPRSEAPE
DGEAPASTKEEPLEEEATTQSRAGREEBEKEQEEEGDVSTLEQG EGRLQLRASVKRKSRPCSLPVSELETVIASACGDPETPRTHYIR IHTLLHSMPSAQGGSAAEEEBGAEEESTLKDSSEKDGLSEVDTV AADPSALEEDREEPEGATPGTAHPGHSGGHFPSLANGAAQDGDT HPSTGSESDSSPRQGGDHSCEGCDASCCSPSCYSSSCYSTSCYS SSCYSASCYSPSCYNGNRFASHTRFSSVDSAKISESTVFSSQDD EEEENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSGHVER SPEGLESPVAGPSNRREGECPILHNSQPVSQLPSLRPEHHHYPT IDEPLPPNWEARIDSHGRVFYVDHVNRTTTWQRPTAAATPDGMR		ĺ		SSESWKPEQLGEGSVPDRPGNQSIELSRPAEEAAVITEAGDQGM
EGRLQLRASVKRKSRPCSLPVSELETVIASACGDPETPRTHYIR IHTLLHSMPSAQGGSAAEEEGGAEEESTLKDSSEKDGLSEVDTV AADPSALEEDREEPEGATPGTAHPGHSGGHFPSLANGAAQDGDT HPSTGSESDSSPRQGGDHSCEGCDASCCSPSCYSSSCYSTSCYS SSCYSASCYSPSCYNGNRFASHTRFSSVDSAKISESTVFSSQDD EEEENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSGHVER SPEGLESPVAGPSNRREGECPILHNSQPVSQLPSLRPEHHHYPT IDEPLPPNWEARIDSHGRVFYVDHVNRTTTWQRPTAAATPDGMR	]			VSVGPEGAGELLAQVQKDIQPAPSAEELAEQLDLGEEASALLLE
EGRLQLRASVKRKSRPCSLPVSELETVIASACGDPETPRTHYIR IHTLLHSMPSAQGGSAAEEEGGAEEESTLKDSSEKDGLSEVDTV AADPSALEEDREEPEGATPGTAHPGHSGGHFPSLANGAAQDGDT HPSTGSESDSSPRQGGDHSCEGCDASCCSPSCYSSSCYSTSCYS SSCYSASCYSPSCYNGNRFASHTRFSSVDSAKISESTVFSSQDD EEEENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSGHVER SPEGLESPVAGPSNRREGECPILHNSQPVSQLPSLRPEHHHYPT IDEPLPPNWEARIDSHGRVFYVDHVNRTTTWQRPTAAATPDGMR		İ		DGEAPASTKEEPLEEEATTQSRAGREEEEKEQEEEGDVSTLEQG
IHTLLHSMPSAQGGSAAEEEDGAEESTLKDSSEKDGLSEVDTV  AADPSALEEDREEPEGATPGTAHPGHSGGHFPSLANGAAQDGDT  HPSTGSESDSSPRQGGDHSCEGCDASCCSPSCYSSSCYSTSCYS  SSCYSASCYSPSCYNGNRFASHTRFSSVDSAKISESTVFSSQDD  EEENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSGHVER  SPEGLESPVAGPSNRREGECPILHNSQPVSQLPSLRPEHHHYPT  IDEPLPPNWEARIDSHGRVFYVDHVNRTTTWQRPTAAATPDGMR			ļ	EGRLQLRASVKRKSRPCSLPVSELETVIASACGDPETPRTHYIR
AADPSALEEDREEPEGATPGTAHPGHSGGHFPSLANGAAQDGDT HPSTGSESDSSPRQGGDHSCEGCDASCCSPSCYSTSCYS SSCYSASCYSPSCYNGNRFASHTRFSSVDSAKISESTVFSSQDD EEENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSGHVER SPEGLESPVAGPSNRREGECPILHNSQPVSQLPSLRPEHHHYPT IDEPLPPNWEARIDSHGRVFYVDHVNRTTTWQRPTAAATPDGMR	] .	ŀ		IHTLLHSMPSAQGGSAAEEEDGAEEESTLKDSSEKDGLSEVDTV
HPSTGSESDSSPRQGGDHSCEGCDASCCSPSCYSTSCYS SSCYSASCYSPSCYNGNRFASHTRFSSVDSAKISESTVFSSQDD EEEENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSGHVER SPEGLESPVAGPSNRREGECPILHNSQPVSQLPSLRPEHHHYPT IDEPLPPNWEARIDSHGRVFYVDHVNRTTTWQRPTAAATPDGMR	}			AADPSALEEDREEPEGATPGTAHPGHSGGHFPSLANGAAODGDT
EEEENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSGHVER SPEGLESPVAGPSNRREGECPILHNSQPVSQLPSLRPEHHHYPT IDEPLPPNWEARIDSHGRVFYVDHVNRTTTWORPTAAATPDGMR	. I			HPSTGSESDSSPRQGGDHSCEGCDASCCSPSCYSSSCYSTSCYS
EEEENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSGHVER SPEGLESPVAGPSNRREGECPILHNSQPVSQLPSLRPEHHHYPT IDEPLPPNWEARIDSHGRVFYVDHVNRTTTWORPTAAATPDGMR	<u> </u>		ł	SSCYSASCYSPSCYNGNRFASHTRFSSVDSAKISESTVFSSODD
SPEGLESPVAGPSNRREGECPILHNSQPVSQLPSLRPEHHHYPT IDEPLPPNWEARIDSHGRVFYVDHVNRTTTWQRPTAAATPDGMR	ļ 1		j	EEEENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSGHVER
IDEPLPPNWEARIDSHGRVFYVDHVNRTTTWORPTAAATPDGMR			į	SPEGLESPVAGPSNRREGECPILHNSQPVSQLPSLRPEHHHYPT
RSGSIQQMEQLNRRYQNIQRTIATERSEEDSGSQSCEQAPAGGG	, ]		j	IDEPLPPNWEARIDSHGRVFYVDHVNRTTTWQRPTAAATPDGMR
	L			RSGSIQQMEQLNRRYQNIQRTIATERSEEDSGSQSCEQAPAGGG

Deginning in clocation corresponding to first amino acid sequence corresponding to first amino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid acid anino acid anino acid acid anino acid acid anino acid acid acid acid acid acid acid acid		SEO	Predicted		
A0: nucleotide location corresponding corresponding corresponding corresponding corresponding corresponding amino acid amino acid amino acid anino acid anino acid anino acid sequence corresponding to first to amino acid anino acid sequence corresponding to the corresponding corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresponding to the corresp				Predicted end	
Corresponding to first anino acid anino acid anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state anino acid sequence state					
corresponding to first amino acid uence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence		110:			
to first anino acid residue of anino acid anino acid anino acid anino acid anino acid sequence    Sequence				corresponding	H=Histidine, T=Tgoleucine, W. r.
amino acid residue of amino acid sequence  ### Typicphin   Teonine, Vevaline, ### Typicphin   ### Typicphin   Teonine, Vevaline, ### Typicphin   ### Typicphin   Teonine, Vevaline, ### Typicphin   ### Typicphin   Teonine, Vevaline, ### Typicphin   ### Typicphin   Teonine, Vevaline, ### Typicphin   ### Typicphin   Teonine, Vevaline, ### Typicphin   ### Typicphin   Teonine, Vevaline, ### Typicphin   ### Typicphin   Teonine, Vevaline, ### Typicphin   ### Typicphin   Teonine, Vevaline, ### Typicphin   ### Typicphin   Teonine, Vevaline, ### Typicphin   ### Typicphin   Teonine, Vevaline, ### Typicphin   ### Typicphin   Teonine, Vevaline, ### Typicphin   ### Typicphin   Teonine, Vevaline, ### Typicphin   ### Typicphin   Teonine, Vevaline, ### Typicphin   ### Typicphin   Teonine, Vevaline, ### Typicphin   ### Typicphin   Teonine, Teonine, ### Typicphin   ### Typicphin   Teonine, Teonine, Teonine, ### Typicphin   ### Typicphin   Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonine, Teonin		1	corresponding		LaLeucine, Mamethionine, Kalysine,
residue of sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence s		1		amino acid	P=Proline O-Clubarian N=Asparagine,
amino acid sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Seque			amino acid	residue of	S=Serine T-Throngine,
sequence    Sequence   Codon, /=possible muclectide   Intention		· I		amino acid	W=Tryptophan v. m
Sequence   Nepossible muclsoride insertion		1			Codon (-man-ital
TIMESFYTULIANYSAYNYTISTICLIMINITACINESATIF TIMESFYTULIANYSAYNYTISTICLIMINITACINESATIF TIMESFYTULIANYSAYNYTISTICLIMINITACINESATIF TIMESFYTULIANYSAYNYTISTICLIMINITACINESATIF TIMESFYTULIANYSAYNYTISTICLIMINITACINESATIF TIMESFYTULIANYSAYNYTISTICLIMINITACINESATIF TIMESFYTULIANYSAYNYTISTICLIMINITACINESATIF TIMESFYTULIANYSAYNYTISTICLIMINITACINESATIF TIMESFYTULIANYSAYNYTISTICLIMINITACINESATIF TIMESFYTULIANYSAYNYTISTICLIMINITACINESATIF TIMESFYTULIANYSAYNYTISTICLIMINITACINES THE THE THE THE THE THE THE THE THE THE			sequence ·		COUCIL, /=DUSSINIE NUCLEOFIAG 3-1-L
NEDLAMPINNEAD TRELEMENGER KTNOOGGENER TOTAL MINERAL TERRETORY TO THE PREVENCE OF THE STATE OF THE PREVENCE OF THE STATE OF THE PREVENCE OF THE STATE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PREVENCE OF THE PR				<del></del>	(=possible nucleotide insertion)
NELLWEPTHNEADTRELIPRICHE TROUGHSTAND AND AUTOMOTES TO TENER THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DEPT THE DE		J	j		GGGGSDSEAESSQSSLDLRREGSLSPVNSQKITLLLQSPAVKFI
TOPRIP FLONGED PRICTIFICAL OCCURRENCE AND TOPRICAL CONTROLLED FROM THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERY		1		í	1 THE PERSONAL SAYRVETSSTCI, KHMTI, MIDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
LARRESELWAL SCHULES SPLAYMOK LVARROPNIFEMALE ROPELARMINE SCHULES SPLAYMOK LARROPNIFEMALE ROPELARMINE SCHULES SPLAYMOK LARROPNIK SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK LIBRORIS SPLAYMOK L		ļ	ŀ	1	1
ROPSLARRIPTER EARLY TREGMINE LECLSCADAUTLISIPEE EINSTOPPLOARFIRE KINT TREGMINE LECLSCADAUTLISIPEE EINSTOPPLOARFIRE KINT TREGMINE LECLSCADAUTLISIPEE EINSTOPPLOARFIRE KINT TREGMINE LECLSCADAUTLISIPEE EINSTOPPLOARFIRE KERTSTER TREGMINE TREGMINE LECT SERVER SERVER FREDER FROM THE STREET SERVER FROM THE LEGGLE THE STREET SERVER FROM THE LEGGLE THE SERVER FROM THE LEGGLE THE SERVER FROM THE SERVER FROM THE LEGGLE THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE SERVER FROM THE		ł	ł		1 THE REPUBLICATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PRO
EINSTYPHOAPPHOAPPHOAPPHOAPPHOAPPHOAPPHOAPPHOA		-		ſ	THE CHOLVEST RESULT FOR THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PA
TREDEFALLEN FIRELAGE AFGOGGOST KILTERPHILEGTEND WAYSRELGRINGLYTTYGEEGLDYSGOSTERFET (LADI WAYSRELGRINGLYTTYGEEGLDYSGOSTERFET (LADI WAYSRELGRINGLYTTYGEEGLDYSGOSTERFET (LADI WAYSRELGRINGLYTTYGEEGLDYSGOSTERFET (LADI HOYLLDAFF) (RPFYKALL) RIPCYD (LASILEYLDGELEN) WARDNIT DILDTFYWEEVFGOVTERLENGRANTOVTEKKEK EYIERMYKMEVERGYVCOTEALVRGFYEVVDSELVSUFDARELG LUTAGTAET (LIDADWALDTYSTRGSYHDELIMFRMAAVERFINE ORLRILGFYTGTSSUPYEGFAADPWEPMGLREFLP * KKWGKTTS LUTAGTAET (LIDADWALDTYSTRGSYHDELIMFYPMAAVERFINE ORLRILGFYTGTSSUPYEGFAADPWEPMGLREFLP * KKWGKTTS LUTAGTAET (LIDADWALDTYSFRTMLYGHT (LATA) VERSTFGT ORLRILGFYTGTSSUPYEGFAADPWEPMGLREFLP * KKWGKTTS LUTAGTAET (LADIA) VERSTFGT (LADIA) VERSTFGT ORLRILGFYTGTSSUPYEGFAADPWEPMGLREFLP * KKWGKTTS LUTAGTAET (LADIA) VERSTFGT (LADIA) VERSTFGT ORLRILGFYTGTSSUPYEGFAADPWEPMGLREFLP * KKWGKTTS FYLMIA VWWGGGKERA VURTURTTYMWTGTPSACCCCCCCCCCCCC LITAGT (LADIA) VALINGT (LADIA) VERSTFGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA) VALINGT (LADIA)		1		ļ	1 WAS DESCRIPTION OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE
MANSHELQRIKLIVIP VEGEDLYSGPREFFFLLSQELEND YYGLFEYSANDTYTVQLSPMSAYEVINLEBERFSGELG\LALI HAVENDAFF\RPYKALL\RFC\D\LSDEYLDEFFRGSLG\LALI HAVENDAFF\RPYKALL\RFC\D\LSDEYLDEFFRGSLG\LALI HAVENDAFF\RPYR\RPYKALL\RFC\D\LSDEYLDEFFRGSLG\LALI HAVENDAFF\RPYR\RPYKALL\RFC\D\LSDEYLDEFFRGSLG\LALI LATAEIDLADBRITTILLDLFTYVGESVFGOVTERELKSGGANTVERKEKS LYTERMYKBVERGVGCTFALVRGFYEVOSRLVSVFDARELE LYTERGYTGTSSVFYEGFAAPDEWBENGTPYVGTERKEKSGANTVERKEKS LYTERGYTGTSSVFYEGFAAPDEWBENGTP\$AKKGKITS CARRICLBREFFTGTKLDFFFAAPDEWBENGTP\$AKKGKITS LYTERGYTGTSSVFYEGFAAPDEWBENGTP\$AKKGKITS LYTERGYTGTSSVFYEGFAAPDEWBENGTF\$AKKGKITS LYTERGYTGTSSVFYEGFAAPDEWBENGTP\$AKKGKITS LYTERGYTGTSSVFYEGFAAPDEWBENGTF\$AKKGKITS LYTERGYTGTSSVFYEGFAAPDEWBENGTF\$AKKGKTS LYTERGYTGTSSVFYEGFAAPDEWBENGTF\$AKKGKTS LYTERGYTGTSSVFYEGFAAPDEWBENGTF\$AKKGTS\$ AKCHLRACHGYELAUTSILTLLALGSIATFEDAVYLYKNYICGF RAGLYGSTLSSAA\CSTLLALWTIGIISRGAYRHILGEDAVYLYKNYICGF RAGLYGSTLSSAA\CSTLLALWTIGIISRGAYRHILGEDAVALYKNYICGF RAGLYGSTLSSAA\CSTLLALWTIGIISRGAYRHILGEDAWGAXFAX LLIEPTLATVUTTBAYTRKONIKVGYSTFSSPDLINKALRENN ATTRISCCCT RAGGARAFYKKTTVVGFPGOSPITRSSHSGAGLLVKNFSTFOFF RAGLYGSTLSSAAAFYKKTTVVGFPGOSPITRSSHSGAGLLVKNFSTFOFF GFHIUGGAGLELL/NVUTHAPPRVULGILFYTLOY THAN THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE					TATEST VEDURATRICATES PROSPOSSED ON CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR O
YYGLPEYSANDTIVUSPMSAYVENHLEWREFSGRILG\LALI HQYLLDAFFY(RPFYKALL)RLPC\D\LSDLEYHDEFHGSLIG\ MKRNRITIOLDLFTYRPYKALL)RLPC\D\LSDLEYHDEFHGSLIG\ MKRNRITIOLDLTYRDEVFGGVTERLKSGGANTQVENKK ETLEMWKWERWERGVQGTEALWRGFYEVUSSELVSVPDAKELE LVIRGTARIOLNDWRINTEVRGSYHDGHLAVRGFYEVUSSELVSVPDAKELE LVIRGTARIOLNDWRINTEVRGSYHDGHLAVRGFYEVUSSELPSVPDAKELE CARLLGFVIGTTSSYPYEGFAAPPWEPMGLRFLP+KKMGKITE LPPRO\HTMCLQPDWDLPVSPRTPMLKLLTM\DEFTSTFGT  ARGLLGFVIGTTSSYPYEGFAAPPWEPMGLKFLP+KKMGKITE LPPRO\HTMCLQPDWDLFVSPRTPMLKLLTM\DEFTSTFGT  ARGLLGFVIGTTSJYPYSUCCFGLMIPESLVLVEMTITSFTAVC IKRTLLWKSSAPTVVSUCCFGLMIPESLVLVEMTITSFTAVC FILLMWNSSAPTVVSUCCFGLMIPESLVLVEMTITSFTAVC RGACLYSGTLSAY/CSTLLALMTLGITHEEDAYLLYKWTICC IKRTLLWKSSAPTVVSUCCFGLMIPESLVLVEMTITSFTAVC RGACLYSGTSSAY/CSTLLALMTLGITHEEDAYLYKWTICC RGACLYSGTSSAY/CSTLLALMTLGITHEEDAYLYKWTICC RGACLYSGTSSAY/CSTLLALMTLGITHEEDAYLYKWTICC RGACLYSGTSSAY/CSTLLALMTLGITHEEDAYLYKWTICC RGACLYSGTSSAY/CSTLLALMTLGITHEEDAYLYKWTICC RGACLYSGTSSAY/CSTLLALMTLGITHEEDAYLYKWTICC RGACLYSGTSSAY/CSTLLALMTLGITHEEDAYLYKWTICCCCPDRL LLILETETHAVLTRINGYSGTLSTLLALMTLGITHEEDAYLYKWTICCCCPDRL LLILETEHTHAVLTRINGYSRIPASTLAGTHAUTGGCCCCPDRL LLILETEHTHAVLTRINGYSRAPLSTLAGHTHIGGCCCPDRL ARGCLLLILILLANGTHIGHTAVARCHAVITGCCCCCPCAPL LLILETEHTHAVLTRINGYSGCGEDITACHTICCHAPACLIFVELUCC CHERGGAAFKYRTTPVOGPEORPTGOKMRGGVELLSPRILCC GFHNVGQACLELL/NVVIHLPRPKVUGLAVARGAULFVELVEUGH SGOPGHYMAGALELL/NVVIHLPRPKVUGLAVARGAULFVELVEUGH SCOVSHEPGOEPTYVULERKSTVAOLPLEYSTRAFRFRPOGFALTH LTALKININIVIKRSSRAPASTLAGTANDFOCGEDITACHTICCHAPACLIFVELUCC CLONIFPPVNITINISNCHSYTEGVSETRASSKYSTHICADA VTSPSFFFF***PL**TAKVENOCAMPEPTVAFFRFRFPPOGFALTH LTALKININIVIKRSSRAPASTATARTEVTVAOLPLEYSTRAFRFRFPPOGFALTH LTALKININIVIKRSSRAPASTATARTEVTVAOLPLEYSTRAFRFRFPPOGFALTH LTALKININIVIKRSSRAPASTATARTEVTVAOLPLEYSTRAFRFRFPPOGFALTH LTALKININIVIKRSSRAPASTATARTEVTVAOLPLEYSTRAFRFRFPPOGFALTH LCLUNIFPPVNITINISNCHSYTTEVTSFTRAFRFRFPPOGFALTH LCLUNIFPPVNITINISNCHSYTTEVTSFTRAFRFRFPPOGFALTH LCLUNIFPPVNITINISNCHSYTTEVTSFTRAFRFRFPPOGFALTH CLUNIFPROMATICATURE SGOPGHYCOACHTATACHARCHATART LCLUNIFPPVNITINISNCHSTTEVTVAOLPTTATAGGMTSMCS		- I	1	ł	TAKE BAKURNE IRKLEAKGROODCKTVI TIDDDII TOOLII
HOYLLDAFFT\RPFYKALL\RLC\DLEWTREEPRIGSION MKDNNITDILDIFFTUNEEVEGOVTERELKSGGANTQUTEKNEK ETIEMWKWEVERGVOCTEALWEGFVUDSELVSUPDARELE LUTACTARIDLENDMRNNTEYRGGYHDGHLUTRFWAAVERFNNE CORLLIGOVTGTSSVYESGAAPPWEURERUFPYKAKGLITS ORDRILGOVTGTSSVYESGAAPPWEURERUFPYKAKGLITS LUTACTARIDLENDMRNNTEYRGGYHDGHLUTRFWAAVERFNNE LUTACTARIDLENDMRNNTEYRGGYHDGHLUTRFWAAVERFNNE LUTACTARIDLENDMRNNTEYRGGYHDGHLUTRFWAAVERFNNE LUTACTARIDLENDMRNNTEYRGGYHDGHLUTRFWAAVERFNNE LUPACHTTAAVEETSTFGT AAQLLRALGSVEIALTSILTLALGS IAIFLEDAVTLYKNTICD IRRTLLMKSSAPTVSUCCFGLHUFBULVENTITSFADY FYLLMLWAVEGGGEAVLETLEDTPMWHTGDCCCCCPCCPLL LUTRKLON,R*CKALSTPS*P*R*SULVIMPMITETPYAVC FYLLMLWAVEGGGEAVLETLEDTPMWHTGDCCCCCPCCPLL LUTRKLON,R*CKALSTPS*P*R*SULVIMPMITETPYAVC FYLLMLIAWSAPTVSUCCFGLHUFSTSTANTOOTTE RGAGLYGSTLSSA/CSTLLALWTLGI ISRQARHHLGEOMMAAP ALFQVLLILTALQR*SISTUSP*S*R*SULVIMPMITETPYAVC GTSAHCHUTRHYYRRKDIKVGYETFSSPSDLDLINKALRMN AMTMRGCTH AAFGENAGAPTXNETPYUVEBPROPTSSTRAGOVANDAPP CCHREGAAPTXNETPYUVEBPROPTGCKHRRGGVSLLSPPLECS GTSAHCHURLDSSSNSPAPAS*LAGTCHARGAVSLLSPPLECS GTSAHCHURLDSSSNSPAPAS*LAGTCHARGAVSLLSPPLEGS GTSAHCHURLDSSSNSPAPAS*LAGTCHARGAVSLLSPPLIGT GTHAKGALGALFITYMFFGCGEDTVADHVASYGVNLYGSYGP SCOVSHEPGGBEPYVULERKETTWOLPLERKFTVOCHPLAFTVIVST GTHAKGALGALFTYMFFGCGEDTVADHVASYGVNLYGSYGP SCOVSHEPGGBEPYVULERKETTWOLPLERKFTFDOPPALTN LAVLKRININIVIKASSATAATNEVPETVVSSSSPUTGGONTIL CLUNNIFPFVNITIWISSCHSVTEGVSETTRSSSPSCHFILLOD VTSSSPFF*S*DL*TAKVONCAGAPTVTVSSSPUTGGONTIL CLUNNIFPFVNITIWISSCHSVTEGVSETTRSSPSCHFILLOD VTSSSPFF*S*DL*TAKVONCAGAPTVTVSSCHTYTSSPUTGGONTIL CLUNNIFPFVNITIWISSCHSVTGEVEDFORDICALSPETUS SGDFCMVCQACWRCGSILPBNILECKLLIPDKAWKYNGHKYNDH FFGLYCICKRPYPDPEBIE IPPENICCVCEDMFFIGHILAGAP SGDFCMVCQACWRCGSILPBNITIAGAUNATICTTTAA WFPLNINSSKLCTCOOMMAYACHTUTTSTAATUNGVATGAT YNPLNINSSKLCTCOOMMAYACHTUTTSTAATUNGVATGAT YNPLNINSSKLCTCOOMMAYACHTUTTSTAATUNGVATGAT YNPLNINSSKLCTCOOMMAYACHTUTTSTAATUNGVATGAT PASARGSPUNAVVNOHTEGRAPARSPCCOOMTVAPILHANSK SGAWMERGT II LIGGSBURTARTSKTVQVYDREADWRAVTVYSG HANDIGGEDFORMSFFKOLGARRAGATTGASDPSCASWUP PHRHLPGLCRPAKTSSTSTOCHARGATAGADGATHANSKSCGULD PRANCAGABANTATTAATUNGU		1	1	l .	) TO TO THE DAMACH VIEW CONTROL TO THE TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOT
MKORNITO LOLDITY THE EVERGUATE ELKSGGANTQUTENNIK ETTERMYKEVERGVOGTEALVRGFYEVUDSENIK ETTERMYKEVERGVOGTEALVRGFYEVUDSENIKSVPDARELE LUTAGTAE ILLNDWENNTEVERGYHOGHLVIRMFWANDERPINNE GERELLOFVGTTSSVPYEGFAAPPWEPMGLERELP KKWGKITE LUPRG HTC.QOPMDLPTVS PRIPTWIK-KLITANVETETSTFOT VAEFAAMEPGRTOTKLOPETVS THALLEVIKETNIGETSTFOT AQCILKALGEVELALISTILLILLAGE HELEVIKETNIGETSTFOT IKRILLMISSABTVVSULCEFGLWI PESILVILWINTICE FILMIUMVERGIGGERAULETUEDTPWHTHOECCCCCCCCPEL LUTERKILLMISSABTVSULCEFGLWI PESILVILWINTICE RGGLYSSTISSA/CSTLLALWITGI ISRQARIHLGEONMGAKE ALFQULLILTRIQPE IFSVLANGGI LISRQARIHLGEONMGAKE ALFQULLILTRIQPE IFSVLANGGI CACCCCCCCPEL LULLETHIMVUTRHYYRKIDIIKVGYETFSSPDLDINLKALREN ATMINGCCTH ALFQULLILTRIQPE IFSVLANGGI CACCCCCCCCPEL LULLETHIMVUTRHYYRKIDIIKVGYETFSSPDLDINLKALREN ATMINGCCTH ALFQULLILTRIQPE IFSVLANGGI CACCCCCCCCCCPEL LULLETHIMVUTRHYYRKIDIIKVGYETFSSPDLDINLKALREN ATMINGCCTH ALFQULLILTRIQPE IFSVLANGGI CACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC		1	1		YYGLFEYSANDTYTVOISPMSAEVENHI EMERGEDET
SYLEMWYMEVERGYCCTERLEGGEMTQUTENNEK  EYLEMWYMEVERGYCCTEALVORGY-VUDSALUS-PRABELE  LYACTAR IDLINGHNINTEYIGGYHDGHLUTREWHANDERNINE  CHELLGOVIGTS SYVEYGERAAPPER GURRERIP E KKRGITS  SPIO 1526 446  VAEFAARHEORTOTELDENTTALLEGERRIP E KKRGITS  LPPRC\HTCLOOPWILDTYSERTPHIYEK\LITA\VEETSTFOT  AQLIRALGOVELALTSILTILLALGS IAI FLEDAYVIL\KYNTLCE  LEPRC\HTCLOOPWILDTYSERTPHIYEK\LITA\VEETSTFOT  AQLIRALGOVELALTSILTILLALGS IAI FLEDAYVIL\KYNTLCE  LITRKLUKSSAPTVYSULCCFGLIN FELDAVVIL\KYNTLCE  FYLIMLWWEGGGEAVLETTEDTPHMVHIGPCCCCCPCCPCIP.  LUTRKLUKSSAPTVYSULCTGELIN FELDAVUTL\KYNTLCE  FYLIMLWWEGGGEAVLETTEDTPHMVHIGPCCCCCPCCPCIP.  ALFQVILLITALOPS IS SYLANGGLIAPCES PYSENTROCVINCALF  RGAGLYGSTLSSA/CSTLLALWTLGI I SRQARLHLGENNGALF  ALFQVILLITALOPS I SYLANGGLIAPCES PYSENTROCVINCALF  RGAGLYGSTLSSA/CSTLLALWTLGI I SRQARLHLGENNGALF  ALFQVILLITALOPS I SYLANGGLIAPCES PYSENTROCVINCALF  RGAGLYGSTLSSA/CSTLLALWTLGI I SRQARLHLGENNGALF  ALFQVILLITALOPS I SYLANGGLIAP CSSPYSENTROCVINCALF  RGAGLYGSTLSSA/CSTLLALWTLGI I SRQARLHLGENNGALF  ALFQVILLITALOPS I SYLANGGLIAP PSYLONGGLIAP PYLOFE  GTISAHCHULALESSINS PIRAS TIGGCHEN PYLOFIC  GTISAHCHULALESSINS PIRAS TIGGCHEN PYLOFIC  GTISAHCHULALESSINS PIRAS TIGGCHEN PYLOFIC  GTISAHCHULALESSINS PIRAS TIGGCHEN PYLOFIC  GTISAHCHULALESSINS PIRAS TIGGCHEN PYLOFIC  GTISAHCHULALESSINS PIRAS TIGGCHEN PYLOFIC  GTISAHCHULALESSINS PIRAS TIGGCHEN PYLOFIC  GTISAHCHULALESSINS PIRAS TIGGCHEN PYLOFIC  GTISAHCHULALESSINS PIRAS TIGGCHEN PYLOFIC  GTISAHCHULAL PROVINCAL  SOLUTION TIGGCHEN PROVINCAL PROVINCAL PROVINCAL  GTISAHCHULAL TIGGCHEN PROVINCAL PROVINCAL PROVINCAL  GTISAHCHULAL TIGGCHEN  GTISAHCHULAL TIGGCHEN  GTISAHCHULAL TIGGCHEN  GTISAHCHULAL TIGGCHEN  GTISAHCHULAL TIGGCHEN  GTISAHCHULAL TIGGCHEN  GTISAHCHULAL TIGGCHEN  GTISAHCHULAL TIGGCHEN  GTISAHCHULAL TIGGCHEN  ALFGELE PROVINCAL TIGGCHEN  GTISAHCHULAL TIGGCHEN  GTISAHCHULAL TIGGCHEN  GTISAHCHULAL TIGGCHEN  GTISAHCHULAL TIGGCHEN  GTISAHCHULAL TIGGCHEN  GTISAHCHULAL TIGGCHEN  GTISAHCHULAL TIGGCHEN  GTISAHCHULAL TIGGCHEN  GTISAHCHULAL TIGGCHEN  GTISAHCHULAL TIGGCHEN  GTISAHCHULAL TIGGCH		ļ		1	HOYLLDAFFT\RPFYKALL\RIRG\D\TCRFFKGRILG\LALI
S910 1526 446 VAEFALDENDWRRNTEYRGYSTHOCHLVIRFWAAVERNNE  CARLLOPYROTESSVEYEGFAAPPWEPMGIRRIP*KKWGKITS LPPRG\PTUTTSSVEYEGFAAPPWEPMGIRRIP*KKWGKITS LPPRG\PTUTTSSVEYEGFAAPPWEPMGIRRIP*KKWGKITS LPRG\PTUTTSSVEYEGFAAPPWEPMGIRRIP*KKWGKITS LPRG\PTUTTSSVEYEGFAAPPWEPMGIRRIP*KKWGKITS VAEFAAMESGRTOIKKDPRYTTADLEVIKKUVGIESAGFSOPPT AQLIKALGEVELALTSIILLIAGSIAIFLEDAYJKWTILOG IKRRILMWSEGGEKEAULRILIAGSIAIFLEDAYJKWTILOG IKRRILMWSEGGEKEAULRILIAGSIAIFLEDAYJKWTILOG IKRRILMWSEGGEKEAULRILIAGSIAIFLEDAYJKWTITSPYAVC LLILETHMYVLIRMYYRKODIKVGGIACSPPYSSKTRSOVMNCH AAPQVLILITALQPSIFSVLANGGGIACSPPYSSKTRSOVMNCH AAPTWGGCTH ALFQVLILITALQPSIFSVLANGGGIACSPPYSSKTRSOVMNCH AAPTWGGCTH AAPTWGGCTH AAPTWGGCTH AAPTWGGCTH AAPTWGGCTH AAPTWGGCTH AAPTWGGCTH AAPTWGGCTH AAPTWGGCTH AAPTWGGCTH AAPTWGGCTH AAPTWGGCTH AAPWGGCTH AAPTWGGCTH AAPTWGGCTH AAPTWGGCTH AAPWGGCTH AAPTWGGCTH AAPTWGGCTH AAPTWGGCTHAQLIFVVF CCHRRGGAAFKYKPTPVVGECGPPYSSKTRSOVMNCH AAPTWGGCTH AAPTWGGCTH AAPTWGGCTH AAPTWGGCTH AAPTWGGCTHAQLIFVVF CCHRRGGAAFKYKPTPVVGECGPTVAGHANGUSLLSPPLECS GTISAHCHLESSSNSPAPAS*LAGITGVCHHAQLIFVVF CCHRRGGAAFKYKPTPVVGECGPTVAGHANGUSLLSPPLECS GTISAHCHLESSSNSPAPAS*LAGITGVCHHAQLIFVVF CCHRRGGAAFKYKPTPVVGECGPTVAGHANGUSLLSPPLECS GTISAHCHLESSSNSPAPAS*LAGITGVCHHAQLIFVVF CCHRRGGAAFKYKPTPVVGECGPTVAGHANGUSLLSPPLECS GTISAHCHLESSSNSPAPAS*LAGITGVCHHAQLIFVVF CCHRRGGAAFKYKPTPVVGECGPTVAGHANGUSLLSPPLECS GTISAHCHLESSSNSPAPAS*LAGITGVCHHAQLIFVVF CCHRRGGAAFKYKPTPVGECGPTVAGHANGUSLLSPPLECT GTHAUAULHUNINKSNSTAATNEVESTVFFSKSVTLGODNTIL IAVLKHANIJVKRSNSTAATNEVESTVFFSKSVTLGODNTIL IAVLKHANIJVKRSNSTAATNEVESTVFFSKSVTLGODNTIL IAVLKHANIJVKRSNSTAATNEVESTVFFSKSVTLGODNTIL IAVLKHANIJVKRSNSTAATNEVESTVFFSKSVTLGODNTIL IAVLKHANIJVKRSNSTAATNEVESTVFFSKSVTLGODNTIL IAVLKHANIJVKRSNSTAATNEVESTVFFSKSVTLGODNTIL IAVLKHANIJVKRSNSTAATNEVESTVFFSKSVTLGODNTIL IAVLKHANIJVKRSNSTAATNEVESTVFFSKSVTLGODNTIL IAVLKHANIJVKRSNSTAATNEVESTVFFSKSVTLGODNTIL IAVLKHANIJVKRSNSTAATNEVESTVFFTSSKSVTLGODNTIL IAVLKHANIJVKRSNSTAATNEVESTVFFTSSKSVTLGODNTIL IAVLKHANIJVKRSNSTAATNEVESTVFFTSSKSVTLGODNTIL IAVLKHANIJVKRSNSTAATNEVESTVFFTSSKSVTLGODNTIL IAVLKHANIJVKRSN			į.	}	MKDNNITDILDI.TETUNEEVECOVERDER VOCATA VOCATA
SPIN 1526 446 VAFFAMERER SVPYREFAAPPENEMERRIEF, KKRØKITS LPPRO\HTCLOPDWDLPTVSPRTFMLYEK\LITAVETTSTOT LPPRO\HTCLOPDWDLPTVSPRTFMLYEK\LITAVETTSTOT VAFFAMERERTOL KLDPRYTOLLEVIKKINGU FSAFFSOPPT AAQLLRAIGSVELALTSILTLAIGS LAIFLEDAYYLYKNYILCE IKRRILMKSSAPTVSVLCCEPULEVIKKINGU FSAFFSOPPT AAQLLRAIGSVELALTSILTLAIGS LAIFLEDAYYLYKNYILCE IKRRILMKSSAPTVSVSVLCCEPULEVIKKINGU FSAFFSOPPTAMTOOTTL REGALVASTILSSA/CSTLLAKINTDS *PR** PWWAFCECCCCCCCPCLPAL LUTRKKAQO\R** CASILLANTDS *PR** PWWAFCECCCCCCCCPAL LUTRKKAQO\R** CASILLANTDS *PR** PWWAFCECCCCCCCCPAL REGALVASTILSSA/CSTLLAKINTDS *PR** PWWAFCECCCCCCCCPAL REGALVASTILSSA/CSTLLAKINTDS *PR** PWWAFCECCCCCCCCCPAL REGALVASTILSSA/CSTLLAKINTOLS *PR** PWWAFCECCCCCCCCCPAL REGALVASTILSSA/CSTLLAKINTOLS *PR** PWWAFCECCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC		1	i	i	EYIERMYKWRYERGWCOTEALWDGRYCHERSGGANTQVTEKNKK
LPPRO\HTCLQPPWDLPTVSPRTPMLYEK\LITA\UVETSTFGT		1		i	LVIAGTAEIDINDUDANTEYDOGUUD
S910   See		1			ORLELLOFUTGTSCUDVEGERARDSHLVIRWFWAAVERFNNE
AQQLERALGEVELALTSITLLALGS IATFLEDAYLIXETICE IRRITLANGSAPTVUSVLCCEGINI PRESIDUENTICE IRRITLANGSAPTVUSVLCCEGINI PRESIDUENTICE IRRITLANGSAPTVUSVLCCEGINI PRESIDUENTICE IRRITLANGSAPTVUSVLCCEGINI PRESIDUENTICE FILLIMINVEGEGGERAURITEDTPMMWHTGPCCCCPCCPRI LLIERRICQN; CYCHALSNITS; **R*PWMACPSSPTASMTQQTTL RGQCIVGSTISSAJCCTLLALANGCQIACSPPYSSKTRSQVMNCH LLIETPLMTVLTRMYYRKDIKVQSETFSSPDLDINIKALRUM ALTMKGCCTI ALTERPTICE GERRGGAAPKYRTPVVQPEGPTGCKHMKGGVSLLSPRLECS GTISAHCNLELPSSSNSPAPAS*LAGITGVCHHAQLIFVFLVET GPHHVQAGLELL,NVUTHLEPVRUGLQA  5912  924  277  MILNKALMIGALALTVWSPCCGGEDIVADHVASYGVNLYQSYGP SQSVSHSPDOBEF PYVDLERRETVWQLP_LFRERRERDEPGFALTN LAVKHNALMIVIKRSNSTAATNEVPEVTVPSKSSYVLGQPNTLI CLVDNIFPPVNHITHLSSGHSVTEGVSETTRSSPKSDHFILQD VTSPSFFFF**DL*TAKVECLGAREPLLKHWGASIPTTL CLVDNIFPPVNHITHLSSGHSVTEGVSETTRSSPKSDHFILQD VTSPSFFFF**DL*TAKVECLGAREPLLKHWGASIPTTL DSERCSYSGOSVRQALYACSTCHEGEBEPAGICLACSYECHOS HKLPELYTKRNERCDCONSFKKNLECKLLDPKAKVNSGNKYNDN FFGLYCICKRPYPDEDBEIPDERGEBEPAGICLACSYECHOS HKLPELYTKRNERCDCONSFKKNLECKLLDPKAKVNSGNKYNDN FFGLYCICKRPYPDEDBEIPDERGEBEPAGICACSYCHOS HKLPELYTKRNERCDCONSFKKNLECKALDPKAKVOLIKKNTAT YWPLNNERSKLCTCQDCHKMYGDLDVLFLTDEDTTVLAYENKGKI AQATTSDFLMDTLSSNNRVQOUTVLEDEDELENEACRYLGGS GDPGEVCCACMKRCSFLMAYAAQLAVTKIST'CMMDWGSTLM E*/DDGEVIKPENSELMASSKGCKLQELKAKQLIKKNTAT YWPLNNERSKLCTCQDCHKMYGDLDVLFLTDEDTTVLAYENKGKI AQATTSDFLMDTLSSNNRVQOUFVLAGGTIYMCBVLGGN GHDYQIGPYRKNLLCYDHRTDVWEERREMTTRAGHHSMCSLGDS IYSIGGSDDNIESMERFDULGVAASFQCUNDTRVAPLLHANSE SGVAWWEGRIYILGGSWBNTAFSTVVQVYDEADKWSGVDLP KAIAGGSACFIAP*SLGGRTRKRAKARGTRIGASDPSCASWDH PRHHPGLCRPAATS IGGSDDNIESMERFDULGVAASFCONOMTRVAPLLHANSE SGVAWWEGRIYILGGSDRTRKRKAKARGTRIGASDPSCASWDH PRHHPGLCRPAATS PASKAEGPVAVVVNGHTEGPAPASAPKPPPGHARPLGSPCPF PQEDPPALGGCPPRNPPSPGFSAVVLLKGTPPPPPFGLVPPIS KPPGFSGLLPSHPPLVSHGPLORYOSPLREVGTOPDLRS PRELPGGEFSAHVHYGGLPAERSPRIPEPPFDGLVPPIS KPPGFSGLLPSHPPLVSHGRFRREFSTLOGUNGTRVDTDPIDLS PRELPGGEFSAHVHYGGLPAERSPRIPEPSPDSTTGTSGKGC TVTGAVNRHLHNIVAGIIPWLHSGLKPTAATAQDQXTSQQYPDH PTRILLQ*NOATABEFSFSLEGEBRIPERSTPTGFFGCPGALQAPH					LPPRG\HTCIODDWDI DTWGDDTDWD PROGERRFLP*KKWGKITS
IRRRITLANGSAPTVUSULCEGIMI PREJULVEMTITSPYAVC FYLLMLUWWEGFGKERAVLRTLRDTPRMUMTISPCCCCCPCEDL LLTRRKLQNR*CWALSNITS***R*P*PWMACPSSPTAMTQQTFI RGAGLYGSTISSA/CSTLLALWTLGI I SRQARLHLGEQNMGAKP ALFQVLLLITALQDS I FSVLANGES PYSSKTRSQVMNCH LLILETPLMTVLTRMYYRKDIKVGYBETSSPDLDIMLKALRIM AMTMIGGCTH  109 595  GDFAFCIQGKGLEMESPKFOSFI IRSSHSGAGLLVKNPSTPVF CCHRRGGARKYKPTFVVGPEGPTGGKHMRGGVSLLSPRLECS GTISSAHCNILLPSSINSPAPAS*LAGITGVCHHAQLIFVFLVET GPHHVGQAGLELL/MVVTHLPRPPKVLGLQA  MILMNALMIGALALTTVMSPCGGEDIVADHVASYGVNLYQSYGP SQQYSHSPDGDEEFTVDLERKETTWQL.PLFRFRRFDPGFALTN IAVLKHNLHVIKRSNSTAANNEVPETVTYSKSPVLLGGPNTLI CLVDNI FSPVVNITHLSXSHSTVEVSETERSSPKSDHFIL.QDQ VTSPSFPFF**DL*TAKVGOLGAWFEDLLKHWGARTPTTL CLVDNI FSPVVNITHLSXSHSTVDVLEEDEELENEACAVLGGS DSEKCSYSQGSVKRQALYACSTCTPEGEBPAGICLACSYECHGS MKLFELYTKRNFRCDCGNSKFKALECKLLDEKAKVNSGNKYNDN PFGLYCICKRPYPDFEDEI PLEMICVCVCDMFHGRHLGATPPE SGDFGBMVQQACMKRCSFLMAYAAQLAVTKIST\GMMDWGTLM E*/DDGVIKENGEHODSTLKAPGGGGKDLAVAGNSEWVGNSEP CAGSSSESDLOTVFKNSLMABSKSCCKLQELKAKQLIKKOTAT YWPLNMRSKLCTCQDCMKMYGGDLEPGGKDDVTREWFRUSGKI AQATCRSDPLMDTLSSMNRVQQVELIC/GIQ*FED GHYQIGFYRNLLCYDHRTDVWEERRPMTTARGWHSMCS*LGM SMANGSACFILAPSTDSWSVAGLPFTTGHAGTIXHOFTY IYSIGSDDNIESMERRPDLUGGADPSTQCMVGMYNAPLHANSE SGYAWEGRIYILGGYSBKNTAFSKTVQVYDREARMSNSCS*LGDE SGYAWEGRIYILGGYSBKNTAFSKTVQVYDREARMSNSCS*LGDE SGYAWEGRIYILGGYSBKNTAFSKTVQVYDREARMSNSCNLDP PHRHLPGLCRPAATS FFGRFTRELKIGGRRRRAALIQAPHCHISPFPCCPPGALQAPEA PASKAEGSCPILAPS*SLGGRTRKRAKAARGTETGASDDSCASWDH PHRHLPGLCRPAATS FFGRFTRELKIGGRRRRRAALIQAPHCHISPFPCCPPGALQAPEA PASKAEGGVAVVNOGHTEGPAPARSAPAPEPGLSFPCTP PQEDPPALGGCPPRPPSPGGSAVVLLKGTPPPPPFGLVPPIS PAPELPGGREPSALPVHQGLPARRRAPAAPDCKTSGGGCR TVTGAVHRHLMHVAGI I PWUHSQLKPTTAADQCKTSGQCPDH PTRILLCYNGATADDCKTSGQCYPDH PTRILLCYNGATADDCKTSGQCYPDH PTRILLCYNGATADDCKTSGQCYPDH		5910	1526	446	VAE FAAMERCETOTICS PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION
IRRRITLANGSAPTVUSULCEGIMI PREJULVEMTITSPYAVC FYLLMLUWWEGFGKERAVLRTLRDTPRMUMTISPCCCCCPCEDL LLTRRKLQNR*CWALSNITS***R*P*PWMACPSSPTAMTQQTFI RGAGLYGSTISSA/CSTLLALWTLGI I SRQARLHLGEQNMGAKP ALFQVLLLITALQDS I FSVLANGES PYSSKTRSQVMNCH LLILETPLMTVLTRMYYRKDIKVGYBETSSPDLDIMLKALRIM AMTMIGGCTH  109 595  GDFAFCIQGKGLEMESPKFOSFI IRSSHSGAGLLVKNPSTPVF CCHRRGGARKYKPTFVVGPEGPTGGKHMRGGVSLLSPRLECS GTISSAHCNILLPSSINSPAPAS*LAGITGVCHHAQLIFVFLVET GPHHVGQAGLELL/MVVTHLPRPPKVLGLQA  MILMNALMIGALALTTVMSPCGGEDIVADHVASYGVNLYQSYGP SQQYSHSPDGDEEFTVDLERKETTWQL.PLFRFRRFDPGFALTN IAVLKHNLHVIKRSNSTAANNEVPETVTYSKSPVLLGGPNTLI CLVDNI FSPVVNITHLSXSHSTVEVSETERSSPKSDHFIL.QDQ VTSPSFPFF**DL*TAKVGOLGAWFEDLLKHWGARTPTTL CLVDNI FSPVVNITHLSXSHSTVDVLEEDEELENEACAVLGGS DSEKCSYSQGSVKRQALYACSTCTPEGEBPAGICLACSYECHGS MKLFELYTKRNFRCDCGNSKFKALECKLLDEKAKVNSGNKYNDN PFGLYCICKRPYPDFEDEI PLEMICVCVCDMFHGRHLGATPPE SGDFGBMVQQACMKRCSFLMAYAAQLAVTKIST\GMMDWGTLM E*/DDGVIKENGEHODSTLKAPGGGGKDLAVAGNSEWVGNSEP CAGSSSESDLOTVFKNSLMABSKSCCKLQELKAKQLIKKOTAT YWPLNMRSKLCTCQDCMKMYGGDLEPGGKDDVTREWFRUSGKI AQATCRSDPLMDTLSSMNRVQQVELIC/GIQ*FED GHYQIGFYRNLLCYDHRTDVWEERRPMTTARGWHSMCS*LGM SMANGSACFILAPSTDSWSVAGLPFTTGHAGTIXHOFTY IYSIGSDDNIESMERRPDLUGGADPSTQCMVGMYNAPLHANSE SGYAWEGRIYILGGYSBKNTAFSKTVQVYDREARMSNSCS*LGDE SGYAWEGRIYILGGYSBKNTAFSKTVQVYDREARMSNSCS*LGDE SGYAWEGRIYILGGYSBKNTAFSKTVQVYDREARMSNSCNLDP PHRHLPGLCRPAATS FFGRFTRELKIGGRRRRAALIQAPHCHISPFPCCPPGALQAPEA PASKAEGSCPILAPS*SLGGRTRKRAKAARGTETGASDDSCASWDH PHRHLPGLCRPAATS FFGRFTRELKIGGRRRRRAALIQAPHCHISPFPCCPPGALQAPEA PASKAEGGVAVVNOGHTEGPAPARSAPAPEPGLSFPCTP PQEDPPALGGCPPRPPSPGGSAVVLLKGTPPPPPFGLVPPIS PAPELPGGREPSALPVHQGLPARRRAPAAPDCKTSGGGCR TVTGAVHRHLMHVAGI I PWUHSQLKPTTAADQCKTSGQCPDH PTRILLCYNGATADDCKTSGQCYPDH PTRILLCYNGATADDCKTSGQCYPDH PTRILLCYNGATADDCKTSGQCYPDH					AAOLI PALCOURI AL TOUR TADLLEVLKTNYGIPSACFSQPPT
LITRIKALO (R*CWALSNTES* R*R*PWMACPSSCCCECCPEL RGACLYGSTLSSA/CSTLLALWTIG] ISROARLHLIGEORMGARY ALFQVILLILATION IS ISROARLHLIGEORMGARY ALFQVILLILATION IS ISROARLHLIGEORMGARY ALFQVILLILATION ISROARLHLIGEORMGARY ANTMISCCTI  109 595 OPLAPCIOGRGLEMRSPKPOSFIIRSSHSGAGLLVKNPSTPVF CCHRRGGARKYRPTPVVGPGORPTOGKHMRGCVSLLSPRLECS GTISAHCHLIPSSNSPPABS*LAGITGVCHHAQLIFVFLVCT GPHHVGQAGLELL/NVVIHLPRPPKVLGLQA  MILINFALMICALALTYTWMSCGEDIVADHVASYGVNLYQSYGP SCQVSHBPDGDEFYVDLERKETVVQLPLFRFRRFDPOFFALTN LAVLKHNLINIVIKRSNSTAATMEVPEVVTFSRSPVTLGGPNTLI CLVDNIPPPVVNITMLSNGHSVTEGVSFTRSSPKDHFILODQ VTSPSFFFF*DL*TAKVBOLGAWFPPLLKHGGABIPTL CLVDNIPPPVVNITMLSNGHSVDVLEEDELEMEACAVLGGS DSEKCSYSQSVKRQALVACSTCTPBGBEPAGICLACSYBCHGS HKLFELYTRINFRCDCGNSKFKNLLSVDVLEEDELEMEACAVLGGS DSEKCSYSQSVKRQALVACSTCTPBGBEPAGICLACSYBCHGS HKLFELYTRINFRCDCGNSKFKNLLADVREGKBUNGSNKFNDN FFGLYCLCKRPYPDPPEDBEIPDEMIQCVVCEDWFHGRHLGAIPPE SGDFOMVCQACMKRCSFLMAYAQLATKIST\GMMDWCGTLM E*/DDGEVIKPRGGHODSTLKEDVPEGKBUNGSRVKKNLATHERITATAKVBNLAKSKSGCLQBLKAKGLIKKDTAT YWPLNMRSKLCTCQDCMMYGDDVFLATBEDMLVAL/GGRN CAGSSESDLQTVFKNESLNAESKSGCLQBLKAKGLIKKDTAT YWPLNMRSKLCTCQDCMMYGDDVFLASIEDMLVAL/GGRN ENGALSSVETTSPKTDSMSVVAGLPRFTYGHAGHTIVADFVYLSG GHDYGIGSTPRKNLCYDHRTDVWBERRFMTTAKGWHSMCSLGDS 1YSIGGSDDNIESBERFPVLVAYAGLPRFTYGHAGTIVADFVYLSG GHDYGIGSTRNKLLCYDHRTDVWBERRFMTTAKGWHSMCSLGDS 1YSIGGSDDNIESBERFPVLVAYAGLPRFTYGHAGTIVADFVYLSG GHDYGIGSTRNKLLCYDHRTDVWBERRFMTTAKGWHSMCSULP KAIAGGSACFTLPSSLGGRTRKRKAKARGTRTGASDPSCASMDH PHRHJBGLGRPAATS  5915 1604 703 FFRFFFELKIGRRKRARITQAPHCHISPRPFCCPFGALQAPEA PASRAEGBVAVVVGGHTEGPAPRSAPKEPPCDPFGLUPPLS SGYAWBEGRTYLLGYSWENTAFSKTVQVYDRABLKWSKVOLLP KAIAGGSACFTLPSSLGGRTRKRKAKARGTRTGASDPSCASMDH PHRHJBGLGRPAATS  5916 256 633 SPRWBEWGDFBLARGEFFSERFFPT PPSPFDSTKTGTGGGCC TVTGAVWRHNHVAGIIPWLHSQLKPTAATAQDQWTSQQYPDH PTRLILQ+NQATABKSFSFEEGERPSRT PPEPSPSTKTGTGGGCC TVTGAVWRHNHVAGIIPWLHSQLKPTAATAQDQWTSQQYPDH				•	TERRITAL MACCA DESIGNATION TO THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF THE TERRITAL OF
LITRIKALO (R*CWALSNTES* R*R*PWMACPSSCCCECCPEL RGACLYGSTLSSA/CSTLLALWTIG] ISROARLHLIGEORMGARY ALFQVILLILATION IS ISROARLHLIGEORMGARY ALFQVILLILATION IS ISROARLHLIGEORMGARY ALFQVILLILATION ISROARLHLIGEORMGARY ANTMISCCTI  109 595 OPLAPCIOGRGLEMRSPKPOSFIIRSSHSGAGLLVKNPSTPVF CCHRRGGARKYRPTPVVGPGORPTOGKHMRGCVSLLSPRLECS GTISAHCHLIPSSNSPPABS*LAGITGVCHHAQLIFVFLVCT GPHHVGQAGLELL/NVVIHLPRPPKVLGLQA  MILINFALMICALALTYTWMSCGEDIVADHVASYGVNLYQSYGP SCQVSHBPDGDEFYVDLERKETVVQLPLFRFRRFDPOFFALTN LAVLKHNLINIVIKRSNSTAATMEVPEVVTFSRSPVTLGGPNTLI CLVDNIPPPVVNITMLSNGHSVTEGVSFTRSSPKDHFILODQ VTSPSFFFF*DL*TAKVBOLGAWFPPLLKHGGABIPTL CLVDNIPPPVVNITMLSNGHSVDVLEEDELEMEACAVLGGS DSEKCSYSQSVKRQALVACSTCTPBGBEPAGICLACSYBCHGS HKLFELYTRINFRCDCGNSKFKNLLSVDVLEEDELEMEACAVLGGS DSEKCSYSQSVKRQALVACSTCTPBGBEPAGICLACSYBCHGS HKLFELYTRINFRCDCGNSKFKNLLADVREGKBUNGSNKFNDN FFGLYCLCKRPYPDPPEDBEIPDEMIQCVVCEDWFHGRHLGAIPPE SGDFOMVCQACMKRCSFLMAYAQLATKIST\GMMDWCGTLM E*/DDGEVIKPRGGHODSTLKEDVPEGKBUNGSRVKKNLATHERITATAKVBNLAKSKSGCLQBLKAKGLIKKDTAT YWPLNMRSKLCTCQDCMMYGDDVFLATBEDMLVAL/GGRN CAGSSESDLQTVFKNESLNAESKSGCLQBLKAKGLIKKDTAT YWPLNMRSKLCTCQDCMMYGDDVFLASIEDMLVAL/GGRN ENGALSSVETTSPKTDSMSVVAGLPRFTYGHAGHTIVADFVYLSG GHDYGIGSTPRKNLCYDHRTDVWBERRFMTTAKGWHSMCSLGDS 1YSIGGSDDNIESBERFPVLVAYAGLPRFTYGHAGTIVADFVYLSG GHDYGIGSTRNKLLCYDHRTDVWBERRFMTTAKGWHSMCSLGDS 1YSIGGSDDNIESBERFPVLVAYAGLPRFTYGHAGTIVADFVYLSG GHDYGIGSTRNKLLCYDHRTDVWBERRFMTTAKGWHSMCSULP KAIAGGSACFTLPSSLGGRTRKRKAKARGTRTGASDPSCASMDH PHRHJBGLGRPAATS  5915 1604 703 FFRFFFELKIGRRKRARITQAPHCHISPRPFCCPFGALQAPEA PASRAEGBVAVVVGGHTEGPAPRSAPKEPPCDPFGLUPPLS SGYAWBEGRTYLLGYSWENTAFSKTVQVYDRABLKWSKVOLLP KAIAGGSACFTLPSSLGGRTRKRKAKARGTRTGASDPSCASMDH PHRHJBGLGRPAATS  5916 256 633 SPRWBEWGDFBLARGEFFSERFFPT PPSPFDSTKTGTGGGCC TVTGAVWRHNHVAGIIPWLHSQLKPTAATAQDQWTSQQYPDH PTRLILQ+NQATABKSFSFEEGERPSRT PPEPSPSTKTGTGGGCC TVTGAVWRHNHVAGIIPWLHSQLKPTAATAQDQWTSQQYPDH		1	1		FYLLMIUMURCHGGWYDY
RGAÇLYGSTLSSA/CSTLLAUMTGIISROARHILGEORMGAKP ALFQVLLILTALQYSIFSVLANGGOIACSPPYSSKTRSOVMNCH LLILSTFEMTVLTRMYXPRKDIKVGYETFSSPDLDIMLKALRNM AMTMKGCTH  109 595 CPLAPCIGKGLEMRSPKPOSTIRSSHSGAGLLVKNPSTIPVE CCHRRGGARYKYRTPVVGPEORPTGOKHMRGGVSILSPRIECS GTISAHCMLRIPSSSMSPAPAS-LAGITGVCHHAQLIFVFLVET CPHRVGQAGLEL/NVVIHLPRPPKVLGLOG SQVSHBFDGDEBTYVDLERKETVAQLPLFRFRFRFDOFALTN IAVIKHALNIVIKRSMSTAATHEVPSTVTLSFSSPVLOGPONTI CLVDNIFPFVVNTTWLSNCHSTVTEGYSETRPSSPKSDHFILOD VTSPSFPFE-VDL-TAKVRGLOKFPPLLKHRGAEIPTTL CLVDNIFPFVVNTTWLSNCHSVTEGYSETRPSSPKSDHFILOD VTSPSFPFE-VDL-TAKVRGLOKFPPLLKHRGAEIPTTL CLVDNIFPFVVNTTWLSNCHSVTEGYSETRPSSPKSDHFILOD VTSPSFPFE-VDL-TAKVRGLOKFPPLLKHRGAEIPTTL CLVDNIFPFVVNTTWLSNCHSVTEGYSETRPSSPKSDHFILOD VTSPSFPFE-VDL-TAKVRGLOKFPPLLKHRGAEIPTTL SSPHSE-VDL-TAKVRGLOKFPPLLKHRGAEIPTTL DERCCSYGGSVKRQALYACSTCTPEGEPAGICLACSYECHGS HKLFELYTKRNFRCDCGMSKFKNLECKLLPDRAKVNSGNNKYNDN FFGLYCICKRPYPDDEBDIFDEMIGCVCEDWFHGRHLGAIPPE CAGSSSSDLOWCACACMKRCSFLMAYAAQLAVTKIST\GMMDMCGTIM E*/DDGEVKVCACMKRCSFLMAYAAQLAVTKIST\GMMDMCGTIM E*/DDGEVKVCACMKRCSFLMAYAAQLAVTKIST\GMMDMCGTIM E*/DDGEVKVCACMKRCSFLMAYAAQLAVTKIST\GMMDMCGTIM E*/DDGEVKVCACMKRCSFLMAYAAQLAVTKIST\GMMDMCGTIM E*/DDGEVKVCACMKRCSFLMAYAAQLAVTKIST\GMMDMCGTIM E*/DDGEVKVCACMKRCSFLMAYAAQLAVTKIST\GMMDMCGTIM E*/DDGEVKVCACMKRCSFLMAYAAQLAVTKIST\GMMDMCGTIM E*/DDGEVKVCACMKRCSFLMAYAAQLAVTKIST\GMMDMCGTIM E*/DDGEVKVCACMKRCSFLMAYAAQLAVTKIST\GMMDMCGTIM E*/DDGEVKVCACMKRCSFLMAYAAQLAVTKIST\GMMDMCGTIM E*/DDGEVKVCACMTRCSTLMAYAAQLAVTKIST\CMMDMCGTIM E*/DDGEVKVCACMTRCSTLMAYAAQLAVTKIST\CMMDMCGTIM E*/DDGEVKVCACMTRCSTLMAYAAQLAVTKIST\CMMDMCGTIM E*/DDGEVKVCACMTRCSTLMAYAAQLAVTKIST\CMMDMCGTIM E*/DDGEVKVCACMTRCSTLMAYAAQLAVTKIST\CMMDMCGTIM E*/DDGENVCACMTRCSTLMAYAAQLAVTKIST\CMMTMCGUTLAVTIGGTN E*/DDGENVCACMTRCSTLAWAACATTTAAGWHSMCCLGGN IYSIGGSDDNICSMERPDVACFIPFYTAAGATTAAGWHSMCCLGGN IYSIGGSDDNICSMERPDVACFIPFYTAAGATTAAGWHSMCCLGGN IYSIGGSDDNICSMERPDVACFIPFYTAAGATTAAGWHSMCCLGGN IYSIGGSDDNICSMERPDVACFIPFYTAAGATTAAGATAACAAAT PASRAEGPVAVVVMGHTEGFAPARSAPKTTCASDPSCASMDH PHRHLDGLCRPAATS PASRAEGPVAVVVMGHTEGFAPARSAPKEPFCPPGLVPPIS PAGLEGSEPSAHD		ľ	1		- TODISDALIVEGEOGREAVISTINGSPONDOGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
ALFQVILITAIQPS IFSVLANGGQIACSPYSSKTRSQVMCH LLILETPIMTVLTRMYRRKDIKVGYETFSSPDLDLNLKALRNM AMTMRGCCH  5911  109  595  OPPLAPCIQGKGLEMESPKPQSFIIRSSHSGAGLLVKNPSTPVF CCHRRGGAFKYKPTPVVGPEQRFTGQKHMRGGVSLLSPRLECS GTISAHCHLRPSSNSDFAPAS*LAGITGVCHHAQLIFVFLVET GFHHVQAGLELL,NVVHLPRPPKVLGLQA MINNZAMLGALATTVMSFCGGEDIVADHVASYGVNLYQSYGP SCQYSHEFDGDEEFYVDLERKETTWQLDLFRFRFRFPDFFALTN IAVLKHNINIVIKRSNSTAATNEVPTVYFSKSPVTLGQPNTLI CLVDNIFPFVVNITWLSNGISVTEGVSETFSSPKSDHFILQDD VTSPSFFFE**DL*TAXVEOLGAWFEPLLKHWGAEIPTTL OLRMAGAEGAAGRGSELEPVVSILVDVLEEDEELBNEACAVLGGS DSEKCSYSQGSVKRQALYACSTCTPEGEEPAGICLACSYECHGS HKLFELYTKRNFRCDCGNSKFKNLECKLLPPKAKVNSGNKYNDN FFGLYCIKRRPPDFEDEEIPDEMIQCVVCEDWFHGRHLGAIPFE SGDFORMVCQACHKRCSFLWAYAAQLAVTKIST\GMNDWGGTLM E*/DDQEVIKPSHGHODSTLKEDVFEQGEDDVREVKVEONSEP CAGSSESDLOTVFKNESLNAESKSCCKLLGELKAQLIKKDTAT YWPLNMRSKLCTCDDCMKWYGDLDVLFLTDEYDTVLAYENKGKI AQATRSDPLMDTLSSMNEVQOVELIC/GIQ*FED  124  NLGGSELPPEEALFIQVASMNQRRVDFYLASIEDMEVAI/GGRN EMGALSSVETYSPKTDSWSYVAGLPFTYGHAGTIYKDFVY1SG GHDYOTGPYRKNLLCYDHKTDVWERRFMTYARGWHSMCSLGDS IYSIGGSDDNIESMRFFDVLGVEAYSPQCNQNTRVAPLLHANSE SGVAWWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGGTKRKAKARGTRTGASDPSCASWDH PRHHDGLCRPAATS  5915  1604  703  FPGRFFFFLKLGRRKRARITQAPHCHSFPRTCFPGALQAFEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPCLYPPLSSFPCPT PQEDFPALGGPCPPRMPSPGFSAVVLKGTPPPPPFGLVPPIS KPPPGFSGLLSPHPVVSDAPPPPPPPPPPPFGLVPPIS KPPPGFSGLLSPHPVSDAPPPPPPPPPPPPFGLVPPIS KPPPGFSGLLSPHPPVSDAPPPPPPPPPCLVPPIS KPPPGFSGLLSPHPPVSDAPPPPPPPPPPCLVPPIS KPPPGFSGLLSPHPPVSDAPPPPPPPPPCLVPPIS FREIBGERPSAHPUHGGLPARRAGPLQRVQEPLRGVGTGPDLRS FPULGELPGERPSAHPUHGGLPARRAGPLQRVQEPLRGVGTGPDLRS  5916  256  633  SPRWWEIWGWHRWESTSLEGEWBERTPEBSPDTKGTSGKGCR TVTGAVHRHLNHVAGITPWHESSTELGEWBERTPEBSPDTKGTSGKGCR FVTGAVHRHLNHVAGITPWHESSTELGEWBERTPEBSPDTKGTSGKGCR FVTGAVHRHLNHVAGITPWUHSGLKPPAATAQDDOWTSQQYPDH FTRILLO*NOATABKNA**CTADLORPHOLLVARNADDOWTSQQYPDH		1			THE TAXABLE VALUE OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPE
LLILETFMTVLTRMYVRRKDIKVGYETFSSPDLDLNIKALRNM AHTMRGCCH  20PLAPCTQGKGLEMRSPKPQSFIIRSSHSGGLLVKNPSTPVF CCHRRGGAPKYKPTPVVGPEQRPTGQKHMRGGVSLLSPRIECS GTISAHCNIRLPSSNSPAPAS*LAGITGVCHHAQLIFVFLVET GFHHVGQAGLELL/NVVIHDRPPKVLGLQA  5912  924  277  MILMKALMLGALALTTVMSPCGGEDIVADHVSYGVNLYQSYGP SGQVSHBFDGDEFYVDLERKETVWQLPLFRRFRFDPGFALTN LAVLKHNINIVIRSNSTAATNEVPEVTVFSKSPVTLGQDNTLI CLVDNIFPPVVNITWLSNGHSVTEGVSETRSSFKSDHFILQDQ VTSPSFFFE*DL*TAKVEGLGAWFEPLLKHWGAEIPPTL CLVDNIFPPVVNITWLSNGHSVTEGVSETRSSFKSDHFILQDQ VTSPSFFFE*DL*TAKVEGLGAWFEPLLKHWGAEIPPTL  5913  46  1198  OLRMAGAEGAAGRGSLEPVUSLVDVLEEDEELENEACAVLGGS DSEKCSYSQSVKRQALYAGSTCTPBEGEEPAGILACSYBCHGS HKLFELLYTKRNFRCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN FFGLYCICKRYPYDPDEDEITDEMIQCVVCEDWFHGRHLGAIPPE SGDFGENVCQACMKRCSFLMAYAAQLAVTKIST'CMMDWGGTLM E*/DDDEVIKPBNGBRODSTLKEDVPFOGKDDVREVKVEQNSEP CAGSSESDLOTVFKNESLHMAYAAQLAVTKIST'CMMDWGGTLM E*/DDDEVIKPBNGBRODSTLKEDVPFOGKDDVREVKVEQNSEP CAGSSESDLOTVFKNESLHAVAAQLAVTKIST'CMMDWGGTLM E*/DDDEVIKPBNGBRODSTLKEDVPFOGKDDVREVKVEQNSEP CAGSSESDLOTVFKNESLHAVXAQLAVTKIST'CMMDWGGTLM E*/DDDEVIKPBNGBRODSTLKEDVPFOGKDDVREVKVEQNSEP CAGSSESDLOTVFKNESLHAVSAQCLAVTISTSTCMTATA AQATDRSDPLMDTLSSMNRVQQVELLC/GIQ*FED  NLGGSSLEPPEEALFJQVABNORRVDFYLASIBEMUAI/GGRN ENGALSSVETYSPKYDSWSVVAGLPRFTYGHAGTIYKDFVY1SG GHDYQIGPYRKKLLCYDHRTDVWEERRPMTTARGHSMCSLGDS 1791GGSDDNIESMERFDVLGVEERRPMTTARGHSMCSLGDS 1791GGSDDNIESMERFDVLGVEERRPMTTARGHSMCSLGDS SGVAWWGRIY1LGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGGTARKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS  FFGRFFPELKLGRRKKARARIQAPHCISPRPFTCPFGALQAPEA PASRAEGPVAVVNGHTTGPAPARSAPKEPELPPPLGSFPCPT PQEDFPALGGPCPPRMPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLBSPHP}VPSDAPPPPPPDPCK/RPRLLPAP/PGLPS PRELIGERPSAHPUHQGLPABRRGPLQRVQEPLRRVCTGPDLRS FPRELIGERPSAHPUHQGLPABRRGPLQRVQEPLRRVCTGPDLRS PPLLQENDPGGEPPGLV*+AAGPAAH  5916  256  633  SPRWEIWGWHRMESFSLEGEWBRIPEFSPDTKGTSGKGCR TVTGAVHRHLMHVAGIIPWVLHSGLERPRATADQDOWTSQQYPDH PTRILLQ*NOATABKN**TULLQLRPDEL**LQPHOPL**LUPPRDS		ì			1 NOT SELECT LOSS AND CSTT. DATE WITE CT TODON TOTAL CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF TH
S911 109 595 CIPLAPCTQRKRIENTRKTYRKDIRKGYSTFSSPDLDLINLKALRIMM COLFRIEND COLFACTOR COLFERENCE CHRISCAPPOSPTIRSSHSGAGLLVKNPSTPVF COHRIGGAPKKKPTPVGPEQRPTGQKHMRGVSLLSPRIECS GTISAHCNLRLPSSSNSPAPAS*LAGITGVCHHAQLIFVFLVET GFHHVGQAGLELL/MVVTHLPRPRVIGLQA  SQYSHEPGGEDEFYVDLERKETVWQLPLPRRFRRFCPPQFALTN LAVLKHLINIVIKRSNSTAATINEVESVTUGGSPSTUGGPNTLI CLVDNIFPPVNNITWLSSGHSVTEGVSETTPSSPSKSPHFILQDO VTSPSFPFE**DL*TAKVEGLGAWFSPLLKHWGAEIPTTL CLVDNIFPPVNNITWLSSGHSVTEGVSETTPSSPSKSHPFILQDO VTSPSFPFE**DL*TAKVEGLGAWFSPLLKHWGAEIPTTL OLRANGAGRAAGRSELEPVVSLVDVLEEDEELENEACAVLGGS DSEKCSYSQGSVKRQALYACSTCTPEGEBPAGICLACSYSCHGS HKLFELYTKRNFRCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN FFGLYGLKRPYPDPEDEIPDEMIGCVVCEDMFFHGHLGAIPPE SGDFORMVCQACMKRCSFLMAYAAQLAVTKIST\GMMDWCGTIM E*/DOBEN'LPENGEHODSTLKEDVPEGGKDDVREVKVEQNSEP CAGSSSESDLOTVFKNESLNABSKSGCKLQBLKAKGLIKKDTAT YWPLNNRSKLCTCQDCMKMYGDLDVLFTDEYDTVLAYENKGKI AQATDRSDPLMDTLSSNNRVQQVBLIC/G1Q*FED  S914 960 124 NLGGSELPPEALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSVAGLPRTTYGHAGTIYKDFVYISG GHDYQIGPYRKNLLCYDHRTDVWEERRFMTTARGHRSMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNOWTRVAPLLHANSE SGWAWEGIYILGGSYSMENTAFSKTYQVYDRAADKWSRGVDLP KAIAGGSACFIAP*SLIGQRYRKKAKARGTTGASDPSCASWDH PRHHPGLCRPAATS  1935 1604 703 FFGRFTFELKGRRRKRARIIQAPHCHSPRPCCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGPFALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGPALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGPFPGPGLQPSPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPFGLVPPIS KPPGFSGLLPSPHLP VBVSPAPPPPPPGCV,RPRLLPAP/PGLPS PRELPGREPSAHPVNGGLPAERGFLQRVQCPCPDLRS PPRELPGREPSAHPVNGGLPAERGFLQRVQCPGPDLRS PPRELPGREPSAHPVNGGLPAERGFLQRVQCPGPDLRS PPRELPGREPSAHPVNGGLPAERGFLQRVQCPGPDLRS PVLOELDEPGAGEPPEGL**AAPAAH  5916 256 633 SPRWEIWGFWRWESFSLEGEWPRIFTESPDSTKGTSGKGCR TVTGAVHRHLMNIVAGIIPWVLTALLORDOWFYSQQYPDH		Ì	į		1 **** X ******************************
5911 109 595 QPLAPCTQGKGLEMRSPKPQSFIIRSSHSGAGLLVKNPSTPVF CHRRGAAFKYKPTPVVGPGQRPTGQKHMRGGVSLLSPRLECS GTISAHCMILPSSSNSPAPAS*LAGITGVCHHAQLIFVFLVET GTISAHCMILPSSSNSPAPAS*LAGITGVCHHAQLIFVFLVET GTISAHCMILPSSSNSPAPAS*LAGITGVCHHAQLIFVFLVET GTISAHCMILPSSSNSPAPAS*LAGITGVCHHAQLIFVFLVET GTISAHCMILPSSNSNPAPAS*LAGITGVCHHAQLIFVFLVET GTISAHCMILLPSSNSPAPAS*LAGITGVCHHAQLIFVFLVET GTISAHCMILPSSNSPAPAS*LAGITGVCHHAQLIFVFLVET GTISAHCMILPSSNSPAPAS*CAGITGSTATATMEVERVTVQLPLFRRFRRFPDFPFALTN IAVLKHNLNIVIKRSNSTAATMEVERVTVPSKSPFVTLGQNTTLI CLVDNIFPPVVNITMLSSGHSVTEGVSETRPSSPKSDHFILLQDO VTSPSFPFE**DL*TAKCQLGAWFEPPLLKHWGAEIPTLL CLVDNIFPPVVNITMLSSGHSVTEGVSETRPSSPKSDHFILLQDO VTSPSFPFE**DL*TAKCQLGAWFEPPLLKHWGAEIPTLL CLVDNIFPPVVNITMLSSGHSVTEGVSETRPSSPKSDHFILLQDO DERKCSSYSQSVKRQALVACSTCTPGEBEPAGICLAGSYSCHGS HKHFELTKRNFRCDCGNSKFKNLECKLLPDKAKWAGNKYNDN FFGLYCICKRPYPDPEDBIPDEMIQCVVCEDWFHGRHLGAIPPE GSPOPWVCQACMKRCSFLWAYAAQLAVTKIST\CMMDWCGTLM E*/DDEVCINCAMSPNGCAKKCSFLWAYAAQLAVTKIST\CMMDWCGTLM E*/DDEVCINCAMSPNGCAKKCSFLWAYAAQLAVTKIST\CMMDWCGTLM E*/DDEVCINCAMSPNGCAKKCSFLWAYAAQLAVTKIST\CMMDWCGTLM E*/DDEVCINCAMSPNGCAKKCSFLWAYAAQLAVTKIST\CMMDWCGTLM E*/DDEVCINCAMSPNGCAKCASFLWAYAAQLAVTKIST\CMMDWCGTLM E*/DDEVCINCAMSPNGCAKCASFLWAYAAQLAVTKIST\CMMDWCGTLM E*/DDEVCINCAMSPNGCAKCASFLWAYAAQLAVTKIST\CMMDWCGTLM E*/DDEVCINCAMSPNGCAKCASFLWAYAAQLAVTKIST\CMMDWCGTLM E*/DDEVCINCAMSPNGCAKCASFLWAYAAQLAVTKIST\CMMDWCGTLM E*/DDEVCINCAMSPNGCAKCASFLWAYAAQLAVTKIST\CMMDWCGTLM E*/DDEVCINCAMSPNGCAKCASFLWAYAAQLAVTKIST\CMMDWCGTLM E*/DDEVCINCAMSPNGCAKCASFLWAYAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA		l	i		DEED IT DIE VETRMY YRRKDIKVGYRTFSSDDI DIATE VAL DELLE
GEPLAPCT QGKGLEMES PROPS IT IRSSHSGAGILVKNESTPVE CCHREGGARFKVRPTPVAGPEGRPTGCKHMRGGVSLLSPRLECS GTISAHCNLRLESSNSPAPAS*LAGITGVCHHAQLIFVFLVET GFHHVQAGLELL/MVVTHLPRPKVLGLQA SGQYSHEPDGDEFYVDLERKETVWQLPLFRFRFRFDPGPALTN IAVLKHNLNIVIKRSSTAATNEVPEVTVYSKSPVTLGQDNTLI CLVDNIPPPVVNITWLSNGHSVTEGVSETRPSSPKSDHFILODQ VTSPSFFFE*PDL*TAKVEGLGAMFEPLLKHWGAETPTTL CLVDNIPPPVVNITWLSNGHSVTEGVSETRPSSPKSDHFILODQ VTSPSFFFE*PDL*TAKVEGLGAMFEPLLKHWGAETPTTL OLRMAGAGAAGRGSLEDVVSLVDVLEEDEELENEAGAVLGGS DSEKCSYSQGSVKRQALYACSTCTPEGEEPAGICLACSYECHGS HKLFELYTKRNFRCDCGNSKFKNLECKLLPDKAKVMSGNKYNDN FFGLYCICKRPYEDPEDEIPEMIQCVVCEDMFHGRHLGAIPPE SGDFORMVCQACMKRCSFLWAYAAQLAVTKIST\GMMDWCGTLM E*/DODEVIKPENGEHDDTILSEDVPEQGKDVREVKVEQNSEP CAGSSSESDLQTVFKNESLNABSKSGCKLQELKAKGLIKKDTAT YWPLNNRSKLCTCQDCMKMYGDLDVLFTDEVDTVLAYENKGKI AQATDRSDPLMDTLSSNNRVQOVBLIC/G1Q*FED CAGSSESDLDTVFKNESLNABSKSGCKLQELKAKGLIKKDTAT YWPLNNRSKLCTCQDCMKMYGDLDVLFTDEVDTVLAYENKGKI AQATDRSDPLMDTLSSNNRVQOVBLIC/G1Q*FED GHDYQIGPYRKNLCYDHRTDVWEERRFMTTARGHSMCS-LGDS INGGSLPPEALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSVAGLGFRTYGHAGTIYKDFVYISG GHDYQIGPYRKNLCYDHRTDVWEERRFMTTARGHSMCS-LGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNOWTRVAPILHANSE SGVAWWEGIYILGGYSWENTAFSKTVQV VIDRADKWSRGVDLP KALAGGSACFIAP*SLGQRTRKKAKARGTTRGSDDSCASWDH PHRHLPGLCRPAATS FFGRTFTPLKLGGRTRKARAIIQAPHCHSPRPT-CPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPFGLPRT-GSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVILKGTPPPPPEGLVPPIS KPPPGFSGLLPSPHLPVSPAPPPPPPGK/PRDLPAPPPPPFGLPPIS FPELPGREPSAHPVHQGLPAERRGPLQRVQCTGPDLRS VLOELEGGARGSACTIAP*SLGGRTRTRABITORYCPPPPPEGLVPPIS FPELPGREPSAHPVHQGLPAERRGPLQRVQCTGPDLRS PRELPGREPSAHPVHQGLPAERRGPLARVQCTGPDLRS PVLOELEGPAGGEPPEGL*AAPAAH  5916 256 633 SPRWEIWGPWHRWESFSLEGGEWPSRIPESPSTKGTSGKGCR TVTGAVHRHLMHIVAGIIPWVLHTALORNOGNYTAATATAQDQWTSQQYPDH PTRILLO-NOATAMOM*TTALLORNOGNYTAATATAALORNOGNYTAAAPA		5911	109	EDE	1 III III MOCCIA
STISAHCNURLESSNSPAPAS*LAGITGVCHHAQLIFVET GFHHVGQAGLELL/NVVIHLPRPBKVLGLQA  MILNKALMIGALALTTVMSPCGGEDIVADVASYGVNLVGSYGP SGQYSHBPDGDEEFYVDLERKETWQLDFLFRFRRRDPDPALTN IAVLKHMLNIVIKRSNSTAATNEVPEVTTVFSKSPVTLGQFNTLI CLVDNIFPPVVNITHUSCHSVTEGVSETRSSPKSDHFILQDQ VTSPSFPFF**DL*TAKVBCLGAWFBPLLKHWGAEIPTTL  5913  46  1198  QLRMAGAEGAAGRGSELEPVVSLVDVLEEDEELENEACAVLGGS DSEKCSYSGSVKROALYACSTCTPEGBEPAGICLACSYECHGS HKLFELYTKRNFCCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN FFGLYCICKRPYPDPEDEIPDMIQCVVCEDWFHGRHLGAIPPE SGDFOGENVCQACMKCSFLMAVAQALAVTKIST\GMMDWCGTLM E*/DDQBVIKPENGEHQDSTLKEDVPEQGKDDVREVKVEQNSEP CAGSSSEDLQTVFKNESLNARSKSGCKLQBLKAKQLIKKDTAT YWPLNNRSKLCTCQDCMKMYGDLDVLFITDEYDTVLAYENKGKI AQATDRSDPLMDTLSSMMRVQOUELIC/GIQ*FED  124  NLGGSELPPEEALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSYVAGLPFFTYGHAGTIYKDFVYISG GHDYQIGPYRKNLCYDHRTDVWEERRPMTTARGWHSMCS-GDS IYSIGGSDDNIESMERFDVLGVEARSPQCNGWTRVAPILHANSE SGVAVWEGRIYILGSYSWENTAFSKTVQVVDREADKWSRGVDLP KAIAGGSACFIAP*SLGORTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS  5915  1604  703  FPGRPTRFLKLGRRRKRARIIQAPHCHISFRPRCCPPGALQAPEA PASRAEGPVAVVVNGHTEGSPAPARSADKEPPDFPGLVPPIS KPPPGFSGLLPSPHP\PVSFAPPPPPPPCK/RPRLPAP/PGLPS PRELIEGEEPSAHVHQGLPABRRGPLQRVQEPLREQVTGPDLRS KPPPGFSGLLPSPHP\PVSFAPPPPPPPCK/RPRLPAP/PGLPS PRELIEGEEPSAHVHGGLPABRRGPLQRVQEPLREGVTGPDLRS VPVLQELPGPAGGEFPSEGL**AAGPAAH  5916  256  633  SPRMWEIWGPWHWESFSLEGEWESRIPEFSFDSTKGTSGKGCR TVTGAVHRHLMHVAGIIPWN*TALLQLRPTAATAQDOWTSQQYPDH  FTRILLQ**VANDAN*TTALLQCHPDALAYAAQDOWTSQQYPDH		i	,	393	QLPLAPCIQGKGLEMRSPKPQSFIIRSSHSGAGLLVKNPSTDVF
5912 974 277 MILNKALMIGALALTVMSPCGGEDIVADHVASYGVNLYQSYGP SCQVSHEPDGDEEFYVDLEKKTYWQLFLLFRFFRFRFDQFALTM IAVLKHNLMIVIKRSSTAATNEVPEVTVFSKPVTLGQPNTLI CLVDNIFPPVVNITMLSNGHSVTEGVSETRPSSPKSDHFILADDQ VTSPSFPFF***DL*TAKVSDLGAWFBPLLKHWGAEIPTTL CLVDNIFPPVVNITMLSNGHSVTEGVSETRPSSPKSDHFILADDQ VTSPSFPFF***DL*TAKVSDLGAWFBPLLKHWGAEIPTTL OLVGNIFPPVVNITMLSNGHSVTEGVSETRPSSPKSDHFILADDQ VTSPSFPFF***DL*TAKVSDLGAWFBPLLKHWGAEIPTTL OLVGNIFPPVVNITMLSNGHSVTEGVSETRPSSPKSDHFILADDQ VTSPSFPFF***DL*TAKVSDLGAWFBPLLKHWGAEIPTTL OLVGNIFPPVSLUTVLEBEERACAVLGGS DSEKCSYSQGSVKRQALYACSTCTPEGEEPAGICLACSYECHGS HKLFELYTKRNFRCDCGMSKFKNLECKLLPPKAKVNSGNKYNDN FFGLYCICKRPYPDPEDEIPDENICCYVCEDWFHGRHLGAIPPE SGDFQENVCQACMKRCSFLWAYAAQLAVTKIST\CWMDWCGTLM E**/DDQEVIKPENGEHDDTLSSMNKYCOVVCLICCYGLQ**FED CAGSSSESDLQTVFKNESLNABSKSGCKLQBLKAKQLIKKDTAT YWPLNWRSKLCTCQDCMKMYGDLDVLFLTDEYDTVLAYENKGKI AQATORSDPLMDTLSSMNNQRVDFYLASIEDMHVAI/GGRN ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVVISG GHDYQIGPYRKNLCYPHRTDVWEERRPMTTARGWHSMCSLGDS INSIGGSDDNIESMERFDVLGVEAYSPQCNOWTRVAPLLHANSE SGYAWWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGYDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS  5915 1604 703 FFGRPTRPLKLGRRRKRARIQAPHCHSFPRTCPPGALQAPEA PASRAGPVAVVVNGHTEGFAPARSAPKEPFGLPRPLSFPPPFCUPPIS KPPPGFSGLLPSPHPLVBIGGPPPPPFPGLVPPIS KPPPGFSGLLPSPHPLVPFGLRYPPPPFPGLVPPIS KPPPGFSGLLPSPHPVPVPSSGFSAVVLLKGTPPPPPPFGLVPPIS KPPPGFSGLLPSPHPVPVPSSGFSAVVLLKGTPPPPPPFGLVPPIS KPPPGFSGLLPSPHPVPVPSSGFSAVVLLKGTPPPPPPFGLVPPIS KPPPGFSGLLPSPHPVPVPSSGFSAPVLLKGTPPPPPPGLVPPIS PRELPGREPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLOELPGPAGGEFFPEGL**AAGPAAH  5916 256 633 SPRWMEIWGPWHWESFSLEGEWFSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLMHVAGIIPWLHASQLPPTAATAQDOWTSQQYPDH PTRILLGAVHANAA		ļ	1		1 OUT THE REAL PLANT IN A COMPANY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PAR
S912   S77   MILINKALMIGALL/ITMSPCGGEDTVADHVASYGVNLYQSYGP   SGQYSHEFDGDEEFYVDLERKETVWQLPLFRRFRRFDPGFALTN   IAVLKHNLNIVIKKSNSTAATNEVESVTVFSKSPVTLGQDRTLI   CLVUNIFPPVVNITWLSNGHSVTEGVSETRPSSPKSDHFILQDQ   VTSPSFPFE**DL*TAKVEGLGAWFEPLLKHWGAEIPTTL   OLSEKCSYSQGSVKRQALYACSTCTPEGEEPAGLACSYECHGS   HKLFELYTKRNFRCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN   FFGLYCICKRPYDPDEIPDEIPDEMIQCVVCEDWFHIGRHLGAIPPE   SGDFQEMVCQACMKRCSFLWAYAAQLAVTKISTGMGMWCGTLM   E*/DDQEVIKPENGEHODSTLKEDVPEQGKDDVREVKVEQNSEP   CAGSSESDLQTVKPENGENAGNGRVVDFYLASIEDMLVAI/GGRN   ENGALSSVETYSPKTDSMSYVAGLPFTTYLASIEDMLVAI/GGRN   ENGALSSVETYSPKTDSMSYVAGLPFFTYGHAGTIYKDFVYISG   GHDYQIGPYRKNLLCYDHRTDVWERRFWTTARGWHSMCSLGDS   IYSIGGSDDNIESMERPDVLGVEAYSPCCNQMTRVAPLLHANSE   SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGJDLP   KAIAGGSACFIAP*SLGQTRKRKAKARGTRTGASDPSCASWDH   PHRHLPGLCRPAATS   SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGJDLP   FPGRPTRPLKLGRRRKRARITQAPHCHISPRPTCPPGALQAPEA   PASRAEGGPVAVVVNGHTEGPAPARSAPKEPEDLPRPLGSFPCPT   PQEDFPALGGPCPPRPPSPGFSAVVLLKGTPPPPPFGLVPPIS   KPPPGFSGLLPSPHP\PVSPAPPPPPPPFQKVPTPIS   KPPPGFSGLLPSPHP\PVSPAPPPPPPPPFCVPPPIS   KPPPGFSGLLPSPHP\PVSPAPPPPPPPPFGVPPPIS   KPPPGFSGLLPSPHP\PVSPAPPPPPPPPFGVPPPIS   KPPPGFSGLLPSPHP\PVSPAPPPPPPPPFGVPPPIS   KPPPGFSGLLPSPHP\PVSPAPPPPPPPPFGVPPPIS   KPPPGFSGLLPSPHPVQCLPBARGPJCAVQEPLRGVQTGPDLRS   PRELPGEEPSAHVHQCLPBARGPJCAVQEPLRGVQTGPDLRS   SPRWWEIWGPWHRWESFSLEGEWPSRIPEFSPDSTKGTSGKGCR   TVTGAVHRHLINTVAGIIPWVHSQLKPTAATAQDOWTSQQYPDH   PTRILIC PNOATANTAATAQDOWTSQQYPDH   PTRILIC PNOATANTAATAQDOWTSQQYPDH   PTRILIC PNOATANTAATAQDOWTSQQYPDH   PTRILIC PNOATANTAATAQDOWTSQQYPDH   PTRILIC PNOATANTAATAQDOWTSQQYPDH   PTRILIC PNOATANTAATAQDOWTSQQYPDH   PTRILIC PNOATANTATALOUPONTSQQYPDH   PTRILIC PNOATANTATALOUPONTSQQYPDH   PTRILIC PNOATANTAATAQDOWTSQQYPDH   PTRILIC PNOATANTAATAQDOWTSQQYPDH   PTRILIC PNOATANTAATAQDOWTSQQYPDH   PTRILIC PNOATANTAATAQDOWTSQQYPDH   PTRILIC PNOATANTAATAQDOWTSQQYPDH   PTRILIC PNOATANTAATAQDOWTSQQYPDH   PTRILIC PNOATANTAATAQDOWTSQQYPDH   PTRILIC PNOATANTAATAATAATAATAATAATAATAATAATAATAATAA			1 1		1 OTTOMICHURDESSSNSPAPAS*LACTTCUCTATACT TOTAL
### ### ##############################		5912	924		I GEHINGOWGREET/MAATHPBBBBKALGI'VY
I IAVLKHNLINIVIKRSINSTAATNEVPEVTYPSKSPVTLGQPNTLI CLVDNIFPPVNITWLSNGHSVTEGVSETRPSSPKSDHFILQDO VTSPSFFF**DL*TAKVEQLGAWFEPLLKHWGAEIPTLL OLRMAGAEGAGGGELEPVUSLVDVLEEDEELENEACAVLGGS DSEKCSYSQGSVKRQALYACSTCTPEGEEPAGICLACSYECHGS HKLFELYTKRNFRCDCCONSKFKNLECKLLPDKAKVNSGNKYNDN FFGLYCICKRPYPDPEDEIPDEMIQCVVCEDWFHGRHLGAIPPE SGDFQEMVCQACMKRCSFLWAYAAQLAVTKIST\GMMDWCGTLM E*/DDQEVIKPENGEHODSTLKEDVPEQGKDDVREVKVEQNSEP CAGSSSESDLQTVFKNESLNAESKSGCKLQELKAKQLIKKDTAT YWPLNWRSKLCTCQDCMKMYGDLDVLFLTDEYDTVLAYENKGKI AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*FED ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGHSMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNOWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQV YDREADKWSRGVUDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTTGASDPSCASWDH PHRHLFGLCRPAATS FPGRPTRFLKLGRRRKRARIQAPHCHISPRPRCCPPGALQAPEA PASRAEGPVAVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPFGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPQK/RPLLPAP/PGLPS PGELFGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGSFPEGL**AACPAAH  5916 256 633 SPRWWEIWGPWHRWESPSLEGEWPSRIPEFSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILQ*NOATADKNN*TTALLQPHOELVSROWN			1 2.3	277	MILNKALMLGALALTTVMSPCGGEDIVADHURGVGIDI
CLVDNIFPPVNITHLSNGHSVTEGYSETRPSSPKSDHFILQDQ VTSPSFPFE**DL*TAKVEQLGAWFEPLLKHKGAEIPTTL QURMAGAEGAAGRGSELEPVUSLVDVLEEDEELENEACAVLGGS DSEKCSYSGOSVKRQALYACSTCTPEGEEPAGICLACSYECHGS HKLFELYTKRNFRCDCGNSKFKNLECKLLPPKAKVNSGNKYNDN FFGLYCLCKRPYPDPEDEIPDEMIQCVVCEDWFHGRHLGAIPPE SGDFOENVCQACMKRCSFLWAYAAQLAVTKIST\GMMDWCGTLM E*/DDQEVIKPENGEHOPSTLKEDVPEQGKDDVREVKVEQNSEP CAGSSSESDLQTVFKNESLNAESKSGCKLQBLKAKQLIKKDTAT YWPLNWRSKLCTCQDCMKMYGDLDVLFLTDEYDTVLAYENKGKI AQATORSDPLMDTLSSMNRVQQVBLIC/GJQ*FED  124 NLGGSELPPEEALFJQVASMNQRRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSYVAGLPFFTYGHAGTIYKDFYYISG GHDYQIGPYRKNLLCYDHRTDVWEERR FPMTTARGWHSMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAPS-SLGQRTRKKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS  5915 1604 703 FPGRFTRPLKLGRRRKRARITIQAPHCHISPRPTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCCT PQEDFPALGGPCPPRNPPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPQK/RPLLPAP/PGLPS PRELPGEEPSAHPVLQGLPARRGPLQRVQEPLRGVGTGPDLRS PVLOELPGPAGGFFPEGL**AAGPAAH  5916 256 633 SPRWBIWGDWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVNHHLINHVAGI IPWUHSQLKPTAATAQDQWTSQQYPDH PTRILIQ*NQATARDKNN*TTALIQBVQHJVADAWRAN			1		1 DOG TOTAL DODGE LIVDLER KETOMOTOT, DI DEDE DE
TIPS WITTER TO A TAKEN CLICAM FEB PLICADO  VTSPSFFFF** ND *TAKVE CLICAM FEB PLICADO  VTSPSFFFF** ND *TAKVE CLICAM FEB PLICADO  VTSPSFFFF** ND *TAKVE CLICAM FEB PLICADO  OLRMAGAEGAAGRQSELEPVVSLVDVLEEDEELENEACAVLGGS  DSEKCSYSQGSVKRQALYACSTCTPEGEEPAGICLACSYECHGS  HKLFELYTKRFRCDCGNSKFKNLECKLLPKAKVNSGNKYNDN  FFGLYCICKRFYPDPEDEITPDEMTQCVVCEDWFHGRHLGAIPPE  SGDFQEWVCQACMKRCSFLWAYAAQLAVTKIST\GMMDWCGTLM  E*/DDQEVIKPENGEHQDSTLKEDVPEQGKDDVREWKVEQNSEP  CAGSSSESDLOTVFKNESLNAESKSGCKLQBLKAKQLIKKDTAT  YWPLNWRSKLCTCQDCMKMYGDLDVLFLTDEYDTVLAYENKGKI  AQATORSDPLMDTLSSWNRVQOVELIC/GIQ*FED  NLGGSELPPEEALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN  ENGALSSVETTYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG  GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS  IYSIGGSDDNIESMERFDVLGGVEAYSPQCNQWTRVAPLLHANSE  SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP  KAIAGGSACFIAP*SLGQRTRKRKAARGTRTGASDPSCASWDH  PHRHLPGLCRPAATS  FPGRPTFPLKLGRYRKRARIIQAPHCHISPRPRTCPPGALQAPEA  PASRAEGGVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT  PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPGLVPPIS  KPPPGFSGLLPSPHP\PVSPAPPPPPPQK/RPRLLPAP/PGLPS  PRELPGGEPSSGLPSPHP\PVSPAPPPPPPQK/RPRLLPAP/PGLPS  PRELPGGEPSGLPSPHP\PVSPAPPPPPDGK/RPRLLPAP/PGLPS  PRELPGGEPSGLPSPHP\PVSPAPPPPPDGK/RPRLLPAP/PGLPS  PRELPGGEPSGREPPEGL**AAGPAAH  5916  256  633  SPRWWEIWGFWHRWESFSLEGEWPSRIPEPSFDSTKGTSGKGCR  TVTGAVHRHLNHVAGILFWLHSQLKPTAATAQDQWTSQQYPDH  PTRILIQ*NQATADKNN*TTALLQBVGLYLVADAMBAR		•	1		1 221 DIGHT DIT VILKSISTAATNEVDEVTTVECKCDVCC
46 1198 QLRMAGAEGAAGRQSLLEPVVSLVDVLEEDEELENEACAVLGGS DSEKCSYSQGSVKRQALYACSTCTPEGGEPAGICLACSYECHGS HKLFELYTKRNFRCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN FFGLYCLCKRPYPDPEDEIPDEMIQCVVCEDWFHGRHLGAIPPE SGDFQEMVCQACMKRCSFLMAYAAQLAVTKIST\GMMDWCGTLM E*/DDQEVIKPENGEHQDSTLKEDVPFQGKDDVREVKVEQNSEP CAGSSSESDLQTVFKNESLMAESKSGCKLQELKAKQLIKKDTAT YWPLNWRSKLCTCQDCMKRYGDLDVLFLTDEYDTVLAYENKGKI AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*FED  124 NLGGSELPPEEALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYS PQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS  5915 1604 703 FPGRPTRPLKGERRKRARIIQAPHCHISPRPTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPFGLPRFLGSFPCPT PQEDFFALGGPCPPRMPSPGFSAVVLLKGTPPPPPFGLVPPIS KPPPGFSGLLPSHPV\QCLPAERRGPLQRVQEPLRGVFPCPT PQEDFFSALGPCPPRMPSPGFSAVVLLKGTPPPPPFGLVPPIS KPPPGFSGLLPSHPV\QCLPAERRGPLQRVQEPLRGVGTGPDLRS PRELEGEEPSAHPVHQCLPAERRGPLQRVQEPLRGVGTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH  5916 256 633 SPRWBEIWGWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWUHNSQLKPTAATAQDQWTSQQYPDH PTRLIQ*NQATADKNN*TTALLQQNDRLAYSQ					1 CHADRIEFFAANTIMUSNOHSAALEAGAGEADAGGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA
DSEKCSYSQGSVKRQALYACSTCTPEGEEPAGICLACSYEHGS HKLFELYTKRNFRCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN FFGLYCICKRPYPDFDEEIPDEMIQCVVCEDWFHGRHLGAIPPE SGDFQEMVCQACMKRCSFLWAYAAQLAVTKIST\GMMDWCGTLM E*/DDQEVIKPENGEHQDSTLKEDVPEQGKDDVREVKVEQNSEP CAGSSSESDLQTVFKNESLNAESKSGCKLQELKAKQLIKKDTAT YWPLNWRSKLCTCQDCMKMYGDLDVLFLTDEYDTVLAYENKGKI AQATDRSDJMDTLSSMNRVQQVELIC/GIQ*FED  124 NLGGSELPPEEALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS IYSIGGSDNIESMERFDVLGVEAYSPQCNQWTRVAPILHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVVDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS  5915 1604 703 FPGRPTTEPLKLGRRRKRARIIQAPHCHSPRPTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPFGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPDFQK/RPRLLPAP/PGLPS PRELEGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH  5916 256 633 SPRWMEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILQ**LONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**CONDONLY**COND	1	5017			I TELEVALAN DUALAKVEOLGAWERDI.I.VUUMANDEN MA
HKLFELYTKRNFRCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN FFGLYCICKRPYPDPEDETPDEMIQCVVCEDWFHGRHLGAIPPE SGDFQEMVCQACMKRCSFLWAYAAQLAVTKIST\GMMDWCGTLM E*/DDQEV!KPENGEHQDSTLKEDVPEQGKDDVREVKVEQNSEP CAGSSSESDLQTVFKNESLNAESKSGCKLQELKAKQLIKKDTAT YWPLNWRSKLCTCQDCMKMYGDLDVLFITDEYDTVLAYENKGKI AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*FED  124 NLGGSELPPEEALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS  5915 1604 703 FPGRPTRPLKLGRRKKARIIQAPHCHSPRPS*CPPGALQAPEA PASRAEGPVAVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPQK/RPRLLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH  5916 256 633 SPRMWEIWGFWHNSTIALJOHORI, VARNHMSE	ı	2313	46	1198	QLRMAGAEGAAGROSELEPVYSLVDVI FEDERY FINA
FFGLYCICKRPYPDPEDEIPDEMIQCVVCEDWFKRHIDN SGDFQEMVCQACMKRCSFLWAYAAQLAVTKIST\GMMDWCGTLM E*/DDQEVIKPENGEHQDSTLKEDVPEQGKDDVREWKVEQNSEP CAGSSSESDLQTVFKNESLNAESKSGCKLQELKAKQLIKKDTAT YWPLNWRSKLCTCQDCMMYGDLDVLFLTDEYDTVLAYENKGKI AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*FED  124 NLGGSELPPEEALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS  5915 1604 703 FPGRPTEPLKLGRRKKRARIIQAPHCHSPRPTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT QCDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPFGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPPPPFGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPPPPPPFGLVPPIS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH  5916 256 633 SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILQ*NQATADKNN*TTALLOPHOPLYAGNUTSQQYPDH	١		1 1		DSEKCSYSOGSVKROALVACSTCTPECEEPAGICE
SGDFQEMVCQACMKRCSFLWAYAAQLAVTKIST\GmMDWCGTLM E*/DDQEVIKPENGEHQDSTLKEDVPEQGKDDVREVKVEQNSEP CAGSSSESDLQTVFKNESLNAESKSGCKLQELKAKQLIKKDTAT YWPLNWRSKLCTCQDCMKMYGDLDVLFLTDEYDTVLAYENKGKI AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*FED  124 NLGGSELPPEEALFIQVASMNQRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYYISG GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS  5915 1604 703 FPGRPTRPLKLGRRRKRARIIQAPHCHSPRPTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPFGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPQK/RPRLPPPFCLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPQK/RPRLPPPPFCLVPPIS PRELPGEEPSAHPVHQGLPAERRGFLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGFFPEGL**AAGPAAH  5916 256 633 SPRWEIWGPHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH	ļ		Í f		HKLFELYTKRNFRCDCGNSKEVNI ECVI I DDWG GERAGICLACSYECHGS
E*/DQEVIKPENGEHQDSTLKEDVPEQGKDDVREVKVEQNSEP CAGSSSESDLQTVFKNESLNAESKSGCKLQELKKQLIKKDTAT YWPLNWRSKLCTCQDCMKMYGDLDVLFLTDEYDTVLAYENKGKI AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*FED  124 NLGGSELPPEALFTQVASMNQRRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG GHDYQIGPYRKNLLCYDHRTDVMEERRPMTTARGWHSMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS  1604 703 FPGRPTRPLKLGRRRKRARIIQAPHCHSPRPTCPPGALQAPEA PASRAEGPVAVVNGHTEGPAPARSAPKEPPGLPRFLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPQK/RPRLLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGAGGEFPEGL**AAGPAAH  5916 256 633 SPRWWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLTLQ*NQATADKNN*TTALLQPHOPL\VSQUYPDARATA	- 1		1		FFGLYCICKRPYPDPEDETEDEMICONICEPUKAKVNSGNKYNDN
CAGSSESDUCTVFKNESLNABSKSGCKLQELKAKQLIKKDTAT YWPLNWRSKLCTCQDCMKMYGDLDVLFLTDEYDTVLAYENKGKI AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*FED  124 NLGGSELPPEEALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS  1604 703 FPGRPTRPLKLGRRKKRARITQAPHCHSPRPTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPFGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPOK/RPRLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH  5916 256 633 SPRWEIWGPWHRWESFSLEGEWPERIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLTLQ*NQATADKNN*TTALLQRDMSLY	1		f i		SGDFOEMVCOACMKPCGELWAYAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
TWPLNWRSKLCTCQDCMKMYGDLDVLFLTDEYDTVLAYENKGKI AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ+FED  124 NLGGSELPPEEALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS  5915 1604 703 FPGRPTRPLKLGRRRKRARIIQAPHCHISPRPTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPFGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPPQK/RPRLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH  5916 256 633 SPRWEIWGPWHRWESFSLEGEWPSRIPEFSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQQCWTSQQYPDH PTRLILQ*NQATADKNN*TTALLOPHORIAYSGNATARARQ	ı		! }	•	E*/DDOEVIKPENGEHODETIKEDUDEG CHIST\GMMDWCGTLM
5914 960 124 NLGGSELPPEEALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS  5915 1604 703 FPGRPTRPLKLGRRRKRARIIQAPHCHISPRPTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPPQK/RPRLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGAGGFPEGL**AAGPAAH  5916 256 633 SPRWEIWGPWHRWESFSLEGEWPSRIPEFSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILQ*NQATADKNN*TTALLOPHORIAVGRUPARARA	1				CAGSSSESDLOTUEVNEST NA REMOGRATION OF THE CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHARLEST AND CHA
5914  960  124  NLGGSELPPEEALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS  5915  1604  703  FFGRPTRPLKLGRRRKRARIIQAPHCHISFRPRTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPPQK/RPRLLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH  5916  256  633  SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQQQWTSQQYPDH PTRLILQ*NQATADKNN*TTALLQPHORLVYCRPMARSQ	1		1		YWPLNWRSKI.CTCODCHIANGED BY
INGGSELPPEEALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS  FPGRPTRPLKLGRRRKRARIIQAPHCHSPRPTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPFGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPOK/RPRLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH  SPRWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLTLQ*NQATADKNN*TTALLORDORL/VGDRMARD	L				AOATORSDRIMOTI GENTRICOLOVEFLTDEYDTVLAYENKGKI
GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLRPAATS  FPGRPTRPLKLGRRRKRARIIQAPHCHISPRPRTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPFGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPPOK/RPRLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH  SPRWWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLTLQ*NQATADKNN*TTALLOPHORIAYGDRARA	ı	5914	960	124	NIGGGEL DEEM PLOWS COMMENCE OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF
GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS  FPGRPTRPLKLGRRKRARITQAPHCHISPRPRTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPFGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPPQK/RPRLLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH  SPRWWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLTLQ*NQATADKNN*TTALLOPHORL\YGDRAGS	1				ENCAL COMETVO PROPERTY OF THE
IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS  FPGRPTRPLKLGRRRKRARITQAPHCHISPRPRTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLIPSPHP\PVSPAPPPPPPQK/RPRLLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH  SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILQ*NQATADKNN*TTALLOPHORLVSGRAGGR	1				- LICENTUS VALUE TO THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL O
SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS  1604  703  FPGRPTRPLKLGRRRKRARITQAPHCHISPRPRTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPPQK/RPRLLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH  5916  256  633  SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILQ*NQATADKNN*TTALLOPHORLVSDRMARSA	1			ì	OTDIGET RANDLACTURE TO VOTE REPORT AND A TOTAL OF A PARTICIPANT AND A TOTAL OF A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PARTICIPANT AND A PA
SOLAWARTH INGSTSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS  FPGRPTRPLKLGRRRKRARI IQAPHCHISPRPRTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPPQK/RPRLLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH  SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGI I PWVLHSQLKPTAATAQQQWTSQQYPDH PTRLILQ*NQATADKNN*TTALLOPHORLVSGLKPTAATAQQWTSQQYPDH	ı			į	TIDIOGSDDNIESMERFDVLGVEAYS DOCNOWTDUA DI LUNGO
5915 1604 703 PHRHLPGLCRPAATS  FPGRPTRPLKLGRRRKRARIIQAPHCHSPRPTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPPQK/RPRLLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH  5916 256 633 SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQQYTSQQYPDH PTRLILQ*NQATADKNN*TTALLOPHOPL\VSPRMASQ	L	í		1	OUTS WEGGI TEGGISWENTAFSKTVOVVDDDADWGDDGGG
5915 1604 703 FPGRPTRPLKLGRRRKRARIIQAPHCIISPRPRTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPPQK/RPRLLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH  5916 256 633 SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILQ*NQATADKNN*TTALLOPHOPL\VSPRMATSQ	ı	ł		l l	TOTAGGGACT TAP* SLGORTRKRKAKAPCTPTCACPDCGACTTC
PPGRPTRPLKLGERRRKRARI IQAPHCHSPRPTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKE PPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPPQK/RPRLLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH SPRMWEIWGPWHRWESFSLEGEWPSR I PEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGI I PWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILQ*NQATADKNN*TTALLOPHOPL\VSPRMASR	Γ	5915	1604	703	THRIBEGUCKPAATS
PQEDFPALGGPCPPRMPSPGFSAVVLLKGTPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPPQK/RPRLLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH  SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILQ*NQATADKNN*TTALLOPHOPL\VSPUMASRA	1			l l	FPGRPTRPLKLGRRRKRARI IQAPHCHSPRPRTCPPGALOADEA
KPPPGFSGLLPSPHP\PVSPAPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP	ı	ł		i i	TAILORD OF VAV V VIGHTEGPAPARSA DEPENDED DEDT COMPANS
PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL*+AAGPAAH  SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILQ*NQATADKNN*TTALLOPHOPL\VSPRMASQ		ł	1		T QUOT FALIGUPCPPRMPPSPGFSAVVI.I.KCTDDDDDDDDDCT.
FREITGESPÄHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL*+AAGPAAH  SPRMEIUGPHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILQ*NQATADKNN*TTALLOPHOPL\VSPLMATSQ	1		ļ		TEFFGEOGLUPSPHP\PVSPAPPPPDDDOW /DDDTTDDD /DOT-
5916 256 633 SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILQ*NQATADKNN*TTALIOPHOPL\YSDRMASQQYPDH	ı	1	í		ENEUFGREESAMPVHOGLPAERRGDI.ADVIADDI DOVAMONTO I
SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILQ*NQATADKNN*TTALLOPHORL\YSDRMARA	Н	5916			* VIQEDPGPAGGEPPEGL**AACDANU
PTRLILQ*NQATADKNN*TTALLOPHOPL\YCRPMAPA	Ι.	2910	256	633	SPRMWEIWGPWHRWESESI.EGEWDED TDETCE
5017 Table Office Table Office Transport		l	ļ	[ ]	TVTGAVHRHLNHVAGTIDWULHGOTUREN
1343 827 AHQILTYLEP/ICLVVNYNKILTVFLTKSVLEI*KFIHTPQTYR	<u> </u>			} .	PTRLILO*NOATADKNIN*TTALLO
	L	5917	1343	827	AHOLLTYLER/TOLINANAKTI MILITALIQPHQRL \VSPRMAEA
					TODA ANTINKI DI ARPLIKSAPET * KEIHIPOTAK

SEQ	Predicted	Predicted end	L Amino poid
ΙĎ	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
ł	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence	_	\=possible nucleotide insertion)
			F*NDFFGIKEVYVSRRLRKTSF/RLAVTFLEQAVVSKECVPVDQ
ł			FMEHLLPSLLSLASDPVPNVRVLLAKALRQMLLEKAYFRNAGNP
		ļ	HLEVIEETILALQSDRDQDVSFFAALEPKRRNIIDTAVLEKQN
5918	13	1247	EGAQVARRASRRQWRAGRCGRGRGGRRAERTGGRGPPGRPPLP
	1	ļ	PGPARRGRRRMETPFYGDEALSGLGGGASGSGGTFASPGRLFPG
1			APPTAAAGSMMKKDALTLSLSEOVAAALKPAPAPASVDDA\ADG
	1		APSAAPPDGLLASPDLGLLKLASPELERLIIOSNGI.VTTTDTCC
		İ	QFLYPKVAASEEQEFAEGFVKALEDLHKONOLGAGRAAAAAA
			AGGPSGTATGSAPPGELAPAAAAPEAPVYA\NLSSY\AGGCPGL
1	l .		RGGAAT\VAFAAEPVPFPPPPPPPGALGPRRP/RLALOGRRPOTV
1		]	PDVP\SFGESP\PLSPIET\DTPRRI\KAKRKRL\RNPOTRAPK
1	ł	}	PASRKLGAQSRALERESEDPS*SPEHGSLASTASLLREQVAQLK
5919	<u> </u>		QKVLSHVNSGCQLLPQHQVPAY
2212	1	4254	TSVQGDSQGTPTSSQGSINMEHWISQAIHGSTTSTTSSSSTQSG
1			GSGAAHRLADVMAQTHIENHSAPPDVTTYTSEHSIOVERPOGST
			GSRTAPKYGNAELMETGDGVPVSSRVSAKIQQLVNTLKRPKRPP
			LREFFVDDFEELLEVQQPDPNQPKPEGAQMLAMRGEQLGVVTNW
			PPSLEAALQRWGTISPKAPCLTTMDTNGKPLYILTYGKLWTRSM
			KVAYSILHKLGTKQEPMVRPGDRVALVFPNNDPAAFMAAFYGCL
1			LAEVVPVPIEVPLTRKDAGSQQIGFLLGSCGVTVALTSDACHKG
			LPKSPTGEIPQFKGWPKLLWFVTESKHLSKPPRDWF\PHIKDAN
1 1			NDTAYIEYKTCK\DGSVLGVTVTRTALLTHCQALTQACGYTEAE
1 1			TIVNVLDFKKDVGLWHGILTSVMNMHVISIPYSLMKVNPLSWI
1	<b>.</b>		QKVCQYKAKVACVKSRDMHWALVAHRDQRDINLSSLRMLIVADG ANPWSISSCDAFLNVFQSKGLRQEVICPCASSPEALTVAIRRPT
			DDSNQPPGRGVLSMHGLTYGVIRVDSEEKLSVLTVQDVGLVMPG
Section 1			AIMCSVKPDGVPQLCRTDEIGELCVCAVATGTSYYGLSGMTKNT
£.,			FEVFAMTSSGAPISEYPFIRTGLLGFVGPGGLVFVVGKMDGLMV
ž.,			VSGRRHNADDIVATALAVEPMKFVYRGRIAVFSVTVLHDERIVI
Lines			VAEQRPDSTEEDSFQWMSRVLQAIDSIHQVGVYCLALVPANTLP
1 - 1	1		KTPLGGIHLSETKQLFLEGSLHPCNVLMCPHTCVTNLPKPRQKQ
1 1	1		PEIGPASVMVGNLVSGKRIAQASGRDLGQIEDNDQARKFLFLSE
} I	İ		VLQWRAQTTPDHILYTLLNCRGAIANSLTCVQLHKRAEKIAVML
1			MERGHLQDGDHVALVYPPGIDLIAAFYGCLYAGCVPITVRPPHP
1 1	1		QNIATTLPTVKMIVEVSRSACLMTTQLICKLLRSREAAAAVDVR
]	į		TWPLILDTDD*PKKRPAQICKPCNPDTLAYLDFSVSTTGMLAGV
1	1		KMSHAATSAFCRSIKLQCELYPSREVAICLDPYCGLGFVLWCLC
j J	ľ		SVYSGHQSILIPPSELETNPALWLLAVSOYKVRDTFCSYSVMEI.
			CTKGLGSQTESLKARGLDLSRVRTCVVVAEERPRIALTOSESKI.
]			FKDLGLHPRAVSTSFGCRVNLAICLOGTSGPDPTTVVVDMPALD
1	1		HDRVRLVERGSPHSLPLMESGKILPGVRIIIANPETKGPLGDSH
j l		•	LGEIWVHSAHNASGYFTIYGDESLQSDHFNSRLSFGDTOTIWAR
			TGYLGFLRRTELTDANGERHDALYVVGALDEAMELRGMRYHPID
1			IETSVIRAHKSVTECAVFTWTNLLVVVVELDGSEQEALDLVPLV
[ ]	j		TNVVLEEHYLIVGVVVVVDIGVIPINSRGEKQRMHLRDGFLADQ
5920	1381	1499	LDPIYVAYNM OLGAVAUAGUSPIDD+LEDDLUDGGG OLVOCUSPUS D
] ]	• • •		QLGAVAHAGVSRIPP+LFPPLHPTFLSLWCLHHKLP/HPPGASM
[ ]			VRPPVVPRRPPAHISSVRQASTQVPRTVPHTQRVANIGTQTTGP
[	1	ļ	SGVGCCTPGRPLLPCKCSSAAHSTYRVQEPAVHIPGQEPLTASM
]			LAAAPLHEQKQMIGERLYPLIHDVHTQLAGKITGMLLEIDNSEL LLMLESPESLHAKIDEAVAVLQAHQAMEQPKAYMH
5921	727	157	VCPGTGGE*GLWGQLGGLPKETPLKPMDAFTGSGLKRKFDDVDV
	İ		GSSVSNSDDEISSSDSADSCDSLNPPTTASFTPTSILKRQKQLR
	ļ		RKNVRFDQVTVYYFARRQGFTSVPSQGGSSLGMAQRHNSVRSYT
<b> </b>		. 1	LCEFAQEQEVNHREILREHLKEEKLHAKKMKLTKNGTVESVEAD
!			GLTLDDVSDEDIDVENVEVDDYFFLQPLPTKRRRALLRASGVHR
1		}	IDAEEKQELRAIRLSREECGCDCRLYCDPEACACSQAGIKCQVD
ſ		i	RMSFPCGCSRDGCGNMAGRIEFNPIRVRTHYLHTIMKLELESKR
1		1	Q\GAAQQPQ*GALPDCQLQPDRSTGL*DPSWIGSKGLSFTGKG
		1	AAATHLIILRVIENRGAEGKRK
5922	2475	495	SYSNWGLFPSVFIQVPRSRTGNLKPIFLFYSYYE\CMETLKG\T
			T CHBI LING (T

The perinning and mucleotide and mucleotide continued by the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of the perinning of		SEQ	I Dynads are		· 
MO: nucleotide location corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corresponding corres		_	Predicted	Predicted end	
Corresponding   Coffee   Corresponding   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffee   Coffe			beginning		(A=Alanine, C=Cvsteire Dansel peptide
corresponding to first amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid acid acid acid acid acid acid acid		"0:			
to first amino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino acid mino a		I			H=Histidine, T=Tsolevaine, G=Glycine,
amino acid sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  seque		1	corresponding		
amino acid sesidue of amino acid sequence  oulded sequence  sequence  condition of the sequence  sequence  condition of the sequence  sequence  condition of the sequence  sequence  sequence  condition of the sequence  condition of the sequence  sequence  condition of the sequence  sequence  condition of the sequence  sequence  condition of the sequence  sequence  condition of the sequence  sequence  condition of the sequence  sequence  condition of the sequence  sequence  sequence  condition of the sequence  sequence  sequence  condition of the sequence  sequence  sequence  sequence  condition of the sequence  sequence  sequence  sequence  condition of the sequence  sequence  sequence  sequence  sequence  condition of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of				amino acid	P=Proline O-Glutamine, N=Asparagine,
## Tryptophan, X-9valine, X-9valine, #=Stop amino acid sequence  ## Tryptophan, X-9valine, X-9valine, #=Stop coon, /=possible nucleotide Sected ediction, /=possible nucleotide Sected ediction, /=possible nucleotide Sected ediction, /=possible nucleotide Sected ediction, /=possible nucleotide Sected ediction, /=possible nucleotide Sected ediction, /=possible nucleotide Sected ediction, /=possible nucleotide Sected ediction, /=possible nucleotide Sected ediction, /=possible nucleotide Sected ediction, /=possible nucleotide Sected ediction, /=possible nucleotide Sected ediction, /=possible nucleotide Sected ediction, /=possible nucleotide Sected ediction, /=possible nucleotide Sected ediction, /=possible nucleotide Sected ediction, /=possible nucleotide Sected ediction, /=possible nucleotide Sected ediction, /=possible nucleotide Sected ediction, /=possible nucleotide Sected ediction, /=possible nucleotide Sected ediction, /=possible nucleotide Sected ediction /=possible nucleotide Sected ediction /=possible nucleotide Sected ediction /=possible nucleotide Sected ediction /=possible nucleotide Sected ediction /=possible nucleotide Sected ediction /=possible nucleotide Sected ediction /=possible nucleotide Sected ediction /=possible nucleotide Sected ediction /=possible nucleotide Sected ediction /=possible nucleotide Sected ediction /=possible nucleotide Sected ediction /=possible nucleotide Sected ediction /=possible nucleotide Sected ediction /=possible nucleotide Sected ediction /=possible nucleotide Sected ediction /=possible nucleotide Sected ediction /=possible nucleotide Sected ediction /=possible nucleotide Sected ediction /=possible nucleotide Sected ediction /=possible nucleotide Sected ediction /=possible nucleotide Sected ediction /=possible nucleotide Sected ediction /=possible nucleotide Sected ediction /=possible nucleotide Sected ediction /=possible nucleotide Sected ediction /=possible nucleotide Sected ediction /=possible nucleotide Sected ediction /=possible nucleotide Sected ediction /=possible		1			F-Figurine, U=GillFamine D_Ai
amino acid sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Sequence  Seque		1	residue of		S=Serine, T=Threonine, V=V=1:ma
Sequence    Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence		1	amino acid		I "= I YPCOPAAN, Y=Tvrosine v_tiple
CITYRATOR MICHOLING INSECTION  CITYRATOR CONTINUENCE PROJECT ANT KENDERGRATTYPE INTELLIGIT  SKITTRIBE CENTROL HIRPERCAALINSKELEIGCSIM PERSANDERGRATTYPE INTELLIGIT  SKITTRIBE CENTROL HIRPERCAALINSKELEIGCSIM PERSANDERGE CHROLYPECT 1-47* KANDINSTYLOKOBEAN  PERSANDERGRATTYPE CHROLING PROJECT INTELLIGION HIRPERCAALINSKELEIGCSIM PERSANDERGE CHROLYPECT 1-47* KANDINSTYLOKOBEAN  LIEGEVIHGE BEPT TYPERLIGIA PAPELLIKKTELIGIA PROJECT INTELLIGION HIRPERCAALINSTELEIGE CHROLING HIRPERCAALINSTELEIGE CHROLING HIRPERCAALINSTELEIGE CHROLING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERCAALING HIRPERC		1		Seducine	"Uddilly / =DOSSIDIE NUCleotide deleti-
CLINATOY KYCSPRNORPACYPSERJATTYFEITSTELLCOSIAN BERS- RYDRYCHESQUEKGAJNISKELISCOSIAN BERS- RYDRYCHESQUEKGAJNISKELISCOSIAN BERS- RYDRYCHESGUEKGAJNISKELISCOSIAN BERS- RYDRYCHESGUEKGAJNISKELISCOSIAN BERS- RYDRYCHESGUEKGAJNISKELISCOSIAN BERS- RYDRYCHESGUEKGAJNISKELISCOSIAN BERS- RYDRYCHESGUEKGAJNISKELISCOSIAN BERS- RYDRYCHESGUEKGASPUTOTYSELIALBAPELIKKTOLIPOLOGUEKGA- LIPLLOGUEKGSPEPUTOTYSELIALBAPELIKKTOLIPOLOGUEKGA- LIPLLOGUEKGSPEPUTOTYSELIALBAPELIKKTOLIPOLOGUEKGA- LIPLLOGUEKGSPEPUTOTYSELIALBAPELIKKTOLIPOLOGUEKGA- LIPLLOGUEKGASPETGEN ANDRESS VEKKOLIVIGAN BERS- LIPLLOGUEKGASPETGEN ANDRESS VEKKOLIVIGAN BERS- KEKGI VI GANKDABENDERELI (A. YOPKANOCON BERS- KEKGI VI GANKDABENDERELI (A. YOPKANOCON BERS- LIPLTON KOLIVATION BERS- LIPLTON KOLIVATION BERS- LIPLTON KOLIVATION BERS- LIPLTON KOLIVATION BERS- LIPLTON KOLIVATION BERS- NSI  5923 137 638 OLGGRAGOGERI LIPLTON BERS- LIPLTON KOLIVATION BERS- NSI  5924 274 2146 ERGENVARIAN BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON BERS- LIPLTON				<del></del>	\-Possible nucleofide incortion\
RVERKYVOLHESSPUCHNOVEN, TANSKKEETGGSEN, HERS- RVERKYVOLHESSPUCHNOVEN, TANSKKEETGGSEN, HERS- RVERKYVOLHESSPUCH STATEMEN OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE			1		CLYNATOYKVCSPRNDRPDACYNDSFDAATTVESTPTOTIL
PSCAAGHONDLILITY TOLDPHYKKGENT ARE YKEKNINGSTYLOKIGAENV LIKGEWIKED FOR TOT JUDDPHYKKGENT GINTGIKFOUVEL LIKGEWIKED FOR TOT JUDDPHYKKGENT GINTGIKFOUVEL LIKGEWIKED FOR TOT JUDGPHYKKGENT GINTGIKFOULAENV LIKGEWIKED FOR THE JUDGT JERGEKOPT I PYGKENGIGGIKINSTYK TIT** DLINITERNIP FOR JARGEKOPT I PYGKENGIGGIKINSTYK REASPYLIKENT I ROUT GIRKEKTA* JAMAGEN POWTYSGIK* JEC RIKASPYLIKEN JARGEKOLI GYTKOS FILLP I KMGELLOFSVYASR EKKGIV I GOWEKED PER GERALI VIGYUGIAWAGGOWA JARGEKORI JED JULIAJAGGOVCKYENT JEGORALI VIGNUL VIGHTULLEVUL PULKENDELES LORMEP PA LOGEKTIL VIGULIVI I STEVLLIKEVUL PULKENDELES LORMEP PA LOGEKTIL VIGULIVI I STEVLLIKEVUL PULKENDELES LORMEP PA LOGEKTIL VIGULIVI I STEVLLIKEVUL PULKAGOSHA KOTATUHAKUT SAMAVATAMINAN JARGEKORE DESS SERIAS LORMEN SAMAVATAMINAN JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKORE PAR JARGEKOR		i	1		1 ONLI THE BENGLERUL LIKE DALLA THE VET DICCOULTY COME.
LIKGSUHRED PADD JO TEELINIPAPELLIKKTROILFIQUARW IFFLIANTES CYROSTT IT FEELINPAPELLIKKTROILFIQUARW IFFLIANTES CYROSTT IT SERNIPAPELLIKKTROILFIQUARW IFFLIANTES CYROST IT SERNIPAPELLIKKTROILFIQUARW IFFLIANTES IT ROYCLARE KORD IT PYCKROLIGOKLYMSTIK ERRAY PELLIPIKRADS CYLOTIK SPYFLLIF KORELLOFS VANSE ERKASI VIONAL EI SINTEGRALIVIANOST GARNATYONRIAL DYLLVARSOV KRITINGCLQINDOGOVYRI VERBITARYONRIAL DYLLVARSOV KRITINGCLQINDOGOVYRI VERBITARYONRIAL DYLLVARSOV KRITINGCLQINDOGOVYRI VERBITARYONRIAL DYLLVARSOV KRITINGCLQINDOGOVYRI VERBITARYONRIAL DYLLVARSOV KRITINGCLGINDOGOVYRI VERBITARYONRIAL DYLLVARSOV KRITINGCLGINDOGOVYRI VERBITARYONRIAL DYLLVARSOV KRITINGCLGINDOGOVYRI VERBITARYONRIAL DYLLVARSOV KRITINGCLGINDOGOVYRI VERBITARYON KRITINGCLGINDOGOVYRI VERBITARYON PLITTY LIKANOSINGE TES CIRCURE KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN AND COLUMBRICAL SERVICIO KRITINGCLIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLGIN KRITINGCLG		1	1		1 ATTACA CALSGO CANCAY W DCV T * ATT * V PATVATO CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARREST CARRE
IFILIAGISCOVERGETT I RESIGNIPABELIKKTROILEIJABNY  ASBF-VILKEI IRROTCI AREGROF I IPGKENDIGORINSTIK  TIT-* DILMITERNIP SEKKUTA- JAMAESH-PONTUSSIK-Y-IC  RIRASTFILMENDADOS I GITKOS PILIP I IRROTCIANSTIK  RIRASTFILMENDADOS I GITKOS PILIP I IRROTCIANSTIK  RIRASTFILMENDADOS I GITKOS PILIP I IRROTCIANSTIK  RIRASTFILMENDADOS I GITKOS PILIP I IRROTCIANSTIK  RIRASTFILMENDADOS I GITKOS PILIP I IRROTCIANSTIK  RIRASTFILMENDADOS I GITKOS PILIP I IRROTCIANSTIK  RIRASTFILMENDADOS I GITKOS PILIP I IRROTCIANSTIK  MANNI I RILAJALEI I SIN GORGALI VIANGETORINAI YORIKAL  DILLANGEGOVER INTINI I GINDOGOVERIN VARINTIANI I GORGANI INTONI  FULLO PILIPONI KGIVATLUNGKI SAMMAVIMININI SI GORGANI I GORGANI  DILLANGOS INSABELESCI DIRI I GENGEVARI KAN LOMVAKKAN JADAPP  LARIOS INSABELESCI DIRI I GENGEVARI KAN LOMVAKKAN JADAPP  LARIOS INSABELESCI DIRI I GENGEVARI KAN LOMVAKKAN JADAPP  LARIOS INSABELESCI DIRI I GENGEVARI KAN LOMVAKKAN JADAPP  LARIOS INSABELESCI DIRI I GENGEVARI KAN LOMVAKKAN JADAPP  LARIOS INSABELESCI DIRI I GENGEVARI KAN LOMVAKKAN JADAPP  LARIOS INSABELESCI DIRI I GENGEVARI KAN LOMVAKKAN JADAPP  LARIOS INSABELESCI DIRI I GENGEVARI KAN LOMVAKKAN JADAPP  LARIOS INSABELESCI DIRI I GENGEVARI KAN LOMVAKKAN JADAPP  LARIOS I GENGEVARI KAN JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JADAPP JA		1	1	1	PSCAAGHCNPLELI ITNPL DDUNYVODDI TO TOTAL TOTAL TOTAL
ASSIP***ULKTS I IRQUIC LARGEROFT I PETOPAPATO CONLINSTIK TIT*****DIAMENDEMPER I IRQUIC LARGEROFT I PETOPAPATO CONLINSTIK TIT*****DIAMENDEMPER I IRQUIC LARGEROFT I PETOPAPATO CONLINSTIK TIT*****DIAMENDEMPER I IRQUIC LARGEROFT I PETOPATO CONLINSTIK RHEAT PER LARGEROFT LARGEROFT IN CHORUNG TOWNEN TYONIN LARGER DIAL LEI IS SETTE TRAITULANCE TOWNEN TYONIN LARGER DEVIAL LEI IS SETTE TRAITULANCE TOWNEN TYONIN LARGER DEVIAL LEI IS SETTE TRAITULANCE TOWNEN THE PETOPATO CONLINSTIKE DEVIAL LEI IS SETTE ALGER TRAITULANCE TOWNEN THE PETOPATO CONLINSTIKE DE LARGER THE PETOPATO CONLINSTIKE DE LARGER TOWNEN TOWNEN AND CONCERNE TO THE INSTITUTE OF THE PETOPATO CONCERNE DE LARGER TOWNEN TOWNEN AND CONCERNE THE LEI SELECTOR SENTEMENTA CONCERNE DE LARGER TOWNEN TOWNEN TOWNEN AND CONCERNE THE LARGER TOWNER OF THE PETOPAPATO CONCERNE THE LARGER TOWNER OF THE PETOPAPATO CONCERNE THE LARGER THE PETOPAPATO CONCERNE THE LARGER THE PETOPAPATO CONCERNE THE LARGER THE PETOPAPATO CONCERNE THE LARGER THE PETOPAPATO CONCERNE THE LARGER THE PETOPAPATO CONCERNE THE LARGER THE PETOPAPATO CONCERNE THE LARGER THE PETOPAPATO CONCERNE THE PETOPAPATO CONCERNE THE PETOPAPATO CONCERNE THE PETOPAPATO CONCERNE THE PETOPAPATO CONCERNE THE PETOPAPATO CONCERNE THE PETOPAPATO CONCERNE THE PETOPAPATO CONCERNE THE PETOPAPATO CONCERNE THE PETOPAPATO CONCERNE THE PETOPAPATO CONCERNE THE PETOPAPATO CONCERNE THE PETOPAPATO CONCERNE THE PETOPAPATO CONCERNE THE PETOPAPATO CONCERNE THE PETOPAPATO CONCERNO CONCERNO CONCERNO CONCERNO CONCERNO CONCERNO CONCERNO CONCERNO CONCERNO CONCERNO CONCERNO CONCERNO CONCERNO CONCERNO CONCERNO CONCERNO CONCERNO CONCERNO CONCERNO CONCERNO CONCERNO CONCERNO CONCERNO CONCERNO CONCERNO CONCERNO CONCERNO CONCERNO CONCERNO CONCERNO CONCERNO CONCERNO CONCERNO CONCERNO CONCERNO CONCERNO CONCERNO CONCERNO CONCERNO CONCERNO CONCE		1			LIKGEVHKCSPKPVFOTEVERINGERVTLGINRTGLKPQVVI
TITY * DIMPITER RUPPESE SELLETA * PALABER DENTY DESCRIPT I PARTICLES VASES RHEAT FELL PRIKADS CVIGTI RUSS FILLET I KNGELLES VASES EKRGI VIGNER KOMEN KOMEN PERE I (19 VEPATHADOS GNOTE). TP / VV MINNET I RICOALLE II SMETGRALTVILAWOETOMINAT YONILAL DIALIZASS GOVER PRAIT FINAL COLLING CONTROL VIGNERILATIVE DES LA GROST SALVEY AND MENT I RICOALLE I SMETGRALTVILAWOETOMINAT YONILAL DIALIZAS GOVER PRAIT FOR THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE V		1	1	1	IFLLNGTSCVVPGGTTTGDDV
TITY * DIMPITER RUPPESE SELLETA * PALABER DENTY DESCRIPT I PARTICLES VASES RHEAT FELL PRIKADS CVIGTI RUSS FILLET I KNGELLES VASES EKRGI VIGNER KOMEN KOMEN PERE I (19 VEPATHADOS GNOTE). TP / VV MINNET I RICOALLE II SMETGRALTVILAWOETOMINAT YONILAL DIALIZASS GOVER PRAIT FINAL COLLING CONTROL VIGNERILATIVE DES LA GROST SALVEY AND MENT I RICOALLE I SMETGRALTVILAWOETOMINAT YONILAL DIALIZAS GOVER PRAIT FOR THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE VICTOR OF THE V		1		1	TALEDING TO CANCELLA (II) RWDWED + DI TIDENDE DE LES CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONTRESE CONT
RIRAY FRLIPKINADSCVI (2017 KPS FFL LIP KMGELLOFS VYASIS  RIKGI V. (GWAKENDEWPERT I (CY VGPATWADGOSKIE/ TP / VYA  MINNI I RICAL ELI I SHETGRAL TULAMOSTOMRINAI YOMIRLAD  DILLIVASGOVCR (FMLTINCCLOI INDOGOVUKHI VERDITLIPCUL  TOVHKE KDEPSL JOKEM PAL IGGYKELI (VALVATIVANITLIANU)  LOVHKE KDEPSL JOKEM PAL IGGYKELI (VALVATIVATICLLE) (VALVATIVANITLIANU)  FLEMOMI KGI VATLUHOKTSAHVIYIMHIYES I GORDIKE EDESE  MSH  5923 137 638 OLGGREGOFFETS I KRMHPI! * RTCPNTINL/ I I LLEGDENO LLEGANGOSKE EDESE  MSH  COGENELMI SLEBHODAL LIMSKYKROMLOMWAKKAVDAEPV  LARHOSHSAH I SEBHODAL LIMSKYKROMLOMWAKKAVDAEPV  LARHOSHSAH I SSELONE (SEMENTANI OVALVATIVANITHY STOROSKE EDESE  MSH  5924 274 2146 PROKKKRAMAHIKI SLESHODAL LIMSKYKROMLOMWAKKAVDAEPV  LARHOSHSAH I SSELONE (SEMENTANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATIVANI OVALVATI		f			1 MAIN VOKISIIKUICIARRICKOFT TOVICKONGTOOM MANAGEMENT
EKWGI VI CONKONDEN PERE I I CYVOPATNA DOS SWGIN, TP / VV MEANI I RIQAILE II ISBETGRALTVIAWOETOMINA I YONILAI DILLVARGOCVER PRILITORIC (JINDGOCVI VENDMILAIPU POLIVAR DE PESIL PER PRICE PRILITORIC (JINDGOCVI VENDMILAIPU I COVINKE PESIL PER PRICE PRILITORIC (JINDGOCVI VENDMILAIPU I COVINKE PESIL PER PRICE PRILITORIC (JINDGOCVI VENDMILAIPU I COVINKE PESIL PER PRILITORIC (JINDGOCVI VENDMILAIPU I COVINKE PESIL PER PRILITORIC (JINDGOCVI VENDMILAIPU I COVINKE PESIL PER PRILITORIC (JINDGOCVI VENDMILAIPU I COVINKE PESIL PER PRILITORIC (JINDGOCVI VENDMILAIPU I COMBREIM I SILEBIODALEL IMSKYR (QMIQUMAKKAUDAEPU CORREGAGEN I SILES CORSECTORIC (JINDGOCVI VENDMILAIPU CORREGAGEN I SILES CORSECTORIC (JINDGOCVI PLISOMGI HIR) OLER SELEGAR (JINDGOPMALVOLETINI (JINDGOCVI PLISOMGI HIR) SVENKKIN PRILITORIC (JINDGOCVI PLISOMGI HIR) SVENKKIN PRILITORIC (JINDGOCVI PLISOMGI HIR) REKULES SILEGAR (JINDGOCVI PLISOMGI HIR) REKULES SILEGAR (JINDGOCVI PLISOMGI HIR) REKULES SILEGAR (JINDGOCVI PLISOMGI HIR) REKULES SILEGAR (JINDGOCVI PLISOMGI HIR) REKULES SILEGAR (JINDGOCVI PLISOMGI HIR) REKULES SILEGAR (JINDGOCVI PLISOMGI HIR) REKULES SILEGAR (JINDGOCVI PLISOMGI HIR) REKULES SILEGAR (JINDGOCVI PLISOMGI HIR) REKULES SILEGAR (JINDGOCVI PLISOMGI HIR) REKULES SILEGAR (JINDGOCVI PLISOMGI HIR) REKULES SILEGAR (JINDGOCVI PLISOMGI HIR) REKULES SILEGAR (JINDGOCVI PLISOMGI HIR) REKULES SILEGAR (JINDGOCVI PLISOMGI PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE PROPORE			1		TITLE DIMITERING PORTSKING TAXABLE DISTRIBUTION TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SEC
MINNT I RIQAILE I I INTEGRATUA GODG SWOTE / TP / VIV  MINNT I RIQAILE I INTEGRATUA GODG SWOTE / TP / VIV  DYLLVABGG VERFILITICCL QIND GOVEN I VENTULI PRILLIPEU    DYLLVABGG VERFILITIC CLAIN DE GOVERNOME TO STAND I VENTULI STAND I VENTULI PRILLIPEU    PLIF OM I KGI VATLUH QKTSAHWYMNIYTS I SORDSK EDESE  NSR  OLGGREGOFFTS I KRMHPI * RTCPNTIL/ I I ILISESTOTIC ILLE ON THE STAND I VENTULI SERVICI PRILIPEU    DELEN BERNER LISES GODG I CEMEG VERKAVQUOD DE CKIA QUE ENKEKER LISES SES LOAR KENKOM LOLWAK KAVADA DE PULTUTI LICHA CHEN LISES SES LOAR KENKOM LOLWAK KAVADA DE PULTUTI LICHA CHEN LISES SES LOAR KENKOM LOCK I PHIS OND HAKE WAN LEIGHBAND I SE SCHARSK HENKLIC SEAR STORD IN LINSI PETS VERN PLITUTI LICHA CHEN SUCKEL KENKOM LOCK I PHIS OND HAKE WAN LEIGHBAND I SUCKEL KENKOM LEIGHBAND SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUCKEL KENKOM LEIGHBAND I SUKKAL ROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE C					
DYLLYARGOVURTIFICATIONAGETQMINATYONIAHVE IDVINIAGEGOVURTIFICACIONAGETQMINATYONIAHVE IDVINIAGEGOVURTIFICACIONAGETATIONAGETQMINATYONIAHVE IDVINIAGEGOVURTIFICACIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETATIONAGETA		1	1	ļ	ENGLY TONWADNEWPRERTTOVVCDATERACTION (TO A COLOR
10VWHKPDPSSLIGKRYPATIGERETHI VOVLUVIRRUTKLHAVUS PLLFQMI KGIVATLVHQKTSHAVNYMNIKYS ISQRDSKSEDESE NSR  OLGGREGGEFETS IKRMHPI*RTCPNTIL/TILISGENTQI ING OGENERUS ILEBEGODALELIMSKYKKAMOLOMOZKAVDADEPU LKANGSISABIESQIDHICEMGEVWRKAVQUDDOCKIQEKIA OLELENKELELISISSESLQARKENKAVQUDDOCKIQEKIA OLELENKELELISISSESSIQARKENKAVQUDDOCKIQEKIA OLELENKELELISISSESSIQARKENKAVQUDDOCKIQEKIA OLELENKELELISISSESSIQARKENTASQAIV PLITVYLILKMVARHHKKLICSKAPSTQLOGKITHSGMGIHHQ SVCMKLKPNTSHIISILMGQPPALIVQLETIAPHTIIOKPOTOD HKKPWKALPHSHHLITSIMGOPPALIVQLETIAPHTIIIOKPOTOD HKKPWKALPHSHHLITSIMGOPPALIVQLETIAPHTIIIOKPOTOD HKKPWKALPHSHHLITSIMGOPPALIVQLETIAPHTIIIOKPOTOD HKKPWKALPHSHHLITSIMGOPPALIVQLETIAPHTIIIOKPOTOD HKKPWKALPHSHHLITSIMGOPPALIVQLETIAPHTIIIOKPOTOD HKKPWKALPHSHHLITSIMGOPPALIVQLETIAPHTIIIOKPOTOD HKKPWKALPHSHHLITSIMGOPPALIVQLETIAPHTIIIOKPOTOD HKKPWKALPHSHHLITSIMGOPPALIVQLETIAPHTIIIOKPOTOD HKKPWKALPHSHHLITSIMGOPPALIVQLETIAPHTIIIOKPOTOD HKKPWKALPHSHLITSIMGOPPALIVQLETIAPHTIIIOKPOTOD HKKPWKALPHSHLITSIMGOPPALIVQLETIAPHTIIIOKPOTOD HKKPWKALPHSHLITSIMGOPPALIVASERPUKEGSPS ANTIFCSINGSHHEPPEQRAKKETISHKGHOVES LABARYKAQSHNESKIFIKHGHOVESHVALIPHTIAPHTIAPHTIAPHTIAPHTIAPHTIAPHTIAPHTI		I	1		I TOWN TEXT VALUE LISING TORAL TURNING TO THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT O
5923 137 636 OLGGREGORFETSIKEMHPI*RTCPNTNL/TILLSCENTORD. COUNTELMISLEHHODALELIMSKYRKOMLOLWYAKKAVDAEPY LEARGYSIKSAETESQIDEICEMGEVIKAVQODDOPCKIOPKLA COUNTELMISLEHHODALELIMSKYRKOMLOLWYAKKAVDAEPY LEARGYSIKSAETESQIDEICEMGEVIKAVQODDOPCKIOPKLA COLEENKELRELLSISSESLOARKENSMOTASQAIK EKGKVKORAGROMISLISISCKSGWSPOSINLENSIPPTSVERN PLITTVYLLKMYARHHKLLCSKAPSTOLOOKIFLHSQOMGIHHO SVCKKLKPNTSHIISIHMOPPMANUCHTAPHTIIOKROTION KREFESLEGOLLIMFVOASS (O.4NOS RINLENSIPPTSVERN PLITTVYLLKMYARHHKLLCSKAPSTOLOOKIFLHSQOMGIHHO SVCKKLKPNTSHIISIHMOPPMANUCHTAPHTIIOKROTION KREFESLEGOLLIMFVOASS (O.4NOS RINLENSIPPTSVERN PLITTVYLLKMYARHHKLLCSKAPSTOLOOKIFLHSQOMGIHHO SVCKKLKPNTSHIISIHMOPPMANUCHTAPHTIIOKROTION KREFESLEGOLLIMFVOASS (O.4NOS RINLENSIPPTSVERN PLITTVYLLKMYARHHKLLCSKAPSTOLOOKIFLHSQOMICH HOR KWEKKNLPIASHHILTSVPOOTVIEKKTGSPEIKLKLITTRIONG RELFESSLEGOLLIMFVOASS (O.5NOS RINLENSIPPTSVERN SSERKSHKIPKLEPPEOMRENERUTVSEKPRESPEIKLKLITTRIONG RELFESSLEGOLLIMFVOASS (O.5NOS RINLENSIPPTSVERN SSERKSHKIPKLEPPEOMRENERUTVSEKPRESPEIKLKKITKTIONG RELFESSLEGOLLIMFVOASS (O.5NOS RINLENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVENDENSIPPTSVE		1	i		1 2 2 2 4 A LOG V CRAF NLTNCCLOTNDOCOMMITTED DAMSET 2 2222
S923 137 638 OLGGRGGRFTSIKEMBPI-RTCPNTINL/IILSQENTOIRDL OGDRRELMISLEEHQDALELIMSKYROMLOMWAKKAVDAEPU LKAHGSHABAIESQIDRICEMGEWARKAVQVDDQFCKIQEKLA OGELENKELEELISISSELQARKSWATAGAEV LKAHGSHABAIESQIDRICEMGEWARKAVQVDDQFCKIQEKLA OGELENKELEELISISSELQARKSWATAGAEV EKGKVKDAGAEQWISLSISSELGKOSMETGFSNELINGITPDTSVRRM PLITVYLLKMVARHHMKLLCKSARTOLQOKIFLHSCMGIHMQ SVCMKLKPNTSHISILIMGQPMALVQLETLAPLITIIDKPQTOD HKKWKNLPLHSHHLHTSVPQTVIPKKTOSFFILIKHTKTIQNG RELFESSLCODLLNRVQASEVOVOSIESREKKKKKNKDSSR ASKIKIPKLEPBEQNRPNERVDTVSKRPREFDVLKEGSPSS ANTIFCSNNGSVHW\FRRQVGLUWSKVGTTFWHEVMSDPQL EVHKKINTGAAEYHVOFFSNQEERAWVIEKVKGHKQYEE LLAEATKQASNIBERGKIKTRPRFSQVI NTQPEGTNAGBVASSLSSTBIRRHGWRTAGWOIGIAHARKALKMT REERIBQYTFIVIDKQPFEALSQAKKSVASKIEVKKTRRPRSVI NTQPEGTNAGBVASSLSSTBIRRHGUELITSTRONGREXPTOS VSSPEATSGSTGSVEKKQQRSIFTRSESEKSTEVVPKKKKKE OVGFLHVES OVGFLHVES 1911 MMTAESREATGISPQAAQEKDGIVIKVEESPEDHIMGQDSTL QDTPPPPPPPIFRQFFTCVMSTFGPBEALSRIKKELCHGMURPP INTREGILBLUVLKQFLSILIPKELQVMLQEYRPDSGSERAVILLE DELDLGGQVPGGVMCPPENLARGMVPLDPVQSSSFDLHHERAT QSHFKISSRKVRLIQSRALPAAHIFSPHSGSPRDAMSALFT ABSQAMVILISMAVSILIEMGCQNLARRHISBRNQENYGSAP PQGGENRMENEESTSKAETBDSAGETTGRSQKEFGERVQLG GKTGERQQKNPBEKTRKERKDSGPALGKDKKTTTGRGPREKGK GLGRSFSSNFTTIPESVFTOKSHRCDEGGKFTTGSSLIFIKK IIHTGEKPYECSSCGRAPKINNS\NLVLHGRITHGRPFECCBE CKARFSISNLILINGHINGSKEPTGCKAFGSGSD)LTKHG RIHTGERFYSCSSCGRAPKSNSVLLLHRRVTTGRPFEKGK GLGRSFSSNFTTIPESVFTOKSHRCDEGGKFTRSSLLIFIK IIHTGEKPYECSSCGRAPKSNSVLLLHRRVTTGRPFEKGK GLGRSFSSNFTTIPESVFTOKSHRCDEGGKFTRSSLLIFIK SSPHHTPVHPPPPENSPRODAMSALFT ANGRUMGRAGGSGSSFAAYCHHARERSPEVSTROKSHRCDEGKFTRSSLLIFIK FRENGRAPHYVHPPPHYPPPPENSPRODAMSALFT ANGRUMGRAGGSGSSFAAYCHHARERSPEVSTROKSHRCDEGKFTRSSLLIFIK IIHTGERFSSCGGRAPKSNSVLLLHRRVTCPKCCK AFFRISTILLHRRITHARERSSEPTSPAGDAFGARKGK VAFFRESSTLTHHRITHARERSSEPTSPAGDAFGARKGK GKRUMGRAGGSGSSFAAYCHHARERSPESCOGGRAPKSERIF TARAGAMGARAGHGGINGHARARGRESSGGGRAFHEEDEV TALALRGGGGGSSVAAPFLGSGGTTAPSSSSGGGRFRIKEESV TALALRGGGGGGFTAMARARAVLKECOLERKRAFGERGEVEFLUV AKKYGKLHEKKRUMGHGINGAMYGGRFSSRGGKFRIKEESV TALALRGGGGGGGFAAMGARGKGLKERLERINRARGCG		1		1	1 TY THING DECOME GAME PATGGER PT. TOOUT TOTAMOS
137 638 OLGGRGGRFTSIKEMHPI*RTCPNTNL/IILLSGENTGIRDL OGENEELMISLESHQDALELIMSKYRKQMLGMVAKKAVDABEPV LARHOSHSAEIESGIBRICEMGEWMRKAVQVDDDOFCKIOEKLA OLELENKELRELLSISSELOARKENSMDTAGOAIK EKKVKOAGAGAGAISISLISGISGISGISGISGISGISTOPSSMLINSIJTPPTSVRRM PLITTVTLLKMVARHHMKLLCSKAPSTOLOGKIFHSGMGIHMG SCMKLKPNTSHIISISLISGISGISGISGISTOPSSMLINSIJTPPTSVRRM PLITTVTLLKMVARHHMKLLCSKAPSTOLOGKIFHSGMGIHMG SCMKLKPNTSHIISISLINGCOPMALVERSTUPITSVRRM PLITTVTLKMVARHHMKLLCSKAPSTOLOGKIFHSGMGIHMG SCHEKSSLCODLUNGVOSE Q*NQSIESRKEKKSNKHDSSR SEERKSHKIPKLEPSGORENVERVDYSKPREEPVLKEGSPSS ANTIFCSNNSSVHWYFKPQVODLVMSKVOTYVHMPCWVSSDPOL EVHYKINTRGAREVHVOPFSNQSRAWHERKVERKYKKKHKOYEE LLABATKQASNNSEKQKIRKYRPRORERAGMDIGIAHAEKALKMT REGEIECYTHYINDKOPFEALISGAKSVASKTEVKKTRREPSVL NTOPEOTNAGEVASLSSTEIRHSGRRITSAEEEPPVLXIAW KTAARKSLPASITHMKSSLDLQKAMSVAVKIEVKVERREPSVL NTOPEOTNAGEVASLSSTEIRHSGRRITSAEEEPPVLXIAW KTAARKSLPASITHMKSSLDLQKAMSVAVKIEVKVERREPSVL OGSFILOFYSTKGIGKTEISVEGODRLIISTPNORNEKPTQS VSSPEATSGSTGSVEKKQORRSIRTTGESERSTEVVPKKKIKKE QVGFLHVES OVSFEATSGSTGSVEKKQORRSIRTRESERSTEVVPKKKIKKE QVGFLHVES OVSFEATSGSTGSVEKKQORRSIRTRESERSTEVVPKKKIKKE QVGFLHVES OSSPEATSGSTGSVEKKQORRSIRTGFPBSERSTEVVPKKKIKKE QVGFLHVES OSSPEATSGSTGSVEKKQORRSIRTGFPBSERSTEVVPKKKIKKE QVGFLHVES OSSPEATSGSTGSVEKKQORRSIRTGFPBSERSTEVVPKKKIKKE QVGFLHVES OSSPEATSGSTGSVEKKQORRSIRTGFPBSERSTEVVPKKKIKKE QVGFLHVES OSSPEATSGSTGSVEKKQORRSIRTGFPBSERSTEVPKKKKKE OSSFFRHSSRLILERGROPPFBCALSRRLLCHOMILPE INTKQJILLLVLKQFISILPKLQVMLQEVPBOGESFPDAMSALFT ABSQMAVILEDMAQUKILDEMGCOMBOLKKYTITGERGFPEKKGK GLGRSFSLSSNFTPREVPTGTKSHRLDDRYGGAP PQGGENNENBESTSKAFTSBDSABRGETTGRSOKEFGERIDGE GKTGERGOKAPGSKFFREKKYENGOGISTVAPPAGKTTGERGFPEKKGK GLGRSFSLSSNFTPREVPTGTKSHRLDLAFGALTKSCV ORGENISASCORSTSVAPPAGKTTGERGFPEKKYCKCK AFTRSSTLILHRI HARERASEFSPASLDAFGALKSCV ORGENISASCORSTSVAPPAGKTTGERRRISEGEAAR KRRLEFIERKKXGNOGISTSVAPPAGKTTRAARPEGG MENVLSAGGGSGVAPPATGGSPATAGGRFRANEREGGG MENVLSAGGGGSGVAPRANGARGRFSSSRGGFRINKEEEV VILABLRGJILLQFFNERGOLIKALGRGGGTLAFSFSSRGGYETHMIFTO MQQRAEDNEAKKREIGRGGLERGRANISCDORGSEADM RRKK\LIEGKLAFERGSSALARMISCDORGSEEDM RRKK\LIEGKLAF		l		i	PLLFQMIKGIVATLVHOKTSAHWWYMNUVBGIGORGE
OLGGERGGFFTSTEKRMHPI FTCPNTNL/IILLGENTOIRDL OQENEELMISLEENGLILLMSYER/CMIQUMVAKKAVDABPV LKAHGSHSABIESQIDRI CEMGEVMRKAVQVDDDQFCKIQEKLA 5924  274  2146  EKGKVKDAGAEQUISLSUSCKGSBEVARRENSMDTASQAIK PLITTVITLLKMVARHHMKLLCSKAPSTOLQGNIFLHSGMGIHHO SYCKLKHPITSHI ISILMGOPMALVOLETIAPLITI IJCKPOTOD HMKFWKALPHSHHLTPSVPGTVIPKKTGSPBILKLTTRIJONG RELFESSLCODLLNRVQASIQ-NO SESREKRKKSKKHEDSSR SEERKSIKIPKJEPEQNRDRWGRVDTVSKPPBEPVLKEGSPBS ANTIFCSNINGSVHW, VERVOUGLUNG SEERKEKKRKSKHEDSSR SEERKSIKIPKJEPEQNRDRWGRVDTVSKPPBEPVLKEGSPBS ANTIFCSNINGSVHW, VERVOUGLUNG SEERKEKKRKSKHEDSSR SEERKSIKIPKJEPEQNRDRWGRVDTVSKPPBEPVLKEGSPBS ANTIFCSNINGSVHW, VERVOUGLUNG SEERKEKKRKSKHEDSSR SEERKSIKIPKJEPEQNRDRWGRVDTVSKPPBEPVLKEGSPBS ANTIFCSNINGSVHW, VERVOUGLUNG SEERKEKKRKSKHEDSSR SEERKSIKIPKJEPSQUPTRAWVIERVYPKWPCWSSDPOL EVHTKINTRGARETHUPPFBRQFRRRDGRAWVIERVERVEKSPBOL EVHTKINTRGARETHUPPFBRQFRRRDGRAWVIERVERVEKSPBOL NTOPEGTNAGEVASLSSTEIRHSGGRRTISSGREDPVKIAW KTARARKSLPASITHHGSSLDLCKKOMSPVVKIERVPALQMATC DGKFIDGFYYSTKGIGNKTEISVRGQDELIISTPNORNEKPPGS VSSPEATSGRIGSVEKKQORRSITENSEERSTEVPKKKIKKE OVOFLHVES  OVFLHVES  1911  MINTGERETATGISPQAAQEKDGIVTVKVEEEDEEDHMWGQDSTL OPPPPPPPPFFRORFRRPCVONTFGPREALSRIKKELCHOMERPE INTRGLIELLJULROPISIIPRELQVWLGEVRPSGEERSTLLLE DLELDLSGGOVPGOVIGPPMLARGWPLDPVQSSSFPLHHEAT QSHFKHSSKRRRLIGSBRAGRETIGRSOKEFGEKDOP GATGEROOKNPEKTKREKRUSGPARMISLSDRINGENVASAP PQGGERNRENEESTSKAFTSEDSASRGETTGRSOKEFGEKDOP GATGEROOKNPEKTKREKRUSGPARMISLSDRINGENVASAP PQGGERNRENEESTSKAFTSEDSASRGETTGRSOKEFGEKDOP GATGEROOKNPEKTKREKRUSGPARMISLSDRINGENVASAP PQGGERNRENEESTSKAFTSEDSASRGETTGRSOKEFGEKDOP GATGEROOKNPEKTKREKRUSGPARMISLSDRINGENVASAP PQGGERNRENEESTSKAFTSEDSASRGETTGRSOKEFGEKDOP GATGEROOKNPEKTKREKRUSGPARMISLTHRINGENVACKKY  11HTGERPYECSSCGKAPNKSYLLIHRRINGTREPYKCTKCCK VAFTESSTLTLHRH HARRERSEYPSPALDAFGALKKCV  SPSPHITPVHPPPEHSAACAPARATCCHVTGEBERKSTEPLERINGARROG GROULSAGGGEVARDAGOKGRKGARFERER INRARROG GROULSAGGGGFVANGEROOKINGERGEPERMISEGON KREMGEFIEKKKONGOIISLAMARGGRESSERGKFNNEEEV VLANLRGRIELOMFHEROOKINGAAMTGGRESSERGKFNNEEEV VLANLRGRIELOMFHEROOKINGAAMTGGRESSRGKFNNEEEV VLANLRGRI		5022	<u> </u>		NSH
1924 274 2146 EIGH IGNEYWRKAYONDOPCKIOEKIA OLELENKELRELIS ISSESIORI CREGWERKAYOVDDOPCKIOEKIA OLELENKELRELIS ISSESIORI CREGWERKAYOVDDOPCKIOEKIA OLELENKELRELIS ISSESIORI CREGWERTASOAIK EKKYKDAGAGEWISLESCKOSWETO SINILISLITPTSVRIM PLITTYTLIKMVARHIMKLICSKAS TOLOOKI PLHSOMGIHO SVCMKLKENTSHI ISIIMGOPMALVOLETLAPLTI II OKPOTOD HMKFWKINLPHSHILTPSVPQTV I PKKTGSPEI KLKITKTIONG RELFESSLCGDLIMWQASS \ O'NOS I SERKEKKKSNNHDSSR SEEKSHKIPKLBPERONRPUTVSEKPREPPULKEGSPS ANTI CSINGSVWI \ FREQVEDLWSK WITTFWRPCMVSSDPOL EVHTKINTRGARESHVQFSSNOGREAWHERWERKGHKQYEE LIABATKQASNHSEKOKI RKPRPORERAWHERWERKGHKQYEE LIABATKQASNHSEKOKI RKPRPORERAWHERWERKGHKQYEE LIABATKQASNHSEKOKI RKPRPORERAWHERWERKGHKQYEE LIABATKQASHSEKOKI SIKTRESSEKSTEVVPKKKIKKE NTOPEGTNAGEVASSLSSTEIRRISGRHTSAEEERPPVKI AN KTAAAAKSLPASI THMKUSLIJOKKOMSPVVKI TEOVALONATG DGKFIDGFYYSTKGIGNKTEISVROODEL IISTPNORNEKPTOS VSSPEATAGSTGSVEKKORRS I RTRSESEKSTEVVPKKKIKKE OVGFLHVES  1911 MYMTAGEREATGLE PQAAQEKINGI VIVKVEEEDEEDHMWGODSTI ODTPPPPPP BI FRORFRRPCYONTFGPREALSKLKELCHOWLRPE INTKEQILELIVLROFUSI LIPKELOWLOEYRPDSGEEAVTILE OLELLISGGOVPGOVHGFEMLAGRUND LIPVORGSSFPLIHEAT QSHFKHSSKKPILLQSRALPAAH PAPPHEGSPRODAMASALFT ANSOMMVKI EDMANUS LILEEBEGOVARGENTI TORROFREKOK GLGRSFSLSSNFTTPBEVPTGTTKSHRCDECGKCFTRSSSLIRIK I HITGEVPYECSGCKAF SINS NILVHQRI NITGRERPEKOK GLGRSFSLSSNFTTPBEVPTGTTKSHRCDECGKCFTRSSSLIRIK I HITGEVPYECSGCKAF SINS NILVHQRI NITGRERPEKOK GLGRSFSLSSNFTTPBEVPTGTTKSHRCDECGKCFTRSSSLIRIK I HITGEVPYECSGCAFPNINSYLLHRRVHTREKPYKCTKCCK AFTRSSTLTHIMHI HARERASPSALDAFGAFLKSCU  DREMLKROSGOPSPPAT/CEPDAPPVVARPERVATORERRISGRAR KREJEFTEKSKOKOOLI SIMKARQMKROSKELLERINBARGO WANGARADINKARBGORSI SWPRAQVITYDAAKYGI PLA YKKYDKALHIKHREPENGOL KARARQWSEFILOR KREMMONKARBGORSI SWPRAQVITYDAAKYGI PLA KKESALGARARGHMI ILONAAMYGGRPSSROGYENYHHAI FDO MOQORAEDNEAXWARSI YRGCLERKKARANSEGCOSSERADM RKK\1ESLKAHANARAAUKSOLERKKRANHSEGCOSSERADM RKK\1ESLKAHANARAAUKSOLERKKRANHSEGCOSSERADM AKGK\1ESLKAHANARAAUKSOLERKKRANHSEGCOGSERADM AKGK\1ESLKAHANARAAUKSOLERKKRANHSEGCOGSERADM AKGKSOLVAPPIGOORISCUSTANAANGEDEKKUNDENLAQEDEKOKON		3323	137	638	QLCGRRGORFRTS I KRMHDI * PTCDYTTY
DELEDINGLIES LISSES LOAR KENSEMTAS QAIK  QUELENKELRELLS ISSES LOAR KENSEMTAS QAIK  EKKEKKDAGABGWISLS LSCKGSWETG SINHLINSLIT PITT-VILKEM YARRHENKLLIC STRY TOLOGK IT HISOMGHHO  SVCHIKLRENTSHII SIIMGO PMALVOLETLAPLTIII OKROTOD  HIKKWINDLINSH LTDS VOR TULL STRY TILL TILL TILL TILL TILL TILL TILL TIL					QUENRELWISLEEHODALELIMONATAL TILLSQENTQIRDL
274  2146  EKGKVKDAGAEOWISISLSCKORWETO PSNIKINSITPTSVRM PLITTVTLIKMVARHHMKLICSKAPSTOLQOKI FLHSQMGIHHO SUCMKLKENTSHI ISILMGAPMALVOLETLAPLI II IOKPOTOD HMKFWKNILPHSHHLTPSVPQTV I PKKTGSPE IKLKITKTIONG RELPERSLCGDLUMPUAGS \( \) O'NGS ISSRKEKKKISNIHDSSR SEERKSIKIPKLEPEQURPUNERVDTVSEKPREPPULKBGSPES ANT IFCSNIGSVUW\RKFQVGDLVMSKVGTYFWWPCMVSSDPOL EVHTKINTGABRYHVQFSROGREAWHEKFWEKYGKGKQVE LLABATKQASNHSEKQKIKRPRPORERAWHEKFWEKYGKGKQVE LLABATKQASNHSEKQKIKKPRPORERAWHEKFWEKYGKGKQVE LLABATKQASNHSEKQKIKRPRPORERAWHEKFWEKYGKGKQVE LLABATKQASHSEKGKIRKPRPORERAWHEKFWEKYGKKYASE ANT IFCSNIGSVEKKQORSISTEIRRHSQRRHTSAEEEEPPVKIAW KTARAAKSLPASITHKGSIDLQKCIMSPVVKIEQVPALQNATG DGKRIDOFVYSTKGIGNITEISVGRPALISTPMORMEKPTOS VSSPEATISGTGSVEKKQORRSISTTRSESSKSTEVVPKKKIKKE QVSPFLIVES  216  1911  MMTAESREATGLSPQAAQEKBGIVVVKVEGDEEDHMWQQDSTL QDTPPPPPPIFFRGRFRFRCYONTTGPREALSRLKELCHQWLRPE INTKEGILBLLVLROPLSIPKELQWLOEYRPDSGEBAVTLLE DLELLLSGQOVPGQVPGFRRFRCYONTTGPREADLSRLKELCHQWRPE INTKEGILBLLVLROPLSIPKELQWLOEYRPDSGEBAVTLLE DLELLLSGQOVPGQVPGFRRFRCYGONTTGPREADLSRLKELCHQWRPE INTKEGILBLLVLROPLSIPKELQWLOEYRPDSGEBAVTLLE QSHFKHSSRKPRLLQSRALPAAHIPAPPHEGSPRDQAMASALFT ANSQAWVKI EDMAVSILLEEWGCONLARRNLSRDMRQENYGSAP QGGERMENNERSTKAETSEBSKGETTGRSQCKFFOKRODE GKTGGRQKNPEKTTRKEKBDSOPAJGKDKKTITGEKGPREKKK GLGGRSFSLSSNFTTPEEVPTOTKSHRCDECKKFTRSSSLIRIK IHTGEKPYECTSCCKCTRSSSLIRIK IHTGEKPYECTSCCKAFNSSNILIHQRIHGREPHEKKK CKGAFSOSSD\LTKHQ RITTGEKPPECNE CKAFFSSNILIHQRIHGREPHEVYKCTKCK \			Į i	•	LKAHOSHSAFIFSOIDBIODAG
274  2146  EKGKVKDAGAEOWISISLSCKORWETO PSNIKINSITPTSVRM PLITTVTLIKMVARHHMKLICSKAPSTOLQOKI FLHSQMGIHHO SUCMKLKENTSHI ISILMGAPMALVOLETLAPLI II IOKPOTOD HMKFWKNILPHSHHLTPSVPQTV I PKKTGSPE IKLKITKTIONG RELPERSLCGDLUMPUAGS \( \) O'NGS ISSRKEKKKISNIHDSSR SEERKSIKIPKLEPEQURPUNERVDTVSEKPREPPULKBGSPES ANT IFCSNIGSVUW\RKFQVGDLVMSKVGTYFWWPCMVSSDPOL EVHTKINTGABRYHVQFSROGREAWHEKFWEKYGKGKQVE LLABATKQASNHSEKQKIKRPRPORERAWHEKFWEKYGKGKQVE LLABATKQASNHSEKQKIKKPRPORERAWHEKFWEKYGKGKQVE LLABATKQASNHSEKQKIKRPRPORERAWHEKFWEKYGKGKQVE LLABATKQASHSEKGKIRKPRPORERAWHEKFWEKYGKKYASE ANT IFCSNIGSVEKKQORSISTEIRRHSQRRHTSAEEEEPPVKIAW KTARAAKSLPASITHKGSIDLQKCIMSPVVKIEQVPALQNATG DGKRIDOFVYSTKGIGNITEISVGRPALISTPMORMEKPTOS VSSPEATISGTGSVEKKQORRSISTTRSESSKSTEVVPKKKIKKE QVSPFLIVES  216  1911  MMTAESREATGLSPQAAQEKBGIVVVKVEGDEEDHMWQQDSTL QDTPPPPPPIFFRGRFRFRCYONTTGPREALSRLKELCHQWLRPE INTKEGILBLLVLROPLSIPKELQWLOEYRPDSGEBAVTLLE DLELLLSGQOVPGQVPGFRRFRCYONTTGPREADLSRLKELCHQWRPE INTKEGILBLLVLROPLSIPKELQWLOEYRPDSGEBAVTLLE DLELLLSGQOVPGQVPGFRRFRCYGONTTGPREADLSRLKELCHQWRPE INTKEGILBLLVLROPLSIPKELQWLOEYRPDSGEBAVTLLE QSHFKHSSRKPRLLQSRALPAAHIPAPPHEGSPRDQAMASALFT ANSQAWVKI EDMAVSILLEEWGCONLARRNLSRDMRQENYGSAP QGGERMENNERSTKAETSEBSKGETTGRSQCKFFOKRODE GKTGGRQKNPEKTTRKEKBDSOPAJGKDKKTITGEKGPREKKK GLGGRSFSLSSNFTTPEEVPTOTKSHRCDECKKFTRSSSLIRIK IHTGEKPYECTSCCKCTRSSSLIRIK IHTGEKPYECTSCCKAFNSSNILIHQRIHGREPHEKKK CKGAFSOSSD\LTKHQ RITTGEKPPECNE CKAFFSSNILIHQRIHGREPHEVYKCTKCK \	- 1				OLELENKEL PELL CICCOST AND THE MINISTER OF THE PROPERTY OF T
PLITTVTLLKYARHHYKLICSKAFSTGLOGKTFLKSOGIHMO SVCMKLKRNTSHIISILMGOPMALVOLDETLAPITIIIOKPOTOD HMKWFWANLPLKSHLITESVPOTVIPKKTGSBET ILKLITTTIIOM RELFESSLCGDLLMBVQASE \Q*NOSISEKKEKKKKNKHOSSR RELFESSLCGDLLMBVQASE \Q*NOSISEKKEKKKKNKHOSSR SEERKSHKIPKLEPEEDMIPBNERVOTVSEKPREEBVIKEGSFSS ANTIFCSNNGSVHW\FKFQVGDLVMSKVGTYFHWPCMVSSDPQL EVHTKINTRGAREYHVQFFSNQFERAWVHEKAVESVKGHKQYEE LLAEATKQASNHSEKKKIKRPRPORERAWVHEKAVESVKGHKQYEE LLAEATKQASNHSEKKKIKRPRPORERAWVHEKAVESVKGHKQYEE LLAEATKQASNHSEKKKIKRPRPORERAWVHEKAVESVKGHKQYEE LLAEATKQASNHSEKKKIKRPRPORERAWVHEKAVESVKGHKQYEE LLAEATKQASNHSEKKKIKRPRPORERAWVHEKAVESVKGHKQYEE LLAEATKQASNHSEKKKIKPRPORERAWVHEKAVESVKGHKQYEE LLAEATKQASNHSEKKKISVASKTEVKKTRVPRSVL NTOPEQTNAGEVASSLSSTSI RSHSGORRIJGAAREEE KTAAARKSLPASITMHKGSLDLQKCNMSPVWIEQVPALQNATG DKKFIDGFVXSTKGIGNKYEIVGCOPLILISTPNQRNEKETOS VSSPEATSGSTGSVEKKQQRRSIRTRSESEKSTEVVPKKKIKKE QVGPLHVES  DGTPPPDPBIFRQRFRRFCYQNTFGPREALSRLKSLCHOHLRPE INTKRGILBLLVLEOPLSILDFELQVHLQEVPDSGEEAVTLLE DLELLLSGQOVPCOVHGPEMLARGWPLDPVOESSSPDLHHEAT QSHFKISSKNPERLUGSRALPANIPAPHEGSPRQAMASALET ADSQAMVKIEDMAVSLILEEMGCQNLARRNLSRNNRGENVGSAP PQGGENRINENEESTSKAETSEDSASRGTTGRSQKEFGEKRDQE GKTGERQQKNPEESTSKAETSEDSASRGTTGRSQKEFGEKRDQE GKTGERQQKNPEESTSKAETSEDSASRGTTGRSQKEFGEKRDQE GKTGERQQKNPEESTSKAETSEDSASRGTTGRSQKEFGEKRDQE GKTGERQQKNPEESTSKAETSEDSASRGTTGRSQKEFGEKRDQE GKTGERQQKNPEESTSKAETSEDSASRGTTGRSGKFEEKOK GLGRSFSLSSNFTTPEEVPTTTKSHRCDCCKCFTRSSSLIRHK IIHTGEKPYECSECGKAPTSINSVILLHRRVHTRKPYKCTKCGK \AFTRESSILTHHRIHAHARERASEYSPASLDAFGAFKKCCK CCKAFSHSSNILHHQRIHGGKPPLCTCHCCKCFTFRSSHS  SDEPHTPVHPPPEHSAACCAPATCCPPPRSSMS  KRIEGEFIEKEKKQKDQIISLMKAEQMKRQKERLERINBAREQG WRNILAGGSGGGGFAPATCCPPPRSSMS  KRIEGEFIEKEKKQKDQIISLMKAEQMKRQKERERKISEERAR KRRLEFIEKEKKQKDQIISLMKAEQMKRGKERLERINBAREQG WRNILAGGGGGGEVAPPLISGTAPSSFSRGGKPRNKEEEV YLARLRQIRLQNFNERQUITGMLARAWGGRESGGGSEEADM RRKK\1ESLKAHANARAAVLKEQLEKKRAYEREKWWEEHLV AKGWSSDVSPPJEQGHTGGSSOKQMSVIJVTSALKEVEVDS SLIDTTETSEEMKKTNALSSKREILERBLKRQUEVDS SLIDTTETSEEMKKTNALSSKREILERBLKRQUEVDS		5924	274	2146	**************************************
SVCMKLRPNTSHIISIMGADLVQLETLARDTIIIORYOTOD HMKFWKMLPLHSHHLTSUNQDTVIPKTGSPBIKLKITKTIONG RELFESSLCGDLLMEVQASS 40 MOSIESRKERKKNKHOSS SERKSHKIPKLPPEBOMR DNERVDTVSEKPREFEVLKEGSPS ANTIFCSNIGSVHW FRFQVODLVMSKCTYPHWPGWSDPQL EVHTKINTGAREYHUQFFSNOFERAWVHEKRVREVKEHKQYEE LLAEATKQASNHSEKGKIRKPRPQRERAWVHEKRVREVKEHKQYEE LLAEATKQASNHSEKGKIRKPRPQRERAWVHEKRVREVKEHKQYEE LLAEATKQASNHSEKGKIRKPRPQRERAWHEKRVREVKEHKQYEE LLAEATKQASNHSEKGKIRKPRPQRERAWHEKRVREVKEHKQYEE LLAEATKQASNHSEKGKIRKPRPQRERAWHEKRVREVKHKKYER REERIEQYTTIJIOKPEBALSQAKKSVASKTEVKTKTRRPSVL NTQPEQTNAGEVASSISSTEIRRIGGRRHTSABEEEPPPVKIAW KITAAARKSLPASITMIKGSLJOKCMMSPVVKIRGVPALQMATG DGKFIDGFVXSTKGIGNKTEISVRGQDRLIISTPRQREKEKTOS GKFIDGFVXSTKGIGNKTEISVRGQDRLIISTPRQREKEKTOS GKFIDGFVXSTKGIGNKTEISVRGQDRLIISTPRQREKEKTOS GVSPLATSGTGSVEKKQQRRSIRTRSESEKSTEVVPKKKIKKE QVGPLHVES  1911 MMTAESREARGLSPQAAQEKOGIVVVKVEEDEDEHMWGDDSTL ONTREGILBLLVLEOPLSILPRELOVWLOEYRPDSGEBAVTLLE LLELLSGQOVPQOVHEPPEMLARRULEPHDOVGSSSPDLHHEAT OSHFKHSSRKPRLLQSRALPAAHIPAPHESPRDQAMASALFT ADSQAMVKIEDMAVSLILEEWGCOMLARRNLSRDNRGENGSAP PQGGENRIENNESSTSKATISDSARGETTGRSQKEFGERRODE GKTGERQOKNPEEKTRKEKRDSGPAIGKKKTITGBRGPREKGK GLGRSFSLSSNFTTPEEVPTGKSRCDCEGKAFTSSSLIRHK IIHTGEKPYECSECGKAFNSTVLILHRRVHTRERPYKCTKCK (AAFTRSSTLITHHIPIHHAERASEYSPASLDAFGAFLKSCV CKARSHSSNLILHQRIHSGEKPYECNECKARSOSSDLITKHO RIHTGEKPYECSECGKAFNSTVLILHRRVHTREPYHCTKCGK (AAFTRSSTLITHHIPIHHAERASEYSPASLDAFGAFLKSCV SPSPHHTPVHPPPPEHSAACPAPATCCPPPRSSMS  KHPSKFGSGALYQLKRPASGONSISWHPAQKTTKRPAKKGIPLA YKKYGDKKLHEKKPLQKHKOAHOTPEKRWITEPRAKITEPAA KRRLEFIEKEKKORDQIISLMKAEQMKRGBKERLERINBARROC WRNULSAGGSGEVAPLAFGGMGILTBSSPSSRGOVEHWHAIFDO MQQQRAEDNERKWRBITGRGLDPRISSRSGGKERADM RRKK\TESLKAHANARAAVLKEQLERKRAVERSKKWEBHLV AKGYGSDVSPPLGQGHTGGSPSSGRGKPRIKEEEV YLALLRQIRLONPNERQUIKAKLGCKKEANNSEGGGESEEDDM RRKK\TESLKAHANARAAVLKEQLEEKRRAVERSKKWEBHLV AKGYGSDVSPPLGQGHTGGSSCOKGMONSIVTSALKEVEUDS SLIDTTETSEEMKKTNNILSSKREILERRLKRQUERUNDS SLIDTTETSEEMKKTNNILSSKREILERRLKRQUENDS	[				DI TERVET I VALLE DE LE CHESTE DE SUPERIOR DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL DE LE CONTROL D
HMKFWKRLDPHSHHLTPSVPOTVIPKKTGSPEIKLKITHTIONG RELFESSLCGDLLMBVQASE Q*NOSIESKEKRKKSNKHDSSR RELFESSLCGDLLMBVQASE Q*NOSIESKEKRKKSNKHDSSR SEERKSHKIPKLPEPEONRPHORVOTVSEKPREEPVLKEGSPSS ANTIFCSNNGSVHW\PKPQVGDLVWSKVGTYPWWPCMVSSDPQL EVHTKINTRGAREYHVQFFSNQFERAQMVIEKKVRSDPQL EVHTKINTRGAREYHVQFFSNQFERAQMVIEKKVGKYEE LLAEATKQASNHSEKKKIRPPRQRBRAQMVIGIAHAEKALMT REBRIEQYTFIYIDKOPERALSQAKKTEVKKTRPRSVL NTQPEQTNAGEVASSLSSTEIRHSGORHTSABEEEPPPVKIAW KTAAARKSLPASITMHKGSLDLQKCNMSPVWRIEQVPALQMATG DKFIDGFVYSTKGIGNKTEISVRGGDBLIISTPMQRMEKPTQS VSSPEATSGSTGSVEKKQQRRSIRTRSSESKETVVPKKKIKKE QVOFPLHVES  216  1911 MMTMEGREATGLSPQAAQEKDGIVTVKVEEEDEEDHMMGQDSTL ODTPPPDPPEIFRQRFRRPCYQNTFGPREALSRLKELCHQMLRPE INTREQILELLVLEQFLSILBRELQVWLOEVRPDSGEBAVTLLE DLELDLSGQOVFCQVHGEPMLARGMVPLDPVQESSFDLHEAT QSHFHISSKKPHLLQSRALPAAHIPAPHEGSPRDQAMASALFT ADSQAMVKIEDMAVSLILEBRAGGKKTITGBRGREKGK GLGRSFSLSSNFTTPEEVPTTTKHRCDECCKCFTRSSSLIRIK IIHTGEKPYECSECGKAP\SLNS\NLVLHORI\HTGEKPHECNE GKAGERQOKNPEDEKTRKEKRDSGPAIGGKKTITGBRGREKGK GLGRSFSSSNILHQRIHGSPYECSECGKAFGOSSDVLTKHQ RIHTGEKPYECSECGKAP\SLNS\NLVLHORI\HTGEKPHECNE CKARSHSSNILLHQRIHGSEVECCCKAFSOSSDVLTKHQ RIHTGEKPYECSECGKAPNRNSYLILHRRVHTREKPYKCTKCGK \AFFTESSTLITHRIHARPHASESFSPASIDAFGAFLKSCV  5926  2 233 DRCLMLKQGSQPGSFPAT/CEPPAPPVQAPCGSCPEPFGAHEP SDSPHITVHPPPPHSAACPAPATCCPPRSSMS  KIFFSFSQALYOKURRPASGOTISMGNETKYPAKYGIPLA YKKYGDKKLHEKKBLQKHKQAHQTPRKRVNTGEERKLSEBAAR KRRLEFIEKEKKGXQDIJGKRAFGSGNOZHHAIFDQ MQQQRABDNEKWRBITGRGLPERGSSRGGKYRKBEEV YLAHLGQIRLQNFNRQGEFGSGFOKOGLAVERAKOVEEPLQR KREMQNKARAEGHMGILGNLAKRGEKKEANISEGGGESEADM RRKK\IESLKAHANARAAVLKCOLLEKKRKAYERSKKWEBHLV AKGYKSDVSPPLGGGHTGGSPSKQQMRSVISYTSALKEVUDS SLIDTTETSEEMKKINNLKAQDKERKREAYERSKWWEBHLV AKGYKSDVSPPLGGGHTGGSPSKQQMRSVISYTSALKEVUDS SLIDTTETSEEMKKINNLKAQDGURKNOSHENDEN	- 1				1 * ## 1 * V I DUNITVAKHHINKLI CSKARSTOI OOMI EI MOOMOTIIII
RELFESSLICEDILINFUQASE\Q*NOSISERKEKKKSNKIDSRS SEEKKSHXIPKLEPEQORPMERUDTVSEKPREEPVLKEGSPSS ANTIFCSNINGSYHW\FKDOGLVWSKVGTYFWWPCMYSSPOL EVHTKINTRGAREYHVQPFSNQPERAWHEKKVEFYKGHKQYEE EVHTKINTRGAREYHVQPFSNQPERAWHEKKVEFYKGHKQYEE LLAEATKQASNHSEKQKIRKPRPGREAQWDIGIAHABKALKMT REERIEQYTFIYIDKQPEALSQAKKSVASKIEVKKTREPRSVL NTQPEQTNAGEVASSLSSTEIRAHSQRRHTSAEEEBPPVKIAW KTAPARKSLPASITMHKGSLDLQKCNMSPVVKIEQVFALQNATG DGKFIDQFVYSTKGIGNKTEISVRGQDELIISTPNQRNEPTQS VSSPEATSGSTGSVEKQQRSIRTRSESEKSTEVVPKKKIKKE QVGFLKVES  1911 MMTAESREATGLSPQAAQEKDGIVIVKVEEEDEEDHMWGQDSTL QDTPPPDPE IFRQRFRFCYQNTTGBREALSRLKELCHQMLRPE INTKEQILELLVLEQFLSILPKELQWLQFYPDSGEBAVTLLE DLELLDSGQQVFGQVHSPEMLARKGMVLDPVQESSSFDLHHEAT QSHFKHSSRKPRILQSRALDAAHIPAPHEGSPRDQAMASALFT ADSQAWVKIEDMAVSLILEEWGCQNLARRNLSRDNRQFRYGSAF PQGGENRENESTSKAETSEDSASRGETTGRSQKSFGEKRDQB GKTGERQQKNPEEKTRKEKRDSGPATGKNKTTTGBREPEKGK GLGRSFSLSNFTTPEVPTGTKSHRCDECGKCFTRSSSLIRHK IIHTGEKPYECSECGKAFNSSNSILIHRRVHTREKPYKCTKCGK \AFTESSTLITHHRIHARERASEYSPASLDAFGAFLKSCV \AFTESSTLITHHRIHARERASEYSPASLDAFGAFLKSCV \AFTESSTLITHHRIHARERASEYSPASLDAFGAFLKSCV \AFTESSTLITHHRIHARERASEYSPASLDAFGAFLKSCV  SDSPHHTPVHPPPEHSAACPAPATCCPPPRSSMS  SDSPHHTPVHPPPEHSAACPAPATCCPPPRSSMS  KREMEFSKEKKGNDQIISLMKAQAHQTPEKRVNTGEERRKISEBAAR KREMEFIEKEKKGNDQIISLMKAQAHQTPEKRVNTGEERRKISEBAAR KREMEFIEKEKKGNDQIISLMARAQMKRQBKERLERINRAREQG WRNVLSAGGSGEVKAPPLGSGGTIAPSSFSRGQVEFNHAFFOQ MQQRAEDNEAKWREITGRGGDTSTAPSSFSRGQVEFNHAFFOQ KREMANKARAREGIMSGILQHLAAMYGGRPSSRGGVEFNKEEV VLARLRGIRFLICHULAAMYGGRPSSRGGVEFNKEEV VLARLRGIRFLICHONLAAMYGGRPSSRGGVERNEEEV VLARLRGIRFLICHONLAAMYGGRPSSRGGVERNEEEV VLARLRGIRFLICHONLAAMYGGRPSSRGGVERNEEEV VLARLRGIRFLICHONLAAMYGGRPSSRGGVERNEEEV VLARLRGIRFLICHONLAAMYGGRPSSRGGVERNEEEV VLARLRGIRFLICHONLAAMYGGRPSSRGGVERNEEEV VLARLRGIRFLICHONLAAMYGGRPSSRGGVERNEEEV VLARLRGIRFLICHONLAAMYGGRPSSRGGVERNEEEV VLARLRGIRFLICHONLAAMYGGRPSSRGGVERNEEEV VLARLRGIRFLICHONLAAMYGGRPSSRGGVERNEEEV VLARLRGIRFLICHONLAAMYGGRPSSRGGVERNEEEV VLARLRGIRFLICHONLAAMYGGRPSSRGGVERNEEV VLARLRGIRFLICHONLAAGPLEKKVWEEHLU AKGVKSDUSSPPLGHERGRSPSKGOLAVERAKAYGEEKKKWEEHLU LSDTFEIN			j J		1 - COMPARTION ISSUED PMAINTING TO THE TOWNS OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY
SEERKSHKIPKLEPEEGNENENDITUSEKPREEPVILEGSPSS ANTIFCSNNGSUHW\FKPQVGDLVWSKVGTYPWWPCMVSSDPQL EVHTKINTRGARETHVUPFSNOPERAWVHEKKPKEYKGHKQYEE LLARATKQASNHSEKOKIRKPRPGRERAQWUIGIAHAEKALKMT REERIEQYTFIYIDKOPEEALSQAKKSVASKIEVKKTREPRSVL NTOPEQTNAGEVASSLISETRIHGKREHTSAEEEEPPPWKIAW KTAAARKSLPASITMHKISJDLOKKIMSPVUKIEOVPALQNATG DGKFIDGFVSTKGIGKKTEISVRGQDRLIISTPNORNERPTOS VSSPEATSGGTGSVEKKQQRRSIRTRESESKSTEVVPKKKIKKE OVGFLHVES  5925 216 1911 MMTAESEEATGLSPQAAQEKDGIVIVKVEEEDEEDHMWGQDSTL QDTPPPDPEIFRQRFRFCYONTFGPREALSRLKELCHGWLRPE INTKEGILELLULEQFLSILJKELQVWLQEYRPDSGEEAVTLLE DLELDLSGQQVFGQVHGPEMLARGMVPLDPVGSSSFDLHHEAT QSHFKHSSRKPRLLGSRALPAAHIPAPPHEGSPRDQAMASALFT ADSQAWVKIEDMAVSILLEEWGCQNLARRAILSDNNGGPWGSAF PQGGENNENEESTSKAETSEDSASRGETTGRSQKEFGEKRQE GKTGGERQOKNPEEKTRKEKRDSOPAIGKDKKTITGBRGPERKGK GLGRSFSLSSNFTTPEEVPTGTKSHCDDEGKGFTKSSSLIRHK I IHTGEKPYECSECGKAF\SLMS\NLVLHQRI\HTGEKPFEKCME CKKAFSHSSNLILHQRIHBGERFYECNGECKAFSOSSD\LTKHQ RIHTGEKPYECSECGKAFNRNSYLILHRRWHTREKPYKCTKCGK \(\frac{VaffrsstilhrhRiharpraseyyspasldafgaflakscv}{VaffrsstilhrhRiharpraseyyspasldafgaflakscv}}  5926 2 233 DRCMLKQGSQPGSPPAT/GEPAPPVVQAPCOSCPEPFGAHEP  SDSPHITPVHPPPEHENAACPAPATCCPPPRSSMS KRIPSKFGSQALYOLKRPASGNISVMPAQKITKPARKYGIPLA YKKYGDKKLHEKKPLQCKHKQAHQTPEKKNNTGERKKKSEBAAR KRRLEFIEKEKKQKDQIISLMKARGMKQGKERLERINRAREOG WRNVLSAGGSGEVKAPFLIGSGGTIAPSSFSSGQYEFNHAIPDO MQQQRAEDNEAKWRGIIGIGGDSSKQMKROKERLERINRAREOG WRNVLSAGGSGEVKAPFLIGSGGTIAPSSFSRGQYEFNHAIPDO MQQQRAEDNEAKWRGIIGIGSPSKQMKQGKRRLERINRAREOG KREMQNKARAREGINGIIGNAMYGGRPSSRGGVRRNKEEEV YLARLRGIRLONPERGQOIKAKLRGRKGEAHHSGOGGSEPADM RKKY\IESLKAHAMARAAVLKEQLERKKWARFERKKWEEHLU AKGVKSDVSPPLGGHTGGSPSKQMKRYSTVSTALKEWGVDS SLIDTRETSEEMGKTNNAISKKREILKRLEENLKAQCLEKKQM LSDTFEITVELPEAKERUSSPBYKURECHECKUNN	- 1				TANKE WINDEDROUGHLIPS V POTVI DE ETER ETER ETER ETER
ANTIFCSNNGSVHW, VEROUGDLYWSKUGTYEWHOWMSSDPOL EVHTKINTRGAREYHVOFFSNOFERAWVHEKRVREYKGHKQYEE LLABATKQASNNSEKUKYRRPORERAWUHEKRVREYKGHKQYEE LLABATKQASNNSEKUKYRRPORERAWUHEKRVREYKGHKQYEE LLABATKQASNNSEKUKYRRPORERAWUHEKRVREYKGHKQYEE REERIEQYTFIYIDKOPEEALSQAKKSVASKTEVKKTRERRSVL NTOPEQITNAGEVASSLSSTEIRHSGRHTSAEEEBPPWKIAW KTAAARKSLPASITHHKGSLDLOKCMMSPVKIEQVPALQNATG DGKFIDGFVYSTKGIGNTTEISURGQDRLIISTPNORNEKPTQS VSSPEATSGSTGSVEKKQORRSITRTSESEKSTEVVPKKKIKKE OVGPLHVES  1911 MMTAESREATGLSPQAAQEKDGIVIVKVEEEDEEDHMWGDSTL QDTPPPPDEIFRORFRRCYONTFGREALSRLKELCHOWLREE INTREQILELLULEQFLSILPKELQVWLQEYPDDSGEEAVTLLEE DLELDLSGQVVPGOVHGPEMLARGWPIDDPVQESSSFDLHHEAT QSHFKHSSRKPRLLQSRALPAAHIPAPPHEGSPRDAMASALFT ADSQAWVKISDMAVSLILEEWGCONLARRNLSRDNRQENYGSAP PQGGENRNEMESTSKAETSEDSASRGETTGRQKEFGEKRDQE GKTGERQQKNPEEKTRKEKRDSGPAIGKDKKTITGERGFREKGK GLGRSFSLSSNFITPEEVPTOTKSHRCDECGKFTRSSSLIRHK IIHTGEKPYECSSCGKAF\SINS\NLULHQRI\HTGEKPHECNE CGKAFSHSSNLILHQRIHSGEKPYECNECGKAFSGSSD\LTKHQ RHHTGKEYPECSSCGKAF\SINS\NLULHQRI\HTGEKPHECNE CGKAFSHSSNLILHQRIHSGEKPYECNECGKAFSGSSD\LTKHQ RHTGEKPYECSECGGAFNNSYLILHRRVHTREKPYKCTKCGK AFTRSSTITLHHRIHAREASFSYPABLDAFGAFLKSCV  5926 2 233 DRCIMLKQGSQPSPPAT/CEPPAPPVVQAPCQSCPEPFGAHEP SSPHHTPVHPPPEHSAACPAPTCOPPPRSSMS  KHFSKFGSQALYQLKRPASGQNISWMPAGKITKPAKYGIPLA YKKYGDKLHEKKPLQKHKQAHOTPEKRVNTGEERRKISEBAAR KRRLEFIEKEKKOKDQIILGNLAAMYGGRPSSSRGGKPRNKEEV YKKYGDKLHEKKPLQKHKQAHOTPERKVNTGEERRKISEBAAR KRRLEFIEKEKKOKDQIILGNLAAMYGGRPSSSRGKPRNKEEEV YLAALLRQIRLQNFNERQQIKAALRGEKKELERINRAREQG WRNVLSAGGSGEVKAPFLGSGTIAPSSPSSRGKYPRKEEEV YLAALLRQIRLQNFNERQQIKAALRGEKKEANFSEGGGSEEADM RRKK\IESLKAHANARAAVLKEQLEKKRAYSREKKWEEHLV AKGVKSDUSPPLGCHETGGSPSKQQMSVISTSTALKEVUDS SLIDTRETSEEMQKTNALSSSRELLRRLNEDLKAQGUEEKKKWE SLIDTRETSEEMQKTNALSSSRELLRRLNEDLKAQGUEEKKKON SLIDTRETSEEMGKRNAISSSSRELLRRLNEDLKAQGUEEKKKN	- 1		[		T NOOT DOODLEGUINKVOASE \ O*NOQ TECHURUNUNG I
EVHYKINTRGAREYHVQFFSNQFERAWHERVRUEYKGHKQYEE  LLAEATKQASNISEKGKIRKPRPQRERAQWDIGIAHAEKALKMT REERIEQYTFIYIDKQPEEALSQAKKSVASKTEVKXTRRPRSVL NTQPQTNAGEVASSLSTEIRHSGRRHTSAEEEEPPPWKIAW KTAAARKSLPASITMHKGSLDLJKKNMSPVVKIEQVFALQNATG DGKFIDQFVSTKGIGNTEISVRGQDRLIISTPNQRNERPTQS VSSPEATSGSTGSVEKKQQRRSIRTTSESEKSTEVVPKKKIKKE QVGFLHVES  1911 MMTMESREATGLSPQAAQEKDGIVIVKVEEEDEEDHMWGQDSTL QDTPPPPDFIFRQKFRRFCYQNTFGPREALSKLKELCHOWLRPE INTKEQILELLVLEQFLSILFKELQVWLQEYRPDSGEEAVTLLE DLELDLSGQQVFGQVHGPMAGRWPLDPVQSSSSFDLHHEAT QSHFKHSSRKPRLLQSRALPAAHIPAPPHEGSPRQAMASALFT ADSQAMVKISDMAVSLIEWGCONLARRNLSRDNRQENYGSAF PQGGENRNENEESTSKAETEDSASRGSTTGRSQKFFGKRDQE GKTGERQQKNPEEKTRKEKRDSGPAIGKDKKTITGERGPREKGK GLGRSFSLSSNFTTPEEVPTGTKSHRCDECGKCFTRSSSLIHKK IHHTGEKPYECSECGKAF\SLNS\NLVHNQRINTGERPHECNE CGKAFSHSNLLIHQRIHSGEKPYECNECGKAFSGSD\LTKHQ RIHTGEKPYECSECGKAF\SLNS\NLVHNQRINTGERPHECNE CGKAFSHSNLLIHQRIHSGEKPYECNECGKAFSGSSD\LTKHQ RIHTGEKPYECSECGKAFQRAPATCCPPRSSMS  5926 2 233 DRCLMLKQGSQFGSPPAT/CEPDAPPVYQAPCQSCPEFFGAHEP  SDSPHHTEVHPPPPHSHSACPAPATCCPPRSSMS SDSPHTTVHPPPPHSHSACPAPATCCPPRSSMS KRFSKFGSQALVQLKRPASGQNSISVMPAQKITKPAAKYGIPLA YKKYGDKKLHEKKPLQKHQAHOTPEKRVNTGEERRKISEBAAR KRRLEFIEKEKKQKDQIISLMKAEQMKRGKELLERINRAREQG WRNVLSAGGSGEVKAPFLGSGTIAPSSFSSRGQYENYBEEV YLARLRQIRLQNFWERQIKAKLGKKEAVERSKQVEEFLOR KREAMQWKARAEGIMGIISLANLAMYGGRFSSRGGKPRIKEEV YLARLRQIRLQNFWERQGIKAALLAMYGGRFSSRGGKPRIKEEV YLARLRQIRLQNFWERQGIKAALLAMYGGRFSSRGGKPRIKEEV YLARLRQIRLQNFWERQGIKAALLAMYGGRFSSRGGKPRREEEV YLARLRQIRLQNFWERGGSFSKQQMRSYSSRGKRENEEEV YLARLRQIRLQNFWERQGIKAALLAMYGGRFSSRGGKRENEEEV YLARLRQIRLQNFWERQGIKAALLAMYGGERKERLERINRAREQG KREAMQWKARAEGIMGILQNLAMYGGRFSSRGGKRENEEEV YLARLRQIRLQNFWERQGIKAALLAMYGGERKERLERINRAEGG SLTDTRETSEEMQKTNNAISSKERLLRRLNEBLKKAQUEDEKKKUND SLTDTRETSEEMQKTNNAISSKERLERILKRDEBLKAQUEDEKKKUND SLTDTRETSEEMQKTNNAISSKERLERILKROULKAQUEDEKKKUND SLTDTRETSEEMQKTNNAISSKERLERCHLWEQLECUL	- 1	i	l l		
LLAEATKQASNHSEKQKIRKPRPQRERAQMDIGIAHAEKALKMT REER IEQYTFYIJDKQPEEALSQAKKSVASKTEVKKTRRPSVL NTOPEQTINAGEVASSLSFEIRRHSQRRTTSAEEBEPPVKIAW KTAAARKSLPASITMHKGSLDLQKCMMSPVKIEQVPALQMATG DGKFIDGFVYSTKGIGNTEISVRGQDRILISTPNQRNEKPTOS VSSPEATSGSTGSVEKKQQRRSIRTRSESEKSTEVVPKKKIKKE QVGFLHVES  1911 MMTAESREATGLSPQAAQEKDGIVIVKVEEEDEEDHMWGQDSTI QDTPPPDPPEIFRQFFRRECYONTFGPREALSKLKELCHOWLRPP INTKEQILELLVLKQFISIIPKELQVWLQEYRPDSGEEAVTLLE DLELDLSGQOVFGQVPBMLARGMVPLDPVQESSFFDLHHEAT QSHFKHSSRKPRLQGSRALPAAH1PAPPHEGSPRDQAMSALFT ADSQANVKISDMAVSLILEBEGCONLARRNLSRDNRQENYGSAP PQGGEMNNEESTSKAETGDSARGETTGRSQKEFGEKRDQE GKTGERQGKNPEEKTRKEKRDSGPAIGKDKKTITGERGPREKGK GLGRSFSLSSNFTTPEEVPTGTKHRCDECGKFTRSSSLIRHK IIHTGEKPYECSECGKAF\SINS\NLVLHQRITGERPHECNE CCKAFSHSSNLILHQRIHGSEKPYECNECGKFTRSSSLIRHK GRITGERYPECSECGKAFNSYLILHRRVHTREKPYKCTKCGK VAFTRSSTLTLHRIHARERASEYSPASLDAFGAFLKSCV  5926 2 233 DRCMLKGGSQPGSPPAT/CEPDAFPVYQAPCQSCPEPFGAHEP SDSPHHTPVHPPPEHSACPAPATCCPPPRSSM  KHFSKFGSQALYQLKRPASGQNSISWMPAQKITKPAKYGIPLA YKKTGDKKLHEKKDLQCHKQAHOTPEKVNTGEERRKISEERAR KRRLEFIEKKKNCHQIILGNLARMYGGRPSVSRGGVEHYHAIFDQ MQQAEDNEAKWKREIYGRGLPERQKGCLAVRARQCVEFFLQR KREAMQNKARAEGHNGILGNLAMYGGRPSVSRGGVEHYHAIFDQ MQQQAEDNEAKWKREIYGRGLPERQKGCLAVRARQVEFFLQR KREAMQNKARAEGHNGILGNLAMYGGRPSSSRGGKPRIKEEV YLAALRQIRLQNFNERQOIKAALRGEKKEANHSEGGEGEEADM RKK\1ESLKHANANARAAVLKEDLEKKKKWWEEHLV AKGVKSDVSPPLGCHETGGSPSKQQMRSVISTSTSALKEVGVUD SLIDTRETSEEMQKTNNAISSKEFLLRRLNEBLKAQCBDEKKKW LLSDTFEINVHEDAKEHREKSVSSDRVWERCCCV	- 1		1		1 - TI COMMOS VAW (FREOVED) AWG KUCTVERIADOR CORRES 1
REERIEQYTFIYINGOPEEALSQAKKVASKYEVKTRRPRSVL NTOPEQTTAGEVASSLSSTEIRRHSQRRHTSAEEEEPPVKIAW KTARARKSLPASITHMKSGDDLIITSPNQRAKEPTOS DGKFIDGFVYSTKGIGNKTEISVRGODDLIITSPNQRAKEPTOS VSSFATTGSTGSVEKKQORSIRTRSESEKSTEVVPKKKIKRE OVGFLHVES  1911 MMTAESREATGLSPQAAQEKDGIVIVKVEEEDEEDHMWGODSTL QDTPPPPDPEIPRQRFRFRFCYONTFGPREALSRLKELCHOWLRPE INTKEQITLELLVLUGDFLSILPKELQVWLQEYPPDSGEEAVTLLE DLELDLSGQQVPGQVHGPEMLARGMVPLDPVQESSSFDLHHEAT QSHFKHSSRKPRLLQSRALPAAHIPAPPHEGSPRDOAMASALFT ANSQAWVKISDMAVSLILEEWGCQNLARRNLSRDNRQENYGSAF PQGGENRNENEESTSKAETSEDSASRGETTGRSQKEFGEKRDQE GKTGERQQKNPEENTRKEKRDSGPAIGKDKKTITGBRGPREKGK GLGRSFSLSSNFTTPEVPTGTKSHRRCDECGKCFTRSSSLIRHK IIHTGEKPYECSEGGKAF\SLNS\NLVLHQRILHTRWHTREKPYKCTKCGK (AFTRSSTLILHQRIHGSEKYYECNECGKAFSQSSD)LTKHQ RIHTGEKPYECSEGGKAFNRSYLLHRRWHTREKPYKCTKCGK (AFTRSSTLTILHRIHARERASEYSPASLDAFGAFLKSCV PRICHERPYECSEGGKAFNRSYLLHRRWHTREKPYKCTKCGK (AFTRSSTTTILHRIHARERASEYSPASLDAFGAFLKSCV SDSPHITDVHPPPEHSAACPAPATCOPPPRSSMS KHFSKFGSQALVQLKRPASGONSISVMPAQKITKPAAKYGIPLA YKKYGDKKHEKKPLQKHKAQHOTPEKRVNTGEERRKISEBAAR KRRLEFIEKEKKQCQIISLMKAAEGMKRGEKERLERINRAREQG WRNVLSAGGSGSVKAPPIGSGGTIAPSSFSSRGQYEHYHAIFDQ MQQRAEDNEAWKREIYRGLPRGRGPREKEEEV YLARLRQIRLQRINGNERQOIKARGEKERANGOVEEFLOR RRKK\TESLKAHANARAAVLKEQLERKKKRAYEREKKVWEEHLV AKGVKSSDVSPPLGCHETGGSPSKQOMFSVISVTSALKSVEGVDS SLIDTRETSEEMQKTNNAISSKREILBRLINRNLKAQEBEKGKQN	- 1				I INCINCE IN VOLUCE IN VOLUCE AND AN ADDRESS OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PRO
NTOPEQTTAGEVASSISSTEIRRISORRHISAGEERPPPVKIAW KTAAARKSLPASITMIKGSLDLQKCNMSPVVKIEQVPALQNATG DGKFIDQFVYSTKGIGNKTEISVRGODELIISTPNORNEKPTOS VSSPEATSGSTGSVEKKQORRSITRTRSESEKSTEVVPKKKIKKE QVGFLHVES  1911 MMTAESREATGLSPQAAQEKDGIVIVKVEEEDEEDHMWGODSTI ODTPPPPDFEIFRQRFRRFCYQNTFGPREALSRLKELCHOWLRPE INTKEQTLIELLVLEQFLSILPKELQVWLQEYRPDSGEEAVTLLE DLELDLSGQQVFGQVHGFWHARGMVPLDPVQESSSFDLHHEAT ADSQAMVKISDMAVSLILEEWGCQNLARRNLSRDNRQENYGSAF PQGGENRENEESTSKAETSEDSASRGETTGRSQKEFGEKRPOE GKTGERQQKNPEEKTRKEKRDSGPATGKDKTTGTGRGPREKGK GLGRSFSLSSNFTTPEEVPTGTKSHRCDECGKCFTRSSSLIRHK IIHTGEKPYECSECGKAF\SINS\NLVLHGRI\HTGERPHECNE CGKAFSHSSNLLHARGHRGERPYECHECGKAFSOSD\LTKHQ RIHTGEKPYECSEGKAFNRNSYLILHRRVHTREKPYKCTKCGK \AFTRSSTLTLHHRIHARERASEYSPASLDAFGAFLKSCV  SDSPHHTPVHPPPEHSAACPAPATCCPPPRSMS  KHFSKFGSQALYQLKEPÄSGGNISVMPAQKITKAPAKYGIPLA KRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERINRAREQG WRNVLSAGGSGEWKAPFLGSGGTAPSSFSSRGVEHYHAIFDO MQQRAEDDNEAWKRGIYGRGLPERQKGQLAVERAKQUEFFLOR KREMQNKARAEGHMGILQNLAAMYGGRPSSSRGGKPRNKEEEV YLARLRQIRLQNFNERQQIISLAKARGEKKEAHNSEGGESEEADM RRKK\TESLKAHANARARAVLKEOLERKKEANFERGGESEEADM RRKK\TSLEHARANARARAVLKEOLERKKEAYEREKKWEEHU AKGWGSDVSPPLGQHETGGSPSKQOMSVISVTSALKEVGUNS SLITDTRETSEEMQKTNNAISSKREILBRILBRNLKAQEBEKGKQN	- [		1		I THE TAXABLE COLOR OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PRO
TRABARKSLPASITMERGSLDLOKCMMSPVVKIEQVFALQNATG DGKFIDQFYYSTKGIGNKTEISVRGQDRLIISTPNQRIKEPTQS VSSPEATGGSTGSVEKKQQRRSIRTRSESEKSTEVVPKKKIKKE QVGFLHVES  216  1911  MMTAESREATGLSPQAAQEKGGIVIVKVEEEDEEDHMWGQDSTL QDTPPPPDPEIFRQRFRRFCYQNTFGPREALSRLKELCHOWLRPE INTKEQILELUVLEQFLSILPKELQVWLOEYPRDSGEEAVTLLE DLELDLSGQOVFGOVHGPEMLARGMVPLDPVQESSSFDLHHEAT QSHFKHSSRKPRLLQSRALPAAHIPAPPHEGSPRDQAMASALFT ADSQAMVKIEDMAVSLILEEWGCONLARRNLSDNRQENYGSAP PQGGENRNENEESTSKAETEGBSASRGETTGRSOKEFGEKRDQE GKTGERQOKNPEKKTKKEKRDSGPAIGKDKKTITGERGPREKGK GLGRSFSLSSNFTTPEEVPTGTKSHRCDECGKGFTRSSSLIRHK IIHTGEKPYECSECGKAF\SINS\NLVLHQRI\HTGEKPHECNE CGKAFSHSSNLILHGRIHGEKPYECNECGKAFSOSSD\LTKHQ RHTGEKPYECSECGKAFNRNSYLLIHRRVHTREPFYKCTKCK AFTRSSTITLHHRIHARERASEYSPASLDAFGAFLKSCV SDSPHHTPVHPPPEHSAACPAPATCCPPPRSSMS  **HFSKRGSQALYQLKRPASGONSISVMPAQKITKPAAKYGIPLA* YKKYGDKKLHEKKPLQKHKQAHOTPEKKVNTGEERKKISEEAAR KRRLEFIEKEKKQKDQIISLMKAEQMKRQBKERLERINRAREQG WRNNLSAGGSGEVKAPFLGSGTIAPSSFSSRGQVEHYHAIFDO MQQQRAEDNAKKREIYGRGLPERQKGQLAVERRKQVEFFLOR KREMQNKARAEGHMGILQNLAAMYGGRPSSRGGKFRNKEEEV YLAALRQIRLQNFNERQQIKAKLGEKKEAMHSEGGGGSEEADM RKKK\IESLKAHMARAAVLKEQLEKKRAYEREKKWEEHLV AKGVKSSDVSPPLGGHETGGSPSKQQMRSVISVTSALKEVGUDS SLIDTRETSEEMQKTNNAISSKREILRRLNENLKAQEDEKGKQN	- [				REERIEQYTFIYIDKOPERALSOAVVOIA CVITTONIA EKALKMT
DGKFIDGFYYSTKGIGNKTEISVRGODRIJGNATG VSSPEATSGSTGSVEKKQORRSIRTRSESEKSTEVPKKKIKKE VSSPEATSGSTGSVEKKQORRSIRTRSESEKSTEVPKKKIKKE OVGFLYUES  1911 MMTAESREATGLSFQAAQEKDGIVIVKVEEEDEEDHMWGQDSTL QDTPPPDPEIFRQRFRRFCYQNTFGPREALSRLKELCHOMLRPE INTKEQILELLVLEQFISILPRELQWWLQEYRPDSGEEAVTLLE DLELDLSGQOVPGOVHGFEMLARGMVPLDPVQESSFDLHHEAT QSHFKHSSRKPRLLQSRALPAAHIPAPPHEGSPRDQAMASALFT ADSQAMVKIEDMAVSLILEEWGCQNLARRNLSRDNRQENYGSAP PQGGENNNENEESTSKAETSEDSASRGETTGRSQKEFGENKDQE GKTGERQQKNPEEKTRKEKRDSGPATGKDKKTITGBRGPREKGK GLGRSFSLSSNFTTPEEVPTGTKSHRCDECCKCFTRSSSLIRHK IIHTGEKPYECSECGKAF\SLNS\NLVLHQRI\HTGEKPHECNE CGKAFSHSSNLILHQRIHSGEKPYECNECGKAFSGSSD\LTKHQ RIHTGEKPYECSECGKAF\SNSYLLHRRVHTREKPYKCTKCGK A\FTRSSTLTLHHRIHARERSASEYSPASLDAFGAFLKSCV SDSPHHTPVHPPPEHSAACPAPATCCPPPRSMS  KHFSKFGSQALYQLKRPASGQNSISVMPAQKITKPAAKYGIPLA YKKYGDKKLHEKKPLQKHKQAHQTPEKRVMTGEERRKISEEAAR KRRLEFIEREKKQNDQIISLMKAEQMKRQEKERLERINRARECG WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGGYEHVHAIFDQ KREAMQNKARAEGHMGILQNLAAMYGGRPSSSRGGKPNKEEEV YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM RRKK\IESLKAHANARAAVLKEQLEKKRAANGEGSESEEADM RRKK\IESLKAHANARAAVLKEQLEKKRAANGEGGSEGEEADM RRKK\IESLKAHANARAAVLKEQLEKKRAAYEREKKVWEEHLUV AKGVKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS SLIDTRETSEEMGKTNNAISSKREILBRLNRENLKAQDEDEKGKON	- 1	ſ			NTOPEOTNAGEVASSI SSTEIR
VSSFEATSGSTGSVEKKQQRRSIRTRSESEKSTEVPKKKIKE  VSSFEATSGSTGSVEKKQQRRSIRTRSESEKSTEVPKKKIKE  OVGFLHVES  MMTAESFEATGLSPQAAQEKDGIVIVKVEEEDEEDHMWGQDSTL QDTPPPPPBIFRQRFRRFCYQNTFGPREALSRLKELCHOMERPE INTKEQILELLVLEQFFSILPKELQVWLQEYRPDSGEEAVTLLE DLELDLSGQQVFGQVHGGFEMLARGMVPLDPVQESSSFDLHHEAT QSHFKHSSRKPRLLQSRALPAAHIPAPPHEGSPRDQAMASALFT ADSQAMVKIEDMAVSLILEEWGCQNLARRMLSRDNRQENYGSAP PQGGENRNENEESTSKAETSEDSASRGETTGRSQKEFGERKDQE GKTGERQQKNPEEKTRKEKRDSGPAIGKDKKTITGERGPREKGK GLGRSFSLSSNFTTPEEVPTGTKSHRCDECGKCFTRSSSLIRHK IIHTGEKPYECSECGKAF\SLNS\NLVLHQRI\HTGEKPHECNE CGKAFSHSSNILHARHIHGEKPYECTECGKAFSOSSD\LTKHQ RIHTGEKPYECSECGKAFNRNSYLILHRRVHTREKPYKCTKCGK \AFTRSSTLTLHHRIHARERASEYSPASLDAFGAFLKSCV SDSPHTPVHPPPHENSAACPAPATCCPPPRSSMS  FSP27  4146  1248  KHFSKRGSQALYQLKRPASGGNSISVMPAQKITKPAAKYGIPLA YKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAAR KRRLEFIERKKKKOKDQIISLMKAAQMKRQBKERLERINRAREQG WRNVLSAGGSGEVXAPFLGSGGTIAPSSFSSRGQYENVHAIFDQ MQQRAEDNEAKWKREIYGRGLPERQKGGLAVERAKQVEEFLOR KREMQNKARAEGHMGILQNLAAMYGGRPSSSRGGKPRNKEEEV YLARRQIRLQNFNERGUIKALRGEKKEANHSEGQEGSEEADM RRKK\IESLKAHANARAAVLKECLOEKKKEANHSEGGEGSEEADM RRKK\IESLKAHANARAAVLKECLOEKKKEANHSEGGEGSEEADM RRKK\IESLKAHANARAAVLKECLOEKKKEAYSTEKKVWEEHLV AKGVKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGYDS SLTDTRETSEEMQKTNNAISSKREILERLNENLKAQEDEKKKON	1	l	. 1		KTAAARKSI PASITMHKGSI DI CKONNA TSAEEEEPPPVKIAW
VSSFEATSGSTGSVEKKQQRRSIRTRSESEKSTEVPKKKIKE  VSSFEATSGSTGSVEKKQQRRSIRTRSESEKSTEVPKKKIKE  OVGFLHVES  MMTAESFEATGLSPQAAQEKDGIVIVKVEEEDEEDHMWGQDSTL QDTPPPPPBIFRQRFRRFCYQNTFGPREALSRLKELCHOMERPE INTKEQILELLVLEQFFSILPKELQVWLQEYRPDSGEEAVTLLE DLELDLSGQQVFGQVHGGFEMLARGMVPLDPVQESSSFDLHHEAT QSHFKHSSRKPRLLQSRALPAAHIPAPPHEGSPRDQAMASALFT ADSQAMVKIEDMAVSLILEEWGCQNLARRMLSRDNRQENYGSAP PQGGENRNENEESTSKAETSEDSASRGETTGRSQKEFGERKDQE GKTGERQQKNPEEKTRKEKRDSGPAIGKDKKTITGERGPREKGK GLGRSFSLSSNFTTPEEVPTGTKSHRCDECGKCFTRSSSLIRHK IIHTGEKPYECSECGKAF\SLNS\NLVLHQRI\HTGEKPHECNE CGKAFSHSSNILHARHIHGEKPYECTECGKAFSOSSD\LTKHQ RIHTGEKPYECSECGKAFNRNSYLILHRRVHTREKPYKCTKCGK \AFTRSSTLTLHHRIHARERASEYSPASLDAFGAFLKSCV SDSPHTPVHPPPHEHSAACPAPATCCPPPRSSMS  FSP27  4146  1248  KHFSKRGSQALYQLKRPASGGNSISVMPAQKITKPAAKYGIPLA YKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAAR KRRLEFIERKKKKOKDQIISLMKAACMKRGKKRAKTIRPACGG WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYENVHAIFDQ MQQRAEDNEAKWKREIYGRGLPERQKGGLAVERAKQVEEFLOR KREMQNKARAEGHMGILQNLAAMYGGRPSSSRGGKPRNKEEEV YLARRQIRLQNFNERGUIKALRGEKKEANHSEGQEGSEEADM RRKK\IESLKAHANARAAVLKECLOEKKKEANHSEGGEGSEEADM RRKK\IESLKAHANARAAVLKECLOEKKKEANHSEGGEGSEEADM RRKK\IESLKAHANARAAVLKECLOEKKKEANHSEGGEGSEEADM RRKK\IESLKAHANARAAVLKECLOEKKKEANHSEGGEGSEEADM AKGVKSSDVSPPLGOHETGGSPSKQQMRSVISVTSALKEVGVDS SLIDTRETSEEMQKTNNAISSKREILERLNENLKAQEDEKGKON LSDTFEINVHEDAKKHERFKSUSSDPAVMEACOUL		j			DGKFIDOFVYSTKGTCNWWDFICE
OVEFLHVES  216  1911  MMTAESREATGLSPQAAQEKDGIVIVKVEEEDEEDHMWGQDSTL QDTPPPPPPEIFRQRFRRFCYQNTFGPREALSRLKELCHQWLRPE INTKEQILELLVLEQFLSILPKELQVWLQEYRPDSGEEAVTLLE DLELDLSGQQVPGQVHGPEMLARGMVPLDPVQESSSFDLHHEAT QSHFKHASRKPRILQSRALPAAHIPAPHEGSPRDQAMASALFT ADSQAMVKIEDMAVSLILEEWGCQNLARRNLSRDNRQENYGSAF PQGGENRNENEESTSKAETSEDSASRGETTGRSOKEFGEKRDQE GKTGERQQKNPEEKTRKEKRDSGPAIGKDKKTITGERGPREKGK GLGRSFSLSSNFTTPEEVPTGTKSHRCDECGKCFTRSSSLIRHK IIHTGEKPYECSECGKAF\SLNS\NLVLHQRI\HTGEKPHECNE CGKAFSHSSNLILHQRIHGGEKPYECNECGKAFSOSSD\LTKHQ RIHTGEKPYECSECGKAFNRNSYLILHRRVHTEKKPYKCTKCGK \AFTRSSTLTLHHRIHARERASEYSPASLDAFGAFLKSCV SDSPHHTPVHPPPEHSAACPAPATCCPPPRSSMS KHFSKTGSQALVOLKRPASGYNSTSVMPAQKITKPAAKYGIPLA YKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAAR KRRLEFIEKEKKOKOQIISLMKAEQMKRQEKERLERINRAREOG WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDO MQQQRAEDNEAKWKREIYGRGLPERQKGOLAVERAKQVEEPLQR KREAMQNKARAEGINGILQNLAAMYGGRPSSRGGKFRNKEEEV YLARLRQIRLQNFNERQOIKAKLRGEKKEANHSEGOGGSEEDADM RRKK\IESLKAHANARARAVLKEQLEKKREAYEREKKVWEEHLV AKGYKSSDUSPPLGQHETGGSPSKQOMRSVISVTSALKEVSVUDS SLIDTRETSEEMQKINNALSSKREILBRLANGLUKAGGDEKKKON	-1	1			1 20th about 121AGIGNKIEISVRGODDI.TICTDMODUCEDER
1911 MMTAESREATGLSPQAAQEKDGIVIVKVEEEDEEDHMWGQDSTL QDTPPPDPEIFRQRFRRFCYQNTFGPREALSRLKELCHQWLRPE INTKEQLIELLVLEQFLSILPKELQVWLQEYRPDSGEEAVTLLE DLEDLSGQQVPGQVHGPEMLARGMVPLDPVQESSSFDLHHEAT QSHFKHSSRKPRLLQSRALPAAHIPAPPHEGSPRDQAMASALFT ADSQAMVKIEDMAVSLILEEWGCQNLARRNLSRDNRQENYGSAF PQGGENRNENEESTSKAETSEDSASRGETTGRSOKEFGEKRDQE GKTGERQQKNPEEKTREKRKDSGPAIGKDKKTITGERGPREKGK GLGRSFSLSSNFTTPEEVPTGTKSHRCDECGKCFTRSSSLIRHK IIHTGEKPYECSECGKAF\SLNS\NLVLHQRI\HTGEKPHECNE CGKAFSHSSNLLHQRIHSGEKYPECNECGKAFSQSSD\LTKHQ RIHTGEKPYECSECGKAFNRNSYLILHRRVHTREKPYKCTKCGK \AFTRSSTLTLHHRIHARERASEYSPASLDAFGAFLKSCV DRCLMLKQGSQPGSPPAT/CEPPAPPVVQAPCQSCPEPFGAHEP SDSPHHTPVHPPPEHSAACPAPATCCPPPRSSMS KHFSKFGSQALYQLKRPASGONSISVMPAOKITKPAAKYGIPLA YKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAAR KRRLEFIEKEKKQKDCJISLMKAEQMKRQEKERLERINRAREQG WRNVLSAGGSGEVKAPFLGSGTIAPSSFSSRGQYEHYHAIFDQ MQQQRAEDNEAKWKREIYGRGLPERQKGQLAVERAKQVEEFLQR KREAMQNKARAEGHMGILQNLAAMYGGRPSSSRGGKPNKEEEV YLARLRQIRLQHIRLDNFNERQQIKAKLRGEKKEANHSEGGGSEEADM RRKK\IESLKAHANARAAVLKEOLEKKRKEAYEREKKVWEEHLV AKGYKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS SLIDTRETSEEMQKITNAISSKREILBRLAUBNLKAQEDEKGKON	L				TOTAL DATE OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY O
INTKEQILELLVLEQFLSTLPKELQVMLQEYRPDSGEEAVTLLE DLELDLSGQQVFGQVHGPEMLARGMVPLDPVQESSSFDLHHEAT QSHFKHSSRKPRLLQSRALPAAHIPAPPHEGSPRQAMASALFT ADSQAMVKIEDMAVSLILEEMGCQNLARRHLSRDNRQENYGSAF PQGGENRNENEESTSKAETSEDSASRGETTGRSQKEFGEKRDQE GKTGERQQKNPEEKTRKEKRDSGPAIGKDKKTITGERGPREKGK GLGRSFSLSSNFTTPEEVPTGTKSHRCDECGKCFTRSSSLIRHK IIHTGEKPYECSECGKAF\SLNS\NLVLHQRI\HTGEKPHECNE CGKAFSHSSNLILHQRIHSGEKPYECNECGKAFSQSSD\LTKHQ RIHTGEKPYECSECGKAFNRNSYLILHRRVHTREKPYKCTKCGK AFTRSSTLTLHHRIHARERASEYSPASLDAFGAFLKSCV  DRCLMIKGGSQPGSPDAT/CEPPAPPVYQAPCQSCPEPPGAHEP SDSPHHTPVHPPEHSAACPAPATCCPPPRSSMS KHFSKRGSQALYQLKRPASGQNSISVMPAQKITKPAAKYGIPLA YKKYGDKKHHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAAR KRRLEFIEKEKKKQKDQIISLMKAEQMKRQEKERLERINRAREOG WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQVEHYHAIFDQ MQQRAEDNEAKWKEIYGRGLPERQKGQLAVERAKQVEEFLQR KRELBFIEKEKKGKDQIISLMKAEQMKRQEKERLERINRAREOG WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQ TLARLRQIRLQNFNERQQIKALRGEKKEANHSEGGESEEADM RRKK\IESLKAHANARAAVLKEQLERKRKEAYEREKKWEEHLV AKGVKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS SLITTRETSEEMKITNALISKREILRRLNENLKAQEDEKKKON LSDTFEINVHEDAKEREKKERSUSCOLUMBLKKACON LSDTFEINVHEDAKEREKKVERGEGGENERUN	Γ	5925	216	1911	6.07.011AP2
INTKEQILELLVLEQFLSTLPKELQVMLQEYRPDSGEEAVTLLE DLELDLSGQQVFGQVHGPEMLARGMVPLDPVQESSSFDLHHEAT QSHFKHSSRKPRLLQSRALPAAHIPAPPHEGSPRQAMASALFT ADSQAMVKIEDMAVSLILEEMGCQNLARRHLSRDNRQENYGSAF PQGGENRNENEESTSKAETSEDSASRGETTGRSQKEFGEKRDQE GKTGERQQKNPEEKTRKEKRDSGPAIGKDKKTITGERGPREKGK GLGRSFSLSSNFTTPEEVPTGTKSHRCDECGKCFTRSSSLIRHK IIHTGEKPYECSECGKAF\SLNS\NLVLHQRI\HTGEKPHECNE CGKAFSHSSNLILHQRIHSGEKPYECNECGKAFSQSSD\LTKHQ RIHTGEKPYECSECGKAFNRNSYLILHRRVHTREKPYKCTKCGK AFTRSSTLTLHHRIHARERASEYSPASLDAFGAFLKSCV  DRCLMIKGGSQPGSPDAT/CEPPAPPVYQAPCQSCPEPPGAHEP SDSPHHTPVHPPEHSAACPAPATCCPPPRSSMS KHFSKRGSQALYQLKRPASGQNSISVMPAQKITKPAAKYGIPLA YKKYGDKKHHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAAR KRRLEFIEKEKKKQKDQIISLMKAEQMKRQEKERLERINRAREOG WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQVEHYHAIFDQ MQQRAEDNEAKWKEIYGRGLPERQKGQLAVERAKQVEEFLQR KRELBFIEKEKKGKDQIISLMKAEQMKRQEKERLERINRAREOG WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQ TLARLRQIRLQNFNERQQIKALRGEKKEANHSEGGESEEADM RRKK\IESLKAHANARAAVLKEQLERKRKEAYEREKKWEEHLV AKGVKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS SLITTRETSEEMKITNALISKREILRRLNENLKAQEDEKKKON LSDTFEINVHEDAKEREKKERSUSCOLUMBLKKACON LSDTFEINVHEDAKEREKKVERGEGGENERUN	1	l	i i	~	OPTION OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SE
DELDLISGOOVPGOVHGPEMLARGMVPLDPVQESSFDLHHEAT  QSHFKHSSRKPRLLQSRALPAAHIPAPPHEGSPRDOAMASALFT  ADSQAMVKIEDMAVSLILEEWGCQNLARRNLSRDNRQENYGSAF  PQGGENRNENEESTSKAETSEDSASRGETTGRSQKEFGEKRDQE  GKTGERQQKNPEEKTRKEKRDSGPAIGKDKKTITGERGPREKGK  GLGRSFSLSSNFTTPEEVPTGTKSHRCDECGKCFTRSSSLIRHK  I 1 HTGEKPYECSECGKAF\SLNS\NLVLHQRI\HTGEKPHECNE  CGKAFSHSSNLILHQRIHSGEKPYECNECGKAFSOSSD\LTKHQ  RIHTGEKPYECSECGKAFNRNSYLILHRRVHTREKPYKCTKCGK  AFTRSSTLITHHRIHARERASEYSPASLDAFGAFLKSCV  DRCLMLKQGSQPGSPPAT/CEPPAPPVYQAPCQSCPEPPGAHEP  SDSPHHTPVHPPPEHSAACPAPATCCPPPRSSMS  KHFSKFGSQALYQLKRPASGONSISVMPAQKITKPAAKYGIPLA  YKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAAR  KRRLEFIEKEKKQKQQIISLMKAEQMKRQEKERLERINRAREQG  WRNVLSAGGSGEVKAPFLGSGTIAPSSFSSRGYEHYHAIFDQ  MQQQRAEDNEAKWREIYGRGLPERQKGQLAVERAKQVEEFLQR  KREAMQNKARAEGHMGILQNLAAMYGGRPSSSRGKPRNKEEEV  YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM  RRKK\IESLKAHANARAAVLKEQLERKKRAYEREKKWWEEHLV  AKGVKSSDVSPLGOHETGGSPSKQQMRSVISVTSALKEVGVDS  SLITDTRETSEEMQKTNNALISSKREILRRLNENLKAQCDEKGKQN	ı	[	J		TO THE TOTAL PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE P
QSHFKHSSRKPRILQSRALPAHIPAPPHEGSPRDQAMASALFT ADSQAMVKIEDMAVSLILEEWGCQNLARRNLSRDNRQENYGSAP PQGGENRENEESTSKAETSEDSASRGETTGRSQKEFGEKRDQE GKTGERQQKNPEEKTRKEKRDSGPAIGKDKKTITGERGPREKGK GLGRSFSLSSNFTTPEEVPTGTKSHRCDECGKCFTRSSSLIRHK IIHTGEKPYECSECGKAF\SLNS\NLVLHQRI\HTGEKPHECNE CGKAFSHSSNLILHQRIHSGEKPYECNECGKAFSQSSD\LTKHQ RIHTGEKPYECSECGKAFNRNSYLILHRRHTREKPYKCTKCGK \AFTRSSTLTLHHRIHARERASEYSPASLDAFGAFLKSCV  DRCLMLKQGSQPGSPPAT/CEPPAPPVYQAPCQSCPEPPGAHEP SDSPHTPVHPPPEHSAACPAPATCCPPPRSSMS  KHFSKFGSQALYQLKRPASGQNSISVMPAQKITKPAAKYGIPLA YKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAAR KRRLEFIEKEKKQKDQIISMKAEQMKRQEKERLERINRAREQG WRNVLSAGGSGEVKAPFLGSGGTIAPSFSSRGQVEHYHAIFDQ MQQQRAEDNEAKWKREIYGRGLPERQKGQLAVERAKQVEEFLQR KREAMQNKARAEGHMGILQNLAAMYGGRPSSSRGGKPRNKEEEV YLARLRQIRLQNPNERQQIKAKLRGEKKEANHSEGQEGSEEADM RRKK\IESLKAHANARAAVLKEQLERKKKAYEREKKVWEEHLV AKGVKSSDVSPPLGOHETGGSPSKQQMRSVISVTSALKEVGVDS SLIDTRETSEEMQKTNNAISSKREILRRLNENLKAQEDEKGKQN LSDTFEINVHEDAKEHEKEKSUSSDRVENBACKOUNDE	1	- 1	1		I THE STUDDING TO BUT INDICATED TO THE TOTAL PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE P
ADSQAMVKIEDMAVSLILEEWGCQNLARRNLSRDINGGERF PQGGENRNENEESTSKAETSEDSASRGETTGRSQKEFGEKRDQE GKTGERQQKNPEKTRKEKRDSGPAIGKDKKTITGERGPREKGK GLGRSFSLSSNFTTPEEVPTGTKSHRCDECGKCFTRSSSLIRHK I IHTGEKPYECSECGKAF\SLNS\NLVLHQRI\HTGEKPHECNE CGKAFSHSSNLILHQRIHSGEKPYECNECGKAFSQSSD\LTKHQ RIHTGEKPYECSECGKAFNRNSYLILHRRVHTREKPYKCTKCGK \AFTRSSTLTLHHRIHARERASEYSPASLDAFGAFLKSCV DRCLMLKQGSQFGSPPAT/CEPPAPPVYQAPCQSCPEPPGAHEP SDSPHTPVHPPPEHSAACPAPATCCPPPRSSMS  KHFSKFGSQALYQLKRPASGQNSISVMPAQKITKPAAKYGIPLA YKKYGDKKLHEKKPLOKHKQAHQTPEKRVNTGEERKISEEAAR KRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERINRAREOG WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQVEHYHAIFDQ MQQQRAEDNAAKWKREIYGRGLPERQKGQLAVERAKQVEEFLQR KREMQNKARAEGIMGILQNLAAMYGGRPSSSRGKKPNKEEEV YLARLRQIRLQNFMERQQIKAKLRGEKKEANHSEGQEGSEEADM RRKK\IESLKAHANARAAVLKEQLERKKKAYEREKKVWEEHLV AKGVKSSDVSPPLGOHETGGSPSKQQMRSVISVTSALKEVGVDS SLIDTRETSEEMQKTNNAISSKREILRRLIRBNLKAQEDEKGKQN	1	ļ	İ		
PQGGENRNENEESTSKAETSEDSASRGETTGRSQKEFGERRDQE GKTGERQQKNPEEKTRKEKRDSGPAIGKDKKTITGBRGPREKGK GLGRSFSLSSNFTTPEEVPTGTKSHRCDECGKCFTRSSSLIRHK IIHTGEKPYECSECGKAF\SLNS\NLVLHQRI\HTGEKPHECNE CGKAFSHSSNILHQRIHSGEKPYECNECGKAFSQSSD\LTKHQ RIHTGEKPYECSECGKAFNRNSYLLHRRVHTREKPYKCTKCGK \AFTRSSTLTLHHRIHARERASEYSPASLDAFGAFLKSCV  5926 2 233 DRCLMLKQGSQPGSPPAT/CEPPAPPVYQAPCQSCPEPPGAHEP SDSPHHTPVHPPPEHSAACPAPATCCPPPRSSMS KHFSKFGSQALYQLKRPASGQNSISVMPAQKITKPAAKYGIPLA YKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAAR KRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERINRAREQG WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGGYEHYHAIFDQ MQQQRAEDNEAKWKREIYGRGLPERQKGQLAVERAKQVEEFLQR KREAMQNKARAEGHMGILQNLAAMYGGRPSSSRGGKPRNKEEEV YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM RRKK\IESLKAHANARAAVLKEQLERKRKEAYEREKKVWEEHLV AKGVKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS SLITDTRETSEEMQKTNNAISSKREILRRLLRBNLKAQEDEKGKQN LSDTFEINVHEDAKEHRKEKSVSSDPRWARRGELHRLERNIKAQEDEKGKQN	1	1		ĺ	TANK ALLO CREEK DE CONCRETE CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTR
GKTGERQQKNPEEKTRKEKRDSGPAIGKDKKTITGERGPREKGK GLGRSFSLSSNFTTPEEVPTGTKSHRCDECGKCFTRSSSLIRHK I I HTGEKPYECSECGKAF\SLNS\NLVLHQRI\HTGEKPHECNE CGKAFSHSSNLILHQRIHSGEKPYECNECGKAFSQSSD\LTKHQ RIHTGEKPYECSECGKAFNRNSYLILHRRVHTREKPYKCTKCGK AFTRSSTLTLHHRIHARERASEYSPASLDAFGAFLKSCV DRCLMLKQGSQPGSPPAT/CEPPAPPVYQAPCQSCPEPPGAHEP SDSPHHTPVHPPPEHSAACPAPATCCPPPRSSMS  KHFSKFGSQALYQLKRPASGQNSISVMPAQKITKPAAKYGIPLA YKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAAR KRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERINRAREQG WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGYEHYHAIFDQ MQQQRAEDNEAKWKREIYGRGLPERQKGQLAVERAKQVEEFLQR KREAMQNKARAEGHMGILQNLAAMYGGRPSSSRGGKPRNKEEEV YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM RRKK\IESLKAHANARAAVLKEQLERKRKEAYEREKKVWEEHLUV AKGVKSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS SLTDTRETSEEMQKTNNAISSKREILRRLNENLKAQEDEKGKON LSDTFEINVHEDAKEHEREKGVSSPRVWEEGCCOV	1	}	}		TODAMININATEDIMANSELLINGUAMINATEDIMI ADDITIONATED - 1
GLGRSFSLSSNFTTPEEVPTGTKSHRCDECGKCFTRSSSLIRHK  I IHTGEKPYECSECGKAF\SLNS\NLVLHQRI\HTGEKPHECNE CGKAFSHSSNLILHQRIHSGEKPYECNECGKAFSQSSD\LTKHQ RIHTGEKPYECSECGKAFNRNSYLILHRRVHTREKPYKCTKCGK \AFTRSSTLTLHHRIHARERASEYSPASLDAFGAFLKSCV  DRCLMLKQGSQPGSPPAT/CEPPAPPVYQAPCQSCPEPPGAHEP SDSPHHTPVHPPPEHSAACPAPATCCPPPRSSMS  HFFSKFGSQALYQLKRPASGQNSISVMPAQKITKPAAKYGIPLA YKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAAR KRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERINRAREQG WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQ MQQQRAEDNEAKWKREIYGRGLPERQKGQLAVERAKQVEEFLQR KREAMQNKARAEGHMGILQNLAAMYGGRPSSSRGGKPRNKEEEV YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM RRKK\IESLKAHANAARAAVLKEQLERKRKEAYEREKKVWEEHLV AKGVKSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS SLTDTRETSEEMQKTNNAISSKREILRRLNBNLKAQEDEKGKON LSDTFEINVHEDAKEHEREKGUSSPRVWHEACCOV			1		- VOODMANDESTSKAETSEDSASDCETTCDDOVEDONIOS - 1
I IHTGEKPYECSECGKAF\SINS\NLVLHQRI\HTGEKPHECNE CGKAFSHSSNLILHQRIHSGEKPYECNECGKAFSQSSD\LTKHQ RIHTGEKPYECSECGKAFNRNSYLILHRRVHTREKPYKCTKCGK \AFTRSSTLTLHHRIHARERASEYSPASLDAFGAFLKSCV DRCLMLKQGSQPGSPPAT/CEPPAPPVYQAPCQSCPEPPGAHEP SDSPHHTPVHPPPEHSAACPAPATCCPPPRSSMS  KHFSKFGSQALYQLKRPASGQNSISVMPAQKITKPAAKYGIPLA YKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAAR KRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERINRAREQG WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQ MQQQRAEDNEAKWKREIYGRGLPERQKGQLAVERAKQVEEFLQR KREAMQNKARAEGHMGILQNLAAMYGGRPSSSRGKPRNKEEEV YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM RRKK\IESLKAHANARAAVLKEQLERKRKEAYEREKKVWEEHLV AKGVKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS SLTDTRETSEEMQKTNNAISSKREILRRLNENLKAQEDEKGKON LSDTFEINVHEDAKEHEREKGVSGSPVANDERACCOVILIBRISK		1		ľ	
CGKAFSHSSNLILHQRIHSGEKPYECNECGKAFSQSSD\LTKHQ RIHTGEKPYECSECGKAFNRNSYLILHRRVHTREKPYKCTKCGK AFTRSSTLTLHHRIHARERASEYSPASLDAFGAFLKSCV DRCLMLKQGSQPGSPPAT/CEPPAPPVYQAPCQSCPEPPGAHEP SDSPHHTPVHPPPEHSAACPAPATCCPPPRSSMS  KHFSKFGSQALYQLKRPASGQNSISVMPAQKITKPAAKYGIPLA YKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAAR KRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERINRAREQG WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQ KREAMQNKARAEGHMGILQNLAAMYGGRPSSSRGGKPRNKEEEV YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM RRKK\IESLKAHANARAAVLKEQLERKRKEAYEREKKVWEEHLV AKGVKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS SLTDTRETSEEMQKTNNAISSKREILRRLNENLKAQEDEKGKON LSDTFEINVHEDAKEHEREKSUSSPRVMEECCOV	1	1		ļ	GLGRSFSLSSNFTTPEEVPTGTKCUDGDEGGVGTTTGERGPREKGK
RIHTGEKPYECSECGKAFNRNSYLILHRRVHITEKPYKCTKCGK  \[ \text{AFTRSSTLTLHHRIHARERASEYSPASLDAFGAFLKSCV} \]  \[ \text{AFTRSSTLTLHRIHARERASEYSPASLDAFGAFLKSCV} \]  \[ \text{DRCLMLKQGSQPGSPPAT/CEPPAPPVYQAPCQSCPEPPGAHEP} \]  \[ \text{SDSPHHTPVHPPPEHSAACPAPATCCPPPRSSMS} \]  \[ \text{SDSPHHTPVHPPPEHSAACPAPATCCPPPRSSMS} \]  \[ \text{KHFSKFGSQALYQLKRPASGQNSISVMPAQKITKPAAKYGIPLA} \]  \[ \text{YKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAAR} \]  \[ \text{KRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERINRAREQG} \]  \[ \text{WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQ} \]  \[ \text{WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQ} \]  \[ \text{KREAMQNKARAEGHMGILQNLAAMYGGRPSSSRGGKPNKEEEV} \]  \[ \text{YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM} \]  \[ \text{RRKK\IESLKAHANARAAVLKEQLERKRKEAYEREKKVWEEHLV} \]  \[ \text{AKGVKSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS} \]  \[ \text{SLTDTRETSEEMQKTNNAISSKREILRRLNENLKAQEDEKGKQN} \]  \[ \text{LSDTFEINVHEDAKEHEREKSUSSPRVMIEGCGOLUMERGKQN} \]	1	- 1		I	I IHTGEKPYECSECGKAE\ SING\ WITTERSSLIRHK
RIHTGEKPYECSECGKAFNRNSYLILHRRVHITEKPYKCTKCGK  \[ \text{AFTRSSTLTLHHRIHARERASEYSPASLDAFGAFLKSCV} \]  \[ \text{AFTRSSTLTLHRIHARERASEYSPASLDAFGAFLKSCV} \]  \[ \text{DRCLMLKQGSQPGSPPAT/CEPPAPPVYQAPCQSCPEPPGAHEP} \]  \[ \text{SDSPHHTPVHPPPEHSAACPAPATCCPPPRSSMS} \]  \[ \text{SDSPHHTPVHPPPEHSAACPAPATCCPPPRSSMS} \]  \[ \text{KHFSKFGSQALYQLKRPASGQNSISVMPAQKITKPAAKYGIPLA} \]  \[ \text{YKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAAR} \]  \[ \text{KRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERINRAREQG} \]  \[ \text{WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQ} \]  \[ \text{WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQ} \]  \[ \text{KREAMQNKARAEGHMGILQNLAAMYGGRPSSSRGGKPNKEEEV} \]  \[ \text{YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM} \]  \[ \text{RRKK\IESLKAHANARAAVLKEQLERKRKEAYEREKKVWEEHLV} \]  \[ \text{AKGVKSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS} \]  \[ \text{SLTDTRETSEEMQKTNNAISSKREILRRLNENLKAQEDEKGKQN} \]  \[ \text{LSDTFEINVHEDAKEHEREKSUSSPRVMIEGCGOLUMERGKQN} \]		- 1	i	İ	CGKAFSHSSNLTLHOR LUCCHUST
5926 2 233 DRCLMLKQGSQPGSPPAT/CEPPAPPVYQAPCQSCPEPPGAHEP 5927 4146 1248 KHFSKFGSQALYQLKRPASGQNSISVMPAQKITKPAAKYGIPLA YKKYGDKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAAR KRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERINRAREQG WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQ MQQQRAEDNEAKWKREIYGRGLPERQKGQLAVERAKQVEEFLQR KREAMQNKARAEGHMGILQNLAAMYGGRPSSSRGGKPRNKEEEV YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM RRKK\IESLKAHANARAAVLKEQLERKRKEAYEREKKVWEEHLV AKGVKSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS SLTDTRETSEEMQKTNNAISSKREILRRLNENLKAQEDEKGKQN LSDTFEINVHEDAKEHEREKGVSSPRVWHEACCOV	ł	- 1	l l		RIHTGEKPYECSECCEN PROVINCIAN ENDERGE RESURE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL
DRCLMLKQGSQPGSPPAT/CEPPAPPVYQAPCQSCPEPPGAHEP  DRCLMLKQGSQPGSPPAT/CEPPAPPVYQAPCQSCPEPPGAHEP  SDSPHHTPVHPPPEHSAACPAPATCCPPPRSSMS  KHFSKFGSQALYQLKRPASGQNSISVMPAQKITKPAAKYGIPLA YKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAAR KRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERINRAREQG WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQ MQQQRAEDNEAKWKREIYGRGLPERQKGQLAVERAKQVEEFLQR KREAMQNKARAEGHMGILQNLAAMYGGRPSSSRGGKPRNKEEEV YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM RRKK\IESLKAHANARAAVLKEQLERKRKEAYEREKKVWEEHLV AKGVKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS SLTDTRETSEEMQKTNNAISSKREILRRLNENLKAQEDEKGKQN LSDTFEINVHEDAKEHEREKGVSSDRKVWEACCOVEN	L			İ	THE COLUMN TECSECONAL TRANSPIRIT TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPER
SDSPHTTPVHPPPEHSAACPAPATCCPPPRSSMS  SDSPHTTPVHPPPEHSAACPAPATCCPPPRSSMS  KHFSKFGSQALYQLKRPASGQNSISVMPAQKITKPAAKYGIPLA YKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAAR KRRLEFIEKEKKQKQDQIISLMKAEQMKRQEKERLERINRAREQG WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQ MQQQRAEDNEAKWKREIYGRGLPERQKGQLAVERAKQVEEFLQR KREAMQNKARAEGHMGILQNLAAMYGGRPSSSRGGKPRNKEEEV YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM RRKK\IESLKAHANARAAVLKEQLERKRKEAYEREKKVWEEHLV AKGVKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS SLTDTRETSEEMQKTNNAISSKREILRRLNENLKAQEDEKGKQN LSDTFEINVHEDAKEHEREKGVSSPRVWHEACCOVEN	1	5926	2	233	AN INCOLUIDABKIHARERASEVGDAGI.DA ECA DI MOGUI
S927  4146  1248  KHFSKFGSQALYQLKRPASGQNSISVMPAQKITKPAAKYGIPLA YKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAAR KRRLEFIEKEKKQKQDQIISLMKAEQMKRQEKERLERINRAREQG WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQ MQQQRAEDNEAKWKREIYGRGLPERQKGQLAVERAKQVEEFLQR KREAMQNKARAEGHMGILQNLAAMYGGRPSSSRGGKPRNKEEEV YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM RRKK\IESLKAHANARAAVLKEQLERKRKEAYEREKKVWEEHLV AKGVKSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS SLTDTRETSEEMQKTNNAISSKREILRRLNENLKAQEDEKGKQN LSDTFEINVHEDAKEHEREKGVSSPRVMEACCOVEN	L	- 1			DRCLIMLKQGSQPGSPPAT/CEDDA PDUVOA DCGGCCCCC
KHFSKPGSQALYQLKRPASGONSISVMPAQKITKPAAKYGIPLA YKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAAR KRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERINRAREQG WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQ MQQQRAEDNEAKWKREIYGRGLPERQKGQLAVERAKQVEEFLQR KREAMQNKARAEGHMGILQNLAAMYGGRPSSSRGGKPRNKEEEV YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM RRKK\IESLKAHANARAAVLKEQLERKRKEAYEREKKVWEEHLV AKGVKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS SLTDTRETSEEMQKTNNAISSKREILRRLNENLKAQEDEKGKQN LSDTFEINVHEDAKEHEFEKSVSSPRVMEACCOVINDER	$\Gamma$	5927	4146		TOTAL TOTAL PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PR
KRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERINRAREQG WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQ MQQQRAEDNEAKWKREIYGRGLPERQKGQLAVERAKQVEEFLQR KREAMQNKARAEGHMGILQNLAAMYGGRPSSSRGGKPRNKEEEV YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM RRKK\IESLKAHANARAAVLKEQLERKRKEAYEREKKVWEEHLV AKGVKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS SLTDTRETSEEMQKTNNAISSKREILRRLNENLKAQEDEKGKQN LSDTFEINVHEDAKEHEREKGVSSDRVMEACCOVMIN	1	- 1		+240	KHFSKFGSQALYOLKRPASGONS I SVMPAOVITEVPANICE STATE
WRNVLSAGGGEVKAPFLGSGGTIAPSSFSRGQYEHYHAIFDQ WRNVLSAGGGEVKAPFLGSGGTIAPSSFSRGQYEHYHAIFDQ MQQQRAEDNEAKWKREIYGRGLPERQKGQLAVERAKQVEEFLQR KREAMQNKARAEGHMGILQNLAAMYGGRPSSSRGGKPRNKEEEV YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM RRKK\IESLKAHANARAAVLKEQLERKRKEAYEREKKVWEEHLV AKGVKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS SLTDTRETSEEMQKTNNAISSKREILRRLNENLKAQEDEKGKQN LSDTFEINVHEDAKEHEFEKSVSSDRVMUEACCOVINDEN	1	- 1	1		
MQQRAEDNEAKWKREIYGRGLIPESFSSRGQYEHYHAIFDQ MQQRAEDNEAKWKREIYGRGLIPERQKGQLAVERAKQVEEFLQR KREAMQNKARAEGHMGILQNLAAMYGGRPSSRGGKPRNKEEEV YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM RRKK\IESLKAHANARAAVLKEQLERKRKEAYEREKKVMEEHLV AKGVKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS SLITDTETSEEMQKTNNAISSKREILRRLNENLKAQEDEKGKQN LSDTFEINVHEDAKEHEFEKSVSSPBYKWEACCOVIN		[		i	**************************************
KREAMONKARAEGHMGILONLAAMYGGRPSSSRGKPRNKEEEV YLAKLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM RRKK\IESLKAHANARAAVLKEQLERKRKEAYEREKKVWEEHLV AKGVKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS SLTDTRETSEEMQKTNNAISSKREILRRLNENLKAQEDEKGKQN LSDTFEINVHEDAKEHEFEKSVSSDRKWEEACCOLUBERSKON	1	1	i	1	THE TOTAL CONTROL OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPE
YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM RRKK\IESLKAHANARAAVLKEQLERKKKAYEREKKVWEEHLV AKGVKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS SLTDTRETSEEMQKTNNAISSKREILRRLNENLKAQEDEKKON LSDTFEINVHEDAKEHEKEKSVSSDRKWEACCOLUBEKKON	1	1	1	İ	MQQQRAEDNEAKWKREIYGDGLDBBQVGGT TAPSSFSSKGQYEHYHAIFDQ
RRKK\IESLKAHANARAAVLKEQLEKKEANHSEGQEGSEEADM RRKK\IESLKAHANARAAVLKEQLEKKKEAYEREKKVWEEHLV AKGVKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS SLTDTRETSEEMQKTNNAISSKREILRRLNENLKAQEDEKGKQN LSDTFEINVHEDAKEHEKEKSVSSDRYKWEACCOLVHARDE	]	ļ	ļ		KREAMONKARAEGHMGILOWARAWGGGCAVERAKQVEEFLQR
AKGVKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS SLTDTRETSEEMQKTNNAISSKREILRRLNENLKAQEDEKGKQN LSDTFEINVHEDAKEHEFEKSVSSDRYWHEACCOLUND ROOM	l	1	İ		YLARLROTHLONENERGOLVAVA BETTER THE THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVAVA BETTER THE TENEDOLVA BETTER THE TENEDOLVA BETTER THE TENEDOLVA BETTER THE TENEDOLVA BETTER THE TENEDOLVA BETTER THE TENEDOLVA BETTER THE TENEDOLVA BETTER THE TENEDOLVA BETTER THE TENEDOLVA BETTER THE TENEDOLVA BETTER THE TENEDOLVA BETTER THE TENED
AKGVKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS SLTDTRETSEEMQKTNNAISSKREILRRLNENLKAQEDEKGKQN LSDTFEINVHEDAKEHEFEKSVSSDRYWHEACCOLUND ROOM		ĺ	ł	1 :	RRKK\ TESLKAHANADANI KERCEKKEANHSEGQEGSEEADM
SLIDTREISEEMQKINNAISSKREILRRLNENLKAQEDEKGKON LSDTFEINVHEDAKEHEFEKSUSSDRYNDEACCOLUND		1	·	1 '	THE OLD THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PR
LSDTFEINVHEDAKEHEKEKSVSSDBKKNEACCOLVINGEN		J	}		······································
I DOLL DELINATEDANCH RECENTAGE OF TALL DELINATED IN THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPER		f	[	, ,	DETERMINE TO SERVICE TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PR
DISFSTTERHTVGEVIKLGPNGSPRRAWGKSPTDSVLKILGFAR		1	ł	1 -	DODITED NOT DAKEHKKEKSUSSIDEVINE ACCOUNT OF THE
					DISPSTTERHTVGEVIKLGPNGSPRRAWGKSPTDSVLKILGEAF

SEQ	Predicted	Predicted end	Amino
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	A=Alanine, C=Cysteine, D=Aspartic Acid, B=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
j	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence	•	\=possible nucleotide insertion)
			LQLQTELLENTTIRSEISPEGEKYKPLITGEKKVQCISHEINPS
			AIVDSPVETKSPEFSEASPOMSLKLEGNLEEPDDLETEILQEPS
	ľ		GTNKDE\SLPCTITDVWISEEKETKETQSADRITIQENEVSEDG
			VSSTVDQLSDIHIEPGTNDSQHSKCDVDKSVQPEPFFHKVVHSE
1	i	1	HLNLVPQVQSVQCSPEESFAFRSHSHLPPKNKNKNSLLIGLSTG
ļ	}	1	LFDANNPKMLRTCSLPDLSKLFRTLMDVPTVGDVRQDNLEIDEI
1	ŀ		EDENIKEGPSDSEDIVFEETDTDLQELQASMEQLLREQPGEEYS
	1		EEEESVLKNSDVEPTANGTDVADEDDNPSSESALNEEWHSDNSD
1	1	]	GEIASECECDSVFNHLEELRLHLEQEMGFEKFFEVYEKIKAIHE
			DEDENIEICSKIVQNILGNEHQHLYAKILHLVMADGAYQEDNDE
5928	4146	1248	KHFSKFGSQALYQLKRPASCQNSISVMPAQKITKPAAKYGIPLA
ĺ	i		YKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAAR
			KRRLEFIEKEKKQKDQIISLMKAEOMKROEKERLERINDADEOC
	l		WKNYLSAGGSGEVKAPFLGSGGTIAPSSFSSPGOVEHYUATEDO
			MQQQRAEDNEAKWKREIYGRGLPEROKGOLAVERAKOVEREL OR
1			KREAMQNKARAEGHMGILQNLAAMYGGRPSSSRGKPPNKEREN
			YLARDRQIRLQNFNERQOIKAKLRGEKKEANHSEGOEGGERADM
1			RRKK\IESLKAHANARAAVLKEOLERKRKEAVEREKKUWEEULU
1			AKGVKSSDVSPPLGQHETGGSPSKOOMRSVISVTSALKEVGUDG
ĺ			SLIDTRETSEEMOKTNNAISSKREILRRINENLKAOEDRVGVON
1 .	ļ		LSDTFEINVHEDAKEHEKEKSVSSDRKKWEAGGQLVIPLDELTL
	İ		DTSFSTTERHTVGEVIKLGPNGSPRRAWGKSPTDSVLKILGEAE
			LQLQTELLENTTIRSEISPEGEKYKPLITGEKKVQCISHEINPS
1 1			AIVDSPVETKSPEFSEASPQMSLKLEGNLEEPDDLETEILQEPS
1 1			GTNKDE\SLPCTITDVWISEEKETKETQSADRITIQENEVSEDG
}	1		VSSTVDQLSDIHIEPGTNDSQHSKCDVDKSVQPEPFFHKVVHSE
1 1			HLNLVPQVQSVQCSPEESFAFRSHSHLPPKNKKKNSLLIGLSTG LFDANNPKMLRTCSLPDLSKLFRTLMDVPTVGDVRQDNLEIDEI
	I		EDENIKEGPSDSEDIVFBETDTDLQELQASMEQLLREQPGEEYS
1 1	1		EEEESVLKNSDVEPTANGTDVADEDDNPSSESALNEEWHSDNSD
1	:		GEIASECECDSVFNHLEELRLHLEQEMGFEKFFEVYEKIKAIHE
			DEDENIEICSKIVQNILGNEHQHLYAKILHLVMADGAYQEDNDE
5929	3	1558	LDFSMTTQLPAYVAILLFYVSRASCQDTFTAAVYEHAAILPNAT
1	1		LTPVSREEALALMNRNLDILEGAITSAADOGAHTIVTDEDATVC
1 [			WNFNKDSLYPYLEDIPDPEVNWIPCNNRNRFGOTPVOPPI.cci \
]			AKNNSIYVVANIGDKKPCDTSDPOCPPDGRYOYNTDVVF\DSOc
1 1	Ĭ.		KDVARIHKQNLFMGENOFNVPKEPEIVTFNTTFGSFGIFTCFDT
1 1			LFHDPAVTLVKDFHVDTIVFPTAWMNVLPHLSAVEFHSAWAMGM
[ ]	1		RVNFLASNIHYPSKKMTGSGIYAPNSSRAFHYDMKTEEGKT.T.C
i i	1		QLDSHPSHSAVVNWTSYASSIEALSSGNKEFKGTVFFDFFTEUV
l f	1		L'IGVAGNYTVCQKDLCCHLSYKMSENIPNEVVALGAEDGLUTTE
ĺ	İ		GRYYLQICTLLKCKTTNLNTCGDSAETASTRFFMFGI.GGTFCTC
		j	YVFPEVLLSENQLAPGEFOVSTDGRLFSLKPTSGPVLTVTLEGP
5930	113	6082	LYEKDWASNASSGLTAQARIIMLIVIAPIVCSLSW
		6062	RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK
			KLVWIPSERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQ
1		į	KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF
İ		ŀ	CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM
l l			LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN
ł			IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV
1	ļ	į	TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL
!		1	KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG
ſ			FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA
1			KATYERLFRWLVHRINKALDRIKRQGASFIGILDIAGFEIFELN
1	ŀ		SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL
		1	DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ
1	İ		GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND
j	1	1	NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT
1	{	1	KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK
		1	LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP

	070			
	SEQ	Predicted	Predicted end	Amino acid second
	ID	beginning	nucleotide	Amino acid segment containing signal peptide
	NO:	nucleotide	location	
	İ	location	corresponding	
	1	corresponding	to first	1 Transport of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the stat
	1	to first	amino acid	1 2 2 2 2 2 11 2 Market Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning Noning
	1	amino acid	residue of	
	J	residue of		1 5-5611He, Talhreonine Wattaline
	1	amino acid	amino acid	"-11 yptopnan, Y=Tyrosina v 11-1
			sequence	Codon, /=possible nucleotide deletion,
		sequence		\=possible nucleotide insertion)
	1			NAIPKGEMDCKONGERNATION)
	1		i	NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH
	1		1	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
	i	]	1	I WAS TO THE TOTAL OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY
	1	1		TO THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF
	i	İ	1	THE TAKEN OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF T
			1	L
	Į.	1		IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE
	i		ł	RLKKEEKTROELEKAKDKI DCERRON COLOR KINKQEVMISDLEE
	1	ļ	1	RLKKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL AKKEELOGALARGREEK
	1	1	1	AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES
	1	1	1	
	Ĭ .	1	ł	I RE CONTROL ENTREMOTOR DATA TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPER
	1	1		
	1		1	I ~ THE TOTAL PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE
				I AT TO DOUG OUT IN THE CONTROL
	i	J	į	
	j	)		
	Į.	ĺ	1 1	HQRQVASNLEKKQ\KKFDQLLAEEKSISARYAEERDRAEAEARE
	ĺ	1	f l	KETKALSLARALEEALEAKEEFERQNKQLRADMEDLMSSKDDVG
		1	ļ	KNVHELEKSKRALEOOU) FERSEREN AUGUSTADMEDLMSSKDDVG
		Į.	i i	KNVHELEKSKRALEQQV\EEMRTQLEELEDELQATEDAKLRLEV
		1		
	İ	1		
			1	
		:		
Į			Į.	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
- 1			! i	
- 1	- 1			
ļ			1	
- !	ļ			
Ì	5931	113		
- 1		113	6082	RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK
-	I	J		
-1	i	i	1	THE DRY SUMMEDICING ASIM PROPERTY AND ASIM
- [	- 1	ı		CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM
	ļ	l	1:	LODREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN
	- 1	ſ	1.	IPGE\LEROLLOANDILEGEONER PRICE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE
		1	1 :	IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV
ı	}	1	1	TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL
	- 1	1	, -	
1	ľ	1		
ı		1		
1		ı	5	
1	1			
ļ	- !			
1	1	j		
1	- 1		1 =	The Dong Court VARLWKDVDR TVCT TOOTTOMORE
1		1	1	
		i	, –	
Ì			N	AIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH
ı	l		L	EEERDLKITDIIIEEONUGUU DRIIIEEGSKIFFRAGVLAH
	İ	į.	N	EEEROLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR
ŀ	1	ļ	E	CAAYLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVK KOTKVEGELEEMED WOOL PLANTE OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CON
1	i	}		
1			I	THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY O
Ì	l	ļ		
	1	}		
l	]			
l	- 1		1	THE STRUCTURE OF THE RESERVE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRUCTURE OF THE STRU
	İ			
	1			
	Į.	1		
	1		FA	KDAASLESOLODTOELLOGETPOWY TO THE TENER KKGIK
				KDAASLESQLQDTQELLQEETRQKLNLSSRIRQLEEEKNSLQ QBEEEEBARKNLEKQVLALQSQLADTKKKVDDDLGTIESLEEA
				DISCULLINGSQUADTKKKVDDDLGTIESLEEA

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1.0.	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
ł	corresponding	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	to first	to first	L-Leucine, M-Mcthionine, N-Asparagine,
	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
		residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Į	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
Ì			KKKLLKDAEALSQRLEEKALAYDKLEKTKNRLQQELDDLTVDLD
			HQRQVASNLEKKQ\KKFDQLLAEEKSISARYAEERDRAEAEAFF
1			KETKALSLARALEBALEAKEEFERONKOLRADMEDLMSSKDDVG
		1	KNVHELEKSKRALEQQV\EEMRTQLEELEDELOATEDAKLRLEV
		Ì	NMQAMKAQFERDLQTRDEQNEEKKRLLIKQVRELEAELEDERKQ
		ì	RALAVASKKKMEIDLKDLEAQIEAANKARDEVIKOLRKI.OAOMK
			DYQRELEEARASRDEIFAQSKESEKKLKSLEAEILQLQEELASS
			ERARRHAEQERDELADEITNSASGKSALLDEKRRLEARIAQLEE
	1		ELEEEQSNMELLNDRFRKTTLQVDTLNAELAAERSAAQKSDNAR
		i	QQLERQNKELKAKLQELEGAVKSKFKATISALEAKIGQLEEQLE
			QEAKERAAANKLVRRTEKKLKEIFMQVEDERRHADQYKEQMEKA
1			NARMKQLKRQLEEAEEEATRANASRRKLQRELDDATEANEGLSR
ŀ			EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK
	1		TSDVNETQPPQSE
5932	33	572	RHLEEICFLFLQKGRKLKLSGPRWEEGKPRGTGGLWVKAEANMG
1	1		FGATLAVGLTIFVLSVVTIIICFTCSCCCLYKTCRRPRPV\APP
1			PHPP/PVVHAPYPQPPSVPPSYPGPSYQGYHTMPPQPGMPAAPY
	1		PMQYPPPYPAQPMGPPAYHETLAGGAAAPYPASQPPYNPAYMDA
į			PKAAL
5933	1	3190	GTRKLKMADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGPSD
ı			SDMPSRTRPKSPRKHNYRNESARESLCDSPHQNLSRPLLENKLK
1 .			AFSIGKMSTAKRTLSKKEQEELKKKEDEKAAAEIYEEFLAAFEG
	ļ		SDGNKVKTFVRGGVVNAAKEEHETDEKRGKIYKPSSRFADQKNP
			PNQSSNERPPSLLVIETKKPPLKKGEKEKKKSNLELFKEELKQI
			QEERDERHKTKGRLSRFEPPQSDSDGQRRSMDAPSRRNRSSGVL
	l i		DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLKKCCCQEFGRFGP
i	<b>:</b>	1	LASVKIMWPRTDEERARERNCGFVAFMNRRDAERALKNLNGKMI
			MSFEMKLGWGKAVPIPPHPIYIPPSMMEHTLPPPPSGLPFNAQP
			RERLKNPNAPMLPPPKNKEDFEKTLSQAIVKVVIPTERNLLALI
			HRMIEFVVREGPMFEAMIMNREINNPMFRFLFENQTPAHVYYRW
-			KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPPLNPYLHGMSEEQ
			ETEAFVEEPSKKGALKEEQRDKLEEILRGLTPRKNDIGDAMVFC
1			LNNAEAAEEIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA
1	ĺ		KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM
1			TCFRAWEDWAIYPEPFLIKLQNIFLGLVNIIBEKETEDVPDDLD
			GAPIEEELDGAPLEDVDGIPIDATPIDDLDGVPIKSLDDDLDGV
			PLDATEDSKKNEPIFKVAPSKWEAVDESELEAQAVTTSKWELFD
			QHEESEEEENQNQEEESEDEEDTQSSKSEEHHLYSNPIKEEMTE
1			SKFSKYSEMSEEKRAKLREIELKVMKFQDELESGKRPKKPGQSF
1			QEQVEHYRDKLLQREKEKELERERERDKKDKEKLESRSKDKKEK
			DECTPTRKERKRRHSTSPSPSRSSSGRRVKSPSPKSERSERSER
			SHKESSRSRSSHKDSPRDVSKKAKRSPSGSRTPKRSRRSRSRSP
]			KKSGKKSRSQSRSPHRSHKKSKGKTNTGRKFFKKAVTYWKCDLF
			LCPERSVF
5934	1	3190	GTRKLKMADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGPSD
} !			SDMPSRTRPKSPRKHNYRNESARESLCDSPHQNLSRPLLENKLK
			AFSIGKMSTAKRTLSKKEQEELKKKEDEKAAAEIYEEFLAAFEG
			SDGNKVKTFVRGGVVNAAKEEHETDEKRGKIYKPSSRFADQKNP
]	l		PNQSSNERPPSLLVIETKKPPLKKGEKEKKKSNLELFKEELKOI
1			QEERDERHKTKGRLSRFEPPQSDSDGQRRSMDAPSRRNRSSGVL
1 1	į		DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLKKCCCQEFGRFGP
1	1	•	LASVKIMWPRTDEERARERNCGFVAFMNRRDAERALKNLNGKMI
<b>;</b>			MSFEMKLGWGKAVPIPPHPIYIPPSMMEHTLPPPPSGLPFNAQP
i	i		RERLKNPNAPMLPPPKNKEDFEKTLSQAIVKVVIPTERNLLALI
] ]		ĺ	HDMTERINDECIMEENMINDETSTONES
] [	f	İ	HRMIEFVVREGPMFEAMIMNREINNPMFRFLFENQTPAHVYYRW
		!	KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPPLNPYLHGMSEEQ
		İ	ETEAFVEEPSKKGALKEEQRDKLEEILRGLTPRKNDIGDAMVFC
1 1			LNNAEAAEEIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA
1 1			KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM
1 1			TCFRAWEDWAIYPEPFLIKLQNIFLGLVNIIEEKETEDVPDDLD
L	<u> </u>		GAPIEEELDGAPLEDVDGIPIDATPIDDLDGVPIKSLDDDLDGV

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
j	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
ł	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of		S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tvrosine, X=Unknown +=cree
ł	sequence	sequence	Codon, /=possible nucleotide deletion
	pedgeuce		\=possible nucleotide insertion)
		1	PLDATEDSKKNEPIFKVAPSKWEAVDESELEAOAUTTCVIELED
ļ	1		UHEESEEEENQNQEEESEDEEDTOSSKSEEHHIJVSNDTVPENUR
-	ļ		SKISKYSEMSEEKRAKLREIELKVMKFODELESGKRDKKDCOCR
İ	i		QEQVEHYRDKLLQREKEKELERERERDKKDKEKLESRSKDKKEK
		1	DECTPTRKERKRRHSTSPSPSRSSSGRRVKSPSPKSERSERSER
ļ	•		SHKESSRSRSSHKDSPRDVSKKAKRSPSGSRTPKRSRSRSRSP
Į.	İ	1	KKSGKKSRSQSRSPHRSHKKSKGKTNTGRKFFKKAVTYWKCDLF
		1	LCPERSVF
5935	3	4493	SYWLSGWRLSRPPROFWAGWRGIGRFGTMAPVHGDDCEIGASAL
1	j		SDSGSFVSSRARREKKSKKGRQEALERLKKAKAGERYKYEVEDF
	1	[	TGVVFFVDFFOVEVIVOARORDENTERLIKKAKAGERYKYEVEDF
ĺ	ĺ		TGVYEEVDEEQYSKLVQARQDDDWIVDDDGIGYVEDGREIFDDD
1		ĺ	LEDDALDADEKGKDGKARNKDKRNVKKLAVTKPNNIKSMFIACA
1	1		GKKTADKAVDLSKDGLLGDILQDLNTETPQITPPPVMILKKKRS
i			IGASPNPFSVHTATAVPSGKIASPVSRKEPPLTPVPLKRAEFAG
			DDVQVESTEEEQESGAMEFEDGDFDEPMEVEEVDLEPMAAKAWD
			KESEPAEEVKQEADSGKGTVSYLGSFLPDVSCWDIDQEGDSSFS
1			VQEVQVDSSHLPLVKGADEEQVFHFYWLDAYEDQYNQPGVVFLF
l i			GKVWIESAETHVSCCVMVKNIERTLYFLPREMKIDLNTGKETGT
			PISMRDVYEEFDEKIATKYKIMKFKSKPVEKNYAFETDDUBENG
			EYLEVKYSAEMPQLPQDLKGETFSHVFGTNTSSLELFLMNRKIK
			GPCWLEVKKSTALNQPVSWCKVEAMAI.KPDI.VNVIKEVERDDI.II
i	l I		VMAFSMKTMQNAKNHONEIIAMAALVHHSFALDKAADKDDDCCK
	i		FCVVSKPKDCIFPYAFKEVIEKKNVKVEVAATERTIJGERIAWI
			HKIDPDIIVGHNIYGFELEVILORINVCKADUWGKICDI KDCDM
1 1			PKLGGRSGFGERNATCGRMICDVEISAKELTRCKSVHT.SELVOO
1 1			LLKIERVVIPMENIONMYSESSOLLYILEHTWKDA\KEILOIMG
	j		ELNVLPLALQITNIAGNIMSRTLMGGRSERNRELLLUARVENDY
1 1			IVPDKQIFRKPQQKLGDEDEEIDGDTNKYKKGRKKGAYAGGLVL
1 1			DPKVGFYDKF1LLLDFNSLYPSI1QEFN1CFTTVQRVASEAQKV
1 1			TEDGEQEQIPELPDPSLEMGILPREIRKLVERRKQVKQLMKQQD
1 1	i		LNPDLILQYDIRQKALKLTANSMYGCLGFSYSRFYAKPLAALVT
$1 \qquad 1$	1		YKGREILMHTKEMVQKMNLEVIYGDTDSIMINTNSTNLEEVFKL
			GNKVKSEVNKLYKLLEIDIDGVFKSLLLLKKKKYAALVVEPTSD
			GNYVTKQELKGLDIVRRDWCDLAKDTGNFVIGQILSDQSRDTIV
1 1	ł.		ENIQKRLIEIGENVLNGSVPVSQFEINKALTKDPQDYPDKKSLP
1	1	i	HVHVALWINSQGGRKVKAGDTVSYVICQDGSNLTASQRAYAPEQ
1 1		i i	LOKODNI-TIDTOVVI-ACCIUDINARI CERTIFICATI
1			LQKQDNLTIDTQYYLAQQIHPVVARICEPIDGIDAVLIATGWEL \DPTQFKVHHYHKDEENDALLGGPAQLTDEEKYRDCERFKCPCP
1	1	j	TCGTENT VDMVEDGGGTDMPDGLTDEEKYRDCERFKCPCP
1	1	[	TCGTENIYDNVFDGSGTDMEPSLYRCSNIDCKASPLTFTVQLSN
1		1	KLIMDIRRFIKKYYDGWLICEEPTCRNRTRHLPLQFSRTGPLCP
]	į		ACMKATLQPEYSDKSLYTQLCFYRYIFDAECALEKLTTDHEKDK
1 1	ļ		LKKQFFTPKVLQDYRKLKNTAEQFLSRSGYSEVNLSKLFAGCAV KS
5936	1124	139	
			RGEEQFDAEFRRFACLGFGERLQEFSRLLRAVHRSRAWTCYLAI
1 1			RMLMATCCPSPTTTACTGPWORAPPLRIJVOKPRADSSCIARAS
1 1		ŀ	NSLCRRKKGLLLRPVAPLRTRPPLLISLPODFROVSSVITOUDIT
	Ţ	ı	PETHRRVRLHKHGSDRPLGFYIRDGMSVRVAPOG\1.EPVPGTBT
Į	ľ	i i	SKLVRGGLAESTGLLAVSDEILEVNGIEVAGKTINOVTDMMUAN
į į		ļ	SHN\LIVTVKPANQRNNVVRGASGRLTGPPSAGPGPAFPDSDDD
			SSDLVIENRQPPSSNGLSQGPPCWDLHPGCRHPGTRSSLPSLDD
5937		·	QEQASSGWGSRIRGDGSGFSL
3337	31	1600	PTSLLKSTVQLMCRLLQDKRYOCVYSLAEIFKVLASFVVII VII
	1	į	IGLTSSYSLWWMLRSSLKQYSFEALREKSNYSDIPDVKNDEART
1		<u>.</u>	LHLADQYDPLYSKRFSIFLSEVSENKLKOINLNNEWTVERI VCV
1	1	1:	LVKNAQDKIELHLFMLNGLPDNVFELTEMEVLSLELIPEVKLPS
	f		AVSQLVNLKELRVYHSSLVVDHPALAFLEENLKILRLKFTEMGK
1	ļ		IPRWVFHLKNLKELYLSGCVLPEQLSTMQLEGFQDLKNLRTLYL
1		1 :	KSSLSRIPQVVTDLLPSLQKLSLDNEGSKLVVLNNLKKMVNLKS
1			LELISCDLERIPHSIFSLONLHELDLRENNLKTVEEIISFQHLQ
1	j	1;	NLSCLKI.WHNNIAYIBAOICAI CAT COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COLOR TO THE COL
		1:	NLSCLKLWHNNIAYIPAQIGALSNLEQLSLDHNNIENLPLQLFL
			CTKLHYLDLSYNHLTFIPEEIQYL\SNLQYFAVTNN1EMLPDG

SEC	Predicted	1	
ID	beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1.0.	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
- 1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
		<del> </del>	LFQCKKLQCLLLGKNSLMNLSPHVGELSNLTHREPIG\NYLETL
			PPELEGCQSLKRNCLIVEENLLNTLPLPVTERLQTCLDKC
5938	395	1865	YKGEGFFCNQEARGERRKKKKAMSSPNIWSTGSSVYSTPVFSQK
l	}		MTVWILLLSLYPGFTSQKSDDDYEDYASNKTWVLTPKVPEGDV
	1	}	TVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGPVNAINME
1	}		YTIDIFFAQTWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRN
			SKKADAHWITTPNRMLRIWNDGRVLYSLRLTIDAECQLQLHNFP
1	1		MDEHSCPLEFSSYGYPREEIVYQWKRSSVEVGDTRSWRLYOFSF
1	1	1	VGLRNTTEVVKTTSGDYVVMSVYFDLSRRMGYFTIOTYIPCTLT
}	}		VVLSWVSFWINKDAVPARTSLGITTVLTMTTLSTIARKSLPKVS
	i		YVTAMDLFVSVCFIFVFSALVEYG\TLHYFVSNRKPSKDKDKKK
	Ì		KNPAPTIDIRPRSATIQMNNATHLOERDEEYGYECLDGKDCASE
İ			FCCFEDCRTGAWRHGRIHIRIAKMDSYARIFFPTAFCLFNLVYW
5939	66		VSYLYL
1 3333	• • • • • • • • • • • • • • • • • • • •	1404	IRPGYLKEVQENSPGHRAGLEPFFDFIVSINGSRLNKDNDTLKD
			LLKANVEKPVKMLIYSSKTLELRETSVTPSNLWGGQGLLGVSIR
			FCSFDGANENVWHVLEVESNSPAALAGLRPHSDYIIGADTVMNE
			SEDLFSLIETHEAKPLKLYVYNTDTDNCREVIITPNSAWGGEGS
			LGCGIGYGYLHRIPTRPFEEGKKISLPGQMAGTPITPLKDGFTE VQLSSVNPPSLSPPGTTGIEQSLTGLSISSTP\PAVSSVLSTGV
			PTVP\LLPPQVNQSLTSVPPMESSYLHLPGLMPFTRQGLPNLPQ
Ĭ	(		PSTFNLPR\PTHSWPGVGLYQEFVKPGVLPPLSSMPPRNLPG\I
1	ł l		APLPLPSEFLPSFPLVPESSSAASSGELLSSLPPTSNAPSDPAT
l			TTAKADAASSLTVDVTPPTAKAPTTVEDRVGDSTPVSEKPVSAA
			VDANASESP
5940	145	717	RRSASRSASPROSAGTAVTTGTRAGGTCLAAAHHRMRWRADGRS
	i		LEKLPVHMGLVITEVEQEPSFSDIASLVVWCMAVGISYISVYDH
ı	1		QGIFKRNNSRLMDEILKQQQELLGLDCSKYSPEFANSNDKDDOV
ł	}		LNCHLAVKVLSPEDGKADIVRAAQDFCQLVAQKQKRPTDLDVDT
5941	13	6146	LA\VYLVQMVVLILI
	"	6147	MCLGRMGASSPRSPEPVGPPAPGLPFCCGGSLLAVVVLLALPVA
1			WGQCNAPEW\LPFARPTNLTDEFEFPIGTYLNYECRPGYSGRPF SIICLKNSVWTGAKDRCRRKSCRNPPDPVNGMVHVIKGIQFGSQ
	1		IKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPP
1 .	1		TITNGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIY
	1		CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL
	ì		NEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPPPD
·1			VLHAERTQRDKDNFSPGQEVFYSCEPGYDLRGAASMRCTPQGDW
	[		SPAAPTCEVKSCDDFMGQLLNGRVLFPVNLOLGAKVDFVCDEGF
}			QLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTG
	i i		KPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPOGNG
		· .	VWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYE
			CRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVH
1			VITDIQVGSRINYSCTTGHRLIGHSSAECILSGNAAHNSTKPPI
.			CORIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKV
			FELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGIL
1			VSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPS
1 !			CSRVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPGYDLRGAA
1	İ		SMRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGA KVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSP
			PVIPNGRHTGKPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTI
!			RCTSDPQGNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASD
1			FPIGTSLKYECRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKT
1			PPDPVNGMVHVITDIQVGSRINYSCTTGHRLIGHSSAECILSGN
1	1		TAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGSVVTYR
1	1	1	CNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKC
} }	1	j	TPPNVENGILVSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQA
] !		İ	LNKWEPELPSCSRVCQPPPEILHGEHTPSHQDNFSPGOEVFYSC
] [		[	EPGYDLRGAASLHCTPQGDWSPEAPRCAVKSCDDFLGQLPHGRV
[		İ	LFPLNLQLGAKVSFVCDEGFRLKGSSVSHCVLVGMRSLWNNSVP
<b></b>			VCEHIFCPNPPAILNGRHTGTPSGDIPYGKEISYTCDPHPDRGM

	SEC	Predicted	Predicted en	d 1 2000
	ID	beginning	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s	
	NO:	nucleotide	nucleotide	
	1	1	location	Glutamic Acid F. Phanes
	ł	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	i	corresponding	to first	
	- 1	to first		D-MCGCLIG, MEMOLINA NO News
	1	amino acid	amino acid	I
	1		residue of	S=Serine, T=Threonine, V=Valine,
	ŀ	residue of	amino acid	Tarmeonine, V=Valine,
	- {	amino acid	sequence	I "-ILYPLOPHAN. Y=Tyrogine V III
	1	sequence	sequence	
		seducine		\=possible nucleotide insertion)
	i			TENTICE CENTER (TENTION)
	1	i	1	TFNLIGESTIRCTSDPHGNGVWSSPAPRCELSVRAGHCKTPEQF
		l	į.	I TO THE TAP AND TO PROGRESS INVECTOR OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE PROGRESS OF THE P
	ĺ	1	1	SVEDNCRRKSCGPPPEPFNGMVHINTDTQFGSTVNYSCNEGFRL
	f	İ	i	IGSPSTTCLVSCMMUTHDEVENDERSTONISCNEGFRL
		J		IGSPSTTCLVSGNNVTWDKKAPICEIISCEPPPTISNGDFYSNN
	1		ĺ	1 TO THE TOTAL OF THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE TAX TO THE
	ĺ	4		TOTAL TOTAL TRANSPORT OF THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE T
	1	l.	}	1 2011 ACCOTMOVM(ADXI/DHC/GDA/QUPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP
			İ	DNFSPGQEVFYSCEPSYDLRGAASLHCTPQGDWSPEAPRCTVKS
	i	l l		CDDFLGOLDHGDVILL DIVISIONAL PQGDWSPEAPRCTVKS
	1	J	1	CDDFLGQLPHGRVLLPLNLQLGAKVSFVCDEGFRLKGRSASHCV
	1	1	1	- COMMISS VEVILED I RUDDIN TI MODITIONE CONTROL
	1		i	1
	1	l .		I
	ł	1	Ī	GFIFCTDQGIWSQLDHYCKEVNCSFPLFMNGISKELEMKKVYHY GDYYTLKCEDGYTLECSPNGGGSFPLFMNGISKELEMKKVYHY
		ř	j	GDYWTLACEDCAMI DOGGOOD ON THE WING ISKELEMKKVYHY
	l	ļ	1	
	ł	İ	1	
	5942	4509		
		4509	688	YLYVRMRANPLAYGISHKAYQIDPPL\RKHREQ\LVIE\VGRKL
	j	ľ		DK\AQMIRFEERTGYFSSTDLGRTASHYYIKYNTIETFNELFDA
	ĺ	1	Į.	HKTECDIES THOUSE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE THE TRUE TO BE
	İ	1	į	
		1	1	
		1		
			ł	
1		1	1	SVMMEAFIQPITRTVLRVTLSIYADFTWNDQVHGTVGEPWWIWV
1			•	EDPTNDHIVHSEVEL AL WYONT OF THE TWNDQVHGTVGEPWWIWV
		1		EDPTNDHIYHSEYFLALKKQVISKEAQLLVFTIPIFEPLPSQYY
		1		T TO THE TOTAL PROPERTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE
- 1		1		The state of the country of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the
- 1			ı	T TO THE TEN THE TEN TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TENT TO THE TE
- 1		·		GKKVIELTGDVTPDMKSIAKADLIVTTPEKWDGVSRSWQNRNYV
- 1		j j		OOVTILI IDETHILGEPRODUT TURNING THE RWEGVSRSWQNRNYV
- 1		1		QQVTILIIDEIHLLGEERGPVLEVIVSRTNFISSHTEKPVRIVG
				1
- 1		] i		T TO THE TOTAL OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF
- 1		1 1		The second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of th
- 1		1 1		I TATE OF THE PROPERTY OF THE PROPERTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF TH
- 1		i i		TEYYDGKTRRYVDFPITDVLQMMGRAGRPQFDDQGKAVILVHDI
- 1		l :		KKDEVKKELVEDEDVEGGEAGRAGRAGRAGEADDOGKAVILVHDI
- 1				
- ]				1 AND IMPSIANICOVS DOLLAR OF COMPANY
- 1				
- 1		1		
1		ļ f	i	DSPHTKAHLLLQAHLSRAMLPCPDYDTDTKTVLDQALRVCQAML
				DVAANOGWIJZTVI NITTVI TOMETO CENTUTOTKI VLIDQALRVCQAML
ı		i i		
1			ŀ	TO THE TRIBERANCE IN THE TOTAL ACCUMENTS
1	ı	ļ	1	
1		1		
	ì	1	J	
1	ł	i	i	PEIPGRYIYTLYFMSDCVLGLDOOVD (N. GODING
-			1	PEIPGRYIYTLYFMSDCYLGLDQQYD/NLSQRYTSESFCTGQHQ
1	5943	1	2274	
	I			DKPTRHKTYLSSSWAKMAAAEGPVGDGELWQTWLPNHVVFLRLR EGLKNOSPTEAEKDASSGLAGGER
1	J			
1	- 1			
	1	1		LSPTQHHVALIGIKGLMVLELPKRWGKNSEFEGGKSTVNCSTTP
1		1	1	VAEREFECCEC IN MAINTAINE TO THE TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTA
1	I	i		
1	- 1	1.		K VIIIVIIIVIIIVIIIVIIIVIIIVIIIVIIIVI
1	i	i		
1	- 1	į.		
ı	- 1	1	j	YHCVVLEGEEEDDHTSEYCODGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
1	- 1	Í	ľ	THE THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPER
l	1	ļ	II 3	
1	- 1	1		TO THE POST OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF
)	Í	ſ	1 '	
1	- 1	1	1.3	· · · · · · · · · · · · · · · · · ·
!	- 1	Í	1 3	IAPPPEECLOLLSPATOVERPOYET
				KKKQLEDLSYCREERKSLREMAERLADKYEEAKEKQEDIMNRMK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
l l	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
į.	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
l	sequence	_	\=possible nucleotide insertion)
			KLLHSPHSELPVLSDSERDMKKELQLIPDQLRHLGNAIKQVTMK
	1		KDYQQQKMEKVLSLPKPTIILSAYQRKCIQSILKEEGEHIREMV
	1	ł	KQINDIRNHVNF
5944	167	3428	FSIATFTDEPEVLTEPPSATTTTTIGISATWTTLAGSHGKRNNT
			ITTTSSKRKNRKNKITPENVQIIFDDPLPISYSQPEKVNGESKS
	1	İ	SSTSESGDSDNMRISSCSDESSNSNSSRKSDNHSPAVVTTTVSS
1		1	KKQPSVLVTFPKEERKSVSGKASIKLSETISEGTSNSLSTCTKS
j			GPSPLSSPNGKLTVASPKRGQKREEGWKEVVRRSKKVSVPSTVI
Ī	1	]	SRVIGRGGCNINAIREFTGAHIDIDKQKDKTGDRIITIRGGTES
	1		TRQATQLINALIKDPDKEIDELIPKNRLKSSSANSKIGSSAPTT
-	t .		TAANTSLMGIKMTTVALSSTSQTATALTVPAISSASTHKTIKNP
	ŀ	1	VN\NVRPGFPVSFP\LAYPPPOFAHALLAAQTFQQIRPPRLPMT
-	•		HFGGTFPPAQSTWGPFPVRPLSPARATNSPKPHMVPRHSNQNSS
	ļ		GSQVNSAGSLTSSPTTTTSSSASTVPGTSTNGSPSSPSVRRQLF
	i		VTVVKTSNATTTTVTTTASNNNTAPTNATYPMPTAKEHYPVSSP
	į		SSPSPPAQPGGVSRNSPLDCGSASPNKVASSSEQEAGSPPVVET
	Ĭ	ļ	TNTRPPNSSSSGSSSAHSNQQQPPGSVSQEPRPPLQQSQVPPP
			EVRMTVPPLATSSAPVAVPSTAPVTYPMPQTPMGCPQPTPKMET
			PAIRPPPHGTTAPHKNSASVQNSSVAVLSVNHIKRPHSVPSSVQ
			LPSTLSTQSACQNSVHPANKPIAPNFSAPLPFGPFSTLFENSPT
	i		SAHAFWGGSVVSSQSTPESMLSGKSSYLPNSDPLHQSDTSKAPG
1			FRPPLQRPAPSPSGIVNMDSPYGSVTPSSTHLGNFASNISGGQM
			YGPGAPLGGAPAAANFNRQHFSPLSLLTPCSSASNDSSAQSVSS
Į.	[		GVRAPSPAPSSVPLGSEKPSNVSODRKVPVPIGTERSARTROTG
1			TSAPSVIGSNLSTSVGHSGIWSFEGIGGNODKVDWCNPGMGNPM
ĺ			IHRPMSDPGVFSQHQAMERDSTGIVTPSGTFHOHVPAGYMDFPK
1			VGGMPFSVYGNAMIPPVAPIPDGAGGPIFNGPHAADPSWNSLIK
			MVSSSTENNGPQTVWTGPWAPHMNSVHMNOLG
5945	1461	197	GVTHLFLFGKRKLRNGIAEDLKGQADFFFLLVSEAVVATGSPRA
			WLTCLILPLPGIIFSVLPKAMSRPLLITFTPATDPSDLWKDGOO
			QPQPEKPESTLDGAAARAFYEALIGDESSAPDSORSOTEPARER
			KRKKRRIMKAPAAEAVAEGASGRHGQGRSLEAEDKMTHRILRAA
1			QEGDLPELRRLLEPHEAGGAGGNINARDAFWWTPLMCAARAGOG
1 1			AAVSYLLGRGAAWVGVCELSGRDAAOLAEEAGFPEVARMVRESH
			GETRSPENRSPTPSLQYCENCDTHFODSNHRTSTAFLLSLSOGP
	•		QPPNLPLGVPISSPGFKLLLRGGWEPSMGLGPRGEGRANDIDTV
i			LKRDQEGLGYRSAPQPRVTHFPAWDTRAVAGRE\TPPRVATLSW
5946			REERRREE\KDRAWERDLRTYMNLEF
3346	541	1666	ILGSYSSIQPEEYS\SVVC\EVVLQDLLA\YVSPK\HSYLRDLP
1		Ì	SEGSPQRVNSIDFV\EL\EHLQPDVLVHAVLRVVDF/TILTEAV
1	1		YSYRGQKQKKVMLTVEQAQDQHYALVLWGPGAAW\YPQLQRKKG
ł I			YIWEFKYLFVQCNYTLENLELHTTPWSSCECLFDDDIRAITFKA
1 1	ł		KFQKSAPSFVKISDLATHLEDKCSGVVLIKAQISELAFPITASQ
	1		KIALNAHSSLKSIFSSLPNIVYTGCAKCGLELETDENRIYKQCF
	1		SCLPFTMKKIYYRPALMTAIDGRHDVCIRVESKLIEKILLNISA
1			DCLNRVIVPSSEITYGMVVADLFHSLLAVSAEPCVLKIQSLFVL
5947	3		DENSYPLOODFSLLDFYPDIVKHGANARL
55.7	, ,	1317	RGIPDRRRRGPIGRVNMDLENKVKKMGLGHEQGFGAPCLKCKEK
1 1			CEGFELHFWRKICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDT
į (		ì	KYTTLIAKLKSDGIPMYKRNVMILTNPVAAKKNVSINTVTYEWA
}	ł		PPVQNQALARQYMQMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD
]	l	J	QDPSKCHELSPREVKEMEQFVKKYKSEALGVGDVKLPCEMDAQG
1		1	PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCCKLSMKEG
1 1	1		DPATYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNBKLYCG
			RHYCDSEKPRCAGCDELIFSNEYTQAENQNWHLKHFCCFDCDSI
1	j	i	LAGEIYVMVNDKPVCKPCYVKNHAVVCQGCHNAIDPEVORVTYN
5948			NFSWHASTECFLCSCCSKCLIGQKFMPVEGMVFCSVECKKRMS
05.60	39	3370	YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPTDO
] [	ľ	1	GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAOAORM
	ł		VEIEIEGRLHRISIFDPLEIILEDDLTAOEMSECNSNKENSERP
			PVCLRTKRHKNNRVKKKNEALPSAHGTPASASALPEPKVRIVEY

	SEQ	Predicted	Predicted end		
	ID	beginning	nu-1		
•	NO:	nucleotide	nucleotide	(A=Alanine, C=Cvsteine, D. A	
	1	uncreoride	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=	
	ſ	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,	
	į	corresponding	to first		
		to first		1 MEDISEDIONING NA NEW COLUMN	
	i .	amino acid	amino acid	1	
	ĺ		residue of	S=Serine, T=Threonine, V=Valine,	
	1	residue of	amino acid	to mental, l'illreonine, V=Valine,	
	İ	amino acid	f	I "" Lypcopnan, Y=Tyrogino v mil	
		sequence	sequence		
		sequence		\=possible nucleotide insertion)	
- 1				SDECARDED DESCRIPTION (SPECION)	
ı		1	1	SPPSAPRRPPVYYKFIEKSAEELDNEVEYDMDEEDYAWLEIVNE KRKGDCVPAVSOSMEER	
- 1		1		1 WOOD O A TURNO CONT. THE PRINCIPLE HERE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHARLES AND COMPANY OF THE CHA	
ļ		ì	1	VCCICMDGECONSNVTLECOMONI AUTOCOMONIA	
ı				VCCICMDGECQNSNVILFCDMCNLAVHQECYGVPYIPEGQWLC/	
J			1	1	
- 1		1	i	I - 1. C. T. A LA LEGISTICA KNI DDADMET TI CATE CAMERATE ASSESSED	
		í	Ì	I RESIDENCE INTROVICACIONALI, VMVMEDUVDI MORGODO-	
			ľ	YCDVHTPPGCTRRPLNIYGDVEMKNGVCRKESSVKTVRSTSKVR	
- 1		1		WYNYWAY A DECEMBER OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STRE	
- 1		1	1	A STAN AND THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE	
		1	1		
J		1		KAAKEKLKYWQRLRHDLERARLLIELLRKREKLKREQVKVEQVA	
- 1		i	1	MET.RI.TDI.TUI I DOVI DOT TOTAL	
			Í		
1		1	i		
- 1		1	İ		
		1		RRPFSWEDVDRLLDPANRAHLGLEEQLRELLDMLDLTCAMKSSG	
		1		SPSKPAKITYKETATT	
ı		1		T = T = T = T = T = T = T = T = T = T =	
		[		1 or proper absente TPDONKKBSDCACCDCDATEER CO	
		J i		1 1	
- 1		1		The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s	
		l l		GQSSMWISTDAAASVLEPLKVVWAKCSGYPSYPALIIDPKMPRV	
				PGHHNGUTTPA DEL DUT "TOTTE LA COGTEST PALITOPEMPRV	
- 1		•		PGHHNGVTIPAPPLDVLKIGEHMOTKSDEKLFLVLFFDNKRSWQ	
Ŀ		1		The second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of th	
	5949	39	3370		
ı	ſ		3370	YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDQ	
- 1				GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAQAQRM	
	į	j		VEIELEGRI-HPISTEDDIETTI DOOL ARSPTRETLTYAQAQRM	
	1	[		VEIEIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP	
- 1					
ĺ	!	į.			
	ł	1			
- 1	- 1	]		VCCICMDGECQNSNVILFCDMCNLAVHQECYGVPYIPEGQWLC/	
f	1	1		RAHCLOSPAPPADCHI CONVICON TOTAL PROPERTY OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF TH	
- 1	ŀ			RAHCLQSRARPADCVLCPNKGGAFKKTDDDRWGHV\VCALW\IP	
- {	- 1	ļ		~ \- ~ \- \- \- \- \- \- \- \- \- \- \- \- \-	
- [	ĺ	ſ	i	* TOTAL A CHOKAGI YMKMPDUVET TOOOTERS	
-	ĺ				
- 1	i	1		KKAKKAKALAEPCAVLPTVCAPYIPPQRLNRIANQVAIQRKKQ	
- 1	Į.	1	ĺ	FVERAHSYWLLKRLSRNGAPLLRRLQSSLQSQRSSQQRENDEEM	
- 1	- 1	i	1	KAAVEVI VYWODI BURK BARKLQSSLQSQRSSQQRENDEEM	
	- 1	i	i		
- 1	1		1	THE PERSON AND A DISTRICT OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF T	
- 1	- 1		i		
- 1	í		ł		
- 1	1	i	ļ	RRPFSWEDVDRLLDPANRAHLGLEEQLRELLDMLDLTCAMKSSG	
- 1	1	ľ		SRSKRAKLI KVETALI BUTT COMPANIE LEDMLDLTCAMKSSG	
1	1		i i	SRSKRAKLLKKEIALLRNKLSQOHSQPLPTGPGLEGFEEDGAAL	
1	J	1	}		
- 1	•		1		
1	i		ĺ		
1			į.	GQSSMWISTDAAASVLEPLKVVWAKCSGYPSYPALIIDPKMPRV	
1	- 1		l	PGHHNGUTI DA DDI DUI KTGOWAKLSGI PSYPALIIDPKMPRV	
	j	ŀ	ł	PGHHNGVTIPAPPLDVLKIGEHMQTKSDEKLFLVLFFDNKRSWQ	
1		1	į,	TOTAL TOTAL STANDARD CONCETTONING TOTAL TOTAL STANDARD CONCETTONING TOTAL TOTAL STANDARD CONCETTONING TOTAL STANDARD CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCETTONING CONCE	
5	950	1166			
1	i	-200	373	ESRS_TMSTSQPGACPCQGAASRPAILYALLSSSLKAVPRPRSR	
1	- 1	1	1 .	CLCRQHRPVQLCAPHRTCREALDVLAKTVAFLRNLPSFWQLPPQ	
1	i i		1 :	DORR LLOGCEGET ECT TOTAL TOTAL VAF LENLPS FWQLPPQ	
1	I	1			
1	- 1	i	1.5		
1	i	ł			
<u> </u>	951	143			
1 3		143	5449 V	WNVKPSLLVVOLEKESDVERHEOVE	
1	i	l	1;	WVKPSLLVVQLFKFSDKEEHEQNDSISGKTGETGVEEMIATRK	
Ī	í	i			
!	Į	ļ	· · · · · · · · · · · · · · · · · · ·	COLDO LECNOSONO IMICITADIO PROPERTO	
i	1	1		CONTRACTOR A DE TITOSINTIE A A DE CALLA DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DE CALLA DATA - CONTRACTOR DATA - CONTRACTOR DE CALLA	
j	Į	1	1 0	THSKONMTTDA PKYTUA A WILLIAM TO THE KONMTTDA PKYTUA A WILLIAM TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL THE TOTAL TO  TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL THE TOTAL TO	
				QNFHRPVKVRKKQIDKEPKIQSCNSGVKSVKNQAHSVLKKTLQ	

SEQ	Predicted	Dwodiahad .	
ID	beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L-Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	bequence	Codon, /=possible nucleotide deletion,
			\=possible nucleotide insertion)
			DQTLVQIFKPLTHSLSDKSHAHPGCLKEPHHPAQTGHVSHSSQK
ŀ	}		QCHKPQQQAPAMKTNSHVKBELEHPGVEHFKEEDKLKLKKPEKN
	[		LQPRQRRSSKSFSLDEPPLFIPDNIATIRREGSDHSSSFESKYM
1	1		WTPSKQCGFCKKPHGNRFMVGCGRCDDWFHGDCVGLSLSQAQQM
İ	l		GEEDKEYVCVKCCAEEDKKTEILDPDTLENQATVEFHSGDKTME
1			CEKLGLSKHTTNDRTKYIDDTVKHKVKILKRESGEGRNSSDCRD
ŀ		İ	NEIKKWQLAPLRKMGQPVLPRRSSEEKSEKIPKESTTVTCTGEK
J	ļ.		ASKPGTHEKQEMKKKKV\EKGVLNVHPAASASKPSADQIRQSVR
			HSLKDILMKRLTDSNLKVPEEKAAKVATKIEKELFSFFRDTDAK
ł	1		YKNKYRSLMFNLKDPKNNILFKKVLKGEVTPDHLIRMSPEELAS
	1		KELAAWRRRENRHTIEMIEKEQREVERRPITKITHKGEIEIESD APMKEQEAAMEIQEPAANKSLEKPEGSEK\RKEEVDSMSKDTTS
1	1		QHRQHLFDLNCKICIGRMAPPVDDLSPKKVKVVVGVARKHSDNE
	1		AESIADALSSTSNILASEFFEEEKQESPKSTFSPAPRPEMPGTV
1			EVESTFLARLNFIWKGFINMPSVAKFVTKAYPVSGSPEYLTEDL
Ì			PDSIQVGGRISPQTVWDYVEKIKASGTKEICVVRFTPVTEEDQI
1	1		SYTLLFAYFSSRKRYGVAANNNKQVKDMYLIPLGATDKIPHPLV
1			PFDGPGLELHRPNLLLGLIIRQKLKRQHSACASTSHIAETPESA
ļ	1		PPIALPPDKKSKIEVSTEEAPEEENDFFNSFTTVLHKQRNKPQQ
1	ļ		NLQEDLPTAVEPLMEVTKQEPPKPLRFLPGVLIGWENQPTTLEL
	ļ i		ANKPLPVDDILQSLLGTTGQVYDQ\AQSVMEQNTVKBIPFLNEQ
	ľ		TNSKIEKTDNVEVTDGENKEIKVKVDNISESTDKSAEIETSVVG
	1 1		SSSISAGSLTSLSLRGKPPDVSTEAFLTNLSIQSKQEETVESKE
	1		KTLKRQLQEDQENNLQDNQTSNSSPCRSNVGKGNIDGNVSCSEN
-	1		LVANTARSPQFINLKRDPRQAAGRSQPVTTSESKDGDSCRNGEK
i	1		HMLPGLSHNKEHLTEQINVEEKLCSAEKNSCVQQSDNLKVAQNS
	ļ .		PSVENIQTSQAEQAKPLQEDILMQNIETVHPFRRGSAVATSHFE
1	1		VGNTCPSEFPSKSITFTSRSTSPRTSTNFSPMRPQQPNLQHLKS
}	]		SPPGFPFPGPPNFPPOSMFGFPPHLPPPLLPPPGFG\FA\ONDM
1	1		VPWPPVV\HLP\GQPQRMMGPLSQASRYIGPONFYOVKD + PP PF
1	1		RRHSDPWGRQDQQQLDRPFNRGKGDRORFYSDSHHLKPFPHFYF
	ļ		WEQESERHRRRDRSQDKDRDRKSREEGHKDKERARLSHCDRGTD
			GKASRDSRNVDKKPDKPKSEDYEKDKEREKSKHREGEKDRDRYH
5952	7006		KDRDHTDRTKSKR
3952	3226	639	PPARRSARDLPRALSMEAARPSGSWNGALCRLL\LVTL\AFLIF
İ			ASDACKNVTLHVPSKLDAEKLVGRVNLKECFTAANLTHSSDEDE
1			QILEDGSVYTTNTILLSSEKRSFTILLSNTENOEKKKIFVFLFU
1			QTKVLKKRHTKEKVLRRAKRRWAPIPCSMLENSLGPFPLFLOOV
1			QSDTAQNYTIYYSIRGPGVDQEPRNLFYVERDTGNLYCTR DVDP
1	Į		EQYESFEILAFATTPDGYTPELPLPLIIKIEDENDNVDIETER
	1		YTFT1FENCRVGTTVGQVCATDKDEPDTMHTRLKYS1IGQVPPS
	• ]		PTLFSMHPTTGVITTTSSQLDRELIDKYOLKIKVODMDGOVEGI.
i I			QTTSTCIINIDDVNDHLPTFTRTSYVTSVEENTVDVETLDVTVE
[			DKDLVNTANWRANYTILKGNENGNFKIVTDAKTNEGVLCVVKPL
1 1			NYEBKQQMILOIGVVNEAPFSREASPRSAMSTATVTVNVEDQDE
[ ]			GPECNPPIQTVRMKENAEVGTTSNGYKAYDPETRSSSGIRYKKL
[	İ		TDPTGWVTIDENTGSIKVFRSLDREAETIKNGIYNITVLASDQG
1 1			GRTCTGTLGIILQDVNDNSPFIPKKTVIICKPTMSSAEIVAVDP
] [	1	j	DEPIHGPPFDFSLESSTSEVQRMWRLKAINDTAARLSYQNDPPF
		1	GSYVVPITVRDRLGMSSVTSLDVTLCDCITENDCTHRVDPRIGG
ļ ļ		i	GGVQLGKWAILAILLGIALFFCILFTLVCGASGTSKQPKVIPDD
			LAQQNLIVSNTEAPGDDXVYSANGFTTQTVGASAQGVCGTVGSG
ĺ	1	į	IKNGGQETIEMVKGGHQTSESCRGAGHHHTLDSCRGGHTEVDNC
5953	330	911	RYTYSEWHSFTQPRLGEESIRGHTLIKN
	330	811	PLLCNPDPGWYWWVKQESEISKESQEMDARPKLDLGFKEGQTIK
			LCIGNITNKKGGASKPRTARGGGLSLLPPPPGGKVTIPPPSS/V
			KLPSTNHVTPPSIPKSNHGGSDADILLDLDSPAPVTTPAPTPVS
5954	32	2720	VSNDLWGDFSTASSSVPNQAPQPSNWVQF
	۵.	2130	PPPPPPKLANMADLEAVLADVSYLMAMEKSKATPAARASKRIVL
- 1	}	i	PEPSIRSVMQKYLAERNEITFDKIFNQKIGFLLFKDFCLNEINE
			AVPQVKFYEEIKEYEKLDNEEDRLCRSRQIYDAYIMKELLSCSH

SEO	15-21		
. ~	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid E DEASpartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	
- 1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
İ	amino acid	residue of	Partorine, Oaglutamine Dangining
l	residue of		S=Serine, T=Threonine, V=V=line
1	amino acid	amino acid	W=Tryptophan, Y=Tyrosine V-III
	sequence	sequence	Couon, /=possible nucleofide deleti
<del></del>	sequence		\=possible nucleotide insertion)
1	j		PFSKQAVEHVQSHLSKKQVTSTLFQPYIEEICESLRGDIFQKFM
ļ		f	ESDKETERCORKNUELNING
ı	1	}	ESDKFTRFCQWKNVELNIHLTMNEFSVHRIIGRGGFGEVYGCRK
i		1	ADTGKMYAMKCLNKKRIKMKQGETLALNERIMLSLVSTGDCPFI
1		1	VCHI IAFATPDKLCFILDLMNGGDI.HVUI GOUGUEGEVEN
1		1	1D11DDEMMARKVVYRDLKPANTLLDEUGRAPTO\ D1 01
Ţ	1		TERRETAS VGTAGIMAPEVI OKGTAVDGGADURGI GOVERN
1	1	Í	LOSSE LANGUE TORMITTONIVE DOTECTED NOT
ł		]	QRDVSKRLGCHGGGSQEVKEHSFFKGVDWQHVYLQKYPPPLIPP
-	j	]	RGEVNAADAFDIGSFDEEDTKGIKLLDCDQELYKNFPLVISERW
]	Ī		COEVTETYVEAVNADTDYLLTADITALITADICDCLQELYKNFPLVISERW
j	1	ŀ	CQEVTETVYEAVNADTDKIEARKRAKNKQLGHEEDYALGKDCIM
İ	J	1	HGYMLKLGNPFLTQWQRRYFYLFPNRLEWRGEGESRQNLLTMEQ
			1 THE VERTOLING RELIGIOUS AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPER
5955	1726		1 TEACHDERRAPRIENKPRSGTVELDEDGLGUDNONGT
	1	444	AREREFRLAVCPLRYPSAYESSPGTELPECGLCRSCORDER CORDER
ļ	I .		L TANKED A DECRETATION AND A LANGE OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROP
	1		THE CANADOG DEGVENETANSEER TO PROTOTE A TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TO
			WASSLHGSLFPHLSLRSEDLIAEFAQVTNWSSCCLRVFAWHPHT
1			NKFAVALLDDSVRVYNASSTIVPSLKHRLQRNVASLAWKPLSAS
]	i i		VLAVACQSCILIWTLDPTSLSTRPSSGCAQVLSHPGHTPVTSLA
1	1		WAPSGGRILSAGRUDA A TRUMPHOMORE TO THE SHORT PUTSLA
	1 1		WAPSGGRLLSASPVDAAIRVWDVSTETCVPLPWFRGGGVTNLLW
į.	1		SPDGSKILATTPSAVFRVWEAQMWTCERWPTLSGRCQTGCWSPD
<u>L</u>			GSRLLFTVLGEPLIYSLSFPERCGEGKG\ALEVQSQQRLWQICL
5956	1705	139	I MAKE TOTAL TO THE PROPERTY OF THE PROPERTY OF
ľ	1	139	GVGVRGARAMATVQEKAAALNLSALHSPAHRPPGFSVAQKPFGA
1	1 1		1
	1 1		1 ZXXXI EGDVDIPKAKVVRVCOALMDVKVEEAVDTVVVVVVVV
	1		1 - DDDGGGGTRF111PNODSOLGKENKT.VCDXDXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
	·		I DISCHED DINENUS LIKEANS PHVNT SATI CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTINION DE CONTANTIN
]	l i		1 DATA DEPENDENT TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPER
1 1	f		AYSDSQEDEWLSAAIDCSEYLPDQMVVEISRSFPEQPDRTDLVK
1			ELLFDAIGRYYSSREPLLNHLSDVHNGIAELLVNGKTEIALEAT
1 1			QLLLKLLDFQNREEFRRLLYFMAVAANPSEFKLQKESDNRMVVK
j į			RIFSKATUDNIKNI SZCIZDI I IZ ST. ANDESEKLOKESDNEMVVK
1 1	1		RIFSKAIVDNKNLSKGKTDLLVLFL\MDHQKDVFKIPGTL\HKI
L	. 1		VS\VK\LMAIQNGRDPNRDAGYIYCQRIDQRDYSNNTEKTTKDE
5957	1479	451	LLNLLKTLDEDSKLSAKEKKK\LLGQFYKCHPDIFIEHFGD
<b> </b>			ELQVAVAMDTLDRVVKPKTKRAKRFLEKREPKLNENIKNAMLIK
1 1	ı	i	GONALAT A LYAPKO ATTENDED ONCE THE
1		j	DIGGODE MEGSHNKKRPNNI.VTGRMVDVDUI.DMTELGTDVD.
]		j	OBIOLINIS CERGITARMLI FAGDDEDUTED VDDI VOLI TERRES
1			FIVENIAL AGLET VLHETALNGKT VED CVVIII VVC CCOMPT 1
l 1	1	1	DEELGESTOUVLKKTHLASDDI.VKI.SMVMDVXI VDVVIVOV
i ,	1	1	1-G111GRIAMORODLSKI,OTRKM\ KGI, KVDDARD I MTDYITTI I
5958			KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL
3336	. 1	3138	AAALGMLLWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD
		1	ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF
j		ı	D'ETNNEKT PINICTE DI DESCRIPTION DE L'ETNNEKT PINICTE DE L'ETNNEKT PINICTE DE L'ETNNEKT PINICTE DE L'ETNNEKT PINICTE DE L'ETNNEKT PINICTE PINICTE DE L'ETNNEKT PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINICTE PINIC
ŀ	1		DTTNNRKIRVNGTKEPIEFKSNQWFG\ATVKA\HKGKSCGPVAP
ļ		ľ	LLFTWRNFLKPTPEKGPVGTCYVAIQNFSAYAEFSPCGNSNADP
1	í	1	TO A STOCK OF STORY KNGDLIVGGPGSFVWOGOVITAN CITARIES
	i		TISE KULLAGEKOTEVAPAS YDDSVI.GVSVA ACEERODOOO
	i	i i	BUVAGIPRGAUNEGIVS I INSYDMTETONETGEOMA GYEGYETTE
İ	1	1	VSDVNSDGLDDVLVGAPLFMEREFESNPREVGOTVI VI OVCCT -
i	i	1	**************************************
j	i		VAGAVULINGNAUGLNTKPFPKFCOCUMA CHAUDCCECOME DOD
ļ	f	i i	SPIDNING PULLVGAFGTGKVAVVRAPDITUTTINAAT TATURET TOO
j		1:	LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD
1	ŀ	1	SLKOKGAIKRTI, FI, DNHOA HBYEDT WAS STANTIVLMAEVQLD
		I i	SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD
1	f	12	ETEFROKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE
		, ,	PARTITION OF THE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY
i		ļ <del>-</del>	A COLUMN TEACHT VM I PECADY VGT FRANK GRADI CORVINGIA I
	i	, .	THE VEDEGREEN VSGTNYSLGIREA VDDI. FETTIME THERE OF DOC
	1	1 -	WENT TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PR
		1	NKDNPDSNFVSLQINITAVAQVEIRGVSHPPQIVLPIHNWEPEE

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
""	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
	1	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Ston
ĺ	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence	1	\=possible nucleotide insertion)
			EPHKEEEVGPLVEHIYELHNIGPSTISDTILEVGWPFSARDEFL
	1		LYIFHIQTLGPLQCQPNPNINPQDIKPAASPEDTPELSAFLRNS
İ		1	TIPHLVRKRDVHVVEFHRQSPAKILNCTNIECLQISCAVGRLEG
j		i	GESAM KURCH WALTER OF THE CONTROL OF THE CLOTS CAVGRLEG
	l		GESAVLKVRSRLWAHTFLQRKNDPYALASLVSFEVKKMPYTDQP
1			AKLPEGSIAIKTSVIWATPNVSFSIPLWVIILAILLGLLVLAIL
5959	1	1166	TLALWKCGFFDRARPPQEDMTDREQLTNDKTPEA
1 3333	1 *	1 1100	GTSGYAAQQLPSLLKEREFHLGTLNKVFASQWLNHRQVVCGTKC
1			NTLFVVDVQTSQITKIPILKDREPGGVTQQGCGIHAIELNPSRT
l			LLATGGDNPNSLAIYRLPTLDPVCVGDDGHKDWIFSIAWISDTM
]	1		AVSGSRDGSMGLWEVTDDVLTKSDARHNVSRVPVYAHITHKALK
ŀ	-		DIPKEDINPDNCKVRALAFNNKNKELGAVSLDGYFHLWKAENTI.
ĺ			SKLLSTKLPYCRENVCLAYGSEWSVYAVGSOAHVSFLDPROPSY
ŀ	1	ļ	NVKSVCSRERGSGIRSVSFYEHIITVGTGOGSLLFYDIRAORFI.
ļ			EERLSACYGSKPRLAGENLKLTTG\KGWLNHDETWRNYFSDIDF
L			FPNAVYTHCYDSSGTKLFVAGGPLPSGLHGNYAGLWS
5960	2853	870	FVWSDGGPRPRRGPAVGAGAAHLSDPWAMTPGTANRATNPLNKE
1	1		LDWASINGFCEQLNEDFEGPPLATRLLAHKIQSPQEWEAIQALT
1	1		VLETCMKSCGKRFHDEVGKFRFLNELIKVVSPKYLGSRTSEKVK
	1 :		NKILELLYSWTVGLPEEVKIAEAYQMLKKQG\IVKSDPKLPDDT
	i .		TFPLPPPRPKNVIFEDEEKSKMLARLLKSSHPEDLRAANKLIKE
1	}		MVQEDQKRMEKISKRVNAIEEVNNNVKLLTEMVMSHSQGGAAAG
1	<b>{</b>		SSEDL\MKEL\YQRCERMRPTLFPTGRVDTEDND\EALAEILQA
1	1		NDNLTQVINLYKQLVRGEEVNGDATAGSIPGSTSALLDLSGLDL
1	(		PPACTTY PAMPTED CROADED CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTRO
1	1		PPAGTTYPAMPTRPGEQASPEQPSASVSLLDDELMSLGLSDPTP
ŀ	! !		PSGPSLDGTGWNSFQSSDATEPPAPALAQAPSMESRPPAQTSLP
			ASSGLDDLDLLGKTLLQQSLPPESQQVRWEKQQPTPRLTLRDLQ
			NKSSSCSSPSSSATSLLHTVSPEPPRPPQQPVPTELSLASITVP
	i I		LESIKPSNILPVTVYDQHGFRILFHFARDPLPGRSDVLVVVVSM
	1		LSTAPQPIRNIVFQSAVPKVMKVKLQPPSGTELPAFNPIVHPSA
			ITQVLLLANPQKEKVRLRYKLTFTMGDQTYNEMGDVDQFPPPET
5961	100		WGSL
3361	198	3147	SGEPRPEPGNMATCIGEKIEDFKVGNLLGKGSFAGVYRAESIHT
1			GLEVAIKMIDKKAMYKAGMVQRVQNEVKIHCOLKHPSILELYNV
1			FEDSNYVYLVLEMCHNGEMNRYLKNRVKPFSENEARHFMHOIIT
			GMLYLHSHGILHRDLTLSNLLLTRNMNIKIADFGLATOLKMPHE
! !			KHYTLCGTPNYISPELATRSAHGLESDVWSLGCMFYTLLIGRPP
1 1	1	!	FDTDTVKNTLNKVVLADYEMPTFLSIEAKDLIHOLLRRNPADRI.
			SLSSVLDHPFMSRNSSTKSKDLGTVEDSIDSGHATISTAITASS
1			STSISGSLFDKRRLLIGQPLPNKMTVFPKNKSSTDFSSSGDGNS
1 1	•		FYTQWGNQETSNSGRGRVIQDAEERPHSRYLRRAYSSDRSGTSN
1 1			SQSQAKTYTMERCHSAEMLSVSKRSGGGENERRYSDTDNNANTE
			NFFKEKTSSSSGSFERPDNNQALSNHLCPGKTPFPFADPTPQTE
1			TVQQWFGNLQINAHLRKTTEYDSISPNRDFQGHPDLQKDTSKNA
	1		WTDTKVKKNSDASDNAHSVKQQNTMKYMTALHSKPEIIQQECVF
1			GSDPLSEQSKTRGMEPPWGYQNRTLRSITSPLVAHRLKPIRQKT
1 1	]		KKAVVSILDSEEVCVELVKEYASQEYVKEVLQISSDGNTITIYY
1 1	1		PNGC/PGEDIA/DDDDCDM/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/DNICD/WCD/WCD/DNICD/WCD/WCD/DNICD/WCD/WCD/DNICD/WCD/WCD/DNICD/WCD/WCD/WCD/WCD/WCD/WCD/WCD/WCD/WCD/W
1 1	1		PNGG\RGFPLA\DRPPSPT\DNISR\YSF\DNLPEKYWRKYQYA
]	1	f	SRFVQLVRSKSPKITYFTRYAKCILMENSPGADFEVWFYDGVKI
1 1	1		HKTEDFIQVIEKTGKSYTLKSESEVNSLKEEIKMYMDHANEGHR
1	į.		ICLALESIISEEERKTRSAPFFPIIIGRKPGSTSSPKALSPPPS
1 !	1		VDSNYPTRDRASFNRMVMHSAASPTQAPILNPSMVTNEGLGLTT
[	į.		TASGTDISSNSLKDCLPKSAQLLKSVFVKNVGWATQ\LTSGAVW
1	Ī	1	VQFNDGSQLVVQAGVSSISYTSPNGQ\TTR\YGENEKLPDYIKQ
H=000			KLQCLSSILLMFSNPTPNFH
5962	20	2447	RVCSSSASTASQAVMADAWEEIRRLAADFQRAQFAEATQRLSER
į i	ļ	İ	NCIEIVNKLIAQKQLEVVHTLDGKEYITPAOISKEMRDELHVRG
1	1	l	GRVNIVDLQQVINVDLIHIENRIGDIIKSEKHVQLVLGQLIDEN
[ ]	j		YLDRLAEEVNDKLQESGQVTISELCKTYDLPGNFLTQALTQRLG
1		j	RIISGHIDLDNRGVIFTEAFVARHKARIRGLFSAITRPTAVNSL
[ ]		j	ISKYGFQEQLLYSVLEELVNSGRLRGTVVGGRQDKAVFVPDIYS
f 1		{	PTOSTWOOSEEPONCY EDDAY OF STREET
			RTQSTWVDSFFRQNGYLEFDALSRLGIPDAVSYIKKRYKTTQLL

	SEQ	Predicted	Predicted end				
•	ID	beginning					
	NO:	nucleotide	nucleotide	I IN-MIGHTUR, CECVSERING Delicantic action and			
	""		location				
	1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,			
	1 .	corresponding	to first				
:	1	to first		b=beucine, M=Methionine N-Acparation			
	1	COTATSC	amino acid	P=Proline, Q=Glutamine, R=Arginine,			
		amino acid	residue of	S=Serine, T=Threonine, V=Valine,			
		residue of	amino acid	w men i leinreonine, V=Valine,			
	1	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop			
	i		sequence	COGOII, /=DOSSIDIE DUCTEOFIA doleti-			
	<u></u>	sequence	ł	\=possible nucleotide insertion)			
	1			PINA GUODE Indication			
	1		ļ	FLKAACVGQGLVDQVEASVEEAISSGTWVDIAPLLPTSLSVEDA			
	1		İ	ALDUCY MARSKUASTVVFSDTVVVSEKE TADORDI DODE			
		1	i	QKAEKEMKNNPVHLITEEDLKQISTLESVSTSKKDKKDERRRKA			
	1	<b>{</b>	1	TEGGGGWDGGGGWDDWGTSTLESVSTSKKDKKDERRKA			
				TEGSGSMRGGGGGNAREYKIKKVKKKGRKDDDSDDESQSSHTGK			
	l i		1	LEGET SEMPODELEDFLEKHIODADERET GELARUT TUDY STORME			
			1	LEVVRSVFMSSTTSASGTGRKRTIKDLQEEVSNLYNNIRLFEKG			
				MKEEADDTONATENGTIANTALTEKG			
	1 1	•		MKFFADDTQAALTKHLLKSVCTDITNLIFNFLASDLMMAVDDPA			
	, ,		1	ALIGERARY TO SKING TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROP			
	}		f	ABACDIMVKRGDKKRERQILFQHRQALAEQLKVTEDPALILHLT			
				SVILLEOFSTHEMI HADEDOUDGE TO THE TOTAL TEMPALITHET			
	ı			SVLLFQFSTHSMLHAPGRCVPQIIAFLNSKIPEDQHALLVKYQG			
				1 DV AQUVSQSAKTGOGDYPLNNET,DKEOFDUACTTDVDI ODI OO			
	5963			1 STRDDVLKSRKSSVTEE			
	2203	62	1130	PWNPQDFPGNRGLMG\QKGEIGPP\GQQGKKGAPGMP\GLMGSN			
- 1	1		I	GSPGOPCEDGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG			
ı	Í		i	GSPGQPGTPGSKGSKGEPGIQGMPGASGLKGEPGATGSPGEPGY			
- 1			·	INGUEGIQGREGORGERGIOGORGERGOCGIOGORGE			
- 1			1	TARGERGERGEPGVRGAIGSKGESGVDGIMGDAGDVCODGDBGDG			
- 1	i		1	GPPGLDGKPGREFSEQFIRQVCTDVIRAQLPVLLQSGRIRNCDH			
- 1	1			CLSONGE DEL DED DESTINATION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DEL CONTRACTION DE LA			CLSQHGSPGIPGPPGPIGPEGPRGLPGLPGRDGVPGLVGVPGRP
- 1	į		ſ	J GVRGDRGDPGRNGEKGSOGFGYDGFOGDDGDDCDBGDDGTG*****			
- 1	į		i	PPGDPGLPGKDGDHGKPGIQGQPGPPGICDPSLCFSVIARRDPF			
H	5964			KROPIVI			
- 1	3364	3	2147	SCRTRGRLSPLQPREAGSSRGSRARSEPPRFGGMEEACQVQTTK			
			j.	REDPHEL PATEL OVA CHENDOSTARS EPPRINGEMEEACQVQTTK			
- 1			ŀ	RGDPHELRNIFLQYASTEVDGERYMTPEDFVQRYLGLYNDPNSN			
	j		ļ	PKIVQLLAGVADQTKDGLISYQEFLAFESVLCAPDSMFIVAFQL			
- [	1			PDROGNOEVIFENVKEIFGOTIIHHHIDENWDCEETDIHEGIDIN			
Į	ŀ			I KKILKI I EF TUFLOELOLEHAROAFAI.KDKGKGCMTCGI DDGD-			
-		i		MVTIRSHMLTPFVEENLVSAAGGSISHQVSFSYFNAFNSLLNNM			
1	1			ELVEKT VSTLAGTENDAGUTURGEN STAGGSTSHQVSFSYFNAFNSLLNNM			
-1				ELVRKIYSTLAGTRKDAEVTKEEFAQSAIRYGQATPLEIDILYQ			
-	j			I MADDINASGRUTLADIERIAPLAEGALDVMIARI ODOGOGOGO			
1	j			FINDSIAESAIRFILGSVAGAVGATAVVDTDIJVZDMONODGGG			
1	ĺ			SVVGELMI KNSFDCFKKVLRYEGFFGLVPGLTDOLTGVA DEKA + 1			
1	l	ł		KLTVNDFVRDKFTRRDGSVPLPAEVLAGGCAGGSQVIFTNPLEI			
i	- 1			AKIRTOAVGETAACOBROATANA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANARA BELANAR			
ı	ľ	J		VKIRLQVAGEITTGPRVSALNVLRDLGIFGLYKGAKACFLRDIP			
ı		i		FSAIYFPVYAHCKLLLADENGHVGGLNLLAAGAMAG\VPAASLV			
ı				I ************************************			
	Į	j		TARKY FROSPORG \ VTLVTYFI.I.ODGDVIDDCCI VD3 GCDDDCC.			
1	j	1		SRIADLPPANPDHIGGYRLATATFAGIENKFGLYLPKFKSPSVA			
L			i	VVQPKAAVAATQ			
1	5965	1	1498	MVPMT.VD E7 DOONS AND A STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE O			
1	- 1			MVTWLYRFLPTSNMAAKLRSLLPPDLRLQFWLHARLQKCFLSRG			
1	ı	i i	ſ	COST COSANAS PLIPGINIAMO I MOCIDIDATO, DE LO CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR			
	1	ſ	- 1	SUMLGRED TRALEPAAPCCCR PHVT.RLAACODD CO. T. C. C.			
ı	ı	ł	İ	EVQVQAPPVVAATPSPTAVPEVASGETADVVQTAAEQSFAELGL			
ı		1	I	GSYTPUGLIONI LEEMIND OF BUILDING TO BUILDING			
ı			1	GSYTPVGLIQNLLEFMHVDLGLPWWGAIAACTVFARCLIFPLIV			
	- 1	1	i	1GERCHARTINHLPEIOKESSRIREAKLAGDUTEVVVA CCEMAT			
ı	!	[		TENNISTALIAPULLIPVTOAPIFISFFIALPEMANT.DVDCt ome			
1		i	i	GLWWFQDLTVSDPIYILPLAVTATMWAVLELGAETGVQSSDLQW			
ĺ	- 1	l		MRNVIRMMPI.TTI.DITMUEDURAVERAVIA COMPANIONE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONT			
ı	í			MRNVIRMMPLITLPITMHFPTAVFMYWLSSNLFSLVQVSCLRIP			
	!			AVRTVLKI PQRVVHDLDKLPPREGFLESFKKGWKNAEMTRQLRE			
	1	l	1	MACHINA COLLAR GPLROTETHNDI LODGKONDONI DEGLACIO			
	5966	102		OSKEKSKI PWHDILG			
		102	1925	RSKQVMARLTKRRQADTKAIQHLWAAIEIIRNQKQIANIDRITK			
	ŀ	i	1	YMSRVHGMHPKETTPOLELAUVDGE			
	1	i i	1	YMSRVHGMHPKETTRQLSLAVKDGLIVETLTVGCKGSKAGIEQE			
	į		į į	OTHER SECTION AND ASSESSMENT OF COMPANY OF A STREET OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION			
	ı	1	1	SDEFRENDSSPWQCPVCRSIKKKNTNKOEMGTVLDETVCDMARD			
		ļ	1	RAID DINKIGKONKHPMYRRLVHSAVDVDTIOEVINGCVVDCVD			
	1	1	1	FKADAQLLLHNTVIFYGADSEQADIARMLYKDTCHEL\DELQLC			
		İ	1.	KNCFYLANAR PDNWFCVPGT TARTILI KUTCHEL DELQLC			
	1	i	1;	KNCFYLANAR PDNWFCYPCI PNHELDWAKMKGFGFWPAKVMQKE			
	1		1 *	DIQUIDURE F GRIHLORAWI PSENTODI TUNTH DI LUVED CACALLER I			
	l		1.	CDEDEDRUKE LKEGREWKSKNEDRGEEEARSSISSISSISSISSISSISSISSISSISSISSISSISSI			
	1		, ,	PERMANGERINOSVEPKKEEPEPETEAVGGGGFT POMPODETER			
			13	SVSTQTKKLSASSPRMLHRSTQTTNDGVCQSMCHDKYTKIFNDF			
				OADS FARIDARS TO TINDGVCQSMCHDKYTKI FNDF			

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
ио:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
l.	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	S-Serine, T-Threonine, V-Valine,
	residue of	amino acid	W=Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Truntophan V Tru
· }	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence		Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			VDDMVCDUVDEREDITION
	ı		KDRMKSDHKRETERVVREALEKLRSEMEEEKRQAVNKAVANMQG
			EMDRKCKQVKEKCKEEFVEEIKKLATQHKQLISQTKKKQWCYNC
5967	102	1925	EEEAMYHCCWNTSYCSIKCQQEHWHAEHKRTCRRKR
ĺ		1,000	RSKQVMARLTKRRQADTKAIQHLWAAIEIIRNQKQIANIDRITK
1	1		YMSRVHGMHPKETTRQLSLAVKDGLIVETLTVGCKGSKAGIEQE
ŀ	1		GYWLPGDEIDWETENHDWYCFECHLPGEVLICDLCFRVYHSKCL
}	1	}	SDEFRLRDSSSPWQCPVCRSIKKKNTNKQEMGTYLRFIVSRMKE
į	1		RAIDLNKKGKDNKHPMYRRLVHSAVDVPTIQEKVNEGKYRSYEE
1			FKADAQLLLHNTVIFYGADSEQADIARMLYKDTCHEL\DELQLC
	Í	1	KNCFYLANARPDNWFCYPCIPNHELDWAKMKGFGFWPAKVMQKE
}	l		DNQVDVRFFGHHHQRAWIPSENIQDITVNIHRLHVKRSMGWKKA
ľ	!	}	CDELELHORFLREGRFWKSKNEDRGEEEAESSISSTSNEQLKVT
			QEPRAKKGRRNQSVEPKKEEPEPETEAVSSSQEIPTMPQPIEKV
ł			SVSTQTKKLSASSPRMLHRSTQTTNDGVCQSMCHDKYTKIFNDF
1			KDRNKSDHKRETERVVREALEKLRSEMEEEKRQAVNKAVANMQG
1	1		EMDRKCKQVKEKCKEEFVEEIKKLATQHKQLISQTKKKQWCYNC
5968	81	1288	EEEAMYHCCWNTSYCSIKCQQEHWHAEHKRTCRRKR
ļ	} i		VRFPRRGGAPPTVLTPGRQQGVFLGPQRPGSEPDIPARGQPHPP RPVGVSTSAQAQVQPPAMHRRRLALGLGFCLLAGTSLSVLWVYL
	1		ENWLPVSYVPYYLPCPEIFNMKLHYKREKPLQPVVWSQYPQPKL
	[ ]		LEHRPTQLLTLTPWLAPIVSEGTFNPELLQHIYQPLNLTIGVTV
1			FAVGN/HFLESAEEFFMRGYRVHYYIFTDNPAAVPGVPLGPHRL
			LSSIPIQGHSHWEETSMRRMETISQHIAKRAHREVDYLFCLDVD
	1		MVFRNPWGPETLGDLVAAIHPSYYAVPRQQFPYERRRVSTAFVA
İ			DSEGDFYYGGAVFGGQVARVYEFTRGCHMAILADKANGIMAAWR
1	}		EESHLNRHFISNKPSKVLSPEYLWDDRKPQPPSLKLIRFSTLDK
			DISCLRS
5969	1126	503	DVGFNIKRKRCDLDVFLESPRKPSGRRDRAPEKQRRIAANKCLC
	[		TGVREGEPPS/TTSQKVKEAGRDFTYLIVVLFGISITGGLFYTI
	1		FKELFSSSSPSKIYGRALEKCRSHPEVIGVFGESVKGYGEVTRR
1			GRRQHVRFTEYVKDGLKHTCVKFYIEGSEPGKQGTVYAQVKENP
			GSGEYDFRYIFVEIESYPRRTIIIEDNRSQDD
5970	316	4712	SQDNIGHRLLQKHGWKLGQGLGKSLQGRTDPIPIVVKYDVMGMG
1 1			RMEMELDYAEDATERRRVLEVEKEDTEELRQKYKDYVDKEKAIA
1 1	Ī		KALEDLRANFYCELCDKQYQKHQEFDNHINSYDHAHKQRLKDLK
1 1			QREFARNVSSRSRKDEKKQEKALRRLHELAEQRKQAECAPGSGP
1			MFKPTTVAVDEEGGEDDKDESATNSGTGATASCGT.GSFFSTDVG
1			GPFTAVQITNTTGLAQAPGLASQGISFGIKNNLGTPLQKLGVSF
<i>!</i>	1		SPAKKAPVKLESIASVFKDHAEEGTSEDGTKPDFKSSDOGLOVK
1			GDSDGSSNLDGKKEDEDPODGGSLASTLSVLVDMVDEDGAGADD
!!	1		PEYYHYIPPAHCKVKPNFPFLLFMRASEOMDGDNTTHDVNADEG
i l			KAGSSPRPRSCIKAAASOGAEKTVSEVSEOPKETSMTPBSPDGG
1	i		KAEAKKALGGDVSDOSLESHSOKVSETOMCESNGGRETELATIDE
[ [	Ī	i	GKESQEGPKHPTGPFFPVLSKDESTALOWPSELLTETKARDETE
	1		YSCNPLYFDFKLSRNKDARTKGTEKPKDIGSSSKDHLOGLDBGE
			PRESERVEGERIVESSEGRMDAPASGSACSGINKOEPGGEVGER
1			TEDTGRSLPSKKERSGKSHRHKKKKKHKKSSKHKRKHKADTERV
1		ļ	SSKAESGEKSKKRKKRKRKKNKSSAPADSRRGDKDFDDGGGGDA
	1	į	PPRRRRAQDDSQRRSLPAEEGSSGKKDEGGGGSSGODUGGBVI
	i	İ	KGELPPSSCQRRAGTKRSSRSSHRSOPSSGDEDSDDASSUBLUG
j	1		KSPSQYSEEEEEEDSGSEHSRSRSRSGRRHSSHRSSRBSYSSE
j			DASSDQSCYSRQRSYSDDSYSDYSDRSRRHSKRSHDSDDSDVAG
ł	1	l	SKHRSKRHKYSSSDDDYSLSCSOSRSRSRSHTRERSPSRCRODE
1	i		SSCSRSRSKRRSRSTTAHSWORSRSYSRDRSRSTPSDSODECED
- 1	ł		KRSWGHESPEERHSGRRDFIRSKIYRSOSPHYFRSGRGRGRGRGVV
j	[		DDGRGDDSKATGPPSONSNIGTGRGSEGDCSPRDKNSVTAVIII
1	]	1	EKIQSRKVERKPSVSEEVOATPNKAGPKLKDPPOGVEGPVI PRO
Ţ		Ī	LGNKPVLPLIGKLPATRKPNKKCEESGLERGERGEGEGEGEGE
1		i	GSSDALFGHQFP\SEETTGPLLDPPPEESKSGEVTADUDVADIC
		1	PPAHFDCYLGDPTISHNYLPDPSDGNTLESLDSSSOPGDVRSSI
			LPIAPDLEHFPSYAPPSGDPSIESTDGAEDA\SLAPLESQPITF
			- Total Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Court in Cour

( <del>  0  </del>			
SE	-	Predicted end	Amino acid segment
- 1	13	nucleotide	
ИО	. I macroocide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	
'	corresponding	to first	
ļ	to first	amino acid	I DEDUCTOR, MEMORNIONING MEMORING
ĺ	amino acid	residue of	1 * = * * * * * * * * * * * * * * * * *
į.	residue of	amino acid	U-Detaile, TellireOnine V-W-1
ļ	amino acid	sequence	"-11yptopnan, YaTvrosine v mal
1	sequence	sequence	
	1 1 1 1 1 1	_	\-PCSSIDIE HUCIPOFIAG inca
ſ	1	l.	TELEMERYSKLOOAAOOHTOOOLLAVOYVA TOS COST
	1		
			PLAQVHHIPQPHLTPISLSHLTHSIIPGHPATFLASHPIHIIPA
			SAIHPGPFTFHDVDHAALVARULARDAATPLASHPIHIIPA
500		1	SAIHPGPFTFHPVPHAALYPTLLAPRPAAAAATALHLHPLLHPI FSGQDLQHPPSHGT
5971	53	2149	SFI-VEVCVDMDND-CONT
	1		SFLYFVGVDMDNPIGNWDGRFDGVQLCSFACVESTILLHINDII PESVTOERPDDVLAFMSDGUSDAGA
ĺ			
- 1	}		I
1	j		T TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPE
i		1	1
ļ	1	1	"
	•	1	1 CONTROL AND SCROLLED BY A CLUDING TO THE COLOR
1	1		
- 1	1	]	
ı			YVCATKIMKLRKILEKVEAASGFTSEEKDPEEFINILFHHILRV
- 1		j	BPLLKIRSAGQKVQDCYFYQIFMEKNEKVGVPTIQQLLEWSFIN
ł	1	ł	SNLKFAFAPSCLITOMPREGNERALENGERVGVPTIQQLLEWSFIN
			SNLKFAEAPSCLIIQMPRFGKDFKLFKKIFPSLELNITDLLEDT
- 1	ł	1	PROCRICGGLAMYECRECYDDPDISAGKIKQFCKTCNTQVHLHP
Ī	· I		I TO TO THE VOLENDER DESCRIPTION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPER
5972	440	1761	I TO
			1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
ſ	1	1	
	•		The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the
1	i i	· ·	
	1		
ı	i i		
l	1 1	ł	
1	1		
İ	1	1	
1	1	1	GQEPPEGVRQGESLESRRGANGPVTPRRGNRVAAPSLAPGMETH
5973	65		
	1 65	-2007	NGDGKDLFGHIWAWRSNGIISNFRRSPHAGMAEDEPDAKSPKTG
1	1	i	
	1 1	Į.	NDKLYLYLQLPSGPTTGDKSSEPSTLSNEEYMYAYRWIRNHLEE
-		<b>!</b>	HTDTCLPKOSVYDAYPKYCESI ACCEST ACCEST
i	1	j	HTDTCLPKQSVYDAYRKYCESLACCRPLSTANFGKIIREIFPDI
	1	1	KARRLGGRGOSKYCYSGIRRKTLVSMPPLPGLDLKGSESPEMGP
1	1		EVTPAPRDELVEAACALTCDWAERILKRSFSSIVEVARFLLQQH
İ	1		
	1 1		
1	1 1		
ł		1	
	1 1		
1	1		
j j	1		
}	! !		
5974	4293		Samonucu Anoszi zukakuanywa
	4253	~200	GLUMHTTSGRIHOAMVTSLNEDNESVERIFFERENT
1 1			
1 1	İ	r	V\ASIKNDPPS\RDNRVVGSARARPSQFPEQFSSAQQNGSV\S
1 1	1	( c	ISPVQAAKKEFGPPSRRKSNCVKEVEKLQEKREKRRLQQQELR
1 1	1	l _E	KRAODVDATNONVEIMCMTDDDDCCC
1		ĺv	KRAQDVDATNPNYEIMCMIRDFRGSLDYRPLTTADPIDEHRIC
j	i	, ,	- MAKE JUNKE JUNKE JUNKE JUNKE JUNKE JUNKE JUNKE JUNKE JUNKE JUNK JUNK JUNK JUNK JUNK JUNK JUNK JUNK
1	l l	,	"YAT NEDIALDUSAPNEMVYRETADDI VEGITEEDIGES I
1 1	j	) W	
1 1	ļ	, -	
1 1	I		O'NC A DD ADADTDIGNSC BLISCOLG WINTEGOD CLIEBAND
1 1	i	1	CONTOUR SELECTION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPE
1 1	1	, ~··	OTTO STATE OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF
, ,	1	,	TO THE LOCAL PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE P
<del></del>		LI	TQWGVGSSPQRDDLKLLCEQNEEEVSPQLFTFHEAVSQMVEM

ſ	SEO	1 -		
	-	Predicted	Predicted end	Amino acid segment
	ID	beginning	nucleotide	Amino acid segment containing signal peptide
	NO:	nucleotide	location	
		location	corresponding	
- 1		corresponding	to first	1 **-***
- 1		to first		D-Deucine, Memethioning N 7
		amino acid	amino acid	T-FLOTING, O=Glutamine, p-Argining
		residue of	residue of	1 5-50 Line, Telline Welling
		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- 1		amino acid	sequence	Codon. /=noscible nusl
L		sequence	_	Codon, /=possible nucleotide deletion,
				\=possible nucleotide insertion)
- 1		1	Ī	CSDMLLER\GPYSAS\VREAKEDEEDEEKIQNEDYHHELSDGDL
		1	1	T TO THE TOP ON THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TOP OF THE TO
		I	1	1 TODE DODING DAAAAGPAGSSHGVVGCCCCD TODDON
		[	1	ATSSLLDIDPLILIHLLDLKDRSSIENLWGLQPRPPASLLQPTA
			1	SYSRKDKDORKOOMMENDEDE VAN 1802 VAN 1802
			ļ	SYSRKDKDQRKQQAMWRVPSDLKMLKRLKTQMAEVRCMKTDVKN
				T TO DIT WOODAN SOUMOTS LESADON AT A ACCORDIGATE ASSESSMENT
- 1				T SOME THE I TRUSTING KENEDINDA DECITA DOLOR DESCRIPTION
	i		1	TARREST TO THE PROPERTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE
- 1			1	I SUCCESSION OF SUIT DAY LABOR OF THE AND AND AND AND AND AND AND AND AND AND
- 1	j	i		1 2 2 CONTROD I GELUPVI PRICASA A DEPERMONDED TRANSFER
	i	-	i	QEEHTSVGGFHDSFMVMTQPPDEDTHSSFPDGEQIGPEDLSFNT
$\vdash$			1	DENSGR
	5979	212	3665	
	i			LPDMTMYLWLKLLAFGFAFLDTEVFVTGQSPTPSPTDAYLNASE
	Į.		I	1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
j	ļ			I AT TAILER VINER V & CGNNT'C'TNNEVHMI. TECTMA CTIC TOTAL
1	- 1			1 - 2 N - 2 - 2 D V F E G V E K V P V H C C S \ O V E O D D C M T UT V C V D T =
			1	I ~ * X** I I I TO YOUNG I VON KETKI ENT. EDEUEVVON ON THE I I I I I I I I I I I I I I I I I I I
- 1	ł		}	I TAMES TO A TOP GO PO
	f	I	,	FTLCYIKETEKDCLNLDKNLIKYDLQNLKPYTKYVLSLHAYIIA
	- 1		;	KVORNGSAAMCHETTECA PROGRESSIONELLE TRYVLSLHAYIIA
- 1	i i			KVQRNGSAAMCHFTTKSAPPSQVWNMTVSMTSDNSMHVKCRPPR
		1		DRNGPHERYHLEVEAGNTLVRNESHKNCDFRVKDLQYSTDYTFK
	T.	1		*** * *** OD * FUGPE LLMHS TSYNCKAT. TART A DT TT: mo == = = = -
- 1	i			
	l	1		
- [	j	1		
	- 1	1	i	TO- INCIT MECINALLY (MINITED FENITALISM
1	- 1	i	i	RAFGECCCKDLTKHKRCP\DYIIQKLNIVNKKEKATGREVTHIQ
ļ	1	1	i	FTSWPDHGVPEDBULLEY BROWN BONNER KATGREVTHIQ
1	i		i	FTSWPDHGVPEDPHLLLKLRRRVNAFSNFFSGPIVVHCSAGVGR
1	- 1	1	ł	TGTYIGIDAMLEGLEAENKVDVYGYVVKLRRQRCLMVQVEAQYI
	. [	į.		
-	İ	1		- z-v r-constant Outling is I have a control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of
1	- 1	1	1	
1			. 1	
		ſ	1	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
	1	i	4	
	Ī	ı	[	LIHCRDGSQQTGIFCALLNLLESAETEEVVDIFQVVKALRKARP
1	i i		į	GMVSTFEQYQFLYDVIASTYPAQNGQVKKNNHQEDKIEFDNEVD
1	1		<b>!</b>	KVKODANCUNDI CA DEKI DEA KOOGOVKKNNHQEDKIEFDNEVD
<u>L</u>		)	i	KVKQDANCVNPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSVNGP ASPALNOGS
1 5	980	3		
	1		, ,	DAWGCKLRRLRFTYGTQTRVSLALPGQYELVHTLVAHQGNWETI
1	Į.	ŀ	1 1	* DEDUC Y VENINEDAAHDI, TET, EVENUUTAT TORUSTERS TO THE
1	1	i	1 '	~ * * D * D O D D V N D F D D V 1 1 Y A L O K D D F C D D D O D F A D M =
1	j	Į.		* * * * * V F NAUGELLIDGOTKKMKSEDEDI VOOT TOT OVA
1				CGAPGQDTKAQSMLVEQSEKLRHLSTFSHQVLQTRLVDAAKALN
1	ľ	1	1	LVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKENELYESLMN
1	- 1		1:	IANRKOEEMKOMINETI MOMENTI I DA DE TRIKKENELYESLMN
ı		1	1 7	IANRKQEEMKDMIVETLNTMKEELLDDATNMEFKDVIVPENGEP
ĺ	- 1		1 '	*OTRETACCTROTORDI ISBINOAVANDI TECHDUT DE
	1		, -	THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY O
ĺ		ŀ	i •	**************************************
i		1	-	TOSER TRUNSSHEAFAASTROLEDGUSCOT EVERDY to
	- 1		,	AMERICAN DESKSLODVIJHRKDKI GOFT GOCOVOTERTE OF THE
	j	ļ	W	GGHFPCALKSVVPPDEKHWNDLALEFHYMRSLPKHERLVDLHG
l	ł	l	! s	VIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIAL
	ı		1	WYEGIRFILHOOL MIDDING WITCH TO THE WITCH THE TRUNCH TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUCK THE TRUC
	- 1		1	A ARGITE PUSOCONTRIBUTE L'ENVILL'UNO MONTRIAL CONTRIBUTION DE
	ı	ŀ	j 4°2	"" OGSI VGI PI HMAPELE IGKYDNSVDVVA PGI I EMVI GGGGGGGG
	-		1 -	FEATERCASKOHLWNNVRRGARPERI.DUFDFFCWOLMD A COLOR
50	81	<del></del>		* DIRECTOR VOPMLOGIMNRLCKS / NSECONDGLODGE
		1	ی ا	KKHSAAMERPWGAADGLSRWPHGLCLILLI OLL DDCTV
	ĺ	[	D.	APPPPAAPLPRWSGPIGVSWGLRAAAA\GGAFPRGGRWRRSAP
	[		G	\EDEECGRVRDEVAKIANNIMIONIANAAA\GGAFPRGGRWRRSAP
		i	-	\EDEECGRVRDFVAKLANNTHQHVFDDLRGSVSLSWVGDSTGV
				LVLTTFHVPLVIMTFGQSKLYRSEDYGKNFKDITDLINNTFIR

SEQ	D		
ID	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning	nucleotide	(A=Alanine, C=Cvsteine, D=Aspartic Acid R
NO:	nucleotide	location	Grutamic Acid, F=Phenylalanine G=Glyging
	location	corresponding	H=H15tlding, I=Isoleucine K=Lysine
1	corresponding	to first	==Leucine, M=Methionine, N=Asparagine
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
			TEFGMAIGPENSGKVVLTAEVSGGSRGGRIFRSSDFAKNFVQTD
	1	l	LPFHPLTQMMYSPQNSDYLLALSTENGLWVSKNFGGKWEEIHKA
ļ	1	j	VCLAKWGGDNTI PETTYANGGGWARA GARANGGKWEEIHKA
1	l .	]	VCLAKWGSDNTIFFTTYANGSCKADLGALELWRTSDLGKSFKTI
ł	1	1	GVKIYSFGLGGRFLFASVMADKDTTRRIHVSTDQGDTWSMAQLP
	ł		SVGQEQFYSILAANDDMVFMHVDEPGDTGFGTIFTSDDRGIVYS
	1		KSLDRHLYTTTGGETDFTNVTSLRGVYITSVLSEDNSIQTMITF
	1	1	DQGGRWTHLRKPENSECDATAKNKNECSLHIHASYSISQKLNVP
			MAPLSEPNAVGIVIAHGSVGDAISVMVPDVYISDDGGYSWTKML
1		1	EGPHYYTILDSGGIIVAIEHSSRPINVIKFSTDEGQCWQTYTFT
- 1	1	ļ	RDPIYFTGLASEPGARSMNISIWGFTESFLTSQWVSYTIDFKDI
İ	]	ĺ	LERNCEEKDYTIWLAHSTDPEDYEDGCTLGYKEOFT.PLPKGGVC
	1		QNGRDYVVTKQPSICLCSLEDFLCDFGYYRPENDSKCVFOPRIK
ŀ	İ		GHDLEFCLYGREEHLTTNGYRKIPGDKCOGGVNPVRFVKDLKKK
ĺ	1		CTSNFLSPEKQNSKSNSVPIILATVGLMI,VTVVAGVI,TVVVVVQ
	1		GGRFLVHLYSVLQQH\AEA\NGVDGVDALDTASHTNKSGYHDDS
5982			DEDITIE
3902	56	2316	ATRPPRGSSWCRQFSRTASAAPGRSNMLRIPVRKALVGLSKSPK
ł	1	Ì	GCVRTTATAASNLIEVFVDGOSVMVEPGTTVLOACEKVGMOTER
			FCIHERLSVAGNCRMCLVEIEKAPKVVAACAMPVMKGWNIT.TMG
ł			EKSKKAREGVMEFLLANHPLDCPICDOGGECDLODOSMMEGNDR
			SRFLEGKRAVEDKNIGPLVKTIMTRCIOCTRCIRFASEIAGVDD
ł			LGTTGRGNDMQVGTYIEKMFMSELSGNTIDTCDVCALTCVDVAR
			TARPWETRKTESIDVMDAVGSNIVVSTRTGEVMRILPRMHEDIN
1			EEWISDKTRFAYDGLKRQRLTEPMVRNEKGLLTYTSWEDALSRV
			AGMLQSFQGKDVAAIAGGLVDAEALVALKDLLNRVDSDTLCTEE
ł	ł		VFPTAGAGTDLRSNYLLNTTIAGVEEADVVLLVGTNPRFEAPLF
Ĭ	1		NARIRKSWLHNDLKVALIGSPVDLTYTYDHLGDSPKILQDIASG
	; I		SHPFSQVLKEAKKPMVVLGSSALQRNDGAAILAAVSSIAQKIRM
	i i		TSGVTGDWKVMNILHRIASQVAALDLGYKPGVEAIRKNPPKVLF
	1		LLGADGGCITRQDLPKDCFIIYQGHHGDVGAPIADVILPGAAYT
i	1		EKSATYVNTEGRACOTYVAVTDOX ADDIVIDED AND TO THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE
ļ	} [		EKSATYVNTEGRAQQTKVAVTPPGLAREDWKIIRALSEIAGMTL
1			PYDTL\DQVRNRLEEVSPNLVRYDDIEG\ANYFQQANELSKLVN
ļ			QQLLADPLVPPQLTMKDFYMTDSISRASQTMAKCVKAVTEGAQA VEEPSIC
5983	248	1763	
1		1,05	EARGDGGRRRHRASGRRAGRGEP\AGLKSQGQRAVPKRAVARGG
			RQ\YSAAIALLEPAGSEIADDLSILYSNRAACYLKEGNCSGCIQ
	1		DCNRALELHPFSMKPLLRRAMAYETLEQYGKAYVDYKTVLQIDC
1	1		GLQLANDSVNRLSRILMELDGPNWREKLSLIPAVPASVPLQAWH
1			PAKEMISKQAGDSSSHRQQGITDEKTFKALKEEGNQCVNDKNYK
]	[		DALSKYSECLKINNKECAIYTNRALCYLKLCOFEEAKODCDOAL
			QLADGNVKAFYRRALAHKGLKNYOKSIJDINKVTIJDPSTIFAK
			MELEEVIRLLNLKDKTAPFNKEKERRKIEIOEVNEGKEEDGPDA
1	l	ľ	GEVSTGCLASEKGGKSSRSPEDPEKLPIAKPNNAYEFGOTTNAL
] ]		ļ	STRKDKEACAHLLAITAPKDLPMFLSNKLEGDTFLJJJOSJKNN
	1		LIEKDPSLVYQHLLYLSKAERFKMMLTLISKGOKELTEOLFEDI
5984			SDIPNNHFILEDIQALKRQYEL
3384	755	1193	SSVCMACTYVSNLGKKQRSVSFLASGLMRVSTGPELRLHHSEVI
1		1	TGDVGRRICRLLVGLFTKGDTSSKRVHPFSPGPCFILCDLAPVC
1	ſ	[	SSPKINVSPFYQN\QTSTQRSCTVFVWQRCSLVGPFQVTVFTMY
<b></b>			FHHSLRSISRFSSG
5985	22	1408	RRVARPGTAEPAKARRTVRRGRARRDLAGAERKAGVSERGDSGR
1	ļ	j	RRPNPSIPSAAAGMSHIQIPPGLTELLQGYTVEVLRQQPPDLVE
1 1	İ	i	FAVEYFTRLREARAPASVLPAATPRQSLGHPPPEPGPDRVADAK
1 1	1	l	GDSESEEDEDLEVPVPSRFNRRVSVCAETYNPDEEEEDTDPRVI
}		ļ	HPKTDEQRCRLQEACKDILLFKNLDQEQLSQVLDAMFERIVKAD
	1		EHVIDOGDDGDNEVVIERCADITUDE ANDDQEQUSQVCDAMFERIVKAD
1 1			EHVIDOGDDGDNFYVIERGTYDILVTKDNQTRSVGQYDNRGSFG
[ ]			ELALMYNTPRAATIVATSEGSLWGLDRVTFRRIIVKNNAKKRKM
1			FESFIESVPLLKSLEVSERMKIVDVIGBKIYKR/DGERIITQGE
1			K\ADSFYIIESGEVSILIRSRTKSNKDGGNQEVEIARCHKGQYF
1 1		Į	GELALVTNKPRAASAYAVGDVKCLVMDVQAFERLLGPCMDIMKR
			NISHYEEQLVKMFGSSVDLGNLGQ

000			
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine Cocyatains Bignal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	oracamic ACIG, F=Phenylalaning C_Cluster
- }	corresponding	to first	I wenter the responding the resident
ł	to first		L=Leucine, M=Methionine N-Agnaragine
i	amino acid	amino acid	F=FIOILING, O=Glubamine D=Argining
		residue of	S=Serine, T=Threonine, V=Valine,
. I .	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon /-nosaible x=Unknown, *=Stop
1	sequence	1	Codon, /=possible nucleotide deletion,
5986	1806	484	\"=possible nucleotide insertion\
	1 2000	484	DAWKSTSLTFHWKLWGRHRGRRRGLAHDKNHLSDOGGREDOUS
į.			SPCCRFDSPRGPPPPRLGLLGALMAEDGVRGSPPVPSGPPMEED
ł		Í	GLRWTPKSPLDPDSGLLSCTLPNGFGGQSGPEGERSLAPPDASI
i	1		LISNICS ICDITIONS PROGRESS TO THE TOTAL PROGRESS LAPPDASI
	ì		LISNVCSIGDHVAQELFQGSDLGMAEEAERPGEK\AGQHSPLRE
i	ļ.	į .	TO A I CAND T POR POLIT A AGE L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT L'ANT
	1		OKKOD V LQLI LQS I QRMPGNAMVRGFRVA V V DBUT TMNNT COT TO
· ·	i		QNWLNDQVMNMYGDLVMDTVPEK\VHFPNSFFY\DKLRTKGYDG
1	1	}	VKRWTKNUDI ENWELLI I DIVIL ENWELLI (VHI FINSFFI (DKLKTKGYDG
Ì	1	l l	VKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSQ
	i	1	LATINARCE ANTAKILOAEAVKKORI DEHOGWKGVEVMNIKA DONDI
	ł	1	DSDCGAF VLQYCKHLALSQPFSFTOODMPKLRROTVKRLCHCVI
5987			TV
3987	1806	484	DAWKSTSLTFHWKLWGRHRGRRRGLAHPKNHLSPQQGGATPQVP
i			SPCCPEDSPERDED OF A CALL CALL
- 1	1	1	SPCCRFDSPRGPPPPRLGLLGALMAEDGVRGSPPVPSGPPMEED
1	1	1	GERWIPESPEDPDSGLESCTLPNGFGGGGGGGFGFDGLADDDAGT
1	Į	ſ	DISHVCSIGURVAONDFOGSDLGMAFFAFFDCCFV\ ACOHORS DE
•	1	j	TEMPTO VOSTEDER LOT VIGSLIPL STDEWNER I. POT POOR PORTS
	i	i	SRKGLVLQLIQSYQRMPGNAMVRGFRVAYKRHVLTMDDLGTLYG
		1	CNWLNDQVMNMYGDLVMDTVPEK\VHFFNSFFY\DKLRTKGYDG
		ł	VKRWTKNUDI ENKELLI IDIIH DITUGA DARAKGYDG
1			VKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSQ
- 1		į.	RTLNRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKMNVARQNN
į	ł	1	1 DEDUCATE VIQUERHIALSQPFSFTOODMPKI,RROTVKRI,CHCVI
5988	1292		_ <del>- </del>
	1232	410	FKKYFLSFLGLLESSHSRDRIHNLVLMFLLATHNLVWWFTCRFQ
		1	REDCTIONAGIMPNPOLNIKALIFGLES   ARGILTOCONTENDO
	1 .	1	LQEVFETDVFGHFILIRELEPLLCHSDNPSQLIWTSSRNARKSN
1	1		FSLEDFQHSKGKEPYSSSKYATDLLSVALNRNFNQQGLYSNVAC
	Į.	J	PCTALTMITYCTI PRETOMET TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE TO BE T
	ŀ	1	PGTALTNLTYGILPPFIWTLLMPAILLLRFPANAFTLTPYNGTE
1	i	ł	1 ADVIDER OR PASSINGLIKY LSATTCECONVINTENCIANDE ANDRE ME
5989	194	1 223	APIQALIBELEKHIRVTIOKTDNOARISGGGT.
		2610	AMDFPQHSQHVLEQLNQQRQLGLLCDCTFVVDGVHFKAHKAVLA
İ	i	1	ACCEPTE VIOLE VIOLED I SNADGI GOVILE PROVED VI OF ORD
1			NVDDVD \AVATELOMODIITACHALKSI.AFDATCDCCMADA
	1	1	EGGDKRAKEEKVATSTLSRLEQAGRSTPIGPSRDLKEERGGQAQ
	ĺ	1	SAASGAEOTEKADADDEDDDUGT KARA
}		i	SAASGAEQTEKADAPREPPPVELKPDPTSGMAAEAEAALSESS
1	ĺ	1 1	EQEMEVEPARKGEEEQKEQEEQEEGAGPAEVKEEGSQLENGEA
1		1	FEENENEESAGTDSGOELGSEARGI DSGTVGDDTDCVAVGC
			WCDDCGREE INTGNERRHIRIHTGERPESCPECCAN ECODAN CO.
1		1	THURST DE LIGHT GUELLEGKSYRLIST, INT. DEVE DE CENTRE DE LE
1		i i	CGKLFTTSGNLKRHQLVHSGEKPYQCDYCGRSFSDPTSKMRHLE
1			THOTOKEHKCPHCOKENOVCHI CONTCORSESDPTSKMRHLE
1		1	THOTOKEHKCPHCDKKFNQVGNLKAHLKIHIADGPLKCRECGKQ
1 1	1		TITOGNUKKHUKIHSGEKPYVCIHCOPOFADDCALOPIRDITES
. [	ĺ	1	DATE OF VINCERAR TOASSLIAHVROUTGEV DVICED CONDONS
			SQUAMBLE REPORTED IN THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPE
1 1	1		LCDKCGRGFNRVDNLRSHVKTVHQGKAGIKILEPEEGSEVSVVT
1			VDDMVTLATEALAATAVTQLTVVPVGAAVTADETEVLKAEISKA
1 1	i		VKOVOEED PATULI VA COCCORDIO DE LA VIADETEVLIKAEISKA
1 1		1	VKQVQEEDPNTHILYACDSCGDKFLDANSLAQHVRIHTAQALVM
l í	1	1	TO THE TOURS OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY O
5990	2		ISPIAPECPPAE
'	<b>~</b> [	4700	FGPGPDSGGGARGSGWGSRSQAPYGTLGAVSGGEQVLLHEEAGD
	į	1	SGFVSLSRLGPSLRDKDLEMEELMLQDETLLGTMQSYMDASLIS
		İ	LIEDFGSLGEVENGLEDBGVDEGD
	i	l	LIEDFGSLGEVEMSLPDPSWDFSPPSFLETSSPKLPSWRPPRSR
j	!	ľ	FRWGQSFFFQQRSUGEEEEEVASFSGOTLAGELDMCVccxpppp
[	į	1	THE THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPER
	ſ		DIAMAGED EDGE OF DUTTE PEGCOVILET VICALATACIDAL EXTRE
		J -	VVRQVSPGPRPVLLDDSLETSSALQLLMPTLESETEAAVPKVTL
[	ſ	1.	CSEKEGI SI NE PEVI DE ACI I VED
	l l	1.7	CSEKEGLSLNSEEKLDSACLLKPREVVEPVVPKEPQNPPANAAP
- 1	i	1.3	SSYRARRGRRRRSKEOPAACVEGYAPPI.PSSSPGOSTVCTPITTE
ŀ	ĺ	1 3	2VDNLQKQPQEELQKESGPLOGKGKPPAWADAWAAAT PNCCDIOL
1	į.	1 *	DERSAGUSSPAKEGPLDLYPKT,ADTTOTNDTDTHI,GIADGAGAG
- 1	i	1 '	FILE VEST EMELIANGEVIAGEVENDEGIANT RETECRITION RELI
			EPVLINPVLADSAAVDPAVVPISDNLPPVDAVPSGPAPVDLALV
			- TOTAL VELSDINGPPVDAVPSGPAPVDLALV

Deginning mucleotide location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location   location	SEQ	Predicted	T 75	
No: nucleotide location corresponding to first amino acid residue of amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence			Predicted end	Amino acid segment containing signal peptide
location of corresponding to first anino acid residue of anino acid residue of anino acid residue of anino acid				(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
COLTESPONDAING to first amino acid residue of amino acid residue of amino acid sequence solve of amino acid sequence solve of amino acid sequence solve of amino acid sequence solve of amino acid sequence solve of amino acid sequence solve of amino acid sequence solve of amino acid sequence solve of amino acid sequence solve of amino acid sequence solve of amino acid sequence solve of amino acid sequence solve of amino acid sequence solve of amino acid sequence solve of amino acid sequence solve of amino acid sequence solve of amino acid sequence solve of amino acid sequence solve of amino acid sequence solve of amino acid sequence solve of amino acid sequence solve of amino acid sequence solve of amino acid sequence solve of amino acid sequence solve of amino acid sequence solve of amino acid sequence solve of amino acid sequence solve of amino acid sequence solve of amino acid sequence solve of amino acid sequence solve of amino acid sequence solve of amino acid sequence solve of amino acid sequence solve of amino acid sequence solve of amino acid sequence solve of amino acid sequence solve of amino acid sequence solve of amino acid sequence solve of amino acid sequence solve of amino acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequen	1.0.	1		Giutamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of amino acid residue of amino acid sequence  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Begunnoc  Be	1			H=Histidine, I=Isoleucine, K=Lysine,
amino acid residue of amino acid sequence  S-Serine, T-Threconine, V-Valide, amino acid sequence  Sequence  Sequence  Deprint Processine Management (Codon, /-possible mucleotide deletion, -possible mucleotide deletion) -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deletion -possible mucleotide deleti				L=Leucine, M=Methionine, N=Asparagine,
### seridue of amino acid sequence   S.Serine, T-Threonine, V-Valine, withknown, *-Stop amino acid sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence	ı			P=Proline, Q=Glutamine, R=Arginine,
Metryptopham, Y-Tyrosine, X-Dukhown, *-Stop	ŀ		residue of	S=Serine, T=Threonine, V=Valine.
amino acid sequence  Codon, /-possible nucleotide insertion)  DPVPNDLTPVDPVUVRSPTDRRGAVSSALGGSAPOLLVESE LDPPKTII 1PVKVVDSLKIESGTSATHTHARPPELSISFYRR RQQRQAETEKKSQUPYGKNP5LPETPTGLADIPCLVIPPSAS  EARLQRSEPTILGILVPVVGPSABSSEPPTVSEVASSPTEQV BERNALDER BYPYGSVSAVPTPSSSALGFSAFOLLVESE LDPPKLLARPSPYGSVSAVPTPSSSALGFSAGGSAPOLLVESE LDPPKLLARPSPYGSVSAVPTPSSSALGFSAGGSAPOLLVESE LDPPKLLARPSPYGSVSAVPTPSSSALGFSAGGSAPOLLVESE LDPPKLLARPSPYGSVSAVPTPSSSALGFSAGGSAPOLLVESE LDPPKLLARPSPYGSVSAVPTPSSSALGFSAGGSAFTE LOPPKLLARPSPYGSVSAVPTPSSSSALGFSAGGSAFTE GPFNVLPLSAGGAPTSPYTVSTVSTSAGGSAGGSAGGSAGGSAGGSAGGSAGGSAGGSAGGSA	· I	1	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Apossible nucleotide insertion	j	amino acid	sequence	Codon, /=possible nucleotide deletion
DPYNNLTYPPYLVKSRYDDRRGAVSSALGGSAPGILLVES  LDPPKXII I PEVKEVDSILKESGYSATHTBARPRELSISFYRRR KQQKQAGATEMESQPYTGKRØSLDFTPTILADI PCLUI PPAGE  KYALQGSFEPTLEI CLVPWOFED SAPS PSP PYSKYSVASSYTTÖV  PSQEMPLLARPSDPVQSVSAVPTPSSMSALDFPAGGLOMPPS  LPPPPLQPPSLIKSMOVLDDFTHKADLSBWCVASSSTTÖV  PSQEMPLLARPSDPVQSVSAVPTPSSMSALDFPAGGLOMPPS  LPPPPLQPPSLIKSMOVLDDFTHKADLSBWCVASSSTTÖV  GELAMGEGGGAPHSTVPPPELDFASIGRAVPOSFMESKGTPA  GPPSNVLPISMAPPLSLGDIGGGAPOTEPTKVEVKPVASSPTT  GELAMGEGGAPHSTVYPPELDFASIGRAVPOSFMESKGTPA  GPPSNVLPISMAPPLSLGDIGGGAPOTEPTKVEVKPVASSPTRY  KVPLATKAVPTPGSTVYKLEAVMFABALKKLSFLPPTRTGSPRR  KVPLATKAVPTPGSTVYKLEAVMFABALKKLSFLPPTRTGSTRRE  KVPLATKAVPTPGSTVYKLEAVMFABALKKLSFLPPTRTGSTRRE  KVPLATKAVPTPGSTVYKLEAVMFABALKKLSFLPPTRTGSTRRE  KVPLATKAVPTPGSTVYKLEAVMFABALKKLSFLPPTRTGSTRRE  KVPLATKAVPTRGSTVYKLEAVMFABALKKLSFLPPTRTGSTRRE  KVPLATKAVPTRGSTVYKLEAVMFABALKKLSFLPPTRTGSTRRE  KVPLATKAVPTRGSTVYKLEAVMFABALKKLSFLPPTRTGSTRRE  KVPLATKAVPTRGSTVYKLEAVMFABALKKLSFLPPTRTGSTRRE  KVPLATKAVPTRGSTVYKLEAVMFABALKKLSFLPPTRTGSTRRE  KVPLATKAVPTRGSTVYKLEAVMFABALKKLSFLPPTRTGSTRRE  KVPLATKAVPTRGSTVYKLEAVMFABALKKLSFLPPTRTGSTRRE  KVPLATKAVPTRGSTVYKLEAVMFABALKKLSFLPPTRTGSTRRE  KVPLATKAVPTRGSTVYKLEAVMFABALKKLSFLPPTRTGSTRRE  KVPLATKAVPTRGSTVYKLEAVMFABALKKLSFLPPTRGSTRRAFLEV  GCGGR-GGRRGBVSSACHNTESSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	i	sequence	] -	\=possible nuclectide insertion\
LDPRITTIFEYKEVYDSIKIESGTSATTHEAPPRILSISSTYRIK ROORGATEMSENSUPPTIKKADE JEPTYTISLAD TEPTYTISLAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTISSAD TEPTYTIS				DPVPNDI TPVDPULVKSPPTDPPRCAVSCAV CCCA POTTUPO
ROORGATTERSOUPPICKIPS. JATOP TO ANTAL GRAPPET PLEICLY VERY ASS STEWS FROM PROBABLIAR PSPEUR SERVING PROBABLIANCE STEWS AS STEWS OF PORT AND ANTAL STEWS AND ANTAL STEWS AS THE SERVING PROBABLE PROPERTY AS THE SERVING PROBABLE PROPERTY PROBABLE PROBABLE PROPERTY PROPERTY PROBABLE PROPERTY PROPERTY PROBABLE PROPERTY PROBABLE PROPERTY PROBABLE PROPERTY PROBABLE PROPERTY PROBABLE PROPERTY PROBABLE PROPERTY PROBABLE PROPERTY PROBABLE PROPERTY PROBABLE PROPERTY PROBABLE PROPERTY PROBABLE PROPERTY PROBABLE PROPERTY PROBABLE PROPERTY PROBABLE PROPERTY PROBABLE PROPERTY PROBABLE PROPERTY PROBABLE PROPERTY PROBABLE PROPERTY PROBABLE PROPERTY PROBABLE PROPERTY PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PRO	1		1	LDDDYTTIDEWEINDELVESES
KTALGRSPETCLEICL.VPVGSSPASPSEPTSVENDASSSTEDU   PSQEMPLLARSPPTQUSVSPADTSPMSALALPPAGGLGMPPS    LPPP-LQPPSTLPLSMGPVLEDPTTTYAPLESMFCYPEIVSPSGYP    LPPP-LQPPSTLPLSMGPVLEDPTTTYAPLESMFCYPEIVSPSGYP    CLPPP-TVVDLVSSTGRAVAVPCTCSVMAPPSTSTGTAY   GPLONGGGQNAPFMSTVPPPLPPASIGRAVPQFKMESRGTPA    GPPSNVLPLSMAPPLSLLGLEVAPPARSKENEVPASPHPK    EKVSALVOSPOMKALACVSAEGYTVERPASERLKFETGETTRRE    KPUPLATKAVTVPTROSTVPKLEMAPARTERLKFETGETTRRE    KPUPLATKAVTVPTROSTVPKLEMAPARTERLKFETGETTRRE    KPUPLATKAVTVPTROSTVPKLEMAPARTERLKFETGETTRRE    KPUPLATKAVTVPTROSTVPKLEMAPARTERLKFETGETTRRE    KPUPLATKAVTVPTROSTVPKLEMAPARTERLFTPHTOGSS    DVVQAFISEIGIRASDLSSLLEGFSKEERKKECPPPAPADSLAV   GNSGGVLIFQEKRIDHRIQAPELAVGAUTTPPHQLMKELA-   AVSILLAKAGSFKSTAGGGTLKFEGOTTSAKIPPAVRLQEGVHGPS    RHVNGSGDDIVCV,VRSRTPPKK,WBALLIF LEPTOPHQLMKELA-   AVSILLAKAGSFKSTAGGGTLKFEGOTTSAKIPPAVRLQEGVHGPS    RHVNGSGDDIVCV,VRSRTPPKK,WBALLIF LEPTOPHQLMKELA-   AVSILLAKAGSFKSTAGGGTLKFEGOTTSAKIPPAVRLQEGVHGPS    RHVNGSGDDIVCV,VRSRTPRKK,WBALLIF LEPTOPHQLMKELA-   AVSILLAKAGSFKSTAGGETLKFEGOTTSAKIPPAVRLQEGGUGGS-   GUQGRAGNSKSVSNOSHSTSEASSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS		ı	İ	POOPONETERICON DESCRIPTION DE PROPERTE DE LA COMPONETERICA DE LA COMPONETERICA DE LA COMPONETERICA DE LA COMPONETERICA DE LA COMPONETERICA DE LA COMPONETERICA DE LA COMPONETERICA DE LA COMPONETERICA DE LA COMPONETERICA DE LA COMPONETERICA DE LA COMPONETERICA DE LA COMPONETERICA DE LA COMPONETERICA DE LA COMPONETERICA DE LA COMPONETERICA DE LA COMPONETERICA DE LA COMPONETERICA DE LA COMPONETERICA DE LA COMPONETERICA DE LA COMPONETERICA DEL COMPONETERICA DE LA COMPONETERICA DE LA COMPONETERICA DE LA COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERICA DEL COMPONETERI
PSQEMELARPSPEVGSVSPANDTPBRAGGLIMPPS   LPPPPTUPES   LEMPPTUPED   LPPPTUPES   LPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLPPPTUPES   CLLPPTUPES   CLLPPTUPES   CLLPPTUPES   CLLPPTUPES   CLLPPTUPES   CLLPPTUPES   CLLPPTUPES   CLLPPTUPES   CLLPPTUPES   CLLPPTUPES   CLLPPTUPES   CLLPPTUPES   CLLPPTUPES   CLLPPTUPES   CLLPPTUPES   CLLPPTUPES   CLLPPTUPES   CLLPPTUPES   CLLPPTUPES   CLLPPTUPES   CLLPPTUPES   CLLPPTUPES   CLLPPTUPES   CLLPPTUPES   CLLPPTUPES   CLLPPTUPES   CLLPPTUPES   CLLPPT		İ	i	MONOR DE SERSEQUE TERMES LE LE TEMES DE LE LE LE LE LE LE LE LE LE LE LE LE LE
LEPPFLQPPSTUPLESMEPTICSTWARP PSTSYTYTY CRIPPSTUPLESMEPTICSTWARP PSTSYTSTTYTY CRIPPSTUPLESMEPTICSTWARP PSTSYTSTTYTY GELOMOGEGUAPFMSTUPPPILIPSAIGRAVPOPKMESRGTPA GEPENVLPISARPHILISLICHAROTOTETHYKEVPISYSTTYTY GELOMOGEGUAPFMSTUPPPILIPSAIGRAVPOPKMESRGTPA GEPENVLPISARPHILISLICHAROTOTETHYKEVPISSTETY KEVSALVOS POMKALACUSAGUTUEPPASERLKPETGTETRRE KEPLPATKAVTPTROSTTYPLANUPARARKENS-FLPTPRTOGSE DVVQAFISEIGIEASDLSSLLEGFEKGERKKECPPPAPADSLAV GINSGGUIPOGLAWVAGATPENOMINKETHOPHOLIMKELA AVSILLAKAGSPKSTAGEGTLKPEOVTSAKIIPAAVRLQEGUMEPS RUHVGSSGIDKOVANSTTSTAKIIPAAVRLQEGUMEPS RUHVGSSGIDKOVANSTTSTAKIIPAAVRLQEGUMEPS RUHVGSSGIDKOVANSTTSTAKIIPAAVRLQEGUMEPS RUHVGSSGIDKOVANSTTSTAKIIPAAVRLQEGUMEPS RUHVGSSGIDKOVANSTTSTAKIIPAAVRLQEGUMEPS RUHVGSSGIDKOVANSTTSTAKIIPAAVRLQEGUMEPS SILLSPRASSCISSISSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	i		1	KIALQRSPETPLEICLVPVGPSPASPSPEPPVSKPVASSPTEQV
CLPPPTYZLUSTRONAPPTAVUSTYSTUTY GGLOMGGGTQHAPWSTUPPPLPPARIOPROPORMESRIPA GPENNLPLSMAPPLSLGLPGHGAPTEPTKYEVKPVPPASHPIK KYSALVOSPOMKALACVSABEOVIVEDASHPIKTEVEKPVPASHPIK KYSALVOSPOMKALACVSABEOVIVEDASHLYRUSTEVPTOGSE DVVQAFISIGIERSOLSSLLEGPEKSEKLPFTOGTEPRE KPPLPATKAVPTPRGSTVPKLPAVHPARLIKLIS-LPTPTTOGSE DVVQAFISIGIERSOLSSLLEGPEKSEKLPFTOGTEPRE KPPLPATKAVPTPRGSTVPKLPAVHPARLIKLIS-LPTPTTOGSE DVVQAFISIGIERSOLSSLLEGPEKSEKLPFOTPATPHOLMKYLA AVSLLAKARSPESTAGEGTEKPEOVT-SAMPAVLLGEVVIGES RVHYGSJÖDHDYC\VRSRTPPKK\MPALLIPEVGSRNNYKRHODI TIKPVISLOPAAPPPPCLAASREPLHREAVAPARLQEVVIGES RVHYGSJÖDHDYC\VRSRTPPKK\MPALLIPEVGSRNNYKRHODI TIKPVISLOPAAPPPCLAASREPLHREAVAPARLQEVVIGES SLLSPBASDCRNDMINTRTPEPSAKORSMCCYRACGASPSSO GWGGRAGNSRSVSIGSINSTESSASSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS		1	1	PSQEMPLLARPSPPVQSVSPAVPTPPSMSAALPFPAGGLGMPPS
GPLONGEGPCHAPPESTUPPPLEPASIGRAYPOPKNESGTPPA GPPENVLPISMAPPLESICLEPGHGAPOTETE WEVEVEVENDAPHER EVESALVOS POMKALACVSAGCUTVERPASIGRATIVES PEPPA ERVASALVOS POMKALACVSAGCUTVERPASIGRALKPETOGSTEPRE KPEPLATKANPTERGSTVEKLPANPARIALIS SLETPTPTOGSE DVVQAFISEIGIBASILSEGPEKSEAKKECPPPAPADSLAV GNGSGUDI POGERFLORIO ADRELLANDALIS SLETPTPTOGSE RVHOSGONDIPOGERFLORIO ADRELLANDALIS SLETPTPTOGSE RVHOSGONDIPOGERFLORIO ADRELLANDALIS SLETPTPTOGSE RVHOSGONDIPOGERFLORIO ADRELLANDALIS SEGNAMINARIO TIKPVUSICAPANPPCILASREPLOHRTS SEQADESAPCLAPE SLLS PEASPERNINDINTTET PEPESAKORS MEGRACINARIO TIKPVUSICAPANPPCILASREPLOHRTS SEQADESAPCLAPE SLLS PEASPERNINDINTTET PEPESAKORS MEGRACINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINARIO SEGNAMINA SEGNAMINA SEGNAMINA SEGNAMINA SEGNAMINA SEGNAMINA SEGNAMINA SEGNAM	1		ļ	LPPPPLQPPSLPLSMGPVLPDPFTHYAPLPSWPCYPHVSPSGYP
GPPENVLPLISMAPPLSLGLICHGHGAPOTEPTKYEVKPVPASHIPK EKVSALVOS POMKALACVSARGVIVERPASKLIPTOTETRER KPELPATKAVPTPRGSTVPKLPAVHPARLIKLIS-LETPTPTOGSE DVVQAFISI GIERSOLIS-LIEGPEKESEKLPFTOGTEPRE KPELPATKAVPTPRGSTVPKLPAVHPARLIKLIS-LETPTPTOGSE DVVQAFISI GIERSOLIS-LIEGPEKTERKEKCPPARPABILAV GNSGGVI POEKRFLDRILOADELANVAGLITPPATPHOLMKYELA AVSILAKAKSPYSTAGGETKLPEVTEVAHAPARLICKUSTOPPE RVHYGSGDHDYC\VRSRTPPKK\MPALLI PEVGSRMYKEHODI TIKPVISLOPAAPPPPCLABRSREDHARVARUGUSVHGPS RVHYGSGDHDYC\VRSRTPPKK\MPALLI PEVGSRMYKEHODI TIKPVISLOPAAPPPECLABRSEDLHIPEVAGENKYKEHODI TIKPVISLOPAAPPPECLABRSEDLAFSESSSSSSSSSSSSSSSSSBRIGGER SLIS-PEASPCRNDWITTPPEFSAKGRMCCYRACGASPSSOL GWGRAGNRSRSVSSGSHRCSSSSSSSSSSSSSSSBRIGGER PSPERSDRRRYSSYNSBURDYRORVUCKKPATEERRVYFIGK IPGRWTRSELKORRSVYGGEIEECTHPRVQCDNYGFYTYR NADE PAPAIESGKHRADABSOPPLC-PGGRRQCKRYSYDLBNRED PAPAVSKRDSLLOPILLERUNDOKALRR APAIESGKHRADABSOPPLC-PGGRRQCKRYSYDLBNRED DPAPVXSKRDSLEDTILLKOADKHAR DLRFOCHMISTITYRNNRI INRMELIKAVITTPECLLILDVRNINK OMERSPLSSHSGOCSPSTYCVTREFORMYTSFERKTELYQELGOAR DLRFOCHMISTITYRNNRI INRMELIKAVITTPECLLILDVRNINKL OMERSPLSSHSGOCSPSTYCVTREFORMYTSFERKTELYQELGOAR ELLERYYTHALDDLSNARERURULDDSGI IFINDDSHRNVMM RIMIGLIMGTTSSUSPEGLATURYTSFERKTELYQELGOAR ELLERYYTHALDDLSNARERURULDGSI IFINDDSHRNVMM RIMIGLIMGTTSSUSPEGLARVITTPECLLILDVRNINKL SILOPILIESTLDALGDFRSVSVORSCHATRVLTWLTTPECLLICHTWITTLGK FORMYSISLITYHLADDLSNARERURULDSGI IFINDDSHRNVMM RIMIGLIMGTTSSUSPEGLARVITTPECLICHMDVK GUKKMPEATRILATIVMLLOFITLCAALMSKLERULTURULT SOODDSEGGLTADOSGININ, SEVLDASSISLOMENLERULTURULTUR GVFFSILATGLLATURGGI KLAPSTYTLIONLAALASTCEPUG GVFFSILATGLLATURGGI KLAPSTYTLIONLAALASTCEPUG GVFFSILATGLLATURGGI KLAPSTYTLIONLAALASTCEPUG GVFFSILATGLLATURGGI KLAPSTYTLIONLAALASTCEPUG GVFFSILATGLLATURGGI KLAPSTYTLIONLAALASTCEPUG GVFFSILATGLLATURGGI KLAPSTYTLIONLAALASTCEPUG GVFFSILATGLLATURULTURURURURURURURURURURURURURURURURUR	ľ			CLPPPPTVPLVSGTPGAYAVPPTCSVPWAPPPAPVSPYSSTCTY
GPPENVLPLISMAPPLSLGLICHGHGAPOTEPTKYEVKPVPASHIPK EKVSALVOS POMKALACVSARGVIVERPASKLIPTOTETRER KPELPATKAVPTPRGSTVPKLPAVHPARLIKLIS-LETPTPTOGSE DVVQAFISI GIERSOLIS-LIEGPEKESEKLPFTOGTEPRE KPELPATKAVPTPRGSTVPKLPAVHPARLIKLIS-LETPTPTOGSE DVVQAFISI GIERSOLIS-LIEGPEKTERKEKCPPARPABILAV GNSGGVI POEKRFLDRILOADELANVAGLITPPATPHOLMKYELA AVSILAKAKSPYSTAGGETKLPEVTEVAHAPARLICKUSTOPPE RVHYGSGDHDYC\VRSRTPPKK\MPALLI PEVGSRMYKEHODI TIKPVISLOPAAPPPPCLABRSREDHARVARUGUSVHGPS RVHYGSGDHDYC\VRSRTPPKK\MPALLI PEVGSRMYKEHODI TIKPVISLOPAAPPPECLABRSEDLHIPEVAGENKYKEHODI TIKPVISLOPAAPPPECLABRSEDLAFSESSSSSSSSSSSSSSSSSBRIGGER SLIS-PEASPCRNDWITTPPEFSAKGRMCCYRACGASPSSOL GWGRAGNRSRSVSSGSHRCSSSSSSSSSSSSSSSBRIGGER PSPERSDRRRYSSYNSBURDYRORVUCKKPATEERRVYFIGK IPGRWTRSELKORRSVYGGEIEECTHPRVQCDNYGFYTYR NADE PAPAIESGKHRADABSOPPLC-PGGRRQCKRYSYDLBNRED PAPAVSKRDSLLOPILLERUNDOKALRR APAIESGKHRADABSOPPLC-PGGRRQCKRYSYDLBNRED DPAPVXSKRDSLEDTILLKOADKHAR DLRFOCHMISTITYRNNRI INRMELIKAVITTPECLLILDVRNINK OMERSPLSSHSGOCSPSTYCVTREFORMYTSFERKTELYQELGOAR DLRFOCHMISTITYRNNRI INRMELIKAVITTPECLLILDVRNINKL OMERSPLSSHSGOCSPSTYCVTREFORMYTSFERKTELYQELGOAR ELLERYYTHALDDLSNARERURULDDSGI IFINDDSHRNVMM RIMIGLIMGTTSSUSPEGLATURYTSFERKTELYQELGOAR ELLERYYTHALDDLSNARERURULDGSI IFINDDSHRNVMM RIMIGLIMGTTSSUSPEGLARVITTPECLLILDVRNINKL SILOPILIESTLDALGDFRSVSVORSCHATRVLTWLTTPECLLICHTWITTLGK FORMYSISLITYHLADDLSNARERURULDSGI IFINDDSHRNVMM RIMIGLIMGTTSSUSPEGLARVITTPECLICHMDVK GUKKMPEATRILATIVMLLOFITLCAALMSKLERULTURULT SOODDSEGGLTADOSGININ, SEVLDASSISLOMENLERULTURULTUR GVFFSILATGLLATURGGI KLAPSTYTLIONLAALASTCEPUG GVFFSILATGLLATURGGI KLAPSTYTLIONLAALASTCEPUG GVFFSILATGLLATURGGI KLAPSTYTLIONLAALASTCEPUG GVFFSILATGLLATURGGI KLAPSTYTLIONLAALASTCEPUG GVFFSILATGLLATURGGI KLAPSTYTLIONLAALASTCEPUG GVFFSILATGLLATURGGI KLAPSTYTLIONLAALASTCEPUG GVFFSILATGLLATURULTURURURURURURURURURURURURURURURURUR		ļ	1	GPLGWGPGPQHAPFWSTVPPPPLPPASIGRAVPQPKMESRGTPA
EXVSALVOS PONKALACVSAGOUTVEEPASERLKPETOGSTEPRE   KPPLPATKAUPTPROGITE VALPATHERATIKS JETPTPTOGSE    DVVQAFISEIGIERS LISELEGPEKSEAKKECPPPAPADELAV   GNGGGUID POEKRIDERI QAPELANVAGILPAVAFILGOVIGES   RVHOGSOUD POEKRIDERI QAPELANVAGILPAVAFILGOVIGES   RVHOGSOUD POEKRIDERI QAPELANVAGILPAVAFILGOVIGES   RVHOGSOUD POEKRIDERI QUE PROGRAMINA PAVELLAKARS PESTAGOGILKPBOVTEAKURADALI PEVGSRANVKRIGOT   TIKPVUSICAPAPPPCIAASREPLOHRTS SEOADESAPCILAPS   SLLSPEAS PERRINDITY TEPPESAKORS REVRACERSA PESSO   GWOGR GGNNSENSUSGSINTSEASSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	1			GPPENVLPLSMAPPLSLGLPGHGAPQTEPTKVEVKPVPASPHPK
REPLANTKAUPTERGSTUPKLEAVBRARLKKLSFLETRITOGSE DVVQAFISEIGIGBAGUSSLLEGPEKRECOPPAPADELAV GNSGUDI PQEKRUDBILQAPELAVKAGLTPPATOHOLMKPLA AVSLLAKAKSPKSTAGETLKEGGYTZAKIPAAVRLQEGVIGPS RVHVGSGDHDYC\VRSRTPPKK\MPALLIPEVGSRMVKRIQDI TIKPVLSLGPAAPPPECTAASREPLDHIRTSSEQADPSAPCLAPS SLLSPEASPCRUDNITTTPEPSPAKORSMRCYEKACRSASPSSO GWGGRGRGNNSRSVSSGSNSRNTSBARSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	1	1	i	FKVSALVQSPQMKALACVSAEGVTVEEPASERI,KPETOETPDDE
DVVQAFTSEIGTEASDLSSILLÖPFKSEAKKECPPPAPADSLAV GNSGGVID PQERFEIDLÖRJAPPELANVETPPATPPHOLIMKPLA AVSLLAKAKSPKSTAGEGTLKPEGYTSAKHIPAAVRIQGEVHIGPS RWHGSGDIDHYC\UNSTYPPKK\MPALIPEAVRIQGE RWHGSGDIDHYC\UNSTYPPKK\MPALIPEAVRIQGE SLLSPEASPCRIDMITTSEGORJAPSACLASP SLLSPEASPCRIDMITTSTEGORJAPSACLASP SLLSPEASPCRIDMITTPPEPSAROSMINCYKAGCRSASPSG GWQGRGRNSRSVSGSNFTSBASSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS		į	1	KPPLPATKAVPTPROSTVPKLPAVHPARI.RKI.SFI.DTPPTOGGE
ONSGGVDIPQERRIDBIAQADGLAPPATOPHOLMKPLA AVSLLAKAKSPASTAQETIAKEPGATAQEQUEVIGES RVHVGSGDHDYC\VRSRTPPKK\MPALLIPEVGSVRIDS RVHVGSGDHDYC\VRSRTPPKK\MPALLIPEVGSVRIDS RVHVGSGDHDYC\VRSRTPPKK\MPALLIPEVGSVRIDVKRRIQDI TIKPVLSLGPAAPPPPCTAASREPLDHIRTSSEQAPPSAPCLAPS SLLSPEASPCRNDMTTTPPETSAGSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS				DVVQAFISEIGIEASDLSSLLEOFEKSEAKKECDDDADADGLAV
AVSILAKAKSPISTAQRETIKEPGYTEAKHIPAAVRIQEGVIGPS RVHYGSGDHDYG\UNSTEPRK\MPALIPEVGSKRNVKRRIQDI TIKPVISIGPAAPPPPCIAASREPLDHRTSSEQAPSAPCIAPS SLISPERSPCRNDMITTSPESSAROSMRCYRKACRSASPSG GWQRAGRNSRSVSGSNRTSBASSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	ŀ	į.		GNSGGVDI POEKRPLORI OA DEL ANVACT TERATRIDUO I WYDT A
RVHYGSGDHDYG\VBRETPPKK\MPALLIPEVGSRMNYKRHQDI TIKPVLSLGPAAPPPCLAASREJHRTSSEQADPSAPCLAPS SLLSPEASPCRIDMITRITPPFSAKORSMRCTKACRSASPSO GWGGRGNSRSWSSUSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	į	İ	ĺ	AVSIJAKAKSDESTAOESTI EDSCHERA MIDA ALDI ODSFERO
TIKPVLSLGPAPPPCTAASREPLDHRTSSDADPSAPCLAPS SLLSPEBASPCRNDMINTETPEPSASRKRCYRKCKRAGASPSSO GWGGRGRNRSWSGUNRTTEASSSSSSSSSSSSSRSRSELSDP HKRWRSSCSSGGERGCSSSSSSSSSSSSSSSRSRSRSE PSPRRSDRRRYSSYSHDHYQRQRVLQKERAIEERRVVFIGK IPGRWTSELKQRFSVFGEIEECTTHFRVGGDNYGFVTYRYAEE AFAAIESGHKLRQADEQFFDLCFGGRGPGCKRSYSDLDSNREDF DPAPVASKPDSLDPTTLKGAQKNLER  75991 334 1379 RLSSHFSOCSPSITVCTNTFPXGCONTSFFRKKTELYQELGLQAR DLRPGHYMSITVRNRRIIMREYLKAVITPRCLLLLDYRNLNLK QWLFRZLPSQLSSEGGULTVTELPFATEALLQVYMITLOGKL SILOPLILETLDALGDPKHSSVDRSKLHHLLORKSLSELETDI KIFKESILEILDEELELELCVEKWSDPQVFRKSSAGIDHAEEM ELLLENYYRLADDLSNAARSLRVLIDDSGSIFFINLDSKRNVMM RLNLQIJTMGTFSLSLFGLMWSDAVGNONTSFFRKKTELYQELGQAR BLLLENYYRLADDLSNAARSLRVLIDDSGSIFFINLDSKRNVMM RLNLQIJTMGTFSLSLFGLMWSDAVGNONTSFFRKKTELYQELGQAR BLLLENYYRLADDLSNAARSLRVLIDDSGSIFFINLSKWMDHYMGGIVEGL GWFSSILBTGLLWHAPGGIKLFGLWSTAFTHFWITTGI MFMGSGLIWRRLLSFLORV/LARSSIASSIANTELKWFAICFUC GVFFSILGTGLLWLPGGIKLFAVFYTLGNLAALASTCFFLMGPVK QLKKMPGATRLLATIVMLCFIFITVANLAFTCFFLAG CKKYMDSTDSGSGANWAGIGAMGGARGAGATGALGWGCKLPSAFCFFGS SVAMDMFQXVEKIGEGTYGVVYKAKNRETGGLVALKKIRLDLEM EGVPSTALREISLLKELKHPNIVRLLDVVRNERKLILVFEFFLSQ DLKKYMDSTPGSELPJELLIKSLIFGLLGGGVSFCHSKRYHRDLK PQMLLINELGAIKLADPGLARAFGVPLRTYTHEVVTLWYRAPEI LLATRFYTTAVDINGCIFANTYTHEVVTLWYRAPEI LLATRFYTTAVDINGCIFANTYTHFVYTLWYRAPEI LLATRFYTTAVDINGCIFANTYTHFVYTLWYRAPEI LLATRFYTTAVDINGCIFANTYTHFVYTLWYRAPEI LLATRFYTTAVDINGCIFANTYTHFVYTLWYRAPEI LLATRFYTTAVDINGCIFANTYTHFVYTLWYRAPEI LLATRFYTTAVDINGCIFANTYTHFVYTLWYRAPEI LLATRFYTTAVDINGCIFANTYTHFVYTLWYRAPEI LLATRFYTTAVDINGCIFANTYTHFVYTLWYRAPEI LLATRFYTTAVDINGCIFANTYTHFYFOXALTFFOXS-TWPL PROFILLGYPSGTYTATTALAPPTFSSPEPSPARGVYVLQRF RH  5994 394 1934 1934 1934 1934 1934 1934 19	1			PVHVGSGDHDVG\ UDGBTDDVV\ MD3 L L TD3 G G G G G G G G G G G G G G G G G G G
SLLSPEASPCRIDMITRIPPEPSAKORSMRYCKRACRSASPSSO GWOGRAGNRISKUSSGSSMRYCSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	[-	1		TIVDU CI CDAADDDCIAA GDDD DUGGSRWNVKRHQDI
GWQGRAGRNSRSVSSGSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	Í	<b>i</b> :		FILEDER COCKETS CONTROL OF THE CONTROL OF THE CONTROL OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF
HKRWRRSSCSSGRSBRCSSSSSSSSSSSSSSSSSSSSSSSSSSS	1			SUBSPEASPCRNDMINTRTPPEPSAKQRSMRCYRKACRSASPSSQ
PSPRRSSDRRRYSSYRSHDHYORGRVLOKERA IEERRVUFICK IPEGMRTSELKORPSVEGIEGETHPRUGGDNOGFVTHYNAEE APAALESGHKLRGADEOPPILCFGGRRGFCKRSYSDLDSNREDF DPAPVKSKFDSLDPTILKQACKHURR  RLSSHFSOCSPSIYCTTREMCGGNVSTSFERKKTELYGELGLOAR DLRRCHMMSITVRNNRII INRMEYLKAVITPECLLILDYRNINLK OWLDFSLPSGLSGGGLVTYPLFSFRRKTELYGELGLOAR DLRRCHMMSITVRNNRII INRMEYLKAVITPECLLILDYRNINLK OWLDFSLPSGLSGGGLVTYPLFSKADPQVFEKSSAGIDHAEEM KIPKESLBEILDEELLEELCYGHTANDFGKSLSELETDI KIPKESLBEILDEELLEELCYSKSDPQVFEKSSAGIDHAEEM RELLLENYYRLADDLSNAARELRVLIDDSGSIIFINDDSHRNYMM RENNLQLIMGTFSLSIFGRUMGAFGMNLESSLEEDHRIFHLITGI SGQDDECGLTADGSOINL/SENSJESPRPHWMGGIVEGL GGVFSILGTGLLWLPGGIKLPRPWMGAMEKLRRVL OLKKMPEATRILATIVMLLCFIFTLCAALMHKKGLAVLFCILG GVFFSILGTGLLWLPGGIKLPRSSLESBEDHRIFHLUFBICFVC GVFFSILGTGLLWLPGGIKLPRSSLESSHAPECFPGS SVAMMAGLGRAGRHMEAGGATGALAVGCKLPSAFCFPGS SVAMMAGNAGIGRAGRHMEAGGATGALAVGCKLPSAFCFPGS SVAMMAGNAGIGRAGRHMEAGGATGALAVGCKLPSAFCFPGS SVAMMAGNAGIGRAGRHMEAGGATGALAVGCKLPSAFCFPGS SVAMMAGNAGIGRAGRHMEAGGATGALAVGCKLPSAFCFPGS SVAMMAGNAGIGRAGRHMEAGGATGALAVGCKLPSAFCFPGS SVAMMAGNAGIGRAGRHMEAGGATGALAVGCKLPSAFCFPGS SVAMMAGNAGIGRAGRHMEAGGATGALAVGCKLPSAFCFPGS SVAMMAGNAGIGRAGRHMEAGGATGALAVGCKLPSAFCFPGS SVAMMAGNAGIGRAGRHMEAGGATGALAVGCKLPSAFCFPGS SVAMMAGNAGIGRAGRHMEAGGATGALAVGCKLPSAFCFPGS SVAMMAGNAGIGRAGRHMEAGGATGALAVGCKLPSAFCFPGS SVAMMAGNAGIGRAGRHMEAGGATGALAVGCKLPSAFCFPGS SVAMMAGNAGIGRAGRHMEAGGATGALAVGCKLPSAFCFPGS SVAMMAGNAGIGRAGRHMEAGGATGALAVGCKLPSAFCFPGS SVAMMAGNAGIGRAGRHMEAGGATGALAVGCKLPSAFCFPGS SVAMMAGNAGIGRAGRHMEAGGATGALAVGCKLPSAFCFPGS ROLLINGLIGSBAKARARTONDALAKKIRLDLEM EGVPSTALREISLLKELKHPNIVRLLDOVUNBEKLLVYGELPG DLKKYMDSTYGSEDIJHNIKGSTGVVAKRRETGOLVALKKIRLDLEM EGVPSTALREISLLKELKHPNIVRLLDOVUNBEKLLVILVEFPLG  BACHGESTAPCHAGATAALAVGCKLPSAFCHAGATGARGANAAA AGBVQLHVWIRGMRIQFQJKAAATIDLDPDFFPGSRFRSCTWPL PRALTATAVONINGICGIFFARGGSRANAMAGSARLANGSFRSLLEGRSALAGGGRGFRERERLPGR SPGPILGARGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	į.	1		UWDURAGENSESVSSGSNRTSEASSSSSSSSSSSSRSRSRSLSPP
IPGRMTRSELKQRSSYGETEECTIHFRQGONYGFUTYRYAEE AFAALESGHKLRQADEQFPLGGGRQGYCKGRYSDLDSNREDF DPAPVKSKFDSLDFDTLKQAQKNLRR  SISSHFSOCSPIYC]TRKGQVNTSFERKKTELYQELGLQAR DLRFQHVMSITVRNNRIIMEMEYLKAVITPECLLILDYRNLANLK QWLFRELPSQLSGEGQLVTYPLFFEFRATEALLQWHINTLQGKL SILQPLILETLDALGDFWRSSVDRSKLHTLLQMGKSLSSLETDI KIFKESILEILDEEGLLEELCVSKWSDPQVFEKSSAGIDHAEEM PLANDALGMGTFSLSFGGHWAPAGMMILGSLEEDHHIFWLITGI KIFKESILEILDEEGLLEELCVSKWSDPQVFEKSSAGIDHAEEM RLNLQLIMGGTFSLSFGGHWAPAGMMILGSLEEDHHIFWLITGI MFMGSGLIWRRLLSFLGGY/LARSSIASYGMKDMVHGGIVGGL GVFFSLGTGLLHNLDGGILKAPTILDSGGIJFIFWHAGAMEKLRRVL SGQDDEGGLTAQDSGINI/SEVLDASSLSFMTRLKWFAICEVC GVFFSLGTGLLHNLDGGILKYFTIGGILAALASTCFIMGPVK QLKKMFFBATRLLATIVMLLCFIFTLCAALMWHKKGLAVLFCILQ FLSMTWYSLSYIPYARDAVIKCSSLS  5993 1650 594 AEGIGSWAVWAGIGWAGGKHMEAGGATGALGVGCKLPSAFCFFGS SVAMDMFQKVEKIGEGTYGVVYKAKANRETGGLVALKKIRLDLEM EGVPSTAIREISLLKELKHPNIVRLLDVVHBERKLYLVFEFLSQ DLKKYMDSTFGSSELPHLIKSYLFGLLGGVSFCHSHRVIHKRDLK PQNLLINELGAI KLADFGIRAFGVPLRTYTHEVVTLLWYAPEI LLATRFYTTAVDIWSIGGIFABMVTRKALFFGDS LEIDQ\LFRI FRINLGTSSEDTHFILKSYLFGLLGGVSFCHSHRVIHKRDLK PQNLLINELGAI KLADFGIRAFGVPLRTYTHEVVTLLWYAPEI LLATRFYTTAVDIWSIGGIFABMVTRKALFFGDS LEIDQ\LFRI FRICHTSSEDTHFILTSSTLLEKSFPKNTRKGLEIVENLEPEG RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQVVLQRF RH AGEVQLHVWIRGMRIQPG/KAAAITDLDPDFEPGSRPRSCTWPL PREIANDPSKPPEVEPDLGEKVHTEGRSEPILLPSRIPEPEAG POPGILGAVTGPRKGSSRNANGSYAELLSGAIESAPERRIT LAQIYSMWNTVPYFKDKGDSNASAGWNSITHHLSLHSKFIKV HNEATAKSSWMMINPEGGKSGKAPRRRAASMDSSKLLRGRSKA PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSNREEADMWTT FRPRSSSNASSVSTRLSPRGSSGALERITESTPASVSYXAGGVPPT LNSGLELLDGIMTSSHSLLESTGGLSGFSLCHPGGTGFSHTYYS SLPSPAEGFLAAGGCTSSSQALEALITSDTPPPADVLMTQVD PILSQAPTLLIGGLFSSSAGAFVFELPEGGTPTSPDD TAMAPPVWASAAPIPKALGTPPVLTPTEAASQDRMPQDLDLDMY MENLECDMDNI ISDLMDEGGCLDPNFPPDP SMAARRGELSLLDGLNAFFDDP SMAARRGEGSARVICTRARGSARVPEDFDP				HKRWRRSSCSSSGRSRRCSSSSSSSSSSSSSSSSSSSSRSRSRS
AFAAIESCHKLRQADEQPFDLCYGGRQTCKRSYSDLDSNREDF DPAPVKSKPDSLDPDTLLKQAQKNLRR  5991 334 1379 RLSSHFSOCSPSIYC/TKFBKQGNVTSFERKKTELYQELGLQAR DLRFQHVMSITVRNNRIIMREYLKAVITPECLLILDYRNIANIK (WLFRSLPSQLSGEGQLVTYDLFFFFRATEALLQYWINTLOGKL SILOPLILETLDALGDPKHSSVDRSKLHTILQORKSLSELETDI KIFFKESTLETILDEELLEELELELCVSKWSDPQVFFKSSAGIHAEEM ELLLENYYRLADDLSNAARELRVLIDDSGSIIFINLDSKRNVMM RLNLQLTMGTFSLSFGLWAFGONLESSLEEDHRIFWLITGI MFMGSGLIWRRLLSFLGR/LARSSIASYGMKDMVHGGIVEGL SGQDDEEQGLTATQDSGINI,SGEVLDASSISFMTRLKWFALGVU GVFFSILGTGLLWLPGGIKLFAVFYTLGALAMHKKGLAVLFCILQ FLSMTWYSLGYIPYARDAVIKCCSSLIS AEGLGSWAVWAGIGWAGRHIMEAGGATGALGVGCKLPSAFCFFGS SVAMDMFQKVEKIGETYGVVYKAKNRETGGLVALKKTRLDLEM EGVPSTAIRSISLLKELKHENIVRLLDVVHNSRKLYLVFEFLSQ DLKKYMDSTGSELPHLHIKSJCLJGLGGVSPCSHRWIHRDLK PQNLLINELGAIKLAPGLARAFGVPLRTYTHEVVTLWYRAPEI LLATRFYTTAVDIWSIGGIFAEMVTRKLFEGDSEIDQ\LFEI FRALGTPSEDTWFGVVQLPVKGSFFKWTRKGLEEIVNLEPEG RDLLMGLLQYDPSQRTTAKTALAHPYFSSPEFSPAARQYVLQRF RH AGBVQLHVWIRGMRIGOPQ/KAAAITDLDPDFFFPGSRFRCTWFL PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSPAGG FOGGILGAVTGFRKGSSRNAMGNGSVAELISQAIESAPERRLT LAQIYEMWATVPYFKDKGDENSSAGWKNSIKHNISLHSKFIKV HNEASTAKSSWMNIPPGGKGSAFRRAANGSSYKLGRSKA PKKKPSGLPAPPEGAPTTSPVGHFAKWSGSPCSRNREEADMWTT FRPRSSSNASVSTRLSPLRPESEVLAEEITPASVSSVAGGVPPT LNEGLELLDGLMLTSSHSLLSGRSGLASELFPASVSSVAGGVPPT LNEGLELLDGLMLTSSHSLLSGRSCLASETPADVSVARGSKA PKKKPSGLPAPPEGABTTSPVGHFAKWSGSPCSRNREEADMWTT FRPRSSSNASVSTRLSPLRPESCVLAEEITPASVSSVAGGVPPT LNEGLELLDGLMLTSSHSLLSGRSCLASETPADVSVARGSKA PKKRPSGLPAPPEGABTTSPVGHFAKWSGSPCSRNREEADMWTT FRPRSSSNASVSTRLSPLRPESCVLAEEITPASVSSVAGGVPPT LNEGLELLDGLMLTSSHSLLSGRSCLSGFSLQHPGVTGPLHTYYS SLPSPAEGFLSAGGCCFSSSQALEALLTSDTPPPPADVLMTQVD PILSQAPTLLLIGGLPSSKALATGVGLCPPKLEAPGPSSLVPPTL SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMBNII 15DLMDEGGGLDPNFPPDP  S995 2 2437 RPFGPGPASGAWLCTRARGSAAFVPPLPFPPSRGARRRRRLPGR GWAALKRGPGSAFGLPRGRARSAAGSRGFSREERGAAAAAAA AEMMELHSLIJDARGRGGLABAFFATGLGGREERGAAAAAAAA AEMMELHSLIJDARGEGLABRFATGLGGREERGAAAAAAAA	ı	]		PSPRRRSDRRRRYSSYRSHDHYQRQRVLQKERAIEERRVVFIGK
DPAPVKSKFDSLDFDTLIKQQCNLER				IPGRMTRSELKQRFSVFGEIEECTIHFRVQGDNYGFVTYRYAEE
DPAPVKSKFDSLDFDTLIKQQCNLER	1 .	<b>)</b> i		AFAAIESGHKLRQADEQPFDLCFGGRRQFCKRSYSDLDSNREDF
DLRFOHMS ITVENNET IMMETYLKAVITPECLILIDYENLINIK  OWLFRIDPSQLSGEGQLUTYPLPEPEFRATEALLQWINTLOGKL SILOPLILETIDALGDPKHSSVDRSKLHILLQMGKSLSELETDI KIFKESILEILDBELGPKHSSVDRSKLHILLQMGKSLSELETDI KIFKESILEILDBELGPKHSSVDRSKLHILLQMGKSLSELETDI KIFKESILEILDBELGELCVSKWSDPQVFEKSSAGIDHAEEM FLANLQLTMGTFSLSLFGLMGVAFGMNLESSLEEDHRIFWLITGI MFMGSGLIWRFLLSFLGR/LARSSLASYGMKDMVHGGIVEGL MFMGSGLIWRRLLSFLGR/LARSSLASYGMKDMVHGGIVEGL GAPDFRILVGVGSGSGFGRGOATEWRPLP PWIGAMREKLREVI SGODDBECGLTAQDSQINL/SEVLDASSLSFNTRLKWFAICFVC GVFFSILGTGLLWLPGGIKLFAVFYTLGNLAALASTCFLMGFVK OLKKMFBATRLLATIVMLCFIFFLCAALWHKKGLAVFCTLO GVFFSILGTGLLWLPGGIKLFAVFYTLGNLAALASTCFLMGFVK OLKKMFBATRLLATIVMLCFIFFLCAALWHKKGLAVFCTLO FLOMTWYSLSYIPYARDAVIKCCSSLLS SVAMDMFOKVEKIGEGTYGVVYKAKNRETGQLVALKKIRLDLEM EGVPSTAIREISLKELKHNNIVHLDDVINNERKLYLVFEFLSQ DLKKYMDSTGSELPHLILSYLFQOLLGGVSFCCHSHRVIKDLK PQNLLINELGAIKLADFGLARAFGVPLRTTTHEVVTLWYRAPBI LLATRFYTTAVDTWSIGCIFADWTTRALPFGDS\EIDQ\LFFR FRALGTBSEDTWPGVTQLPPYKGSFPKWTRKGLEEIVPNLEPEG RDLLMQLLQVDPSQRITAKTALAHPYTSSPEFSPAARQYVLQRF RH AGEVQLHWIRGMRIQFQ/KAAAITDLDPDFEPQSRPRSCTWPL PREPLANOPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAGG PQDGILGAVTGPRKGGSRRNAMGNSYAELISQAIESAPEKRLT LAQIYEMWTRTVYFKDKGDSNSSAGWKNSIRNLSLHSKFIKV HEBATOKSSWMMINPEGGSSGKAAPRRAASMDSSKLLRGRSKA PKKKPSGLPAPPEGATPTSFVGHFAKWSGSPCSRRREEADMWTT FRRRSSNNASVSTRLSPRESEVLAESTPASVSSYAGGVPPT LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHFGVTGPLHTYSS SLFSPAGGFLSAGGGCFSSSQALEALLTSDTPPPPADVLMTQVD PLLSQAPTLLLGGLPSSSKLATGVGLCPKPLEAPGFSLVPTL SMIAPPPVWASAPIPKAGGFPNEPESVLAPSTLTPSFSVTPLT SMIAPPPVWASAPIPKAGGFPNEPESPASCORMPQDLDLDMY MENLECDMONI ISDLANDEGGLDFNPEPDF SMAPSPOWASAPIPKAGGSRGRARRRRREREPGR GWAALKRGGCSAPGLEARAFYTGLGVKKGPDLNSESNOSI. AEMMELHSLIDPN RRGELLDARFYTGLGVKKGPSRAAAAAAAA AEMMELHSLIDPN RGRELLDARFYTGLGVKKGPSNSESNOSI.				DPAPVKSKFDSLDFDTLLKQAQKNLRR
DLRFGHYMSITYRNNRIIMREYLKAVITPECLILLIDYRNLAIK OWLPRIBGUSGEGOLTYPELPFEFRATEALLQYWINTLQGKL SILOPLILETLDALGDPKHSSVDRSKLHILLQNGKSLSELETDI KIFKESILEILLDEELLEELCVSKWSDPQVEEKSSAGIDHAEEM ELLLENYYRLADDLSNAARELRVLIDDSGYIFINLOBHRNYMM RINLQLTWGTFSLSIFGLMGVAFGMNLESSLEEDHRIFWLITIGI MFMOSGLIWRLLSFLGFLMGVAFGMNLESSLEEDHRIFWLITIGI MFMOSGLIWRLSFLGFLMSSLESSMENDWHGGIVEGL SGODDERQLTAQDSQINL/SEVLDASSLSFNTTILKWFAICFVC GVFFSILGTGLWLPGGIKLFAVFYTLGNLAALASTCHMGFVK OLKKMFEATRILATIVMLCPIFTLCAALWHKKGLAVLFCILQ FLSMTWYSLSYIPVARDAVIKCSSLLS  SVAMDMPQKVEKIGEGTYGVYYKAKNETGGLVALKKTRLDLEM EGVFSTALRSISILKELKHNIVRLDLDVHMERKILYLVFEFLSQ DLKKYMDSTFGSELPHHLIKSYLFOLLQGVSFCHSHRVIHRDLK PQNLLINELGAIKLADFGLARAFGVPLRTTTHEVVTLWYRAPEI LLATRFYTTAVDIWSIGCIFAEMVTRKALFFGDS\EIDQ\LFFR FRNLGTFSEDTWPGVTQLPPYKGSFFFWTRKGLEEIVPNLEPEG RDLLMQLLQVDPSQRITAKTALAHPYFSSPEPSPAARQVVLQRF RH  AGEVQLHVWIRGMRIQPQ/KAAAIIDLDPDFEPQSFRSCTWPL PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSLAFERRLT LAQ1YBMWARTVPYFKDKGDSNSAGWKNSIRNINLSLHSKTIKV HNEATGKSSWMINPEGGKSGKAFRRAASMDSSSKLLRGRSKA PKKKPSGLPAPPEGATFTSPVGHFAKWSGSPCSRNREEADMWTT FFRRSSNASSVSTRISPRESEVLAESIPASVSSXAGGVPPT LNGGLELLDCINLTSSHSLLSRGLGFSLQHPGVTGPLHTYSS SLFSPAEGPLSAGEGCFSSQLAGHFSVATGGVPT LNGGLELLDCINLTSSHSLLSRGLGFSLQHPGVTGPLHTYSS SLFSPAEGPLSAGEGCFSSSQLALITSDTPPPPADVLMTQUD PILSQAPTLLLLGGLPSSSKALATGVGLCFRPLEAPGPSSLUPTL SMIAPPPVMASAPIPRAGGFPNFEPDFERSTUPTL SMIAPPPVMASAPIPRAGGFPNFEPDFFPFSRGARRRRRPLFGR GVAALKRGFGSAPGLLFARFYTGLGVKKPLBAFGFSLVPTL SMIAPPPVMASAPIPRAGGFPNFEPDFFPFSRGARRRRRPLFGR GVAALKRGFGSAPGLLFARFYTGLGVKKGPLNSESNOSI. AEMMELHSLIPPN TISDLADGEGLDFNFEPDF	5991	334	1379	RLSSHFSQCSPSIYC\TKFDKQGNVTSFERKKTELYOELGLOAR
OWLFRELDSQLSGEGGLVTYPLFFFRAIEALLGYWINTLGGKL SILOPLILETLDALGDPKHSSUDRSKLHTLLQNGKSLSELETDI KIFKESILEILDEBELLEELCVSKWSDPQVFEKSSAGIDHAEEM ELLLENYYRLADDLSNAARELEKULDDSGSIIFINLDSHRIVMM RLNLQLIVMGTFSLSIFEGMWAFGMNLESSLEEDHIFWLITGI MFMGSGLIWRRLLSFLGR/LARSSIASYGMKDMYHGGIVEGL SGPDFRLVCGVSGSGFFGGRGGOATENFPLRFWNGAMEKLRVL SGQDDEEGGLTAQDSQINL/SEVLDASSLSFNTRLKWFAICFVC GVFFSILGTGLLWLPGGIKLFAFTTLGNLAALASTCFLMGFVK OLKKMFEATRLLATIVMLLCFIFTLCAALWHKKGLAVLFCILQ FLSMTWYSLSYIPYARDAVIKCCSSLLS SVAMDMFQKVEKIGGETVYVKAKNRETGGLVALKKIRLDLEM EGVPSTAIREISLLKELKHPNIVRLLDVVHNERKLYLVFEFLSQ DLKKYMDSTPGSELPHHIKTPOLLGCVSCHSHRVIHRDLK PQNLLINELGAIKLADFGLARAFGVPLRTYTHEVVTLWYRAPEI LLATRFYTTAVDINSIGCIFAEMVTRKALFPGDS\EIDQ\LFRI FRNLGTBSEDTWPGGYLDPKGSPPKWTRKGLEIVYNLEPEG RDLLMQLLQVDPSQRITAKTALAHPYFSSPEPSPARQYVLQRF RH AGRVQHHWIRGMRIQPG/KAAAIIDLDPDFEPGSRPSCTWPL PRPEIANOPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAGG POPGILGAVTGPRKGGSRRNAWGNSYAELISQAIESAPEKRIT LAQIYEMWATVPYFKDKGDSNSSAGWNSIRHNLSHLSFIKV HNEATGKSSWMINNPEGGKSGKAPRRAASMDSSSKLLRGRSKA PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRREEADMWTT FRPRSSSNASSVSTRLSPLRFESSVLAEEIPASVSSYAGGVPPT LNEGLELLDGLNLTSSHSLLSRSELSGFSLGHGVTGPHTYSS SLPSPAEGPLSAGEGGFSSQALEALLTSDTPPPPADVLIMTQVD PILSQAPTLLLLGGLPSSKLATVGLCPKPLEAFGPSSLVPTL SMIAPPPVMASAPIPKALGTTVLTPTTEAASGORMPOLDLDMY MENLECDMONIISDLMDGGGGLDPNFFPDP  5995 2 2437 RPPGPGPASGAWLCTRARGSAAFVPPLFRPSRGRARRRRREPGR GVAALRRGPGSAFGLPRGRAERSAAGSGGRERERGAAAAAAA AEMMELLALVLD\DYNRCGLLEARPYTGLGVSKGPLNSESSNOSI	•			DLRFQHVMSITVRNNRIIMRMEYLKAVITPECLLILDYRNINIK
SILOPLILETLDALGDPKHSSUDRSKLHTLLQNGKSLSELETDI KIFKESILBILDEEBLEQVSKWSDPQVFEKSSAGIDHAEEM ELLLENYYRLADDLSNAARELRVLIDDSGSIIFINLDSHRIVMM RLNLQLTMGTFSLSLFGLMGVAFGWNLESSLEEDHRIFWLTGI MFMGSGLIWRRLLSFLGR/LARSSIASYGMKDMMGGVEGL SGDDEEQGLTAQDSQINL/SSLSFNTRLKWFAICFVC GVFFSILGTGLHW.PGGIKLFAVFTIGNLAALASTCPLMGPVK QLKKMFEATRLLATIVMLLCFIFTLCAALWWHKKGLAVLFCILQ FLSMTWYSLSYIPYARDAVIKCCSSLS  SVAMDMFQKVEKIGEGTYGVVYKAKNRETGQLVALKKIRLDLEM EGVPSTAIREISLLKELKHVIRLDVVHNEKKLIVLFFLSQ DLKKYMDSTFGSELPHHIKSYLFQLQGVSPCHSHRVIHRDLK PQNLLINELGAIKLADFGLARAFGVPLRTYTHEVVTLWYRAPEI LLARTFYTTAVDIWSIGGIFAEMVTRKALFPGDS\EIDQ\LFRI FRNLGTPSEDTWPGVTQLPDYKGSFPKWTRKGLEETVPNLEPEG RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQYVLQRF RH  1934 AGEVQLHVWIRGMRIQPQ/KAAAIIDLDPDFEPQSRPRSCTWPL PRFEIANQPSKPPSVEPDLGEKVHTEGRSEPILLPSRLPEPAGG PQPGILGAVTOPRKGSRRNAWGNGSYAELISQAIESAPEKRLT LAQIYEMMVRTVPYFKDKGDSNSAGWNSIRHINLSLHSKFIKV HNBATGKSSWMMLNPEGGKSGKARARRAASMDSSSKLLRGRSKA PKKKPSGLPAPPEGATFTSPVGHTAKMSGSPCSNREEADMWTT FRPRSSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPPT LANGIELLLDGLNLTSSHSLLSRSGLGGFSLGHPGVTGPLHTYSS SLPSPAEGPLSAGEGGFSSGALERLLTSDTPPPPADLVLMTQUD PILSQAPTLLLLGGLPSSKLATGVGLCPKPLEAPGPSSLVPTL SMIAPPPVMASABIPKALGTTVLTPTTEAASGDRMPQDLDLDMY MENLECDMONIISDLMDEGGGLDPNFEPDP  SPPSES 2 2437 RPSPGGBASGAWLCTRARGSAAFVPPLPRPSRGARRRRRLFGR GVAALRRGPGSAFGLPRGRAERSAAGSGGGREREERGAAAAAAA AEMMEELHSL\DP\RRQELLBARP\SESSNOSI				QWLFRELPSQLSGEGQLVTYPLPFEFRATEALLOYWINTLOCKI.
KITKESILEILDEEELLEELCVSKWSDPQVFEKSSAGIDHAEEM ELLLENYRLADDLAAREENVLIDDGGS I FINLDSHRNVMM RLNLQLTMGTFSLSLFGLMCAFGMNLESSLEEDHRIFWLITGI MFMGSGLTWRRLISFLGY/LARSSIASYGMKDMVHGGIVEGL AGPDFFLVCGVSGSGFFGGGGGATENPELF PWIGAMEKLERVL SGQDDEEGGLTAQDSQINL/SEVLDASSLSFNTRLKWFAICFVC GVFFSILGTGLLWLPGGIKLFAVFYTLGNLAALASTCFLMGPVK OLKKMFEATRILATITWMLCFIFFICAALWMKKGLAVLFCILQ FLSMTWYSLSYIPYARDAVIKCCSSLS  SVAMDMFQKVEKIGEGTYGVYYKAKNRETGGLVALKKIRLDLEM EGVPSTAIREISLLKELKHENIVRLLDVVHBERKLYLLVFEFLSQ DLKKYMDSTPGSELPHLIKSYLFOLLGGVSFCHSHRVIHRDLK PQNLLINELGAIKLADFGLARAFGVPLRTYTHEVVTLWYRAPEI LLATRFYTTAVDIWSIGGIFAEMVTRKALFFGDS\EIDQ\LFRI FRNLGTISEDTWPGVTQLPPYKGSFPKWTRKGLEETUPRLEPEG RDLLMQLLQYDPSQRITAKTALAHPYFSSPEFSPAARQYVLQRF RH  AGEVQLHVWIRGMRIQPQ/KAAAIIDLDPDFEPQSRPRSCTWPL PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPPEAG PQPGILGAVTGPRKGSRRNAWGNGSYAELISQAIESAPEKRIT LAQIYEMMVRTVPYFKDKGDSNSSAGWKNSIRHNISLHSKFIKV HNEATGKSSWMMLNPEGGKSGKAPRRRAASMDSSSKLIRGRSKA PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWTT FRPRSSNASSVSTRLSPLRPESEVLAEEIPASVSYAGGVPPT LMEGLELLDGLNLTSSHBLLSRSGLSGFSLCHPGGTFGPHTYSS SLPSPAEGFLSAGEGCFSSQALEALLTSDTPP PPADVLMTQVD PILSQAPTLLLLGGLPSSKLATGVGLCPKPLEAPGFSSLVPTL SNIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECCHOMNI ISDLMGEGGLDFNFEPDP  S995 2 2437 RPPGPGPASGAWLCTRARGSAAFVPPLFRPPSRGARRRRLPGR GVAALRRGGGSAPGLPRGRAERSAAGGSGPSREERGAAAAAAA AEMMEELHSLVDP, RROELLEARFYTGLGGVSGFJNSESNOSI				SILOPLILETLDALGDPKHSSVDRSKIHTLLONGKSLSELETDI
ELLLENYYRLADDLSNAARELRVLIDDSGSITFINLDSHRNVMM RLNNQ-ITMSTFSLSEDLMGVAFGMNLESSLEEDHRIFWLITGI MFMGSGLIWRRLISFLGF/LARSSIASYGMKDMVHGGIVEGL SGODDEGCGLTAQDSIJN/SEVLDASSLSFNTRLKWFAICFVC GVFFSILGTGLLWLPGGIKLFAVFYTLGNLAALASTCFLMGPVK OLKKMFEATRLLATIVMLLCFIFTLCAALWWHKKGLAVLFCILQ FLSMTWYSLSYIPYARDAVIKCCSSLS  5993 1650 594 AEGLGSWAVWAGLGWAGRHMEAGGATGALGVGCKLPSAFCFPGS SVAMDMFCKVEKIGEGTYGVVYKAKNRETGOLVALKKIRLDLEM EGVPSTATRE ISLLKKHPNIVRLLDVHNERKKLLIVFEFLSQ DLKKYMDSTPGSELPLHLIKSYLFQLLQGVSFCHSHRVHKRDLK FQNLLINELGAIKLADFGLARAFGVPLRTYTHEVVTLWYRAPEI LLATRFSTTATVDNISGCIFAEMVTRKNLFFGOS\EIDQ\LFRI FRNLGTPSEDTWPGVTQLPDYKGSFPKWTRKGLEEIVPRLEPEG RDLLMQLLQYDPSGRITAKTALAHPYSSPEPSPAARQVVLQRF RH  AGEVQLHVWIRGMRIQPG/KAAAIIDLDPDFEPQSRPRSCTWPL PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLDEPAGG PQPGILGAVTOPRKGGSRRNAWGNGSYAELISQAIESAPEKRIT LAQIYEMMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKV HNEATGKSSWWMLMPEGGKSGRKARRRAASMDSSSKLIRGRSKA PKKKPSGLPAPPEGATPTSPVGHFAKWGSPCSRRNEEADMWTT FRPRSSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPPT LNEGLELLDGLNLTSSHSLLSRGLSGFSLCHPGVTTGPLHTYSS SLPSPAEGPLSAGEGCFSSQALEALLTISDTPPPADVLMTQVD PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPTL SMIAPPPVMASAPIPKALGTPVLTPFTEAASQDKMPQDLDLDMY MENLECOMDNI ISDLWDEGGGLDFNFEPDP  5995 2 2437 RPPGPGPASGAVLCTRARGSAAFVPPLFRPPSRGARRRRLPGR GVAALRRGPGSSAFGLPRGRAERSAAGSGRSPSREERGAAAAAAAA AEMMEELHSL\DP\RQBELEARF\TGGLGSVGSNSSINGSI	1	·		KIFKESILEILDEEELLEELCVSKWSDPOVEEKSSACIDUAERW
RLINLQLTMGTFSLSLFGLMQAFGMNLESSLEEDHRIFWLITGI MFMGSGLIWRRLLSFLGR/LARSSIASYGMKDMVHGGIVEGL  SGOPPFRLVGGVSGSGFPGRQGQGATTNFPLRPWNGAMEKLRRVL SGOPDECQLTAQDSQINL/SEVLDASSLSFNTRLKWFAICFVC GVFFSILGTGLLWLPGGIKLFAVFYTLGNLAALASTCFLMGPVK QLKKMFEATRLLATIVMLLCFIFTLCAALWHKKGLAVLFCILQ FLSMTWYSLSYIPYARDAVIKCCSSLLS  SQADMECGATGAUGGCKLPSAFCFFGS SVAMDMFQKVEKIGGTYGVVYKAKNRETGGLVALKKIRLDLEM EGVPSTATREISLLKELKHPNIVRLLDGVHNERKLYLVFEFLSQ DLKKYMDSTPGSELPHLIIKSYLFOLLGGVSFCHSHRVIHRDLK FQNLLINELGAIKALDFGLARAFGGVPLRTVTHEVVTLWYRAPEI LLATRFYTTAVDIWSIGCIFAEMVTRKALFFGDS\EIDQ\LFRI FRNLGTPSEDTWPGVTQLPDYKGSFPKWTKKGLEEIVENLEPEG RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPARQYVLQRF RH  AGEVQLHVWIRGMRIQPQ/KAAAITDLDPDFEPQSRPRSCTWPL PRPEIANQPSKPPSVEPDLGEKVHTEGRSEPILLPSRLPEPPAG PQPGILGAVTGPRKGSRRNAWGNQSYAELISQAIESAPEKRLT LAQIYEMMVRTVPYFFKDKGDSNSSAGWKNSIRHNLSLHSKFIKV HNEATGASSWMMLNPEGGKSGKAPRRAASMDSSSKLLRGRSKA PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWTT FFPRSSSNASSVSTRLSPLRPESSVLAEEIPASVSSYAGGVPPT LMGGLELDGLNLTSSHSLLSRGGLSGFSLQHPGVTGPLHTYSS SLFSPAEGPLSAGGCFSSSQALEALLTSDTPPPPADVLMTQVD PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPTL SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNIISDLMDEGGGLDFNFFPDP SPPPFGGGSAPGLAFERGAAAAAAA AEMMEELHSL\DP\RRQGAPGRARERSAAGSGRGPSREERGAAAAAAAA AEMMEELHSL\DP\RRQGAPGLEARRFYAGGSRGPINSEERGAAAAAAAA AEMMEELHSL\DP\RRQGAPGLEARRFYAGGSRGPINSEERGAAAAAAAA	1 1	}	-	ELLLENYYRIADDI.SNAAREI.PVI.TDBGGGITETNI.DCUDARAM
5992 2 609 AGPDFRLVGGVSGGFPGGRGGATENRPLRFNGAMEKLRRUL SGQDDEEQGLTAQDSQINL/SEVLDASSLSFNTRLKWFAICFVC GVFFSILGTGLLWLPGGIKLFAVFYTLGNLAALASTCFLMGPVK QLKKMFEATRLLAITUWLLCFIFTLCAALWWHKKGLAVLPCILQ FLSMTWYSLSYIPYARDAVIKCCSSLLS 5993 1650 594 AEGLGSWAVWAGLGWAGRHMEAGGATGALGWGCKLPSAFCFPGS SVANDMFQKVEKIGEGTYGVVYKAKNRETGQLVALKKIRLDLEM EGVPSTAIREISLLKELKHPNIVRLLDVVHNERKLYLVFEFLSQ DLKKYMDSTPGSELPLHIIKSYLFOLLQGVSFCHSHRVIHRDLK PQNLLINELGAIKLADPGLARAFGVPLRTYTHEVVTLWYRAPPI LLATRFYTTAVDIWSIGCIFAEMVTRKALFPGDS\EIDQ\LFRI FRNLGTPSEDTWPGVTQLPPVKGSFPKWTRKGLEEIVPNLEPPG RDLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQVVLQRF RH AGBVQLHVWIRGMRIQPQ/KAAAITDLDPDFEPQSRPRSCTWPL PREIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPPAGG POPGILGAVTGPRKGSSRRNAWGNGSYAELISQAIESAPEKRIT LAQIYEMMVRTVPYFKDKGDSNSSAGWKNSIRINLSLHSKFIKV HNEATGKSSWMMLNPEGGKSGKRRAASMDSSSKLRGSRA PKKKPSGLPAPPEGATPTSFVGHFAKWSGSPCSRNREEADMWTT FRPRSSSNASSVSTRLSPLRPESEVLAEEIPPASVSSYAGGVPPT LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYSS SLFPSPAEGPLSAGGCFFSSQALEALLTSDTPPPPADWITQVD PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPTL SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNIISDLMDEGGGLDPNFFPDP SPPEGGRGAARARAAA AEMMEELHSL\DP\RPGPFFPSRGARRRRRLPGR GVAALRRGPGSAPGLPGGRESAAGSGGGPSREERGAAAAAAAA AEMMEELHSL\DP\RPGPFFPSRGARRRRRLPGR GVAALRRGPGSAPGLPGGRESAAGSGGGPSREERGAAAAAAAA				RINIOT TMGTESI SI EGI MGWA EGMIT EGGI DEDUD TIWI TIMA
AGPDFRLVCGVSGSGFPGGRQGATENRPLRPWNGAMEKLRRVL SGQDDEEQGLTAQDSQINL/SEVLDASSLSFNTRLKWFAICFVC GVFFSILGTGLLWLPGGIKLFAVFYTLGNLAALASTCFLMGPVK QLKKMFEATRLLATIVMLLCFIFTLCAALWWHKKGLAVLFCILQ FLSMTWYSLSYIPYARDAVIKCCSSLLS  5993 1650 594 AEGLGSWAVWAGLGWAGRHMEAGGATGALGVGCKLPSAFCFPGS SVAMDMFQKVEKIGEGTYGVVYKAKNRETGQLVALKKIRLDLEM EGVPSTAIREISLLKELKHPNIVRLLDVVHNERKLYLVFEFLSQ DLKKYMDSTPGSELPHHIKSYLFQDLLQGVSFCHSHRVIHRDLK PQNLLINELGAIKLADFGLARAFGVPLRTYTHEVVTLWYRAPBEI LLATRFYTTAVDIWSIGGIFAEWVTRKALFPGDS\EIDQ\LFRI FRHLGTFSEDTWPGVTQLPPVKGSFPKWTRKGLEEIVPNLEPEG RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQYVLQRF RH  394 1934 AGEVQLHVWIRGMRIQPQ/KAAAIIDLDPDFEPQSRPRSCTWPL PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAGG PQPGILGAVTGPRKGGSRRNAWGNQSYAELISQAIESAPEKRLT LAQIYEMMVRTVPYFKDKGDSNSSAGWKNIKHNLSLHSKFIKV HHEATGGSSSWMMINSPEGGKSGKAPRRRAASMDSSSKLLRGRSKA PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWTT FRPRSSSNASSVSTRLSPLRESEVLAEEIPASVSSVAGGVPPT LNEGLELLDGLMLTSSHSLLERGLGFFSLQHPGVTGPLHTYSS SLFSPAEGPLSAGEGCFSSQALEALLTSDTPPPPADVLMTQVD PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPTL SMIAPPPWMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNIISDLMDEGGGLDFNFEPDP 5995 2 2437 RPPGPGPASGAWLCTRRRGSAAFVPPLFPPSRGARRRRLPGR GVAALRRGSLHSL\DP\RRQELLEARF\TGLGVSKGPLNSESSNOSL	)			MEMGSGI.TWDDLI.SET.GD/LADSSTAGVOWYDAWHGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
SGQDDEEQGLTAQDSQINL/SEVLDASSLSFNTELKWFAICFVC GVFFSILGTGLLWLPGGIKLFAVFYTLGNLAALASTCFLMGPVK QLKKMFEATRLATIVMLLCFIFTLCAALWWHKGLAVLPCILQ FLSMTWYSLSYIPVARDAVIKCCSSLLS SVAMDMFQKVEKIGEGTTGVVYKAKNRETGQLVALKKIRLDLEM EGVPSTAIREISLLKELKHPNIVRLLDUVHNERKLYLLVFEFLSQ DLKKYMDSTPGSELPLHLIKSYLFQLLQGVSFCHSHRVIHRDLK PQNLLINELGAIKLADFGLARAFGVPLRTYTHEVVTLWYAPEI LLATRFYTTAVDIWSIGCIFAEMVTRKALFPGDS\EIDQ\LFRI FRHLGTFSEDTWEVVTQLPDYKGSFPKWTRKGLEEIVPNLEPEG RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQYVLQRF RH  AGBVQLHVWIRGMRIQPG/KAAAIIDLDPDFEPQSRPRSCTWPL PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAGG PQDGILGAVTGPRKGGSRNAMGNQSYAELISQAIESAPEKRLT LAQIYEMWVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKV HHEATGKSSWMMLNPEGGKSGKAPRRAASMDSSSKLLRGRSKA PKKKPSGLPAPPEGATPTSPVCHFAKWSGSPCSRNREEADMWTT FRPRSSSNASSVSTRLSPLRPESEVLAEIPRSVSSYAGGVPPT LEGGLELLDGLNITSSHSLLSRSGLSGFSLCHPGVTGPLHTYSS SLPSPAEGPLSAGEGCFSSQALEALLTSDTPPPPADVLMTQVD PILSQAPTLLLLGGLPSSKLATGVGLCPKPLEAPGEPSLVPTL SIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNIISDLMDEGGGLDFFNFEPDP  5995 2 2437 RPPGPGPASGAWLCTRARGSAAFVPPLPFPPPSRGARRRRLPGR GVAALRRGPGSAPGLPRGRAERSAAGSGRGPSREERGAAAAAAA AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGPINRESSNOSI	5992	- 2	509	ACRIPER VCCVCCCCPRCCPRCCPRCCPRCCPRCCPRCCPRCCPRCC
GVFFSILGTGLLWLPGGIKLFAVFYTLGNLAALASTCFIMGPVK QLKKMFEATRLLATIVMLLCFIFTLCAALWWKKGLAVLFCILQ FLSMTWYSLSYIPYARDAVIKCCSSLLS  594  AEGIGSWAVWAGLGWAGRHMEAGGATGALGVGCKLPSAFCFFGS SVAMDMFQKVEKIGEGTYGVVYKAKNRETGGLVALKKIRLDLEM EGVPSTAIREISLLKELKHPNIVRLLDVHMERKLYLVFEFLSQ DLKKYMDSTPGSELPLHLIKSYLFQLLQGVSFCHSHRVIHRDLK PQNLLINELGAIKLADFGLARAFGVPLRTYTHEVVTLWYRAPEI LLATRFYTTAVIUNSIGCIFAEMVTRKALFFGDS\EIDQ\LFRI FRNLGTPSEDTWPGVTQLPDYKGSFPKWTRKGLEEIVPNLEPEG RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQYVLQRF RH  AGEVQLHVWIRGMRIQPQ/KAAAIIDLDPDFEPQSRPRSCTWPL PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAGG POPGILGAVTGPRKGGSRRNAWGRGSYAELISQAIESAPEKRLT LAQIYEMWYTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKV HNEATGKSSWWMLNPEGGRSGKARRRAASMDSSSKLLRGRSKA PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWTT FRPRSSSNASSVSTRLSPLRPESEVLAEEIFASVSSYAGGVPPT FRPRSSNASSVSTRLSPLRPESEVLAEEIFASVSSYAGGVPPT LMGGLELLDGLNLTSSHSLLSRSGLSGFSLQHFGVTGPLHTYSS SLFSPAEGPLSAGEGCFSSQALEALLTSDTPPPPADVLMTQVD PILSQAPTLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPTL SMIAPPPWMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNIISDLMDEGGGLDFNFEDDP  5995 2 2437 RPPGFGPASGAWLCTRARGSAAFVPPLFPPSGRGARRRRRLPGR GVAALRRGPGSAPGLPRGRAERSAAGSGRGPSREERGAAAAAAA AEMMEELHSL\PP\RRQELFARGSAAFVPPLFPPSGRGARRRRLPGR GVAALRRGPGSAPGLPRGRAERSAAGSGRGPSREERGAAAAAAA AEMMEELHSL\PP\RRQELFARGSAAFVPPLFPPSGRGARRRRLPGR		_	603	GCODDECOL TO OBCOTAL (OTTO DE CARPLE PWNGAMEKLRRVL
OLKKMFEATRILATIVMLLCFIFTLCAALWHKKGLAVLFCILQ FLSMTWYSLSYIPYARDAVIKCCSSLLS  AEGIGSWAVWAGIGWAGRHMEAGGATGALGUGCKLPSAFCFPGS SVAMDMFQKVEKIGEGTYGVVYKAKNRETGQLVALKKIRLDLEM EGVPSTAIREISLLKELKHPNIVRLLDUVHNERKLYLDVFEFLSQ DLKKYMDSTPGSELPLHLIKSYLFQLLQGVSPCHSHRVIHRDLK PQNLLINELGAIKLADPGLARAFGVPLRTYTHEVVTLWYRAPPEI LLATRFYTTAVDIWSIGCIFAEMVTRKALFPGDS\EIDQ\LFRI FRNLGTPSEDTWPGVTQLPDYKGSFPKWTKGLEEIVPNLEPEG RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQYVLQRF RH  S994  394  1934  AGBVQLHVWIRGMRIQPQ/KAAATIDLDPDFEPQSRPRSCTWPL PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAGG POPGILGAVTGPRKGGSRRNAWGNQSYABLISQAIESAPEKRLT LAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKV HNEATGKSSWWMLNPEGGKSGKAPRRAASMDSSSKLLRGRSKA PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNEEADMWTT FRPRSSNASSVSTRLSPLRPESEVLAEEIPASUSSYAGGVPPT LNEGLELLDGLNLTSSHSLLSRGLSGFSLQHPGVTGPLHTYSS SLFSPAEGPLSAGEGCFSSSQALEALLTSDTPPPPADVLMTQVD PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPTL SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNIISDLMDEGEGLDFNFPDDP  5995  2 2437  RPPGPGPASGAWLCTRARGSAAFVPPLPRPPSRGARRRRRLPGR GVAALRRGPGSAPGLPRGRAERSAAGSGRGPSREERGAAAAAA AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGPLNSESSNOSL	1 1	1		SGODDEEQGLTAQDSQINL/SEVLDASSLSFNTRLKWFAICFVC
FLSHTWYSLSYIPYARDAVIKCCSSLLS  5993  1650  594  AEGLGSWAVWAGLGWAGRHMEAGGATGALGVGCKLPSAFCFPGS SVAMDMFQKVEKIGEGTYGVVYKAKNRETGQLVALKKIRLDLEM EGVPSTAIREISLLKELKHPNIVRILDVVHMERKLYLVFEFLSQ DLKKYMDSTPGSELPLHLIKSYLFQLLQGVSFCHSHRVIHRDLK PQNLLINELGAIKLADFGLARAFGVPLRTYTHEVVTLWYRAPBI LLATRFYTTAVDIWSIGGIFAEMVTRKALFPGDS\EIDQ\LFRI FRNLGTPSEDTWPGVTQLPDYKGSFPKWTRKGLEEIVPNLEPEG RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQYVLQRF RH  AGBVQLHVWIRGMRIQPQ/KAAAIIDLDPDFEPQSRPRSCTWPL PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAGG PQPGILGAVTGPRKGGSRRNAWGNQSYAELISQAIESAPEKRLT LAQIYEMWVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKV HNEATGKSSWWMLNPEGGKSGKAPRRAASMDSSSKLRGGRSKA PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWTT FRPRSSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPPT LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYSS SLFSPAEGPLSAGEGCFSSSQALEALLTSDTPPPADVLMTQVD PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPTL SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNIISDLMDEGEGLDFNFEPDP  5995  2 2437  RPPGPGPASGAWLCTRARGSAAFVPPLPFRPSRGARRRRLPGR GVAALRRGPGSAPGLPRGRAERSAAGSGRGPSREERGAAAAAA AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGPLNSESSNOSL	1 1			GVFFSILGTGLLWLPGGIKLFAVFYTLGNLAALASTCFLMGPVK
1650  594  AEGLGSWAVWAGLGWAGRHMEAGGATGALGVGCKLPSAFCFPGS SVANDMFQKVEKLIGEGTYGVVYKAKNRETGQLVALKKIRLDLEM EGVPSTAIREISLLKELKHPNIVRLLDVVHNERKLYLVFEFLSQ DLKKYMDSTPGSELPLHILKSYLFQLLQGVSFCHSHRVIHRDLK PQNLLINELGAIKLADFGLARAFGVPLRTYTHEVVTLWYRAPEI LLATRFYTTAVDIWSIGCIFAEMVTRKALFFGDS\EIDQ\lffi FRNLGTPSEDTWPGVTQLPDYKGSFPKWTRKGLEEIVPNLEPEG RDLLMQLLQYDPSQRITAKTALAHPYFSSPEFSPAARQYVLQRF RH  AGEVQLHVWIRGMRIQPQ/KAAAITDLDPDFEPQSRPRSCTWPL PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAGG PQDGILGAVTGPRKGGSRRNAWGNQSYAELISQAIESAPEKRLT LAQIYEMWVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKV HNEATGKSSWMLNPEGGKSGKAFRRAASMDSSSKLLRGRSKA PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWTT FRPRSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPPT LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYSS SLFSPAEGPLSAGEGCFSSQALEALLTSDTPPPPADVLMTQVD PILSQAPTLLLGGLPSSKLATGVGLCPKPLEAPGPSSLVPTL SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNIISDLMDEGEGLDFNFEPDP  5995 2 2437 RPPGPGPASGAWLCTRARGSAAFVPPLPRPSRGARRRRLPGR GVAALRRGPGSAPGLPGRAERSAAGSGRGPSREERGAAAAAAA AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGPLNSSSNOSL	1 -1			QLKKMFEATRLLATIVMLLCFIFTLCAALWWHKKGLAVLFCILQ
SVAMDMFQKVEKIGEGTYGVVYKAKNRETGQLVALKKIRLDLEM EGVPSTAIREISLLKELKHPNIVRLLDVVHNERKLYLVFEFLSQ DLKKYMDSTPGSELPLHLIKSYLFQLLQGVSFCHSHRVIHRDLK PQNLLINELGAIKLADFGLARAFGYPLRTYTHEVVTLWYRAPEI LLATRFYTTAVDIWSIGCIFAEMVTRKALFPGDS\EIDQ\LFRI FRMLGTPSEDTWPGVTQLPDYKGSFPKWTRKGLEEIVPNLEPEG RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQYVLQRF RH  AGEVQLHVWIRGMRIQPQ/KAAAIIDLDPDFEPQSRPRSCTWPL PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAGG PQPGILGAVTGPRKGGSRRNAWGNQSYAELISQAIESAPEKRLT LAQIYEMMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKV HNEATGKSSWWMLNPEGGKSGKAPRRAASMDSSKLLRGRSKA PKKKPSGLPAPPEGATTTSPVGHFAKWSGSPCSRNREEADMWTT FRPRSSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPPT LNEGLELLGCINLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYSS SLFSPAEGPLSAGEGCFSSQALEALLTSDTPPPPADVLMTQVD PILSQAPTLLLLGGLPSSKLATGVGLCPKPLEAPGPSSLVPTL SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNIISDLMDEGEGLDFNFEPDP  5995 2 2437 RPPGPGPASGAWLCTRARGSAAFVPPLFRPPSRGARRRRLPGR GVAALRRGPGSAPGLPRGRAERSAAGSGRGPSREERGAAAAAAA AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGPLNSSSSNOSL	F003			FLSMTWYSLSYIPYARDAVIKCCSSLLS
SVAMDMFQKVEKIGEGTYGVYYKAKNRETGQLVALKKIRLDLEM EGVPSTAIREISLLKELKHPNIVRLLDVVINBERKLYLVFEFLSQ DLKKYMDSTPGSELPLHLIKSYLFQLLQGVSFCHSHRVIHRDLK PQNLLINELGAIKLADFGLARAFGVPLRTTTHEVVTLWYRAPEI LLATRFYTTAVDIWSIGCIFAEMVTRKALFPGDS\EIDQ\LFRI FRNLGTPSEDTWPGVTQLPDYKGSFPKWTRKGLEEIVPNLEPEG RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQYVLQRF RH  AGEVQLHVWIRGMRIQPQ/KAAAITDLDPDFEPQSRPRSCTWPL PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAGG POPGILGAVTGPRKGGSRRNAWGNQSYAELISQAIESAPEKRLT LAQIYEMWVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKV HNEATGKSSWMMINPEGGKSGKAPRRRAASMDSSSKLLRGRSKA PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWTT FRPRSSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPPT LNEGLELLDGINTSSHSTLLSRSGLSGFSLQHPGVTGPLHTYSS SLPSPAEGPLSAGEGCFSSSQALEALLTSDTPPPPADVLMTQVD PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPTL SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNIISDLMDEGGLDFNFEPDP  5995 2 2437 RPPGGPASGAWLCTRARGSAAFVPPLPRPPSRGARRRRRLPGR GVAALRRGPGSAPGLPRGRAERSAAGSGRGPSREERGAAAAAAA AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGPLNSESSNOSL	3333	1650	594	AEGLGSWAVWAGLGWAGRHMEAGGATGALGVGCKLPSAFCFPGS
EGVPSTAIREISLLKELKHPNIVRLLDVVHNERKLYLVFEFLSQ DLKKYMDSTPGSELPHLIKSYLFQLLQGVSFCHSHRVIHRDLK PQNLLINELGAIKLADFGLARAFGVPLRTYTHEVVTLWYRAPEI LLATRFYTTAVDIWSIGCIFAEMTTRKALFPGDS\EIDQ\LFRI FRMLGTPSEDTWPGVTQLPDYKGSFPKWTRKGLEEIVPNLEPEG RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQYVLQRF RH  S994  394  1934  AGEVQLHVWIRGMRIQPQ/KAAAIIDLDPDFEPQSRPRSCTWPL PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAGG PQPGILGAVTGPRKGGSRRNAWGNQSYAELISQAIESAPEKRLT LAQIYEMWYRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKV HNBATGKSSWWMLNPEGGKSGKAPRRAASMDSSSKLLRGRSKA PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWTT FRPRSSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPPT LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYSS SLFSPAEGPLSAGEGCFSSQALEALLTSDTPPPADVLMTQVD TILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPTL SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNIISDLMDEGEGLDFNFEPDP  S995  2  2437  RPPGPGPASGAWLCTRARGSAAFVPPLPRPPSRGARRRRLPGR GVAALRRGPGSAFGLERRSAAGSGRGPSREERGAAAAAA AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGPLNSESSNOSL				SVAMDMFQKVEKIGEGTYGVVYKAKNRETGQLVALKKIRLDLEM
DLKKYMDSTPGSELPHLIKSYLFQLLQGVSFCHSHRVIHRDLK PQNLLINELGAIKLADFGLARAFGVPLRTYTHEVVTLWYRAPEI LLATRFYTTAVDIWSIGCIFAEMVTRKALFPGDS\EIDQ\LFRI FRMLGTPSEDTWPGVTQLPDYKGSFPKWTRKGLEEIVPNLEPEG RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQYVLQRF RH  S994 394 1934 AGEVQLHVWIRGMRIQPQ/KAAAIIDLDPDFEPQSRPRSCTWPL PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAGG POPGILGAVTGPRKGGSRRNAWGNQSYAELISQAIESAPEKRLT LAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKV HNEATGKSSWWMLNPEGGKSGKAPRRAASMDSSSKLLRGRSKA PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWTT FRPRSSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPPT LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHFGVTGPLHTYSS SLPSPAEGPLSAGEGCFSSQALEALLTSDTPPPPADAVLMTQVD PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPTL SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNIISDLMDEGEGLDFNFEPDP  5995 2 2437 RPPGFGPASGAWLCTRARGSAAFVPPLPFPSRGARRRRRLPGR GVAALRRGPGSAPGLPRGRAERSAAGSGRGPSREERGAAAAAAA AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGPLNSESSNOSL	1	1		EGVPSTAIREISLLKELKHPNIVRLLDVVHNERKLYLVFEFLSO
PQNLLINELGAI KLADFGLARAFGVPLRTYTHEVVTLWYRAPEI LLATRFYTTAVDIWSIGCI FAEMVTRKALFPGDS\EIDQ\LFRI FRMLGTPSEDTWPGVTQLPDYKGSFPKWTRKGLEEI VPNLEPEG RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPS PAARQYVLQRF RH  394 1934 AGEVQLHVWIRGMRIQPQ/KAAAITDLDPDFEPQSRPRSCTWPL PRPEIANQPSKPPEVEPPLGEKVHTEGRSEPILLPSRLPEPAGG PQPGILGAVTGPRKGGSRRNAWGNQSYAELISQAIESAPEKRLT LAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKV HNEATGKSSWWMLNPEGGKSGKAPRRRAASMDSSSKLLRGRSKA PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWTT FRPRSSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPPT LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYSS SLFSPAEGPLSAGEGCFSSSQALEALLTSDTPPPPADVLMTQVD PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPTL SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNIISDLMDEGEGLDFNFEPDP  5995 2 2437 RPPGFGPASGAWLCTRARGSAAFVPPLPRPPSRGARRRRLPGR GVAALRRGPGSAPGLPRGRAERSAAGSGRGPSREERGAAAAAAA AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGPLNSESSNOSL	ſ	· · · · · · · · · · · · · · · · · · ·		DLKKYMDSTPGSELPLHLIKSYLFOLLOGVSFCHSHRVIHRDIK
LLATRFYTTAVDIWSIGCIFAEMVTRKALFPGDS\EIDQ\LFRI FRMLGTPSEDTWPGVTQLPDYKGSFPKWTRKGLEEIVPNLEPEG RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQYVLQRF RH  5994  394  1934  AGEVQLHVWIRGMRIQPQ/KAAAITDLDPDFEPQSRPRSCTWPL PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAGG PQPGILGAVTGPRKGGSRRNAWGNQSYAELISQAIESAPEKRLT LAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKV HNEATGKSSWWMLNPEGGKSGKAPRRRAASMDSSSKLLRGRSKA PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWTT FRPRSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPPT LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYSS SLFSPAEGPLSAGEGCFSSQALEALLTSDTPPPPADVLMTQVD PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPTL SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNIISDLMDEGEGLDFNFEPDD  S995  2  2437  RPPGPGPASGAWLCTRARGSAAFVPPLPRPPSRGARRRRLPGR GVAALRRGPGSAPGLPRGRAERSAAGSGRGPSREERGAAAAAA AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGPLNSESSNOSL		į		PONLLINELGAIKLADFGLARAFGVPLRTYTHEVVTLWYRADET
FRMLGTPSEDTWPGVTQLPDYKGSFPKWTRKGLEEIVPNLEPEG RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQYVLQRF RH  394  1934  AGEVQLHVWIRGMRIQPQ/KAAAIIDLDPDFEPQSRPRSCTWPL PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAGG PQPGILGAVTGPRKGGSRRNAWGNQSYAELISQAIESAPEKRLT LAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKV HNEATGKSSWWMLNPEGGKSGKAPRRRAASMDSSSKLLRGRSKA PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWTT FRPRSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPPT LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYSS SLFSPAEGPLSAGEGCFSSQALEALLTSDTPPPPADVLMTQVD PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPTL SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNIISDLMDEGEGLDFNFEPDP  5995  2  2437  RPPGPGPASGAWLCTRARGSAAFVPPLPRPPSRGARRRRLPGR GVAALRRGPGSAPGLPRGRAERSAAGSGRGPSREERGAAAAAAA AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGPLNSESSNOSL	1 1	1		LLATREYTTAVDIWSIGCIFAEMVTRKALFPGDS\ETDO\LEBT
RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQYVLQRF RH  394  1934  1934  AGEVQLHVWIRGMRIQPQ/KAAAITDLDPDFEPQSRPRSCTWPL PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAGG PQPGILGAVTGPRKGSRRNAWGNQSYAELISQAIESAPEKRLT LAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKV HNEATGKSSWWMLNPEGGKSGKAPRRAASMDSSSKLLRGRSKA PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWTT FRPRSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPPT LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYSS SLPSPAEGPLSAGEGCFSSQALEALLTSDTPPPPADVLMTQVD PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPTL SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNIISDLMDEGEGLDFNFEPDP  5995  2  2437  RPPGPGPASGAWLCTRARGSAAFVPPLPRPPSRGARRRRRLPGR GVAALRRGPGSAPGLPRGRAERSAAGSGRGPSREERGAAAAAA AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGPLNSESSNOSL	1 1			FRMLGTPSEDTWPGVTOLPDVKGSFPKWTPKGLEFTVPNLEDEC
S994 394 1934 AGEVQLHVWIRGMRIQPQ/KAAAIIDLDPDFEPQSRPRSCTWPL PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAGG PQPGILGAVTGPRKGGSRRNAWGNQSYAELISQAIESAPEKRLT LAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKV HNEATGKSSWMMLNPEGGKSGKAPRRRAASMDSSSKLLRGRSKA PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWTT FRPRSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPPT LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYSS SLPSPAEGPLSAGEGCFSSSQALEALLTSDTPPPPADVLMTQVD PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPTL SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNIISDLMDEGEGLDFNFEPDP  5995 2 2437 RPPGPGPASGAWLCTRARGSAAFVPPLPRPPSRGARRRRLPGR GVAALRRGPGSAPGLPRGRAERSAAGSGRGPSREERGAAAAAAA AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGPLNSESSNOSL	1 1	1		RDLLMOLLOYDPSORTTAKTALAUDVESCREBERAAROVIII ODD
5994  394  1934  AGEVQLHVWIRGMRIQPQ/KAAAITDLDPDFEPQSRPRSCTWPL PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAGG PQPGILGAVTGPRKGGSRRNAWGNQSYAELISQAIESAPEKRLT LAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKV HNEATGKSSWWHLNPEGGKSGKAPRRRAASMDSSSKLLRGRSKA PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWTT FRPRSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPPT LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYSS SLFSPAEGPLSAGEGCFSSQALEALLTSDTPPPPADVLMTQVD PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPTL SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNIISDLMDEGEGLDFNFEPDP  7995  2 2437  RPPGPGPASGAWLCTRARGSAAFVPPLPRPPSRGARRRRLPGR GVAALRRGPGSAPGLPRGRAERSAAGSGRGPSREERGAAAAAA AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGPLNSESSNOSL	1 1	1		
PRPEIANQPSKPPEUPDLGEKVHTEGRSEPILLPSRLPEPAGG PQPGILGAVTGPRKGGSRRNAWGNQSYAELISQAIESAPEKRLT LAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKV HNEATGKSSWWMLNPEGGKSGKAPRRAASMDSSSKLLRGRSKA PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWTT FRPRSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPPT LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYSS SLFSPAEGPLSAGEGCFSSSQALEALLTSDTPPPPADVLMTQVD PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPTL SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNIISDLMDEGEGLDFNFEPDP  5995 2 2437 RPPGPGPASGAWLCTRARGSAAFVPPLPRPPSRGARRRRLPGR GVAALRRGPGSAPGLPRGRAERSAAGSGRGPSREERGAAAAAA AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGPLNSESSNOSL	5994	394	1934	
PQPGILGAVTGPRKGGSRRNAWGNQSYAELISQAIESAPEKRLT LAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKV HNEATGKSSWWMLNPEGGKSGKAPRRAASMDSSSKLLRGRSKA PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWTT FRPRSSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPPT LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYSS SLFSPAEGPLSAGEGCFSSQALEALLTSDTPPPPADVLMTQVD PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPTL SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNIISDLMDEGEGLDFNFEPDP RPPGPGPASGAWLCTRARGSAAFVPPLPRPPSRGARRRRLPGR GVAALRRGPGSAPGLPRGRAERSAAGSGRGPSREERGAAAAAA AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGPLNSESSNOSL	1 1		1334	DEDELANOR CONTRIBUTE OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PR
LAQIYEMMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKV HNEATGKSSWMMLNPEGGKSGKAPRRRAASMDSSSKLLRGRSKA PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWTT FRPRSSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPPT LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYSS SLFSPAEGPLSAGEGCFSSQALEALLTSDTPPPPADVLMTQVD PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPTL SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNIISDLMDEGEGLDFNFEPDP  5995 2 2437 RPPGPGPASGAWLCTRARGSAAFVPPLPRPPSRGARRRRLPGR GVAALRRGPGSAPGLPRGRAERSAAGSGRGPSREERGAAAAAA AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGPLNSESSNOSL		į		PORCHAMOPSKYPEVEPDLGEKVHTEGRSEPILLPSRLPEPAGG
HNEATGKSSWWMLNPEGGKSGKAPRRRAASMDSSSKLLRGRSKA PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWTT FRPRSSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPPT LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYSS SLFSPAEGPLSAGEGCFSSSQALEALLTSDTFPPPADVLMTQVD PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPTL SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNIISDLMDEGEGLDFNFEPDP  5995 2 2437 RPPGPGPASGAWLCTRARGSAAFVPPLFRPPSRGARRRRLPGR GVAALRRGPGSAPGLPRGRAERSAAGSGRGPSREERGAAAAAAA AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGPLNSESSNOSL		1		POPULLGAVTGPRKGGSRRNAWGNQSYAELISQAIESAPEKRLT
PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWTT FRPRSSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPPT LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYSS SLFSPAEGPLSAGEGCFSSQALEALLTSDTPPPPADVLMTQVD PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPTL SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNIISDLMDEGEGLDFNFEPDP  5995 2 2437 RPPGPGPASGAWLCTRARGSAAFVPPLPRPPSRGARRRRLPGR GVAALRRGPGSAPGLPRGRAERSAAGSGRGPSREERGAAAAAA AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGPLNSESSNOSL	] [	- 1	1	LAQ1YEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKV
PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWTT FRPRSSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPPT LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYSS SLFSPAEGPLSAGEGCFSSQALEALLTSDTPPPPADVLMTQVD PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPTL SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNIISDLMDEGEGLDFNFEPDP  5995 2 2437 RPPGPGPASGAWLCTRARGSAAFVPPLPRPPSRGARRRRLPGR GVAALRRGPGSAPGLPRGRAERSAAGSGRGPSREERGAAAAAA AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGPLNSESSNOSL	1			HNEATGKSSWWMLNPEGGKSGKAPRRRAASMDSSSKLLRGRSKA
FRPRSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPPT LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYSS SLFSPAEGPLSAGEGCFSSSQALEALLTSDTPPPPADVLMTQVD PILSQAPTLLLLGGLPSSKLATGVGLCPKPLEAPGPSSLVPTL SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNIISDLMDEGEGLDFNFEPDP SP95 2 2437 RPPGPGPASGAWLCTRARGSAAFVPPLPRPPSRGARRRRLPGR GVAALRRGPGSAPGLPRGRAERSAAGSGRGPSREERGAAAAAA AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGPLNSESSNOSL	j	[·		PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWTT
LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYSS SLFSPAEGPLSAGEGCFSSQALEALLTSDTPPPPADVLMTQVD PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPTL SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNI ISDLMDEGEGLDFNFEPDP  5995 2 2437 RPPGPGPASGAWLCTRARGSAAFVPPLPRPPSRGARRRRLPGR GVAALRRGPGSAPGLPRGRAERSAAGSGRGPSREERGAAAAAA AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGPLNSESSNOSL	1	i		FRPRSSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPPT
SLPSPAEGPLSAGEGCFSSSQALEALLTSDTPPPPPADVLMTQVD PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPTL SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNI ISDLMDEGEGLDFNFEPDP SP95 2 2437 RPPGPGPASGAWLCTRARGSAAFVPPLPRPPSRGARRRRLPGR GVAALRRGPGSAPGLPRGRAERSAAGSGRGPSREERGAAAAAA AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGPLNSESSNOSL	1 1			LNEGLELLDGLNLTSSHSLLSRSGLSGFSLOHPGVTGPLHTVCC
PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPTL SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNIISDLMDEGEGLDFNFEPDP SP95 2 2437 RPPGPGPASGAWLCTRARGSAAFVPPLPRPPSRGARRRRLPGR GVAALRRGPGSAPGLPRGRAERSAAGSGRGPSREERGAAAAAA AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGPLNSESSNOSL	1 1			SLPSPAEGPLSAGEGCFSSSOALFALLTSOTDDDDADULMTOTT
SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY MENLECDMDNIISDLMDEGEGLDFNFEPDP  5995 2 2437 RPPGPGPASGAWLCTRARGSAAFVPPLPRPPSRGARRRRLPGR GVAALRRGPGSAPGLPRGRAERSAAGSGRGPSREERGAAAAAAA AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGPLNSESSNOSL	1			PILSOAPTLLLLGGLPSSSKLATGVGLCDKDLPA DCDCGLTDD
MENLECDMDNI ISDLMDEGEGLDFNFEPDP  5995 2 2437 RPPGPGPASGAWLCTRARGSAAFVPPLPRPPSRGARRRRLPGR GVAALRRGPGSAPGLPRGRAERSAAGSGRGPSREERGAAAAAAA AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGPLNSESSNOSL	1			SMIAPPPVMASADIPVALCTRU TRADERA CORRESPONDA
5995 2 2437 RPPGPGPASGAWLCTRARGSAAFVPPLPRPPSRGARRRRLPGR GVAALRRGPGSAPGLPRGRAERSAAGSGRGPSREERGAAAAAAA AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGPLNSESSNOSL	1 1		į	MENTECOMONI I COL MODGE OF DEVENDO
GVAALRRGPGSAPGLPRGARRAGSGRGPSREERGAAAAAA AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGPLNSESSNOSL	5995	2	2427	
AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGPLNSESSNOSL			243/	RPFGFGFASGAWLCTRARGSAAFVPPLPRPPSRGARRRRLPGR
AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGPLNSESSNOSL	j l		l	GVAALKKGPGSAPGLPRGRAERSAAGSGRGPSREERGAAAAAA
1	1 1		Į.	AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGPLNSESSNQSL
CSVGSLSDKEVETPEKKQNDQRNRKRKAEPYETSQGKGTPRGHK	<u> </u>	<u>-</u> -		CSVGSLSDKEVETPEKKQNDQRNRKRKAEPYETSQGKGTPRGHK

- 1	SEQ	Predicted	1 15 - 31	
	ID	beginning	Predicted end	
٠ ا	NO:	nucleotide	nucleotide	I WATER ANTING, CECOSEDING DEDANGERS - 1 1 1
		location	location	Torucamic Acid, Fabrery alaning Codissis
J		corresponding	corresponding	/ """ Value of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of
- 1		to first	to first	D=Leucine, M=Methionine, N=Asparagion
		amino acid	amino acid	F=F1011ne, U=Glutamine P=brgining
		residue of	residue of	S=Serine, T=Threonine, V=Valine
- 1		amino acid	amino acid	W=ITyptophan, Y=Tyrosine y-unb
- 1		sequence	sequence	Codon, /=possible micleotide deleti-
- +		sequence		/ /~Possible nucleoride incertion/
- 1		-		ISDYFERRVEOPLYGLDGSAAKFATEFOCAL DTLAGE
- 1				DTEQLAQRGAGLCFTFVSAQQNSPSSTGSGNTEHSCSSQKQISI
- 1				QHRQT\QSDLTIEKISALENSKNSDLEKKEGRIDDLLRANCDLR
				RQI\DEQQKMLEKYK\ERLNRCFDNEPRNFLIEKSKQEKMACRD
			]	KSMQDRLRLGHFTTVRHGASFTEQWTDGYAFQNLIKQQERINSQ
		1	·	REEIERQRKMLAKRKPPAMGQAPPATNEQKQRKSKTNGAENETL
		}		TLAEYHEOEET EKI DI CUL KKEEDETONDI DOOR KINGAENETL
- 1				TLAEYHEQEEIFKLRLGHLKKEEAEIQAELERLERVRNLHIREL KRIHNEDNSOFKDURTI NDRVI IVII
		[		KRIHNEDNSQFKDHPTLNDRYLLLHLLGRGGFSEVYKAFDLTEQ
- 1				RYVAVKIHQLNKNWRDEKKENYHKHACREYRIHKELDHPRIVKL
- 1				YDYFSLDTDSFCTVLEYCEGNDLDFYLKQHKLMSEKEARSIIMQ
				IVNALKYLNEIKPPIIHYDLKPGNILLVNGTACGEIKITDFGLS
- 1		ĺ		KIMDDDSYNSVDGMELTSQGAGTYWYLPPECFVVGKEPPKISNK
				VDVWSVGVIFYQCLYGRKPFGHNQSQQDILQENTILKATEVQFP
L				1 * NE V VIELAKAFIKKULAYRKKORIDVOOLACDDVI I DIITOVIII
	5996	1612	981	1 DIDSPAGAMIASISGASNNSSSN
- 1				DQQACILGLMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCE
- 1				DEST V V F GS I V IN SG Y LNSASEGEE F C T VNIDNIDATA CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONCUENT CONC
- 1				AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA
		i		THAT IMPIGUSCYL \ANOWOVSKPKDWDI.NPCTDACDCDDCCCCC
	5997	1612	981	1 + v > + v + v + v + v + v + v + v + v +
- [		í	201	DQQACLIGIMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCE
	1	1		
- 1		ł		THE DICHOLD VIETO ISSVKDRKK AUT COUDING CONTINUE TO
				TWILD TODOCTO (ANOWOVSKPKDNDINECTOR CROPPORTS
	5998	1612	981	1
- 1	1		301	DQQACLLGLMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCE
				DEST VEGST VNEGY LINSASEGER POT UNIDATION A CONTROL OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PRO
		<b>,</b>		THE DICCOLLARDOV & POLISSVKDRKK AVI SCHOLAROGERSTER
L		- 1		THAT DWF IGUSCIL (ANOWOVSKDKDNDINECTED) CDCDDCCCC
	5999	2	1790	1 O - I MODIAALAVKRIKIII SEOEEVQTE PD/ AGAOD
		ŀ		RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP
1		į		1 COURSELLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE BELLEVILLE
1				1 MI VEGISCIR (QIEAKALKVROADITPETUOVEVOUT OUT 1
1				1 ~ Denicular Langue Elektrist I Striker, Vermore des es
	}	į.		V 1 DGDGFRDDVLHFRHKGLJJ.FKI,TJ.FKKIT DVFGDFD
1.				1 ***** VESEPPERILENGESDESOYRDRKSMSPDCGI OROND == - 1
1	- 1	1		FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLFQVEDSS
1	i	į		KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE
1	ļ	1		I ADODATIVE LUZANZA SERIBITA ODDU VILGORIA TECH AND THE
1	- 1	1		DOXIGHT LATE INGY I CHOYMAT OOUGHT I COMMON
}		}		MINGGROUDD AT VEVERAL TOTAL DELIVER TRANSPERS
1	- 1			I THE TELEVICION OF ADGICANCE CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A CONTINUE OF A
<u></u>			ľ	LFRIVNVAKKIGNVMVTT\SRNVVQTGK\AVGQSVGGAFS\SAK TA\MSSWLSTFTTSTSQSLTEPPDEKP
6	000	101	1561	TEPCRTAENCTATMOENTEPPDEKP
1	ı	.		TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL
				DDFEDKVFYRTEFQNREFKATMCNLLAYLKHLKGQNEAALECLR
		}		KAEELIQQEHADQAEIRSLYTWGNYAWYYHMGRLSDVQIYVDK
	1	ĺ	İ	VKHVCEKFSSPYRIESPELDCEEGWTRLKCGGNQNERAKVCFEK
1	- 1	i		ALEKKPKNPEFTSGLAIASYRLDNWPPSQNAIDPLRQAIRLNPD
1		i	j	NQYLKVLLALKLHKMREEGEEGEGEK\LVEEALEKAPG\VTDV
1	1			LRSAA\KFYRGKDEPDKAIELLKKALEYIP\NNAYLHCQIGCCY
	ì	i	Ĭ	RAKVFQVMNLRBNGMYGKRKLLELIGHAVAHLKKADEANDNLFR
		1	1	VCSILASLHALADQYEDAEYYFQKEFSKELTPVAKQLLHLRYGN
	-	i	1	TOBLOW ACCOUNT HELEGYKINOKS REKERMYDYLOVI AVIANOS
		ŀ		SINCADSEALHVEAF LQELNEKMQQADEDSERGIFSGSI.TDGAC
6	001	176		Circa
	- 1	İ		AFAHSPSRGHRHTHIHTPRHTPRCTMAESHLQSSLITASQFFEI
			f	WEIT DADGSGILEGKELONLIOELOOARKAGI PI CDENUMENT
<u> </u>		j	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s	*10210DGICIGIVELAHVI.PTEENFI.I.I.FPCOOI.VCCE\ =======
			·	WRKYDTDHSGFIETEELKNFLKDLLEKANKTVDDTKLAEYTDLM

SEO	Predicted	I Design and the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the s	
ID	beginning	Predicted end nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
ł	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
i	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
ı	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
İ	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
J	sequence	bequence	Codon, /=possible nucleotide deletion,
<b> </b>	<del>                                     </del>	<del></del>	\=possible nucleotide insertion)
			LKLFDSNNDGKLELTEMARLLPVQENFLLKFQGIKMCGKEFNKA
i	ı		FELYDQDGNGYIDENELDALLKDLCEKNKQDLDINNITTYKKNI
6002	977	81	MALSDGGKLYRTDLALILCAGDN
		"	LAPPGGGLHIPPRTPLSHSRPPPSHHAPHPSPLPLPPADLHPHS
		ĺ	SMAQRSDLLELDCQLTRDRVVVVSHDENLCRQSGLNRDVGSLDF
1	İ	ł	EDLPLYKEKLEVYFSPGHFAHGSDRRMVRLEDLFQRFPRTPMSV
1	į.	ľ	EIKGKNEELIREQ/VLVRRYDRNEITIWASEKSSVMKKCKAANP
}			EMPLSFTISRGFWVLLSYYLGLLPFIPIPEKFFFCFLPNIINRT
			YFPFSCSCLNQLLAVVSKWLIMRKSLIRHLEERGVQVVFWCLNE
6003	140	1000	ESDFEAAFSVGATGVITDYPTALRHYLDNHGPAARTS
""	1 110	4098	GKLRAFRGMRRLICKRICDYKSFDDEESVDGNRPSSAASAFKVP
1			APKTSGNPANSARKPGSAGGPKVGAGASKEGGAGAVDEDDFIKA
1	<b>[</b>		FTDVPSIQIYSSRELEETLNKIREILSDDKHDWDQRANALKKIR
			SLLVAGAAQYDCFFQHLRLLDGALKLSAKDLRSQVVREACITVA
	1		HLSTVLGNKFDHGAEAIVPTLFNLVPNSAKVMATSGCAAIRFII
			RHTHVPRLIPLITSNCTSKSVPVRRRSFEFLDLLLQEWQTHSLE
	1		RHAAVLVETIKKGIHDADAEARVEARKTYMGLRNHFPGEAETLY
j	]		NSLEPSYQKSLQTYLKSSGSVASLPOSDRSSSSSSSSSINDDECC
i			KWSTANPSTVAGRVSAGSSKASSLPGSLQRSRSDIDVNAAAGAK
1			AHHAAGQSVRSGRLGAGALNAGSYASLEDTSDKLDGTASEDGRV
1			RAKLSAPLAGMGNAKADSRGRSRTKMVSQSQPGSRSGSPGRVLT
j.	1		TTALSTVSSGVQRVLVNSASAOKRSKIPRSOGCSPEASDSDLett
ŀ	j į		ARSSRIPRPSVSQGCSREASRESSRDTSPVRSFOPLASPHUSES
Í	1 [		TGALYAPEVYGASGPGYGISOSSRLSSSVSAMRVINTGSDVFFA
	1		VADALLEGDIRTKKKPARRRYESYGMHSDDDANSDASSACSEDS
			YSSRNGSIPTYMRQT\EDV\AEVLNRCASSNWSERKEGLLGLON
	1 1		LLKNORTLSRVELKRLCEIFTRMFADPHGKRVFSMFLETINDET
	}		QVHKDDLQDWLFVLLTQLLKKMGADLLGSVOAKVOKALDVTRES
1 .	1		FPNDLQFNILMRFTVDQTQTPSLKVKVAILKYIETLAKOMDRCD
1			FINSSETRLAVSRVITWTTEPKSSDVRKAAOSVLISI.FEI.NTDF
	ì		FTMLLGALPKTFQDGATKLLHNHLRNTGNGTOSSMGSDLTPDTD
	[		RSPANWSSPLTSPTNTSQNTLSPSAFDYDTENMNSEDIVSSLDC
1			VTEAIQNFSFRSQEDMNEPLKRDSKKDDGDSMCGGPG\MSDPPn
	i i		GGDATDSSQTAL\DNKASLLHSMPTHSSPRSRDVNDVNVSDgie
1			PFNKSALKEAMFDDDADOFPDDLSLDHSDLVARLIKELSNHNED.
			VEERKIALYELMKLTQEESFSVWDEHFKTILLLLLETIGDKEDT
1			IRALALKVLREILRHQPARFKNYAELTVMKTLEAHKDPHKEVVR
1			SAEEAASV\LATSI\SPEQCIKVLCPIIOTADVPINIAAIKMOT
]	ļ		KVIERVSKETLNLLLPEIMPGLIOGYDNSESSVRKACVFCLVAV
			HAVIGDELKPHLSQLTGSKMKLLNLYIKRAQTGSGGADPTTDVS
6004	740		GQS
"""	140	4098	GKLRAFRGMRRLICKRICDYKSFDDEESVDGNRPSSAASAFKVP
l [		İ	APKTSGNPANSARKPGSAGGPKVGAGASKEGGAGAVDEDDFIKA
	1		FTDVPSIQIYSSRELEETLNKIREILSDDKHDWDQRANALKKIR
1 1	[	ſ	SLLVAGAAQYDCFFQHLRLLDGALKLSAKDLRSOVVREACTTVA
i	·		HLSTVLGNKFDHGAEAIVPTLFNLVPNSAKVMATSGCAAIRFII
i	1	1	RHTHVPRLIPLITSNCTSKSVPVRRRSFEFLDLLLOEWOTHSLE
	f		RHAAVLVETIKKGIHDADAEARVEARKTYMGLRNHFPGEAETIV
}			NSLEPSYQKSLQTYLKSSGSVASLPOSDRSSSSSOESI,NPDF99
j	ļ	•	KNSTANPSTVAGRVSAGSSKASSLPGSLORSRSDIDVNAAAGAK
ŀ	ì	i	AHHAAGQSVRSGRLGAGALNAGSYASLEDTSDKLDGTASEDGRV
			RAKLSAPLAGMGNAKADSRGRSRTKMVSOSOPGSRSGSPCDVITT
		Ī	TTALSTVSSGVQRVLVNSASAQKRSKIPRSOGCSRRASPSRISV
ļ		}	ARSSRIPRPSVSQGCSREASRESSRDTSPVRSFOPLASRHHSRS
j	j	ļ	TGALYAPEVYGASGPGYGISQSSRLSSSVSAMRVLNTGSDVERA
}		1	VADALLLGDIRTKKKPARRYESYGMHSDDDANSDASSACSERS
1	1	į	YSSRNGSIPTYMRQT\EDV\AEVLNRCASSNWSERKEGLLGLQN
1		1	LLKNORTLSRVELKRLCEIFTRMFADPHGKRVFSMFLETLVDFI
1		Ī	QVHKDDLQDWLFVLLTQLLKKMGADLLGSVQAKVQKALDVTRES
1		ŀ	FPNDLQFNILMRFTVDQTQTPSLKVKVAILKYIETLAKQMDPGD
			FINSSETRLAVSRVITWTTEPKSSDVRKAAQSVLISLFELNTPE
		<del></del>	

	SEQ	Predicted	Predicted end	
	ID	beginning	nucleotide	
	NO:	nucleotide		I Manageriale, CECVSCRIBE Delegartic hair n
			location	Glutamic Acid E-Phonylalania
	1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	i	ccrresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	!	to first		Debeucine, Memethionine Newscars
			amino acid	P=Proline, Q=Glutamine, R=Arginine,
		amino acid	residue of	Seserine Tomber
		residue of	amino acid	S=Serine, T=Threonine, V=Valine,
		amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
			sequence	Couon, /=possible miclentide deleti-
1		sequence	!	\=possible nucleotide insertion)
				FEMILION NUMBER (1)
			1	FTMLLGALPKTFQDGATKLLHNHLRNTGNGTQSSMGSPLTRPTP
			1	LOS PANOS PLISPINISONTI SPSAFDVDTENMICED TVOOTER
ĺ			i	VTEAIONESEPSOEDMIEDT KEDGWEDD OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SEL
l			İ	VTEAIQNFSFRSQEDMNEPLKRDSKKDDGDSMCGGPG\MSDPRA
ı			1	1 CODATOS QUAD UNICAS LLHSMPTHS SPP S DOWN DVING DOTA
- 1	J		ĺ	T THROADREAMFDDDADOFPDDISIDESDIVARTIVEL COURSE
٠ ا	l l		1	VEERKIALYELMKLTQEESFSVWDEHFKTILLLLETLGDKEPT
- 1	1			TRALAL WILL DESCRIPTION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE
			j .	I TRALIALIK V DREILERHOPARFKNYAEL TVMKT-EAUVDDIVEDVER
- 1			i	SACEAASV (LAISI (SPEOCIKVI CPT TOTADVDTNI A A TIMEOR
- 1	- 1		1	KVIERVSKETLNLLPEIMPGLIQGYDNSESSVRKACVFCLVAV
	1		İ	UNVICED VENT COLUMN STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF THE STATES OF
- 1			1	HAVIGDELKPHLSQLTGSKMKLLNLYIKRAQTGSGGADPTTDVS
ı	6005	122		605
	0005	133	5955	RSSGRROEOLGOEPGPEPVCMACCLGGPGPG
- 1	1		ĺ	RSSGRRQEQLGQFFGRERKGMASGLGSPSPCSAGSEEEDMDALL
ı			ŀ	THE DEFENDENCE DESCRIPTION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY O
- 1	ŀ			ARVAREMULCAOLGDSSGEGPERVERERRYALDGDGEGGDSSC
1	1			GKKKKKLGPKKEKKSKSKRKEEEEEDDDDDDDSKEPKSSAQLL
- 1	1			EDWGMED TOHNEGEED VERM TRANSPORTED TO THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TOTAL OF THE TO
- 1		i		EDWGMEDIDHVFSEEDYRTLTNYKAFSQFVRPLIAAKNPKIAVS
- 1	1			KMMMVLGAKWREFSTNNPFKGSSGASVAAAAAAAVAVVESMVTA
- 1		ŀ		1EVAPPPPPVEVPIRKAKTKEGKGPNARRKPKGSDPVDDAKKDK
- (	i	- 1		PKKVAPLKIKLGGFGSKRKRSSSEDDDLDVESDFDDASINSYSV
- 1	i			SDGSTSDSSBSBVITTO
ĺ	l l	I I		SDGSTSRSSRSRKKLRTTKKKKKGEEEVTAVDGYETDHQDYCEV
- 1	ľ	i		L CONGRETTICOTCERATHMOCTUDEDMERY DEGRACODITORISME
- 1	i	1		Authvernoegeettreckeedleeebunnmeedbrokboom
-				CDTCPSSYHIHCLNPPLPEIPNGEWLCPRCTCPALKGKVQKILI
1	į.			WKWCODDCDTDVDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
ł	l	Į.		WKWGQPPSPTPVPRPPDADPNTPSPKPLEGRPERQFFVKWQGMS
1		i		I THESE VOLUMEDHOUSE VOLUME TO THE TERM OF THE PROPERTY IN
	1	1	i	D /MARAYADPATAEMEER FYRYGTKDEW/ MMTUDTY MITOTOLING
	- 1		l	HVHYLIKWRDLPYDQASWESEDVEIQDYDLFKQSYWNHRELMRG
- 1	1			FEGRE DOWN WHITE THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY
-	Ť	J		EEGRPGKKLKKVKLRKLERPPETPTVDPTVKYERQPEYLDATGG
	i			* DIF I VILGUINWERF SWAOGTOTT LADEMCT CYTYOTT VOT
1	•	1		YKEGHSKGPFLVSAPLSTIIN\WEREFEMWAPDMYV\VTYVGDK
	1	ľ	1	DSRAIIRENEFS\FEDNAIRGGKKASRMKKEASVKFHVLLTSYE
ļ	ļ	1		LITIDMATI CCIDUR CI TITTE CON CONTROCK ASKMIKKEASVKFHVLLTSYE
1	- 1		i	LITIDMAILGSIDWACLIVDEAHRLKNNQSKFFRVLNGYSLQHK
1	į.	Į.	1	THE TOTAL CONNERS SHIP WAS TAKEN TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPER
1	1	Į.		QIKKLHDMLG\PHMLRRLKADVFKNMPSKTELIV\RVELSPM\Q
1		1	f	KKYYK\YILHSKFLKALN\ARGGGNQVSLLNVVMDLKKCCNHPY
			1	LEDVA AMEA DIVALENT ARGGGNQVSLLNVVMDLKKCCNHPY
	- 1	ł		DEF VARIOUS NIJENGMYDGSALTRASGRIJI I OVMY 1017 100 0000
	1	1	i	WATER O'S ALL VALUE OF PERFECT KAES TECHNOLOGY TO THE
1	ĺ	j	1	FNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQ
	I	F		AFSRAHRIGONKUMTURETERA
1			1	AFSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMMLTHLVV
İ		Į.		WEGGGSWIGSWSKOEFDDIIFKEGAEBIEKUEWADOGGDYWANGOOO
1		{	· · · · · · · · · · · · · · · · · · ·	DOVINIUD NATERILIDANO DETERMENTO CONTRA CORRESPONDENT
1	i	i		REEEMGEEEEVEREIIKQEESVDPDYWEKLLRHHYEQQQEDLAR
1	- 1	1		NI CKCKD I DYCODIO CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CO
i	İ		1:	NLGKGKRIRKQVNYNDGSQEDRDWQDDQSDNQSDYSVASEEGDE
1		ľ	1 .	DE DERSEAPERRYSKKGLRNDKDKDI,DDI,I,ADUGCMTBUT GERRAL
1	i	1		QRKAFLNAIMRYGMPPQDAFTTQWLVRDLRGKSEKEFKAYVSLF
1	1	i i	l i	MRHICEPGADGAETEADCUADEGE CARAMETERIA VSI.F.
I	ļ	ĺ	13	MRHLCEPGADGAETFADGVPREGLSRQHVLTRIGVMSLIRKKVQ
[	1	ľ	1 .	EL PULLUCKA SMISETAE VEENKKASODG CD CDATTOTO COLORDO
	1	1	1 -	NIFAPVPPAELGIKIEENSLKEEESTEGEKEVVCTADDTA TOOM
I		1	I	DAPAPASEDEKVVVEPPEGEEKVEKAEVKERTEEPMETEPKGKG
	I	ł	1 3	AADVEKVEEKCATDI EDITATIONALA VEKTEEPMETEPKGKG
Ī	l	ſ	*	THE VERY PERSON TOTAL TAKEN A PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMENT OF THE PERSON TO A COMMEN
	j	1	1 -	DONDER QRENIT ROREMENT ADDRESS A TRANSPORT OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY O
	Ī	l	1 -	THE TAXABLE WALLAGE IN THE CYARWOD TOND DOWN IT WE DRIVE TO
		1	l n	VRGNFLEIKNKFLARREKTI POATUTEROV
		į į	-	NRGNFLEIKNKFLARRFKLLEQALVIEEQLRRAAYLNMSEDPSH
	l	1	1 4	STATION I REAL VECLARISHOHI, SKESMAGNUDANATIT TIPLE TO
	1	ļ	} ==	SECULIONICADVIRLIPATIARIPPVAVRI OMCEDNITI CDI DATO DE L
<del></del> ,			. I E	PTPQQVAQQQ
6	006	1	965	NOFT PARTURED NAME OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF THE PARTURE OF
	ı	1		NDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVHPC
	I	1	ا ا	READINIVIE LEGKEHOLKELHPLHRIDRITSGULMED VER DAG
	1	ŀ	1 5	KIREVYRUKQLEKEYVCRVEGEFPTEEVTCKEDIIJUKWUKU
	1	ľ	l c	RVDPRGKPCETVFQRLSYNGQSSVVRCRPLTGRTHQIRVHLQF
			1.	GHPILNDPIVNCYMCDODODODOO
				GHPILNDPIYNSVAWGPSRGRGGYIPKTNEELLRDLVAEHQAK

SEO	Predicted	Predicted end	l amino and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second a second and ------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown *=Ston
ļ	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
1			QSLDVLDLCEGDLSPGLTDSTAPSSELGKDDLEELAAAA\QKME
			EVAEAAPQELDTIALASEKAVETDVMNQ\RQT\TLCRVPAGATG SLAPRPCDVPTCPTL
6007	3	2351	
İ		1 2332	HELGQVEYVFTDKTGTLTENEMQFRECSINGMKYQEINGRLVPE GPTPDSSEGNLSYLSSLSHLNNLSHLTTSSSFRTSPENETELIK
1	[		EHDLFFKAVSLCHTVQINNVQTDCTGDGPWQSNLAPSQLEYYAS
			SPDEKALVEAAARIGIVFIGNSEETMEVKTLGKLERYKLLHILE
-			FDSDRRRMSVIVQAPSGEKLLFAKGAESSILPKCIGGEIEKTRI
ļ	j		HVDEFALKGLRTLCIAYRKFTSKEYEEIDKRIFEARTALQQR\E
į			EKLAAVFQFIEKDLILLGATAVEDRLODKVRETIEALRMAGIKV
İ	}	ł	WVLTGDKHETAVSVSLSCGHFHRTMNILELINOKSDSECAEOLR
	1	İ	QLARRITEDHVIQHGLVVDGTSLSLALREHEKLFMEVCRNCSAV
			LCCRMAPLQKAKVIRLIKISPEKPITLAVGDGANDVSMIOFAHV
			GIGIMGKEGRQAARNSDYAIARFKFLSKLLFVHGHFYYIRIATL
1			VQYFFYKNVCFITPQFLYQFYCLFSQQTLYDSVYLTLY\NICFT
			SLPILIYSLLEQHVDPHVLQNKPTLYRDISKNRLLSIKTFLYWT
1			ILGFSHAFIFFFGSYLLIGKDTSLLGNGQMFGNWTFGTLVFTVM VITVTVKMALETHFWTWINHLVTWGSIIFYFVFSLFYGGILWPF
			LGSQNMYFVFIQLLSSGSAWFAIILMVVTCLFLDIIKKVFDRHL
			HPTSTEKAQLTETNAGIKCLDSMCCFPEGEAACASVGRMLERVI
			GRCSPTHISRSWSASDPFYTNDRSILTLSTMDSSTC
6008	4554	1089	AGVRRAGARRGPGRALFAGATAVPPPSARRRRRCPAPEHAGDAR
i			ASRPSQETMFQLPVNNLGSLRKARKTVKKILSDIGLEYCKEHIE
			DFKQFEPNDFYLKNTTWEDVGLWDPSLTKNODYRTKPFCCSACP
			FSSKFFSAYKSHFRNVHSEDFENRILLNCPYCTFNADKKTLETH
			IKIFHAPNASAPSSSLSTFKDKNKNDGLKPKQADSVEQAVYYCK
			KCTYRDPLYEIVRKHIYREHFQHVAAPYIAKAGEKSLNGAVPLG
			SNAREESSIHCKRCLFMPKSYEALVQHVIEDHERIGYQVTAMIG HTNVVVPRSKPLMLIAPKPQDKKSMGLPPRIGSLASGNV\RSLP
			SQQMVNRLSIPKPNLNSTGVNMMSSVHLQQNNYGVKSVGQGYSV
1			GQSMRLGLGGNAPVSIPQQSQSVKQLLPSGNGRSYGLGSEQRSQ
1 1			APARYSLQSANASSLSSGOLKSPSLSOSOASRVLGOSSSKDAAA
! !			ATGPPPGNTSSTQKWKICTICNELFPRNVYSVHFEKEHKAEKUD
1 1			AVANYIMKIHNFTSKCLYCNRYLPTDTLLNHMLIHGI.SCPYCPS
1 1			TFNDVEKMAAHMRMVHIDEEMGPKTDSTLSFDLTLOOGSHTNIH
			LLVTTYNLRDAPAESVAYHAQNNPPVPPKPQPKVQEKADIPVKS
1 1			SPQAAVPYKKDVGKTLCPLCFSILKGPISDALAHHLRERHQVIQ
Ì			TVHPVEKKLTYKCIHCLGVYTSNMTASTITLHLVHCRGVGKTQN GQDKTNAPSRLNQSPSLAPVKRTYEQMEFPLLKKRKLDDDSDSP
1 [	1		SFFEEKPEEPVVLALDPKGH\EDDSYEARKSFLTKYFT\KQPYP
1 1	ł		TRREIEKLAASLWV\WK\SDIASHFSNKRKKCVRDCEKYKPGVL
<b>1</b>			LGFNMKELNKVKHEMDFDAEGLFENHDEKDSRVNASKTADKKIN
1 1		i	LGKEDDSSSDSFENLEEESNESGSPFDPVFEVEPKISNDNPERH
			VLKVIPEDASESEEKLDQKEDGSKYETIHLTEEPTKLMHNASDS
			EVDQDDVVEWKDGASPSESGPGSOOVSDFEDNTCEMKPGTWSDF
1	1	İ	SSQSEDARSSKPAAKKKATMQGDREQLKWKNSSYGKVEGFWSKD
		ļ	QSQW:NASENDERLSNPQIEWQNSTIDSEDGEQFDNMTDGVAEP MHGSLAGVKLSSQQA
6009	4272	1534	CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC
ļ l			HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW
[	ł		EAYTLGHQHWNMFPIQRPPLVMKGRRIMCGKCEKG*VSDSVTGG
			RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL
	ļ		NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG
	ľ		NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWODHA
			VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLOGEPTTTSVSI.
1	Ĭ	į	FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP
	1	1	I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHOLFAEVN
i		ĺ	AVTRGSAVQRRPSITISSIHVDTKIOQELHDVMVAGADGVVOWG
ļ	}	ļ	DPFVVGLAGIFHLIDDPLHQIELSFORRV*EOCOGVKPDSOPVP
- 1		i	RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT
			RDLLRGGDRGHVVVIVLCRLGSLVGGLGTDBLLWFGGR*LIIIG

Г	SEO	Predicted	Predicted end	
- 1	ID	beginning	nucleotide	
	NO:	nucleotide	location	I MANAGEMENT COUNTRY TO THE TOTAL TO THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK TH
- 1		location	corresponding	Gracamic Acid, Faphenylalaning A_Al
- 1		corresponding	to first	"="Istidine, i=Isoleucine V-lucine
- 1		to first	amino acid	Debeucine, Memethionine Memaragine
		amino acid	residue of	P=Proline, Q=Glutamine, P-Argining
		residue of	amino acid	S=Serine, T=Threonine, V=Valine
- 1		amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- 1		sequence	sequence	codon, /=possible nucleofide deletion
			<del></del>	\=Possible nucleotide insertion\
- 1		i	1	1**RGRLSGEWGCGLGRGELFQVSIGIGVSIVHIGQGDHEVLGG
- 1		ł ·	1	AGDVERGALHATGOGVEALVOOLLDVGPACALGT.CDGAATECOCK
				GRAGGEPARGEOVCITEVAOWRMHDGRELGGAEWDWOAT TGART
- I				CGVGGATLLKALSQYFLKGG*RLWCAPCO*DVKVDODDWDG+WD
- 1				R'NGDITHUEN*LL*GAVCCRLVILRWCGI.T.PRUCKROM+TICA
- 1				GSFPGRLWP*PFISQERPNGHCQWEFRLAVPSWKCRWSRWRVRG
- 1				TWRIGNPLLNLL*GAWLGGAACGGOOGGPI.STWOACTGDGOAAD
	6010	1	3533	DEFE QUACKPRIQUECKIWVCPIAWROLLAVTPD
i		_	3555	IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM
- 1				AGISQNAKTGULPAFGECVGIASKALCGI.TFAAAAAAAVI.VG.TED
			1	PNSQAGHQGLVDP1QFARANOAIOMACONI,VDDGGGDGOULGAN
ı				1 1 VAKHI SAUCNACRIASSKTANDVAKDHEVOCA VEVANOMANT
- [	- 1			VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEFVS
- 1	i			IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP
	1			PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC
- 1				IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP
- 1				IATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHQQQM
	- 1			TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAAQLMK
	l l			EAVDDIMVTI.NEAASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG TFVDYQTTVVKYSKAIAVTAQEMMTKSVTNPBELGGLASQMTSD
- 1				YGHLAFQGQMAAATAEPEEIGFQIRTRVQDLGHGCIFLVQKAG\
1	1			ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI
	ŀ			TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHRENILKTA
		ļ		KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA
ı	1			SIGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM
	- 1	1		YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALEATIECIKQ
- 1	i			ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQE
				DVIAIANLSKKAVSDMLTACKOASFHDDVSDEVDTDALDEGTDG
1		1		I IGILDELEHVLVII-OKPTPELKOOLAAFGKDUAGAUTET TOAR
	i	ł		EAMAGTEWOOPEDPTVIAETELLGAAAGTEAAAKKI.BOT KARAK
	- 1			FROM THE EQUILEARKS I ADD TO THE ADD TO THE TOTAL
	-	ļ		VGSIPANAADDGQWSQGLISAARMVAAATSSLCRAANASTOGTA
1		1		SEEALLSSAKQVAASTAOLLVACKVKADODSEAMDDLONAGNALL
ı	- 1	į		KASDNIVRAAQKAAFGKADDDDVVVKTKFVGGIAOIIAAGEEM
	011	445		DKAEKELEEAKKKLAQIRQQOYKFLPTELREDEG
"		446	1835	LLQPAMRKSPGLSDCLWAWILLLSTLTGRSVGORSLODELKDWG
	İ			IVEIKLUDKLLDGYDNRLRPGLGERVTEVKTDIEVTERODYODY
1		1		DMEITIDVERROSWKDERLKFKGPMTVI.PI.MNI.MA CVILIEDDUR
1	1	i		FINGRASVAHIMIMPNKLLRITEDGTT.I.VTMPITUD\ ADGDAAD
				GRUF PM \D\AHACPLKFGSYAYTRAEVVYEWTDEDADCIARIAED
1		į	ļ	GSRLINGIDLLGOTVDSGIVOSSTGEVVIAMTTURUI VEVI ATTUTT
1	i	!		QTILPCIMIVILSQVSFWLNRESVPARTVEGUTTU TMTTT GTR
ł				ARNSLPRVAYATAMDWFIAVCYAFVESAI.TERATINIVETTO
1	ŀ			WDGKSVVPEKPKKVKDPLIKKNNTYAPTATSYTPNLARGDPGLA
1			1	TIAKSATIEPKEVKPETKPPEPKKTFNSVSKIDDISDIADDIA
60	012	351	5013	GIFNLVYWATYLNREPQLKAPTPHQ
1	- 1	'	2013	PAELFQSFAIWHKELYDWRLGPWNQCQPVISKSLEKPLECIKGE
	ł	1		EGIQVREIACIQKDKDIPAEDIICEYFEPKPLLEQACLIPCQQD
1	ļ	1		CIVSEFSAWSECSKTCGSGLQHRTRHVVAPPQFGGSGCPNLTEF
ı		ł	1	QVCQSSPCEAEELRYSLHVGPWSTCSMPHSRQVRQARRRGKNKE
1	- 1			REKDRSKGVKDPEARELIKKKRNRNRQNRQENKYWDIQIGYQTR
	ŀ	[	1	EVMCINKTGKAADLSFCQQEKLPMTFQSCVITKECQVSEWSEWS
1		1		PCSKTCHDMVSPAGTRVRTRTIRQFPIGSEKECPEFEEKEPCLS
ļ	I		•	QGDGVVPCATYGWRTTEWTECRVDPLLSQQDKRRGNQTALCGGG
	j			IQTREVYCVQANENLLSQLSTHKNKEASKPMDLKLCTGPIPNTT
	1	ļ	1	QLCHIPCPTECEVSPWSAWGPCTYENCNDQQGKKGFKLRKRRIT
	1		J;	NEPTGGSGVTGNCPHLLEAIPCEEPACYDWKAVRLGDCEPDNGK
				ECGPGTQVQEVVCINSDGEEVDRQLCRDAIFPIPVACDAPCPKD
	- 1		1;	CVLSTWSTWSSCSHTCSGKTTEGKQIRARSILAYAGEEGGIRCP
			ſ,	NSSALQEVRSCNEHPCTVYHWQTGPWGQCIEDTSVSSFNTTTTW NGEASCSVGMQTRKVICVRVNVGQVGPKKCPESLRPETVRPCLL

SEQ	Predicted	Predicted end	Amino acid segment conto
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H-Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
			PCKKDCIVTPYSDWTSCPS\SCKEGDSSIRKOSRHRVITOLPAN
1	Į		GGRDCTDPLYEEKACEAPQACOSYRW\KTHKW\HRCO\LVP\WS
l			VQQDSP\GAQEGCGPGRQARAITCRKODGGQAGIHECLQYAGDV
1			PALTQACQIPCQDDCQLTSWSKFSSCNGDCGAVRTRKRT;VGKS
1			KKKEKCKNSHLYPLIETQYCPCDKYNAQPVGNWSDCILPEGKVE
-			VLLGMKVQGDIKECGQGYRYQAMACYDQNGRLVETSRCNSHGYI
			EEACIIPCPSDCKLSEWSNWSRCSKSCGSGVKVRSKWLREKPYN
			GGRPCPKLDHVNQAQVYEVVPCHSDCNQYLWVTEPWSICKVTFV
			NMRENCGEGVQTRKVRCMQNTADGPSEHVEDYLCDPEEMPLGSR
1			VCKLPCPEDCVISEWGPWTQCVLPCNQSSFRQRSADPIRQPADE
			GRSCPNAVEKEPCNLNKNCYHYDYNVTDWSTCQLSEKAVCGNGI
			KTRMLDCVRSDGKSVDLKYCEALGLEKNWQMNTSCMVECPVNCQ LSDWSPWSECSQTCGLTGKMIRRRTVTQPFQGDGRPCPSLMDQS
1		l	KPCPVKPCYRWQYGQWSPCQVQEAQCGEGTRTRNISCVVSDGSA
	1		DDFSKVVDBEFCADIBLIIDGNKNMVLEESCSQPCPGDCYLKDW
		1	SSWSLCQLTCVNGEDLGFGGIQVRSRPVIIQELENQHLCPEQML
			ETKSCYDGQCYEYKWMASAWKGSSRTVWCQRSDGINVTGGCLVM
Ī		1	SQPDADRSCNPPCSQPHSYCSETKTCHCEEGYTEVMSSNSTLEQ
1			CTLIPVVVLPTMEDKRGDVKTSRAVHPTOPSSNPAGRGRTWFI.O
1			PFGPDGRLKTWVYGVAAGAFVLLIFIVSMIYLACKKPKKPORRO
6013			NNRLKPLTLAYDGDADM
9073	1161	710	GAFIAGVPVQPVLIRYPNSLDTTSWAWRGPGVLKVLWLTASQPC
			SIVDVEFLPVYHPSPEESRDPTLYANNVQRVMAQALGIPATECE
	ļ		FVGSLPVIVVGRLKVALEPQL/WGTGKSASEGWAVRWLCGRWGR
6014	2857	613	ARPESNDQPGRVCQAATAL EAVAGGMEKSRMNLPKGPDTLCFDKDEFMKEDFDVDHFVSDCRK
		015	RVQLEELRDDLELYYKLLKTAMVELINKDYADF\VNLSTNLVGM
			DKALNQLSVPLGQLREEVLSLRSSVSEGIRAVDERMSKQEDIRK
1			KKMCVLRLIQVIRSVEKIEKILNSQSSKETSALEASSPLLTGQI
			LERIATEFNQLQFHACQSK\GMPLLDKVRPRIAGITAMLQQSLE
1			GLLLEGLQTSDVDIIRHCLRTYATIDKTRDAEALVGOVLVKPYI
1			DEVIIEQFVESHPNGLQVMYNKLLEFVPHHCRLLREVTGGAISS
1			EKGNTVPGYDFLVNSVWPQIVQGLEEKLPSLFNPGNPDAFHEKY
1			TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKWNLPVYFQI
			RFREIAGSLEAALTDVLEDAPAESPYCLLASHRTWSSLRRCWSD
1 !			EMFLPLLVHRLWRLHSGRFWARYSVFV\N\ELSLRPISNESPKE
1			IKKPLVTGSKEPSITQGNTEDQGSGPSETKPVVSISRTQLVYVV
1			ADLDKLQEQLPELLEIIKPKLEMIGFKNFSSISAALEDSQSSFS
			ACVPSLSSKIIQDLSDSCFGFLKSALEVPRLYRRTNKEVPTTAS SYVDSALKPLFQLQSGHKDKLKQAIIQQWLEGTLSESTHKYYET
j l			VSDVLNSVKKMEESLKRLKQARKTTPANPVGPSGGMSDDDKIRL
1	ł		QLALDVEYLGEQIQKLGLQASDIKSFSALAELVAAAKDQATAEQ
<u> </u>			P
6015	13	2237	AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC
j	İ		VKGKGSLPLSAHGIVVAWLSRAEWDQVTVYLFCDDHKLORYALN
! !			RITVWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDELRLLY
			GMALVRFVNLISERKTKFAKVPLKCLAOEVNIPDWIVDLRHELT
[ [			HKKMPHINDCRRGCYFVLDWLQKTYWCRQLENSLRETWELEEFR
1 1			EGIEEEDQEEDKNIVVDDITEQKPEPQDDGKSTESDVKADGDSK
			GSEEVDSHCKKALSHKELYERARELLVSYEEEQFTVLEKFRYLP
1	į		KAIKAWNNPSPRVECVLAELKGVTCENREAVLDAFLDDGFLVPT
] [			FEQLAALQIEYEENVDLNDVLVPKPFSQFWQPLLRGLHSQNFTQ
			ALLERMLSELPALGISGIRPTYILRWTVELIVANTKTGRNARRF
	}		SAGQWEARRGWRLFNCSASLDWPRMVESCLGSPCWASPQLLRII
			F\KAMGQGLQDE\EQEKLLRICSIYTQSGENSLVQEGSEASPIG KSPYTLDSLYWSVKPASSSFGSEAKAQQQEEQGSVNDVKEEEKE
			EKEVLPDQVEEEEENDDQEEEEEDEDDEDDEEEDRMEVGPFSTG
	1	j	QESPTAENARLLAQKRGALQGSAWQVSSEDVRWDTFP\LGRMPR
,	ļ		SRPRTPAELMLENYDTHVIFWTKPVL\EQRLEPSTCK\TDTLGL
	l		\SCGVGS\GNCSNSSSSNFRGAFLLEARGSLH\GL\KTGLOLF
6016.	13	2237	AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC

SE	Q Predicted		
I		Predicted end	
		nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ИО		location	Glutamic Acid, E=
İ	location	corresponding	
í	corresponding	to first	
- 1	to first		D-Deucine, M=Methionine N-Aconomic
	amino acid	amino acid	i
	marid acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan V=Typnoins variation
- 1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	j -	Codon, /=possible nucleotide deletion,
			\-Possible nucleofide incorpion\
Į.	ľ		VKGKGSLPLSAHGIVVAWLSRAEWDOVTVVI BODDVIKI ODVINI
	1		TATIVING ROUND DIAVASTADI, TROUT, TOURGOT OFFICE
	i		GMALVRFVNLISERKTKFAKVPLKCLAQEVNIPDWIVDLRHELT
1	1		HKKMPE INDCPROCYEVE DWY OVERWARD OF THE LT
	1	1	HKKMPFINDCRRGCYFVLDWLQKTYWCRQLENSLRETWELEEFR
	1	1	EGIEEEDQEEDKNIVVDDITEQKPEPQDDGKSTESDVKADGDSK
	1	-	1 COLD VOORCARALSHKELYERARELLINGVEREORDER DECENS
- }	J	İ	T 1031 1030 MILES PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF
ļ	i		I PARABATE I PENADPINDATA DAL MARIA
- 1	1		
ŀ			SAGQWEARRGWRLFNCSASLDWPRMVESCLGSPCWASPQLLRII
ı	}	1	F/KAMGOGLODE/EGEVILDIGGEVEN SPOLLRII
			F\KAMGQGLQDE\EQEKLLRICSIYTQSGENSLVOEGSEASPIG
	i	i	1 TODOUT WOVEPASSSEGSEAKACOOFFOCOUNTRY
i		!	T NEW TED CAREER NOTO ENERGE EDED DE DE DE DESTRUCTION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DE LA COMPANSION DEL COMPANSION DE LA
1		1	I OW KIEST DINDEN I DIRVIEW TKDW. / PODI PDOMOVS man-
601	7 203		1 10 CO 100 (GNCSNSSSNERGAFI.T.FADGGI 11) GT \ TIMGE 65 -
001	, 203	3469	SHQEIEQNSAMAPRKRGGRGISFIFCCFRNNDHPEITYRLRNDS
1	1 .		NFALOTMEPAL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL DARBUEEL
1	1	4	NFALQTMEPALPMPPVEELDVMFSELVDELDLTDKHREAMFALP
1			AEKKWQIYCSKKKDQEENKGATSWPEFYIDQLNSMAARKSLLAL
l	1	i i	LANDED DE LA LESER LA
1	i		1
- 1	i	1 1	OCCUPANT VAVATOR TRICANCILA DESCRIPACIONA OFFICA ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOMOS ANTICOM
İ		1	**** VIDINDUDASIGRYRI) EVSI, VTX TMCDTXXXXX GCG2
		1 1	DFILEFAKERET HILLER THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THAT THE THE THE THE THE THE THE THE THE TH
1	1		DELEFAKRFELVHIDTKSATOMPELTRKRLTHSEAYPHFMSILH
1	1	1 1	HCLOMPYKRSCNTVOVWLLLDDIZGGZUZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZ
	- I	1	HCLQMPYKRSGNTVQYWLLLDRIIQQIVIQNDKGQDPDSTPLEN
		1	THE PARTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF T
1		1 1	
l	ł.	! !	
i		1 1	~~~~~ TE DE FOGEPPEPGPPPLGA TMDDDCA DMCT AT VVICE
		i	TITE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRAC
İ			STANDARD OF THE WASHINGTON TO THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF T
1	1	1 1	QNCNILLSRLKLSNDEIKRAILTMDEQEDLPKDMLEQLLKFVPE
1	1	1	KSDIDLLEEHKHELDRMAKADRFLFEMSRINHYQQRLQSLYFKK
ł	1	1 1	KFAERVAEVKRYUEA TROGGEREN SRINHYQQRLQSLYFKK
	1	1	KFAERVAEVKPKVEAIRSGSEEVFRSGALKQLLEVVLAFGNYMN
ĺ		1 1	**************************************
1	1		O VINDING SURDIPUAAKVNMTELDKEI STI. DOGI WALKONDA DAGA
1	1	i i	NOW FOR VSVVSOFITVASESESDIVED I A EARLY POST
	1	1	THE CHARGET CALL TO BE CONTRACTED TO THE CONTRACT OF THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE CALL THE
1	į	[ { '	THE THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPER
6018	13		DDDCKDKKKK K I IMIMIII QQDDDDTMVT 31-
	1 43	2510	TISQSGGIRRREAVWFEVVNMDFSRIHMYSPPQCVPENTGYTY ALSSSYSSDALDEFTEHY DRIVEDSRIHMYSPPQCVPENTGYTY
i	1		ALSSSYSSDALDFETEHKLDPVFDSPRMSRRSLRLATTACTLGD
ľ	1 1	1	GEAVGADSGTSSAUGI KARA ARTENSARSLRLATTACTLGD
ı	1	-	GEAVGADSGTSSAVSLKNRAARTTKQRRSTNKSAFSINHVSRQV
1	1		
ľ		, ,	DIRGGIRAMIOGNGDVGAGAATCHNCEECCNOMY CONTROL
	1	1 -	THE TENT OF VORVISKURNOKCODOCKGROUT, DATIDOD A CONTINUE OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE
1	1	-	
Í	i .	4 **	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,
1	1	ļI	SLRGQG\NFFSFLPVLNWASMHRTQRVDDPQDVFKPTTSRLKQ
	1 1	l p	PLOGDSEAFPWHWMSGVEOOVAGLOGGGGTTTTSRLKQ
ł	1	1 7.	PLQGDSEAFPWHWMSGVEQQVASLSGQCHHHGENLRELTTLLQK
1	1 1	1.5	QARVDQMEGGPAGPSASVRDAVGQPPRETDFMAFHQEHEVRMS
1	1 1	1 **	DEDITION DREASEALUKELEOTKOKTICAUGEOTT DESIRENT
I	1	~	POSTUCIOS WELL KICKLAD MODDID MOMBINIST FOR THE
1	1 1	) ×	ACCOPPAND ALL SOUP ASKEDI OTMINITORI OF OTT DESIGNATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE
!	1	-	**************************************
ł	1		VDFALESGGGSTI.STPCSETVETVETVETVETVETVETVETVETVETVETVETVETVE
l	1	1 37	VDFALESGGSILSTRCSETYETKTALMSLFGIPLWYFSQSPR
1	}	į •	VINE TO THE ONCHAP KISCHSTYT, VADIL COMMITTED AND CONTROL OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF T
L	1	,	* TOM TOO AFROM AVYOUR ROLENDE VOTE COLUMN CONTRACTOR AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL AND A TOTAL
6019	2		DENTEDOTATOT VEHICLES I FENNICHDE VTCI VD PRINTARE I
	<u> </u>	1066 T	PNDREPPPQRPPSSRRASHLAQEITSAASLGDQTQILGSLTTA
			ALITSPITATORNOLOGICA

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ì	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
1			PVITSAIRSMPGISSQILTNAQGOVIGTLPWVVNSASVAADADA
}			QSLQVQAVTPQLLLNAQGOVIATLASSPI,PPPVAVRK\ PSTBRC
1	1	ł	LLKSEVQPIKPTPTVPQPAVVIASPAPAAKPSASAPTPTTCSFT
	Ť.	1	PTVSQLVSKPHTPSLDEDGINLEEIREFAKNFKIRRLSLGLTOT
			QVGQALTATEGPAYSQSAICRFEKLDITPKSAOKLKPVI.FKWLN
			EAELRNQEGQQNLMEFVGGEPSKKRKRRTSFTPQAIEALNAYFE
İ	1	}	KNPLPTGQEITEIAKELNYDREVVRVWFCNRRQTLKNTSKLNVF
6020	4953	549	QIP
1	1	349	EAIQFEVSIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYYLPW
1			AHTKPVVTLTSYWEDISHRLDAVNTLLAMAERLQTNIEALKSGI
i			QGKIPANQLAELWLKLIDEVIEDTRYTLPLTEGKANVTVLDTQI
Į	ł		RKLRSRSLSQIHEAAVRMRSEATDVKSTLAEIEDWLDKLMQLTE EPQNSMPDIIIWMIRGEKRLAYARIPAHQVLYSTSGENASGKYC
ł	i		GKTQTIFLKYPQEKNNGPKVPVELRVNIWLGLSAVEKKFNSFAE
1			GTFTVFAEMYENQALMFGKWGTSGLVGRHKFSDVTGKIKLKREF
			FLP2KGWEWEGEWIVDPERSLLTEADAGHTEFTDEVYQNESRYP
	i		GGDWKPAEDTYTDANGDKAASPSELTCPPGWEWEDDAWSYDINR
			AVDEKGWEYGITIPPDHKPKSWVAAEKMYHTHRRRRLVRKRKKD
			LTQTASSTAGAMEELQDQEGWEYASLIGWKFHWKORSSDTERPR
1 1			RWRRKMAPSETHGAAAIFKLEGALGADTTEDGDEKSLEKOKHSA
1			TTVFGANTPIVSCNFDRDYIYHLRCYVYOARNLLAIDKDSFSDD
1 1			YAHICFLHRSKTTEIIHSTLNPTWDOTIIFDEVEIYGEPOTVLO
-			NPPKVIMELFDNDQVGKDEFLGRSIFSPVVKINSEMDITPKILL
1 ]			HPVMNGDKACGDVLVTAELILRGKDGSNLPILPPORAPNI.VM/P
]			QGIRPVVQLTAIEILAWGLRNMKNFQMASITSPSLVVBCGGERV
1 1			ESVVIKNLKKTPNFPSSVLFMKVFLPKEELYMPPLVIKVIDHRQ
			FGRKPVVGQCTIERLDRFRCDPYAGKEDIVPQLKASLLSAPPCR
1 1			DIVIEMEDTKPLLASKCLSSMSTALSKMASPATVHLTEKEEEIV
1 1			DWWSKFYASSGEHEKCGQYIQKGYSKLKIYNCELENVABFEGLT DFSDTFKLYRGKSDENEDPSVVGBFKGSFRIYPLPDDPSVPAPP
1 1	ľ		ROFRELPDSVPQECTVRIYIVRGLELQPQDNNGLCDPYIKITLG
)	1		KKVIE DRDHYI PNTLNPVFGRMYELSCYLPQEKDLKISVYDYD
] ]	l		TFTRDEKVGETIIDLENPF\LSRFG\SHCG\IPEEYCVSGVNTW
1			RDSLR\PTQ\LLQNVARFKGFPQPILSEDGSRIRYGGRDYSLDE
			FEANKILHQHLGAPEERLALHILRTQGLVPEHVETRTLHSTFQP
1			NIS\RYYLRVIIWNTKDVILDEKSITGEEMSDIYVKGWIPGNEF
1	İ		NKQKTDVHYRSLDGEGNFNWRFVFPFDYLPAEOLCIVAKKEUFW
	i		SIDQTEFRIPPR\LIIOIW\DNDKFS\LDDVIGPPPTITCPUTT
1			HFLQKSPGGNC/RGLDMIPDLKAMNPLKAKTASLFEOKSMKGNW
[	1		PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDERNMND
			KLDLPNRPETSFLWFTNPCKTMKFIVWRRFKWVIIGLLFLLILL
6021	4953	549	LFVAVLLYSLPNYLSMKIVKPNV
			EAIQFEVSIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYYLPW
1 1	1		AHTKPVVTLTSYWEDISHRLDAVNTLLAMAERLQTNIEALKSGI QGKIPANQLAELWLKLIDEVIEDTRYTLPLTEGKANVTVLDTQI
		•	RKLRSRSLSQIHEAAVRMRSEATDVKSTLAEIEDWLDKLMQLTE
1 !	1	l	EPQNSMPDIIIWMIRGEKRLAYARIPAHQVLYSTSGENASGKYC
[ [	1	ļ	GKTQT1FLKYPQEKNNGPKVPVELRVNIWLGLSAVEKKFNSFAE
1			GTFTVFAEMYENQALMFGKWGTSGLVGRHKFSDVTGKIKLKREF
	1		FLPPKGWEWEGEWIVDPERSLLTEADAGHTEFTDEVYONESPVD
1 1	[		GGDWKPAEDTYTDANGDKAASPSELTCPPGWEWEDDAWSYDIND
		İ	AVDEKGWEYGITIPPDHKPKSWVAAEKMYHTHRRRRLVRKRKKD
] ]			LTQTASSTAGAMEELQDQEGWEYASLIGWKFHWKORSSDTFRPR
1 1		[	RWRRKMAPSETHGAAAIFKLEGALGADTTEDGDEKSLEKOKHSA
1 1		1	TTVFGANTPIVSCNFDRDYIYHLRCYVYOARNLLALDKDSFSDD
] ]	l	J	YAHICFLHRSKTTEIIHSTLNPTWDOTIIFDEVEIYGEPOTVLO
<b>[</b>	İ	ľ	NPPKVIMELFDNDQVGKDEFLGRS I FSPVVKLNSEMD I TDKI.I.W
† †			HPVMNGDKACGDVLVTAELILRGKDGSNLPILPPORAPNI.VMVP
		!	QGIRPVVQLTAIEILANGLRNMKNFQMASITSPSLVVECGGERV
	1	i	ESVVIKNLKKTPNFPSSVLFMKVFLPKEELYMPPLVIKVIDHRQ
	<u></u>	<u>_</u>	FGRKPVVGQCTIERLDRFRCDPYAGKEDIVPQLKASLLSAPPCR

	SEQ	Predicted	Predicted end	
	ID	beginning	nucleotide	
4	NO:	nucleotide	location	I MATERIAL CECUSTOINO DENOMESTA NELLA MATERIALMANTE DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DEL CONTRACTOR DE LA CONTRACTOR DE LA C
ı		location	corresponding	Tacamic Acta, Febrery alanine Ceclicaine
		corresponding	to first	
ı		to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
- 1		amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- 1		amino acid	sequence	Codon, /=possible nucleotide deletion,
-		sequence		\=possible nucleotide insertion)
ĺ	İ			DIVIEMEDTKPLLASKCLSSMSTALSKMASPATVHLTEKEEEIV
				DWWSKFYASSGEHEKCGQYIQKGYSKLKIYNCELENVAEFEGLT
			1	DFSDTFKLYRGKSDENEDPSVVGEFKGSFRIYPLPDDPSVPAPP
- 1				TRUP REDPUS VPQECTVRIYIVRGI.EL.ODODAMICI CDDVIVETTE -
				ARVIE (DRUHILPNTLNPVFGRMYELSCVI.DOEVDI VI GIURIA
	1			1 TT TADER VGET TIDLENPF \ LSRFG \ SHCG \ TDEEVCHOOTERS
- [				TRUSTIK (PTQ \LLONVARFKGPPOPTI, SEDGSPTDVGGDDVG-
-	}			TEANXIDIQUEGAPEERLALHII.RTOGI.VDRUVETDTI UORDON
- 1	1			1 NIO NII DRVII WATKOVI LDEKSTTGEEMSDI VIVOUT DOWN
	}		ı	I NAOKI DVH I KSLDGEGNENWREVEDEDVI. DAEGI CITTA KKRITERI
	l			SIDGIESKIPPK (LIIOIW (DNDKFC) I.DDVI CEDDOR MCDIM-
	[			I TO TO TO THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER O
	- 1			FCIAEROGARVMAGKVEMTLETINEKEARPRDACYCRAPRANCE
				KLDLPNRPETSFLWFTNPCKTMKFIVWRRFKWVIIGLLFLLILL LFVAVLLYSLPNYLSMKIVKPNV
- [	6022	4953	549	ENTOFFUSIONVCOVENERAL
- 1	1			EAIQFEVSIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYYLPW
	- 1			AHTKPVVTLTSYWEDISHRLDAVNTLLAMAERLQTNIEALKSGI QGKIPANQLAELWLKLIDEVIEDTRYTLPLTEGKANVTVLDTQI
-	f			RKLRSRSLSQIHEAAVRMRSEATDVKSTLAEIEDWLDKLMQLTE
- 1	- 1			EPQNSMPDIIIWMIRGEKRLAYARIPAHQVLYSTSGENASGKYC
-	- 1			I CATELLE LATPOEKNNGPKVPVELRVNTWIGT CAUBUURENGE
				GIFIVFAEMIENQALMFGKWGTSGLVGPHKEEDVECKTKI KDDD
	1			1 THE ENGINE WEGEWIYDPERSLLTEADAGHTERTDEUVONDORUS !
1	1			OUDINE ABDITION GO KAASPSELT COD CWDWD TO THE I
				AVDEAGME YGITIPPDHKPKSWVAAEKMVHTUDDDDI UDVDVO
1				1 DIQIASSIAGAMEELODOEGWEYASI.TGWKEUWYODGODWODD
	ı	İ		RWRRANDAPSETHGAAAIFKLEGALGADTTEDGDEVCLEVONGS
	!	1		TTVFGANTPIVSCNFDRDYIYHLRCYVYQARNLLALDKDSFSDP
	- 1	i		YAHICFLHRSKTTEIIHSTLNPTWDQTIIFDEVEIYGEPQTVLQ
ŀ	J	1		NPPKVIMELFDNDQVGKDEFLGRSIFSPVVKLNSEMDITPKLLW HPVMNGDKACGDVLVTABLILRGKDGSNLPILPPQRAPNLYMVP
	1			QGIRPVVQLTAIEILAWGLRNMKNFQMASITSPSLVVECGGERV
1				ESVVIKNLKKTPNFPSSVLFMKVFLPKEELYMPPLVIKVIDHRQ
ì	1			PURKEY VGQCTAERLDRFRCDPYACKPDTVDOT VACTY CARDON
	ı			DIVIEWEDIKPHLASKCLSSMSTALSKMASDAMMIN WORDS
1		Ī		DWISKE IASSCENERCGOYIOKGYSKI, KTVNCEL ENTIN BEDGE
1	1	1	i	DISDIFACING ASDENEDPSVVGEFKGGFDIVDI DODDOVIDA DO
		į		MALVERDOANDECLARIATION OF THE CONTRACT CONTRACTOR
1				WKV + II \DKDH I I PN I LNPV F GRMYFI SCVI DOFFDI VI CINOND
1	- 1	•		TEACHER VGELLIDDENER/INSTER/SHCG/IDERVOYOR
	1	,		RDSLR\PTQ\LLQNVARFKGFPQPILSEDGSRIRYGGRDYSLDE
1	1		1	FEANKILHQHLGAPEERLALHILRTQGLVPEHVETRTLHSTFQP NIS\RYYLRVIIWNTKDVILDEKSITGEEMSDIYVKGWIPGNEE
l			•	NKOKTDVHYRSLDGEGNFNWRFVFPFDYLPAEQLCIVAKKEHFW
	.			DIDGIEST REK (DI 101 M / DNDKES / LDDVI CEDDUI MODIUM
			I	MI DONGE GONC / RGLOMIPDI.KAMNPI.KAKTASI PROVONYONIN
	- 1		1	*CIACADGARVEAGREENTLETINEREADEPDAGGGDDEDAGG
				KUDUPNKPETSFLWFTNPCKTMKFIVWPPFKMITICTI DIT TO
-	023	102		DE ANAUDISCENAT SWKIAKDMA
		102	916	SQELGMFVELNNLLNTTPDRAEOGKLTLLCDAZZDCGGYLTT
			1	DE LIBRANCE VCE VALIOSESHYST VCORT CVCT TMAD COOKER 1
	- 1			DEGLI I V CSGR \ VFOAOKEPHPI OPI PFANACHI VDI PERIMPA
	-		į	ERF VOSCEARWITPVLLVDDLSVIJISI.GMCAVAVI.DETUVCDAM
		1		VCHEDROMMVVLVHDSGDAEDEENDTI.I.NGI.GUOGUI II DADOT
			1.	AIGICKDVHGQLKILWRRPSOPAVHRDOSFTVOVKTODVCVCER
6	024	3		AKGMSEAVL
		1		FLSFLCYPRFRCLFCLQFAIPASRMEQLNELELLMEKSFWEEAE
	}		1 .	DEALUE VANV VASE PRTVLSTGMDNRVI AT ATMITTECHTE CONTINUE OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE
			1	RLVITASQSLENKELCILRNDWCSVPVEPGDIIHLEGDCTSDTW
				IIDKDFGYLILYPDMLISGTSIASSIRCMRRAVLSETFRSSDPA FROMLIGTVLHEVFOKAINNSFAPEKLOELAFOTIOEIRHLKEM

SEQ	Predicted	Predicted end	1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and 1 Amin and
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
l		corresponding	H=H1Stldine, I=Isoleucine, K=Lvsine
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	}   -	\=possible nucleotide insertion)
			YRLNLSQDEIKQEVEDYLPSFCKWAGDFMHKNTSTDFPQMQLSL
			PSDNSKDNSTCNTEINENDETCKNAGDFMHKNTSTDFPQMQLSL
1		ļ	PSDNSKDNSTCNIEVVKPMDIEESIWSPRFGLKGKIDVTVGVKI
			HRGYKTKYKIMPLELKTGKESNSIEHRSQVVLYTLLSQERRADP
1			EAGLLLYLKTGQMYPVPANHLDKRELLKLRNQMAFSLFHRISKS
1			ATROKTQLASLPQIIEEEKTCKYCSQIGNCALYSRAVEQQMDCS
İ	)		SVPIVMLPKIEEETQHLKQTHLEYFSLWCLMLTLESQSKDNKKN
	<b>!</b>		HQNIWLMPASEMEKSGSCIGNLIRMEHVKIVCDGOYLHNFOCKH
[	1		GAIPVTNLMAGDRVIVSGEERSLFALSRGYVKEINMTTVTCLLD
			RNLSVLPESTLFRLDQEEKNCDIDTPLGNLSKIMENTFVSKKID
	}		DLIIDFREPQFISYLSSVLPHDAKDTVACILKGLNKPQRQAMKK
	1		VLLSKDYTLIVGMPGTGKTTTICTLVRILYACGFSVLLTSYTHS
1			AVDNILLKLAKFKIGFLRSR\QIQKVHPAIQQFTEHEICRSKSI
1	1		KS\LALLEELYTSQLIDATTCMGINHPIFSRKIFDFCIVDEASQ
	i I		ISQPICLGPLFFSRRFVLVGDHQQLPPLVLNREARALGMSESLF
	1		KDI FONKS MUOT THOU DINGS THE TOTAL STATE THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL STATE OF THE TOTAL
			KRLEQNKSAVVQLTVQYRMNSKIMSLSNKLTYEGKLECGSDKVA
1	l i		NAVINLRHFKDVKLELEFYADYSDNPWLMGVFEPNNPVCFLNTD
1 i			KVPAPEQVEKGGVSNVTEAKLIVFLTSIFVKAGCSPSDIGIIAP
1 .			YRQQLKIINDLLARSIGMVEVNTVDKYQD\RDKSIVLVSFVRSN
	1		KDGTVGELLKDWRRI NVAITRAKHKLILLGCVPSLNCYPPLEKL
6025	3977		LNHLNSEKLIIDLPSREHESLCHILGDFQRE
""	3377	89	GGFPAQSDHLPPVFPLRSDLLITMSTLYVSPHPDAFPSLRALIA
	i		ARYGEAGEGPGWGGAHPRICLOPPPTSRTSFPPPRIDALEOGDG
1 1			GLWVWGATAVAQLLWPAGLGGPGGSRAAVLVOOWVSYADTELTP
1 1	}		AACGATLPALGLRSSAQDPQAVLGALGRALSPLEEWIRI.HTVI.A
	į		GEAPTLADLAAVTALLLPFRYVLDPPARRIWNNVTRWFVTCVRQ
1 1	i		PEFRAVLGEVVLYSGARPLSHQPGPEAPALPKTAAQLKKEAKKR
			EKLEKFQQKQKIQQQQPPPGEKKPKPEKREKRDPGVITYDLPTP
			PGEKKDVSGPMPDSYSPRYVEAAWYPWWEQQGFFKPEYGRPNVS
1 1			AANPRGVFMMCIPPPNVTGSLHLGHALTNAIQDSLTRWHRMRGE
1 1	1	i	TILWNPGCDHAGIATQVVVEKKLWREQGLSRHQLGREAFLQEVW
l i			KWKEEKGDRIYHQLKKLGSSLDWDRACFTMDPKLSAAVTEAFVR
!			LHEEGIIYRSTRLVNWSCTLNSAISDIEVDKKELTGRTLLSVPG
1 1	1	i	YKEKVEFGVLVSFAYKVQGSDSDEEVVVATTRIETMLGDVAVAV
1 1	1		HOKOTOVOU KCKOUTUURI SUGI DEEVVVATTRIETMLGDVAVAV
1	1		HPKDTRYQHLKGKNVIHPFLSRSLPIVFDEFVDMDFGTGAVKIT
1 1			PAHDQNDYEVGQRHGLEAISIMDSRGALINVPPPFLGLPRFEAR
		į	KAVLVALKERGLFRGIEDNPMVVPLCNRSKDVVEPLLRPQWYVR
	1	ſ	CGEMAQAASAAYTRGDLRILPERHQRTWHAWMDNIRE\WCMFPG
	1	}	KLWWG\HR\IPAYFVTVSDPAVPPGEDPDGRYWVSGRNEAEARE
1			KAAKEFGVSPDKISLQQDEDVLDTWFSSGLFPLSII.GWPNOSED
1	İ		LSVFYPGTLLETGHDILFFWVARMVMLGLKLTGRLPFREVYI.HA
1	i		IVRDAHGRKMSKSLGNVIDPLDVIYGISLOGLHNOLLNSNLDPS
1			EVEKAKEGQKADFPAGIPECGTDALRFGLCAVMSOCPDINIDUM
1	1	1	RILGYRHFCNKLWNATKFALRGLGKGFVPSPTSOPGGHESLVDP
1 1	ł	}	WIRSRLTEAVRLSNQGFQAYDFPAVTTAOYSFWLYELCDVVLEC
ţ		i	LKPVLNGVDQVAAECARQTLYTCLDVGLRLLSPFMPFVTEELEO
]		İ	RLPRRMPQAPPSLCVTPYPEPSECSWKDPEAEAALELALSTTPA
1 1		İ	VRP\LRADYNLHPESGPTCFLEVAD\EATGALASAVSGYVQGPG
		J	QAQVVVAVAEPWGLPAP\QGCAVALASDRCSI\HLQLQG\LLDP
1		}	ARELG\KLQ\AKRVEAQ\RQAQ\RLR\ERRA\ASGNPVKVPL\E
<u> </u>			VQEADEAKLQQTEAELRKVDEAIALFQKML
6026	2674	514	GPITFLKKKAKMKDMPLRIHVLLGLAITTLVQAVDKKVDCPRLC
			TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQ
1 1	ļ		THAT AKTEYSTORDING MOT BY COURT CONTROL OF THE PART PART PART PART PART PART PART PART
į f	1		TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV
[	1		YLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHN
!!!	j	İ	LLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK
1	İ		PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH
	ļ		VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL
		ĺ	ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESIMI.
	ł		NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMNMNKTN
[			IRFMEPDSLFCVDPPEFQGONVROVHFRDMMEICLPLIAPESFP
<u> </u>			SNLNVEAGSYVSFHCRATA\EPQPEIYWITPSGQKLLPNT\LTD
		······································	

SEC	2 Predicted		
ID		Predicted end	
NO:	1	nucleotide	
1 110:	· · · · · · · · · · · · · · · · · · ·	location	
1	location	corresponding	H=Histiding T-To-landine, G=Glycine,
į.	corresponding	to first	
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	I TELULINE, UEGIUCAMINE DENVESSES
ŀ	residue of	amino acid	J-Serine, Tellineonine V-Valine
	amino acid		Walryptophan, Yarvrosine variations
1	sequence	sequence	COCOL, /=possible micleoride deleti-
<u> </u>	sequence		_Possible nucleofide incombion\
- 1	į.		KFYVHSEGTLDINGVTPKEGGLYTCIATNLVGADLKSVMIKVDG
		<b>f</b>	SFPODNINGSLATKIPDIOANSKI KUDG
ı	1		SFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFVK
	1	ĺ	
	1		TARGET A TENGLISH DOKE YER UNTERTAIN OF COLL OF TOTAL
1	-	ŀ	TODO ENWINDERS I VRNYLOK PTFALCET. VDDT TNI WED CTOTO
6027	5254	4148	[ YOUKVEAT VIGEPTNMS
- 1	5251	4148	GGRRAPGRPGRSIKDEEEETVFREVVSFSPDPLPVRYYDKDTTK
í	ł	1	
			LLCHDMMGGYLDDRFIQGSVVQTPYAFYHWQCIDVFVYFSHHTV
			TIPPVGWTNTAHRHGVCVLGTFITEWNEGGRLCEAFLAGDERSY
1		1	OAVADRIMOTT\ BEEBEDOWLTWT
ì	1		QAVADRLVQIT\RFFRFDGWLINIENSLSLAAVGNMPPFLRYLT
ľ	1		TOLHROVPGGLVLWYDSVVQSGQLKWQDELNQHNRVFFDSCDGF
- 1		i	I * **********************************
- )	]	1	T THE COURT REPORT OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROP
6028	120		1 22 VIBRINCEAPARTCH
	1	3432	NCLLLQAKGFHGEIEDLQQWLTDTERHLLASKPLGGLPETAKEQ
		1	1 ANT THE TOP OF BARBETY KS IMOKEDOMI. A DEDUCA DONATED AS A SECOND OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PRO
Í		1	TANDRONGED VETKLINER / KT/ KT. PENTAL A / MODIFICAL /
1	i	1	WLTQAEQTLNVASRPSLILDTVLFQIDEHKVFANEVNSHREQII
ļ			ELDKTGTHLKYFSQKQDVVLIKNLLISVQSRWEKVVQRLVERGR
- 1	}		SLDDARKRAKOFURANCKI MENI DEGENERAVORLVERGR
1	1	ì	SLDDARKRAKQFHEAWSKLMEWLEESEKSLDSELEIANDPDKIK
l l			TQLAQHKEFQKSLGAKHSVYDTTNRTGRSLKEKTSLADDNLKLD
1	<b>}</b>	1	DMLSELRDKWDTICGKSVERQNKLEEA\LLFSGQFTDALQALID
ł		1	THE ANY DE VENEDUP VHGD I DILVMNI. TONIUM FOREIT GROWN OF THE
Į.		ł	T TO THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF T
j		]	DELICATION VALUE IN THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROP
1			I DED STINGT IN ALLEGARARIAN RATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PRO
1	į i		I TATAL TOUR PER VERWARDHOORT, A SATIACT TAYOUT THE TATAL
}	1		( 'S
1			I THE THE CONDESSION IN THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PR
1	í i		QIETKNPRVNLLVSKWQQVWLLALERRRKLNDALDRLEELREFA
1	1		NFDFDIWRKKYMRWMNHKKSRVMDFFRRIDKDQDGKITRQEFID
1			GILSSKFPTSRLEMSAVADIFDRDGDGYIDYYEFVAALHPNKDA
1		ĺ	YKPITDADKIEDEUTROWA KOKOT TO TOTAL YEFVAALHPNKDA
j	l	ľ	YKPITDADKIEDEVTRQVAKCKCAKRFQVEQIGDNKYRFFLGNQ
i	1	ŀ	FGDSQQLRLVRILRSTVMVRVGGGWMALDEFLVKNDPCRAKGRT
Į.	1 1	j	
1	1		- X- 3-X-D-S-Y VALLITPK LIHOL/PDNVCPD6H myovana
	1 1	· · · · · · · · · · · · · · · · · · ·	
i	1	ļ	
-	1		TEST TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE TEST TO THE T
6029	1 1		20100100
	( + )	3533	IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM
	1	1	- VIOLUSIANT GULPAPGECIVICI ACKALOOT PERSON NA SANCARE.
	l	i i	THOUSENDED TOP ARANGATOMA CONTENDED CONTRACTOR
l	1	ł	TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL
l	1	l	VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEFVS
	1	1	IPAOI SEEGGODORDII VON KOKETATAPLI EAVENLTAFASNPEFVS
			IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP
	1	j	PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC
		1	IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP
		1 '	TATACHGERAULGHKGTOLASYFFDT TT XXIIOUX OVER DOOL OF
		*	
	ĺ	, ·	DDITT TONEMADEVGLV(GMVDATAFAMORT DEGESS
	ļ l	, ,	** VD1V11VVRISKAJAVTAORMMTKCITRIDEET doz z a
	1	1 '	TOTAL QUENTALIBEETGFOTPTPMDDICUCCTET MOTOR AND
ł	1	1.*	THE VOLUME TO STAND THE CARACTERIZET ON CARROTTE AND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE
į	1	) n	TAATAVSGIIADLDTTIMFATAGTLNABNSETFADHRENILKTA
1	1	i r	CALVEDTKLLVSGAASTEDVI ACAROGET FADHRENILKTA
ľ		ء ا	KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA
ſ	1		TOO DO TO A CONTRACT RESTRICT TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY
-	i	, -	QUACASTA VIIVINVISLLKTVKAVEDEA TRANSA TRANSA I
			TT TE SOLUTE PENTSSPEES I PMTVCTTMATTA VALVA A CONTRACTOR I
		——————————————————————————————————————	VIATANLSRKAVSDMLTACKQASFHPDVSDEVRTRALRFGTEC

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Į.	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
}	sequence	sequence	\=possible nucleotide insertion)
		<del> </del>	TLGYLDLLEHVLVILQKPTPELKQQLAAFSKRVAGAVTELIQAA
		[	EAMKGTEWVDPEDPTVIAETELLGAAASIEAAAKKLEQLKPRAK
	]		PKQADETLDFEEQILEAAKSIAAATSALVKSASAAQRELVAQGK
1			VGSIPANAADDGQWSQGLISAARMVAAATSSLCEAANASVQGHA
1	1	1	SEEKLISSAKQVAASTAQLLVACKVKADQDSEAMRRLQAAGNAV
1			KRASDNLVRAAQKAAFGKADDDDVVVKTKFVGGIAQIIAAQEEM
1	1	1	LKKERELEEARKKLAQIRQQQYKFLPTELREDEG
6030	3	1777	FPGRGSPALQLEVLICLGLMGLERALNVLAPIFYRNIVNLLTEN
İ			APWNSLAWTVTSYVFLKFLQGGGTGSTGFVSNLRTFLWIRVQQF
	}		TSRRVELLIFSHLHELSLRWHLGRRTGEVLRIADRGTSSVTGLL
ł	ì	1	SYLVFNVIPTLADIIIGIIYFSMFFNAWFGLIVFLCMSLYLTLT
			IVVTEWRTKFRRAMNTQENATRARAVDSLLNFETVKYYNAESYE
1			VERYREALIKYQGLEWKSSASLVLLNQTQNLVIGLGLLAGSLLC
ľ			AYFVTEQKLQVGDYVLFGTYIIQLYMPLNWFGTYYRMIOTNFID
		1	MENMFDLLKK\ETEVKDLPGAGPFRFQKGRIEFENVHFSYADGR
	1		ETLQDVSFTVMPGQTLALVGPSGAGKSTILRLLFRFYDISSGCI
		<u> </u>	RIDGQDISQVTQALFRFSHWELCPKDTVLFNDTIADNIRYGRVT
· l	1		AGNDEVEAAAQAAGIHDAIMAFPEGYRTQVGERGLKLSGGEKQR
İ			VAIARTILKAPGIILLDEATSALDTSNERAIQASLAKVCANRTT
			IVVAHRLSTVVNADQILVIKDGCIVERGRHEALLSRGGVYADMW
6031	1.60		QLQQGQEETSEDTKPQTMER
0031	160	1694	LRMSENLDKSNVNEAGKSKSNDSEEGLEDAVEGADEALQKAIKS
1			DSSSPQRVQRPHSSPPRFVTVEELLETARGVTNMALAHEIVVNG
1			DFQIKPVELPENSLKKRVKEIVHKAFWDCLSVQLSEDPPAYDHA
	]		IKLVGEIKETLLSFLLPGHTRLRNQITEVLDLDLIKQEAENGAL
1			DISKLAEFIIGMMGTLCAPARDEBVKKLKDIKEIVPLFREIFSV
	•		LDLMKVDMANFAISSIRPHLMQQSVEYERKKFQEILERQPNSLD FVTQWLEEASEDLMTQKYKHALPVGGMAAGSGDMPRLSPVAVQN
1			YAYLKLLKWDHLQRPFPETVLMDQSRFHELQLQ\REQLTILGAV
1	•		LLVTFSMAAPGISSQADFAEKLKMIVKILLTDMHLPSPHLKDVL
1			TTIGEKVCLEVSSCLSLCGSSPFTTDKETVLKGQIQAVASPDDP
j			IRRIMESRILTFLETYLASGHQKPLPTVPGGLSPVQRELEEVAI
			KFARLVNYNKMVFCPYYDAILSKILVRS
6032	39	2415	AARLCRAQPTKSAWMIRDLSKMYPQTRHPAPHQPAQPFKFTISE
			SCDRIKEEFQFLQAQYHSLKLECEKLASEKTEMQRHYVMYYEMS
			YGLNIEMHKQAEIVKRLNAICAQVIPFLSQEHQQQVVQAVERAK
			QVTMAELNAIIGQQQLQAQHLSHGHGLPVPLTPHPSGLOPPAIP
		,	PIGSSAGLLALSSALGGQSHLPIKDEKKHHDNDHQRDRDSIKSS
1		ļ ,	SVSPSASFRGAEKHRNSADYSSESKKQKTEEKEIAARYDSDGEK
1			SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP
			ASIASSSSTPSSKSKELSLNEKSTTPVSKSNTPTPRTDAPTPGS
			NSTPGLRPVPGKPPGVDPLASSLRTPMAVPCPYPTPFGIVPHAG
1			MNGELTSPGAAYAGLHNISPQMSAAAAAAAAAAAYGRSPVVGFD
			PHHHMRVPAIPPNLTGIPGGKPAYSFHVSADGQMQPVPFPPDAL
1			IGPGIPRHARQINTLNHGEVVCAVTISNPTRHVYTGGKGCVKVW
1	ļ		DISHPGNKSPVSQLDCLNRDNYIRSCRLLPDGRTLIVGGEASTL
		i	SIWDLAAPTPRIKAELTSSAPACYALAISPDSKVCFSCCSDGNI
	ĺ	,	AVWDLHNQTLVRQFQGHTDGASCIDISNDGTKLWTGGLDNTVRS
]			W\DLREGRQLQQHD/FFTSPVFSLGYCP\TEEWLAVGMENSN\V
]			EVLHVTKPDKYQLHLHESCVLSLKFAHCGKWF\VSTGKDNLLNA
			W\RTPYG\ASIF\QSKESSS\VLSCDI\SVDDKYIVTGS\GDK\ RATVYEVIY
6033	39	2415	AARLCRAQPTKSAWMIRDLSKMYPQTRHPAPHQFAQPFKFTISE
		CIFS	
j l			SCDRIKEEFQFLQAQYHSLKLECEKLASEKTEMQRHYVMYYEMS YGLNIEMHKQAEIVKRLNAICAQVIPFLSQEHQQQVVQAVERAK
] [		ĺ	QVTMAELNAIIGQQQLQAQHLSHGHGLPVPLTPHPSGLOPPAIP
1			PIGSSAGLLALSSALGGQSHLPIKDEKKHHDNDHQRDRDSIKSS
ļ l			SVSPSASFRGAEKHRNSADYSSESKKQKTEEKZIAARYDSDGEK
			SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP
			ASIASSSSTPSSKSKELSLNEKSTTPVSKSNTPTPRTDAPTPGS
			NSTPGLRPVPGKPPGVDPLASSLRTPMAVPCPYPTPFGIVPHAG
		·	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s

ſ	SEQ	Predicted	Predicted end	1 Amin
. 1	ID	beginning	nucleotide	
1	NO:	nucleotide	location	( ''' ALANAME, CECVSEEINE DENonameia xeis a
- 1		location	corresponding	Officiality Acid, Febbenylalanine C_Classic
		corresponding	to first	1 "-nistiding, l=180(eucine K-lucine
- 1		to first		Lateucine, Mamethionine Nagaragine
1		amino acid	amino acid	F=FFOilne, U=Glutamine R-Argining
		residue of	residue of	S=Serine, T=Threonine, V=V=line
- 1		amino acid	amino acid	W=Tryptophan, Y=Tyrosine Y-inknown + at-
			sequence	Codon, /=possible nucleotide deletion,
-		sequence	_}	\=possible nucleotide insertion)
				MNGELTSPGAAYAGLHNISPQMSAAAAAAAAAAYGRSPVVGFD
		i		PHILIMPUPA TOPMI MOTTOGENES PONSAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
- 1			ĺ	PHHIMRVPAIPPNLTGIPGGKPAYSFHVSADGQMQPVPFPPDAL
			İ	IGPGIPRHARQINTLNHGEVVCAVTISNPTRHVYTGGKGCVKVW
		ļ		DEBREGNASEVSQLDCLNRDNYTRSCRIADDCDTT.TVCCRA.cm
- [		i	}	STWDDAMPIPKIKAELTSSAPACYALATSDDSVICESCOOD ONE
- }		]	Ī	AVAIDANQTEVROFOGHTDGASCIDISNDGTET WEGGI DAWEN O
ì				W VDDREGROLOOHD/FFTSDVFSLGVCD/ TERMIT ALCOHOLOOL
		ĺ	]	EVERVIKEDRYQLHLHESCVISLKFAHCGKUR\ VERGVENT
- 1		1	J	W\RTPYG\ASIF\QSKESSS\VLSCDI\SVDDKYIVTGS\GDK\
<u> </u>	6034			RATVYEVIY
- 1	6034	2683	714	ESGRRRLKRRRSPCPGTAGGPGETNPGPGACPRGPREEAAAAM
				ETAPOFA PROPERTIES DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DEL CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DEL CONTRA DE LA CONTRA DE LA CONTRA DEL CONTRA DE LA NTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA C
				EIAPQEAPPVPGADGDIEEAPAEAGSPSPASPPADGRLKAAAKR VTEPSPEDINGSWEDVER
				VTFPSDEDIVSGAVEPKDPWRHAQNVTVDEVIGAYKQACQKLNC
J	- 1	1		I AVIENDUKULUEFIDLGHRI DCI DI KCEKI DVVVODA I DDI IIIII
	ı			1 DOF AV VOLCOTALDEDGASAL FOMTEVVECARGITAT ANTERNAL
-1	- 1			T MONOMENT MARKETS CLOYI I DARN'TOT, DUCA DEGRADA TO THE
				THE DEMASTS GRAPHITLATALKMNINT DETAIL A DATE TO SEE
-		İ		DOAQUONILLA INCSLOI LOT RNNHVI.DSGI.AVI CEGI VOODVO-
-	- 1			VID VUMINULTHIGMAFI GMTI DUTOCI ETI XI CIDID YOUR CONTROL
- 1	- 1	1		I TOTAL CONTROL OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERT
-				DOKENETATGGLMALSLALKVNHST.T.PT.DT.DDEDVVEAVVCDID
- 1	J.			1 2 ALLIAE LUNGUKRNI VLARERERKEODDOI CACMDERON TOTAL
	1	,		VPDDEPAAGVQNGAPSPAPSPDSDSDSDSDSDGPPPPPPPPPPPPPPPPPPP
				1 FOGATOTROTGSSEPOPPPEPPRSGDDT.DNGT.VDPDATATORNO (
1-	-			PPGPEVKGGSCGLEHELSCSKNEKELEELLLEASQESGQETL
	6035	19	404	SVTYLGIILHKNTGALPADPVQLISQTPTPSTKQQLLSFLGMVG
	ı	I		YEALMIDGES IT TANK ON THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE
L				YFYLWIPGFAILTKPLCKLTKENLADAIDPKSFSHSSFRSLKTA
	6036	1745	356	LENASTLALPDSSQPF\SLHTAEVQGCVVEILTQGLGPLPV
ı	- 1	i	220	LPDVEKLGRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLQRN
1				I DRUGGERGVERPPHLAALILARGGSKGTDT.ENTERT AGENT TOTAL
1	İ			VDICAMEDSUMFUSVWVSTDHDETENVAKORCAOMINDOGRESSES
	- 1	1		COLOURITE TONIHNE VOIVGNIOATS DCI. HDTDI OKUR DATE
1		i		DDG:D3VF3VVKKHOFRWSETOKGVPEVFEDINI NDAVDDDDOD
1	ļ	1		I WOULD LENGS FIRAKRHILL EMGYLOGGKMAVVENDARIOUS TOTAL
1	. 1	ŀ	i	DIDATIACURVIRIGIEGKEKLKETKI.INONTOCCI TMOTITICE I
1	ł			GDQREIISIDVKDAIGISLIKKSGTFVDI.TCPDACCVORT COT
ļ	i		ı	EDCAME VS VSDKLAV VDEWRKEMGI, CWKENA VI CATERIOD DOCUMENTS
1	İ			RIGISOMPADACSTAUKAVGYICKCNGGDGA \ TDDDADITEA \
<del>ا</del> ــــــ	037			MEKGLINFMPKNRNLAVNIGEKK
١ ١	037	2936	1919	WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA
	- 1	ľ		GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAPALSSRDSRFRDR
1		i	1	SFSEGGERI LUTOVORCOCOURTGERANDE PAPALSSRDSRFRDR
		i	1	SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG
[	i	i		DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI
	J	f	f	HNAEERRALAGARDLSADRPRLQHSFSFAGFPSAAATAAATGLL
ŀ	į		ŀ	DSPTSITPPPILSADDLLGSPTLPDGTNNPF\AFSSQELASLFA
ŀ		1		FEMOLIPGICS PITTLIFR PMSESPHMFDS PPS PODE COLOR OF STATE OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF TH
6	038	1450	426	55555H5G5DSPTLDNSRRLPIFSRLSTSDD
	- 1		426	SSALQEFGTRNHTFGVPLPHRRKQIISCNICQLRFNSDSQAAAH
	İ	ı	1	1 NO 1 NOAKKUKALEAMKNKOKSVTAKNE A KOOPPOCTOON TO THE TANKE
	[	- 1	1	SURIDGIAGIPAISTTTTVEIRKSSUMTTETTCVITTVODORT TO
	- 1	1	j	NSSCPSTETEEBKAKRLL\YCSLCKVAVNSASQLEAHNSGTKHK
	1	]		TMLEARNGSGTI KAFPRAGVKGKGPVNKGNTGLQNKTFHCEICD
	1	j	ı	VHVNSETOLKOHISSPRHKDRAACKDAKOKUTGEQNKTFHCEICD
	1	1	1	VHVNSETQLKQHISSRRHKDRAAGKPPKPKYSPYNKLQKTAHPL GVKLVFSKEPSKDLAPPILIPNDLAAAKPPKPKYSPYNKLQKTAHPL
			ĺ	GVKLVFSKEPSKPLAPRILPNPLAAAAAAAAVAVSSPFSLRTAP
61	039	4073	1000	AATLFQTSALPPALLRPAPGPIRTAHTPVLFAPY
	- 1	J	4 '	LDEYEARLTLANLDDFEEDNEDDDENRVNQEEKAAKITELINKL
			1.	NE DDEAEADLATVNSNPFDDPDAAELNPFGDPDGFFPTTPTTA CD
	,		1.4	RATEDSFINNSYNPFKEVOTPOYINPFDEDEAEVELVDSDDOG
	1	1		
	1		1 .	NAMI RPVDMSKYLYADSSKTEEEEI DESNDEVEDVOTDDDDD
			1 .	KXKNIRPVDMSKYLYADSSKTEEEELDESNPFYEPKSTPPPNNL VNPVQELETERRVKRKAPAPPVLSPKTGVLNENIVSAGKDLSTS

SEO	Predicted	Drodieted and	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +-C+on
1	amino acid	sequence	Codon, /=possible nucleotide deletion
<u> </u>	sequence		\=possible nucleotide insertion)
ı			PKPSPIPSPVLGRKPNASQSLLVWCKEVTKNYRGVKITNFTTSW
ļ			RNGLSFCAILHHFRPDLIDYKSLNPODIKENNKKAYDGEASTGI
	1	1	SRLLEPSDMVLLAIPDKLTVMTYLYQIRAHFSGQELNVVQIEEN
			SSKSTYKVGNYETDTNSSVDQEKFYAELSDLKREPELQQPISGA
Ì			VDFLSQDDSVFVNDSGVGESESEHQTPDDHLSPSTASPYCRRTK
		İ	SDTEPQKSQQSSGRTSGSDDPGICSNTDSTQAQVLLGKKRLLKA ETLELSDLYVSDKKKDMSPPFICEETDEQKLQTLDIGSNLEKEK
		İ	LENSRSLECRSDPESPIKKTSLSPTSKLGYSYSRDLDLAKKKHA
			SLRQTESDPDADRTTLNHADHSSKIVQHRLLSRQEELKERARVL
1			LEQARRDAALKAGNKHNTNTAAPFCNRQLSDQQDEERRRQLRER
ſ			ARQLIAEARSGGKMSELPSYGERAAEKLKERSKASGDENDNIET
ł			DINEEIPEGFVVGGGDELTNLENDLDTPEONSKLVDI.KI.KKI.I.R
			VQPQVANSPSSAAQKAVTESSEQDMKSGTEDLRTERLOKTTERE
ļ			RNPVVFSKDSTVRKTQLQSFSQYIENRPEMKRORSIOEDTKKGN
1	}		EEKAAITETQRKPSEDEVLNKGFKDS\SQYVVGELAALENEQKQ
Į			IDTRAALVEKRLRYLMDTGRNTEEEEAMMQEWFMLVNKKNALIR
j	]		RMNQLSLLEKEHDLERRYELLNRELRAMLAIEDWOKTEAOKRRE QLLLDE_VALVNKRDALVRDI.DAQEKQAEEEDEHLERTLEQNKG
			KMAKKEEKCVLQ
6040	475	1052	PTALMTAPSCAFPVQFRQPSVSGLSQITKSLYISNGVAANNKLM
1	i		LSSNQITMVINVSVEVVNTLYEDIQYMQVPVADSPNSRLCDFFD
1	1		PIADHIHSVEMKQGR\TLLHCAAGVSRSAALCLAYLMKYHAMST.
1			LDARTWTKSCRPIIRPNSGFWEQLIHYEFQLFGKNTVHMVSSPV
6041	2	2006	GMIPDIYEKEVRLMIPL
] ""	'	3886	TEKDEKTAHNLENVLIHFWERLSEICVAKISEPEADVESVLGVS
			NLLCVLQKPKGSLKSSKKKNGKVRFADEILESNKENEKCVSSEG
1			EKIECWELTTEPSLTHNSSGLLSPLRKKPLEDLVCKLADISINY
Į.			VNERKSEQHLRFLSTLLDSFSSSRVFKMLLGDEKQSIVQAKPLE
ļ	!		IAKLVQKNPAVQFLYQKLIGWLNEDQRKDFGFLVDILYSALRCC DNDMERKKVLDDLTKVDLKWNSLLKIIEKACPSSDKHALVTPWL
			KGDILGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ
1 1			HVKNDYLIGDVYVERIIVRLHETLFKTKKLSEAESSDSSVSFIC
1			DVAYNYFSSAKGCLLMPSSEDLLLTLFOLCAOSKEKTHI.PDFI.7
1 1			CKLKNTWLSGVNLLVHQTDSSYKESTFLHLSALWLKNOVOASSI
1			DINSLOVLLSAVDDLLNTLLESEDSYLMCVYTGSVMPNDSEWER
	ļ		MRQSLPMQWLHRPLLEGRLSLNYECFKTDFKEODIKTI.PSHI.CT
1			SALLSKMVLIALRKETVLENNELEKIIAELLYSLQWCEELDNPP
1 1			IFLIGFCEILQKMNITYDNLRVLGNMSGLLQLLFNRSREHGTLW
1 1			SLIIAKLILSRSISSDEVKPHYKRKESFFPLTEGNLHTIQSLCP FLSKEEKKEFSAQCIPALLGWTKKDLCSTNGGFGHLAIFNSCLQ
1 1			TKSIDDGELLHGILKIIISWKKEHEDIFLFSCNLSEASPEVLGV
]			NIEIIRFLSLFLKYCSSPLAESEWDFIMCSMLAWLETTSENQAL
1 1			YSIPLVQLFACVSCDLACDLSAFFDSTTI.DTTCNT.PVNT.TCFWZ
] }			EFFSQGIHSLLLPILVTVTGENKDVSETSFONAMIKPMCETTTY
i I	İ		ISKEQLLSHKLPARLVADOKTNLPEYLOTLLNTLAPLLLEDARD
] }			VQIAVYHMLYKLMPELPQYDQDNLKSYGDEEEEPALSPPAALMS
1			LISIQEDLLENVLGCIPVGQIVTIKPLSEDFCYVLGYLLTWKLI
		. !	LTFFKAASSQLRALYSMYLRKTKSLNKLLYHLFRLMPENPTYAB
l i		ſ	TAVEVPNKDPKTFFTEELQLSIRETTMLPYHIPHLACSVYHMTL KDLPAMVRLWWNSSEKRVFNIVDRFTSKYVSSVLSFQEISSVQT
[	ł	1	STQLFNGMTVKARATTREVMATYTIEDIVIELIIQLPSNYPLGS
		İ	IIVESGKRVGVAVQQWRNWMLQLSTYLTHQNGSIMEGLALWKWN
		ļ	VDKRFEGVEDCMICFSVIHGFNYSLPKKACRTCKKKFHSA\CLY
			KWFTSSNKSTCSLCRETFF
6042	1306	253	MAELAPASPSDIKASVSNGDTTLLCSRROSCGMNEVROVSLTVD
1		1	GSPAPSHSLPLQPRSGGSLCPSRAW/PDPHOLFDDTSSAOSPGV
		J	GAQRAPGGLSYPAASPTPHAAFLADPVSNMAMAYGSSLAAGGER
			LVDKNIDRFIPITKLKYYFAVDTMYVGRKLGLLFFPYLHODWEV
ĺ			QYQQDTPVAPRFDVNAPDLYIPAMAFITYVLVAGLALGTODRFS
	1	1	PDLLGLQASSALAWLTLEVLAILLSLYLVTVNTDLTTIDI.VARI.
	···	<u>_</u>	GYKYVGMIGGVLMGLLFGKIGYYLVLGWCCVAIFVFMIRTLRLK

SEQ	Predicted	Dwodiebed	
ID	beginning	Predicted end	
NO:	nucleotide	nucleotide location	I MERITALIS, CECVETEINA DENSANDE NELL NELL NELL
	location		1 didcamic Acid, Febhenvialaning C-Cl.
	corresponding	corresponding	1 """ TELECTOTIE, I=ISOIEUCIDE V"I'"
1	to first	to first	L=beucine, M=Methionine N=Acronsories
i	amino acid	amino acid	F=Froline, O=Glutamine p-Arginine
	residue of	residue of	S=Serine, T=Threonine, V-Valine
1		amino acid	W=Tryptophan, Y=Tvrosine Y-Unknown to
ł	amino acid	sequence	Coupir, /=possible nucleotide deletion
<del></del>	sequence		\=possible nucleotide insertion\
			ILADAAAEGVPVRGARNQLRMYLTMAVAAAQPMLMYWLTFHLVR
6043	403	599	LCLFFFFPCATPVLPLPSLISAL/CLSHLSVSSWFCPCQPPLPC
			PLPPLONKTAKGSLSTEQSERG
6044	793	412	KLEMWNFTLISKVKISREVTMIASKFGIGQQVRHSLLGYLGVVV
1	j	1	DIDPVYSLSEPSPDELAVNDELRAAPWYHVVMEDDNGLPVHTYL
	1	1	AEAQLSSELQDEHP\EQPSMDELAQTIRKQLQAPRLRN
6045	155	2299	SPI. DOVA AMBLY DODA OPENDELAQTIRKQLQAPRLRN
			SPLPQVAAMNYLRRRLSDSNFMANLPNGYMTDLQRPQPPPPPPG AHSPGATEGORIAN
ŀ			AMSSGATEGEGTATAERSSGVAPAASPAAPGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
J			SNAVRQI TAAAAATESEOVGGGGGGGGGGGGGGGAGGGGTTTTTDEDTTE
	}		DWARTERGAKTHGEIDIKVEOAFFSDININADANGGBGUDADA
			ANGVAVVRSLAPDEVLIROHAFSMARNGDVPSLVTGIOVAGERO
1	1		VISUASVINF CDKPWVFAOMVRIHKKT GTFFFFF TDOTEVDAVAS
	<u> </u>		EMISS LITTLY VVKMGHGTLWGWGK7K7/DNOUDEOD TA GIRLA CO
	1		TATABET LUAKTUVRVOKIGONYKAYMRTSUSCHURTHTOCA
1	1		MILECIA SORIKLWYDTCSEIFGGI.DICAVEALUCYDCDULLTD
- (	i I		I VVGSS.MPLIGDHQDEDKOLIVELVVVKMAQALDBORODDA CDGD
			1 GONGGI FOFGALFLUKOTSOODAGDDAOODDDDOOGDDOOGDDO
	ļ		ArgateriggReffeeGOOHLSGLGPPACSDLDOpt.Bcpmcapoon
			I TO ATTURE I AGORNOSK BANGTOLODO VALUE I
	,		ATRYTOVOGPAPPKASGAPPGGOOROGDDOKDDGDACDTDOACO
1 1			AGPPPRTGPPTTQQPRPSGPGPAGRPKPQLAQKPSQDVPPPATA
1 1	]		AAGGPPHPQLNKSQSLTNAFNLPEPAPPRPSLSQDEVKAETIRS
J			I THURSTAGUESU
6046	212	1075	EGLTGPCERVPFLLGRGPPHGATRAGHRAVRWAGPESLPPLPR
1	ļ		SLIMDSPRAGTHQGPLDAETEVGADRCTSTAYQEQRPQVEQVGK
i	j		OAPLS PGI PAMGGPGPGPGPGPDPAGA GG
} }			QAPLS PGLPAMGGPGPGPCEDPAGAGGAGAGGSEPLVTVTVQCA
1 1	1		FTVALRARGADLSSLRALLGQALPHQ\AQLGQLSYLAPGEDGH
]			WVPIPEESLQRAWQDAAACPRGLQLQCRGAGGRPVLYQVVAQH
L 1			SYSAQGPEDLGFRQGDTVDVLCEVDQAWLEGHCDGRIGIFPKCF VVPAGPRMSGAPGRLPRSQQGDQP
6047	49	1405	DULUGGI DMD DA DMI DOM
1			PVLVTSLRMREADTLRPPQLMEVSADIISTVEFNHTGELLATGD
]		ł	KGGRVVIFQREPESKNAPHSQGEYDVYSTFQSHEPEFDYLKSLE
1 1	1	1	IEEKINKIKWLPQQNAAHSLLSTNDKTIKLWKITERDKRPEGYN
1	ľ		TRUBEGREEN TENTOUR TO THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROT
	ļ		THO IS AN SUCCE TIME ADD LICENTARY TO THE TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL
1 1		}	MIEDELEVITASEPHPHHCNI, FVVSSSKCSI, DI COMPA DE COMP
i l	i		MONDE DEPENDED NKSFFSEIIS \ SVSDVKFSUGDDVMT 700\ Diet
·		·	TVAVWDD \NMCARPIETYOVHDYLRSKI.CGI.VENDCTEDVERGA
1 1	}		MAGSDS VIMIGA VINNEFRMEDRNTKRDUTI VENCRECKREALL
1	1		DEPER VC VGGKRKRDDISVDSLDFTKKTI, HTAWHDAENTTATAA
6048	1		IMMLITEODKANSDWH
1	_ [	3134	GIRTPKFCDSPTSDLEMRNGRGRGKRMRPNSNTPVNETATASDS
		1	AGISHOSAI RAGANSKGRRGSONSSEHR PPAGGTGERNTVAGRGG
1 1	i		ANARAM RELIGIONE LINESSEDSKOSKRVPTNOMOGA TODI DOMICI.
, ,		3	PET VEDRICES PVLIDCPH PNCMKKVKUTNCT VVIIO ATTAINED 1
	ſ	Į.	SAPEADGUSEYGEEPILHADI.GSCNG\ ASVCOV\ GGI GDADGA
1 /	1		PROKE VEPHSPSPSSKFSTKGLCKKKL.CCECDEDLCAL OVERSE
		1 .	DGPS VMDE I SNUAFDSLERKCMEKEKCKKDCGI VDEVIDAVA
	1		OAKEI/AFUAIPPOOIYTEOTATETAASDGGGGGGT TATURAANIA
1		1 -	NOTODATIQUE TO MGEPFT VNDATATO A KOKKKY KOKKKY KOKKOKKO
1	1	1 -	DESPET PGRVCRAEEGKSPFRESSGNGMKMEGT I NGCCDDUGGD
į l	ļ	1 -	LAST CALADKI YS FTDNAPSPSTECCCOL ENTERNOOD TOOL TOOL
1			QUGARASSVKINSPAYSDISDAGEDGEGKUDGUKEVDA FOT THE
	j	1	EGAKKTLFPPQPQSKDSPYYQGFESYYSPSYAQSSPGALNPSSQ
j	1	1 2	AGVESQALKTKRDEEPESIEGKVKNDICEEKKPELSSSSQQPSV
		13	TOORPNMYMOST VYNOVAVVERVOUS CONTROL OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE S
1		1	CORPRMYMQSLYYNQYAYVPPYGYSDQSYHTHLLSTNTAYRQQ
1		1	CEQQKRQSLEQQQRGVDKKAEMGLKEREAALKEEWKQKPSIPP
1		1 2	TLTKAPSLTDLVKSGPGKAKEPGADPAKSVIIPKLDDSSKLPGQ
			APEGLKVKLSDASHLSKEASEAKTGAECGRQAEMDPILWYRQEA
			PRMWTYVYPAKYSDIKSEDERWKEERDRKLKEERSRSKDSVPK

SEQ	Predicted	Drodies	
ID	beginning	Predicted end	
NO:	nucleotide	nucleotide	M=Alanine, C=CVsteine, N=Assertic Asia =
	location	location	Glutamic Acid, F=Phenylalanine G-Glucino
j	corresponding	corresponding	H=H1Stldine, I=Isoleucine, K=Tyeine
İ	to first	to first	L=Leucine, M=Methionine, N=Asparagine
	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine
İ	residue of	residue of	S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion
<del></del>	bequence	<u> </u>	\=possible nucleotide insertion)
}	+		EDGKESTSSDCKLPTSEESRLGSKEPRPSVHVPVSSPLTQHQSY
1	1	ł	1 PYMHGYSYSQSYDPNHPSYRSMPAVMMONYPGSYLDGGYGGG
			YGSKVSGGEDADKARASPSVTCKSSSESKALDTLOOMSCHUNGK
•			SPITSDKTSOERDRGGCGVVGGGGGCSCSSVGGAGGGDGVDDDDD
	[		SPSQRLMSTHHHHHHLGYSLLPAQYNLPYAAGLSSTAIVASOOG
6049	215		STPSLYPPPRR
1 0043	215	1089	AMTGVFDRRVPSIRSGDFQAPFQTSAAMHHPSQESPTLPESSAT
1			DSDYYSPTGGAPHGYCSPTSASYG\KALNPYOYOYHGYMGSACS
1	•		YPAKAYADYSYASSYHQYGGAYNRVPSATNOPEKEVTEDENDMY
			NGKPKKVRKPRTIYSSFQLAALQRRFOKTQYLALPFPAFLAget.
	ļ		GLTQTQVKIWFQNKRSKIKKIMKNGEMPPEHSPSSSDPMACNED
1	ì		QSPAVWEPQGSSRSLSHHPHAHPPTSNOSPASSVI.FNSASWYTC
5050			AASSINSHLPPPGSLQHPLALASGTLY
6050	566	1718	KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWYL
į			PNTAMKKKVLLMGKSGSGKTSMRSIIFANYTARDTPRICATTID
ĺ	1		RIHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVRFLGNIAU NIK
	1 i		DCGGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESRELEKDMUV
	]		YOSCLEAILQNSPDAKIFCLVHKMDLVOEDORDI.TEKERERII D
	1		RESEPTECS CERTS I WDETLY KAWSSIVYOLT PNYCOT PMNT DN
	j		FAETTEADEVLLFERATFLVISHYOCKEORDAHREEKTSMITKO
1			FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTVAMAAMEDDOT
6051			PSAATLINIRNARKHFEKLERVDGPKOCLLMR
6021	566	1718	KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWUL
1			PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRDIGATILD
			RIHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVPFT.CNI.VI.MI.W
			DCGGQDTFMENYFTSQRDNIFRNVEVLTVVFDVFSDFT.FVDMUV
-			1 YQSCLEAILQNSPDAKIFCLVHKMDLVOEDORDI.TEKERERDI.D
[ ]	1		RESEPTECSCERTSINDETLYKAWSSIVYOLIPMYOOLEMNIDM
1			FAETLEADEVLLFERATFLVISHYOCKEORDAHRERKISMITEO
			FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTVVMVAMSDDET
			PSAATLINIRNARKHFEKLERVDGPKQCLLMR
6052	566	1718	KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEDGVGSI CWV
1 1	}		PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRRLGATILD
1			RIHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVPFLCNLVLNLU
1 1	Į.		DCGGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESRELEKDMHY
1			YQSCLEAILQNSPDAKIFCLVHKMDLVOEDORDIJEREPERDIR
			RLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQQLEMNLRN
1	ļ		FAEIIEADEVLLFERATFLVISHYQCKEQRDAHRFEKISNIIKQ
1 1	(		FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVMSDPSI
			PSAATLINIRNARKHFEKLERVDGPKQCLLMR
6053	201	1704	KGTEMNKSRWQSRRRHGRRSHQQNPWFRLRDSEDRSDSRAAQPA
	I		HDSGHGDDESPSTSSGTAGTSSVPELPGFYFDPEKKRYFRLLPG
	1		HNNCNPLTKESIRQKEMESKRLRLLQEEDRRKKIARMGFNASSM
1 1	1		LRKSQLGFLNVTNYCHLAHELRLSCMERKKVQIRSMDPSALASD
1 1	· [		RFNLILADTNSDRLFTVNDVTVGGSKYGIINLQSLKTPTLKVFM
1 1	1		HENLYFTNRKV\NSVCWASLNHLDSHILLCLMGLAETPGCATLL
1			PASLFVNSHPAGIDRPG\MLCSFRIPGANSCAWSLNIQANNCFS
1 1	1		TGLSRRVLLTNVVTGHRQSFGTNSDVLAQQFALMAPLLFNGCRS
J i	j		GEIFAIDLRCGNQGKGWKATRLFHDSAVTSVRILQDEQYLMASD
1 1	1	I	MAGKIKLWDLRTTKCVRQYEGHVNEYAYLPLHVHEEEGILVAVG
1			QDCYTRIWSLHDARLLRTIPSPYPASKADIPSVAFSSRLGGSRG
	1	İ	APGLLMAVGQDLYCYSYS
6054	1	1054	P?IARLQEFGTSRRHMAAPSGVHLLVRRGSHRIFSSPLNHIYLH
1	Í		KOCCCOORDINEEEDDODDECTOR TO THE TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTA
] [	J		KQSSSQQRRNFFFRRQRDISHSIVLPAAVSSAHPVPKHIKKPDY
į (	1	Í	VTTGIVPDWGDSIEVKNEDQIQGLHQACQLARHVLLLAGKSLKV
j	į		DMTTEEIDALVHREIISHNAYPSPLGYGGFPKSVCTSVNNVLCH
	ł		GIPDSRPLQDGDIINIDVTVYYNGYHGDTSETFLVGNVDECGKK
}		J	LVEVARRCRDEAIAACRAGAPFSVIGNTISHITHQNGFQVCPHF
	}		VGHGIGSYFHGHPEIWHHANDSDLPMEEGMAFTIEPIITEGSPE
		l	FKVLEDAWTVVSLD/TSKVSAQFEHTVLITSRGAQILTKLPHEA

SEO	Predicted						
ID	beginning	Predicted end					
NO:	nucleotide	nucleotide	( A-Alguille, CECVSCEINE D-Acabasia alia a				
1.0.	location	location	Gracamic Acid, Febbenylelening C Glassia				
·	corresponding	corresponding	n=nistidine, l=Isoleucine V-lugine				
Į.	to first	to first	L=Leucine, M=Methionine, N-Aspassaine				
	amino acid	amino acid	Paproline, OsGlutamine, Reargining				
1		residue of	S=Serine, T=Threonine V-Valine				
- 1	residue of	amino acid	W=Tryptophan, Y=Tvrosine Y=Unknown + G=				
Í	amino acid	sequence	COGOII, /=DOSSIDIE NUCleotide doloriam				
	sequence		\=possible nucleotide insertion)				
6055	421	2364	PPYFLLSFLAWWLYGQSDRTETDISQSAGPPPGTLQCSALHHDP				
1	i	1	GCANCSRFCRDCSPPACQCHTHVFPGNALNGVQPPELSRTLALI				
ļ	1	1	SSREPPRKKKKSQTETGKERERTSFLTQGGKRFELQHGLAGICM				
- }	1	1	TLLITGDSIVSAEAVWDHVTMANRELAFKAGDVIKVLDASNKDW				
	1		WWGQIDDEEGNFPASFVRLWVNHEDEVEEGPSDVQNGHLDPNSD				
į			CLCLGRPLQNRDQMRANVINEIMSTERHYIKHLKDICEGYLKQC				
ĺ			RKRRDMFSDEQLKVIFGNIEDIYRFQMGFVRDLEKQYNNDDPHL				
l			SEIGPCFLEHQDGFWIYSEYCNNHLDACMELSKLMKDSRYQHFF				
1	į		EACRLLQQMIDIA\IDGFLLTPVQKICKYPLQLAELLKYTAQDH				
Į.	1		SDYRYVAAALAVMRNVTQQINERKRRLENIDKIAQWQASVLDWE				
i	[		GEDILDRSSELIYTGEMAWIYQP\YGRNQQRVFFLFDHQMVLCK				
			KDLIRRDILYYKGRIDMDKYEVVDIEDGRDDDFNVSMKNAFKLH				
	1		NKETEETHLEEAKKI EEKIDGU DASGARDDDFNVSMKNAFKLH				
1	1		NKETEEIHLFFAKKLEEKIRWLRAFREERKMVQEDEKIGFEISE				
L	<u>                                     </u>		NQKRQAAMTVRKVPKQKGVNSARSVPPSYPPPQDPLNHGQYLVP \DGIAQSQVFEFTEPKRSQSPFWQNFSRLTPFKK				
6056	43	3358	SGCPCPUPUPCEOLOPOAROUS				
	1		SGGRGPVRVRSEQLSPSAEQVSQISQISLGRRPLSSLPPPPSRA LAPTRAPDTALTIMEVAEVESPLNPSCKIMTFRPSMEEFREFNK				
1	1 1		YLAYMESKGAHRAGLAKVIPPKEWKPRQCYDDIDNLLIPAPIQQ				
1	J		MVTGQSGLFTQYNIQKKAMTVKEFRQLANSGKYCTPRYLDYEDL				
	<u> </u>		ERKYWKNLTFVAPIYGADINGSIYDEGVDEWNIARLNTVLDVVE				
1	1		EECGISIEGVNTPYLYFGMWKTTFAWHTEDMDLYSINYLHFGEP				
1	1		KSWYAIPPEHGKRLERLAQGFFPSSSQGCDAFLRHKMTLISPSV				
	! 1		LKKYGIPFDKITQEAGEFMITFPYGYHAGFNHGFNCAESTNFAT				
	l		VRWIDYGKVAKLCTCRKDMVKISMDIFVRKFQPDRYQLWKQGKD				
	<b>!</b>		IYTIDHTKPTPASTPEVKAWLQRRRKVRKASRSFQCARSTSKRP				
	1		KADEEEEVSDEVDGAEVPNPDSVTDDLKVSEKSEAAVKLRNTEA				
	l		SSEEESSASRMQVEQNLSDHIKLSGNSCLSTSVTEDIKTEDDKA				
	i		YAYRSVPSISSEADDSIPLSTGYEKPEKSDPSELSWPKSPESCS				
			SVAESNGVLTEGEESDVESHGNGLEPGEIPAVPSGERNSFKVPS				
			IAEGENKTSKSWRHPLSRPPARSPMTLVKQQAPSDEELPEVLSI				
1 1			EEEVEETESWAKPLIHLWQTKPPNFAAEQEYNATVARMKPHCAI				
			CTLLMPYHKPDSSNEENDARWETKLDEVVTSEGKTKPLIPEMCF				
i i			IYSEENIEYSPPNAFLEEDGTSLLISCAKCCVRVHASCYGIPSH				
	1		EICDGWLCARCKRNAWTAECCLCNLRGGALKQTKNNKWAHVMCA				
] !	1		VAVPEVRFTNVPERTQIDVGRIPLQRLKLKCIFCRHRVKRVSGA				
1 1	j		CIQCSYGRCPASFHVTCAHAAGVL\MEPDDWPYVVNITCFRHKV				
			MENVASAACEKVISVGOTVITKHRNTRYVSCOMMAUTEOGEWEY				
! !			MFDDGSFSRDTFPEDIVSRDCLKLGPPAFGFINOUVMPDGVI VO				
1 1	1		ALIPGSNIAHMYOVEFEDGSOIAMKREDIVTIDEELDEDIVADD				
1			VSAGRCHLGTCQVNSLSSPHVSQAQQETYLGFWINSKKSQCNIF				
6057			13611				
603/	1	853	FVARLKEQEGEGGLGPRKEKGRARGRERRRKMQLTRCCFVFLVQ				
] [			CODIDATE COODDOLLE CONTROLLE DATE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTROLLE DE LA CONTRO				
1	f	1	RPHANSTILGLEAPPGEAWGILGOPPNRPNHSDDDSAVIVVIEG				
1	!		WGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFOUNATCOONTA				
1 1		}	ISUVPPSKAVEFHOEOOIFIEAKASKIFNC\ DMEMBELLE\ DCDD				
1			15 I I I DPAKI CSRDHAOSSATWSCSOPFKING TV TARVETDUD				
6058			LVQKVCPDYNYHSDTPYYPSG				
6038	1	986	HPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLDKPPPAPVCGP				
1 1			SGUAASSI PPSTRFPGVAIYLVEPRMGRSRRAFI.TGT. A DEVGTO				
	İ	i	VUDACSSEATHVVMEETSAEEAVSWOERRMAAADDGCTDDALLD				
1 1		İ	ISWLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAWMPAYACQR				
1	1	1	PTPLTHHNTGLSEALEILAEAAGFEGSEGRLLTFCRAASVLKAL				
!	1		PSPVTTLSQLQGLPHFGEHSSRVVQELLEHGVCEEVERVRRSE/				
1	j	1	RLFTQ1FGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGEP				
6059			SREAGPWASLNCTLDPSASTP				
8609	2	3650	QQDFESLADLTDHRAHRCPGDGDDDPQLSWVASSPSSKDVASPT				
	1	J ,	QNIGDGCDLGLGEEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH				
		1:	SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS				
- 1	J	1 -	KSDHDKIHDKIHSSSKPFKCTVCKPCFSSTSSI OSUMONUVIDIR				
		1	EHLAKSEKEAKKDDFMCDYCEDTFSQTEELEKHVLTRHPQLSEK				
	-		THE THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE TENER TO THE THE TENER TO sponding   cofirst   sain acid   defined   cotation   corresponding   cofirst   sain acid   defined   cotation   corresponding   cofirst   sain acid   defined   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation   cotation	SEO	Predicted	Predicted end	Amino acid comest costsisis
--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------	----------	---------------	---------------	---------------------------------------------------			
No:leotide   Cortesponding to first amino acid residue of amino acid residue of amino acid sequence   Secrime, Manchionine, Nasparagine, Perpoine, Quitumine, Rarginine, Secrime, Territorine, Vevaline, amino acid sequence   Secrime, Territorine, Vevaline, Secrime, Territorine, Verylophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yerytophan, Yer	_	1		(A=Alanine C=Cysteine D=Aspartic Acid E=			
Continue				Glutamic Acid. F=Phenylalanine. G=Glycine			
Corresponding to first amino acid residue of amino acid residue of amino acid sequence   S-Serine, T-Threonine, V=Valine, S-Serine, T-Threonine, V=Valine, S-Serine, T-Threonine, V=Valine, S-Serine, T-Threonine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=V	1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,			
to first amino acid residue of amino acid residue of amino acid anino acid sequence  sequence  sequence  sequence  sequence  sequence  Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nuclectide deletion Codon, /=possible nuclectide deletion Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nuclectide deletion Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nuclectide dissertion Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Alterphophan, Y=Tyrosine, X=Unknown, *=Stop Alterphophan, Y=Tyrosine, X=Unknown, *=St	Ì	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,			
amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequen			amino acid	P=Proline, Q=Glutamine, R=Arginine,			
amino acid sequence  Codon, /-possible nucleotide deletion, /-possible nucleotide insertion  ADACCHICCEVFUDENTILIAHIRGAHANCHECRMCPE(OFSS /- NEGSTPDS:SHAVEY DENTILIAHIRGAHANCHECRMCPE(OFSS)  ARACYCHIDS:ROPDS:SHAVEY DEPUZ:SVARSASTPDS:SASY REGSTPDSTLKP:RGOKKMRDDGGWT:KVYSCPYCS:KRPDPS:SASY REGSTPDSTLKP:RGOKKMRDDGGWT:KVYSCPYCS:KRPDPS:SASY REGSTPDSTLKP:RGOKKMRDDGGWT:KVYSCPYCS:KRPDPS:SASY REGSTPDSTLKP:RGOKKMRDDGGWT:KVYSCPYCS:KRPDPS:SASY REGSTPDSTLKP:RGOKKMRDDGGWT:KVYSCPYCS:KRPDPS:SASY REGSTPDSTLKP:RGOKKMRDDGGWT:KVYSCPYCS:KRPDPS:SASY REGSTPDSTLKP:RGOKKMRDDGGWT:KVYSCPYCS:KRPDPS:SASY REGSTPDSTLKP:RGOKKMRDDGGWT:RSUSGHI:KVSHCGPNS:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGhi:KVSHCGPN:RSUSGhi:KVSHCGPN:RSUSGhi:KVSHCGPN:RSUSGhi:KVSHCGPN:RSusghi:KVSHCGPN:RSusghi:KVSHCGPN:RSusghi:KVShccanii:KVShccanii:KVShccanii:Kvshcgn:Rsusghi:Kvshcgn:Rsusghi:Kvshcgn:Rsusghi:Kvshcgn	İ			S=Serine, T=Threonine, V=Valine,			
amino acid sequence  Codon, /-possible nucleotide deletion, /-possible nucleotide insertion  ADACCHICCEVFUDENTILIAHIRGAHANCHECRMCPE(OFSS /- NEGSTPDS:SHAVEY DENTILIAHIRGAHANCHECRMCPE(OFSS)  ARACYCHIDS:ROPDS:SHAVEY DEPUZ:SVARSASTPDS:SASY REGSTPDSTLKP:RGOKKMRDDGGWT:KVYSCPYCS:KRPDPS:SASY REGSTPDSTLKP:RGOKKMRDDGGWT:KVYSCPYCS:KRPDPS:SASY REGSTPDSTLKP:RGOKKMRDDGGWT:KVYSCPYCS:KRPDPS:SASY REGSTPDSTLKP:RGOKKMRDDGGWT:KVYSCPYCS:KRPDPS:SASY REGSTPDSTLKP:RGOKKMRDDGGWT:KVYSCPYCS:KRPDPS:SASY REGSTPDSTLKP:RGOKKMRDDGGWT:KVYSCPYCS:KRPDPS:SASY REGSTPDSTLKP:RGOKKMRDDGGWT:KVYSCPYCS:KRPDPS:SASY REGSTPDSTLKP:RGOKKMRDDGGWT:RSUSGHI:KVSHCGPNS:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGHI:KVSHCGPN:RSUSGhi:KVSHCGPN:RSUSGhi:KVSHCGPN:RSUSGhi:KVSHCGPN:RSUSGhi:KVSHCGPN:RSusghi:KVSHCGPN:RSusghi:KVSHCGPN:RSusghi:KVShccanii:KVShccanii:KVShccanii:Kvshcgn:Rsusghi:Kvshcgn:Rsusghi:Kvshcgn:Rsusghi:Kvshcgn				W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop			
ADLICHIC PEVPURENTILIAHIHOAHANIQKHICKPROPE OF SASV \ \[ AGVYCHIOSINGED SIMHSY EDVILGYANABASTPOSSASY \ \text{BGSTDSTLKPLRGCKMRDDGGGMTKVYSCFYCSKRDFNSIL AVLEHIHATILARKQGSHTGCLIDSMTIJINGHTKYKLHKN \ \text{AALPEVAGPONISAFHCNYCDEMFADINSIGEHIKVSHGCPRANGY \ \text{BGSTDSTLKPLRGCKMRDDGGGMTKVYSCFYCSKRDFNSIL \ \text{AALPEVAGPONISAFHCNYCDEMFADINSIGEHIKVSHGCPRANGY \ \text{BGSTMSTSTLKPLTRHIKENIKNIPLARKGAT \ \text{BGSTMSTSTLKPLTRHIKENIKNIPLARKGAT \ \text{BGSTMSTSTLKPLTRHIKENIKNIPLARKGAT \ \text{BGSTMSTSTLKPLTRHIKENIKNIPLARKGAT \ \text{BGSTMSTSTLKPLTRHIKENIKNIPLARKGAT \ \text{BGSTMSTSTLKPLTRHIKENIKNIPLARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGSTMSTARKGAT \ \text{BGST			sequence	Codon, /=possible nucleotide deletion,			
AGOVECHOSHROPDSSHHSVSTPDVILGSVASMASATTPDSSAFE   ERGSTPDSTLENERGCKEMENDOGGMYKUVYSCYCSKRDFNSL   AVLEHHLKTHIADKPQGSHTCQICLDSMFTLYNLINGHVRKLING   AVLEHHLKTHIADKPQGSHTCQICLDSMFTLYNLINGHVRKLINGH   HAYPVMGFORIASAFCHNYCEMEADINSLGGHIKVSHCGPNANF   SDGNNAFFCNCCSMGFLTESSLTEHIQQQAHCSVGSKALLESPV   VOPTOSFMEVYSCYCTISSIFICSILLITHIKUSHCGPNANF   SDGNNAFFCNCCSMGFLTESSLTEHIQQQAHCSVGSCALLESPV   VOPTOSFMEVYSCYCTISSIFICSILLITHIKUSHCGPNANF   SDGNNAFFCNCCSMGFLTESSLTEHIQQQAHCSVGSCALLESPV   VOPTOSFMEVYSCYCTISSIFICSILLITHIKUSHCGPNANF   SKKARAGSFVSSDVEVSSPRGRLSASANSISNGEVPCNCCOLL   KKSARAGSFVSSDVEVSSPRGRLSASANSISNGEVPCNCCOLL   COEVPDSKYSIJ (VOHLAVNGENERKMYSCTACHGHITTHKKYNT   VMTTSTHYVCESCOXGFSSVDD\LQNI\LLDMPHPLCCTHCTL\   COEVPDSKYSIJ (VOHLAVNGENERKMYSCTACHGHITTHKKYNT   VMTTSTHYVCSSCOXGFSSVDD\LQNI\LLDMPHPLCCTHCTL\   COEVPDSKYSIJ (VOHLAVNGENERKMYSCTACHGHITTHKKYNT   VMTKHSHLGNFAKAKHCI (CGERFPSSLIDICHTTHKKYNT   VMTKHSHLGNFAKAKHCI (CGERFPSSLIDICHTTHKKYNT   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VALUENTER   VAL		sequence		\=possible nucleotide insertion)			
ERGSTDSTLKPLRGCKEMPROGGONTKVYSCCYCSKRDFNSL AVLEHILKTHIARPRQSHYCOLCDSMITTLYHDYKLHKN HAYPVMGFONISAFHCNYCDEMFADINSLGEHIKVSHGOPHAKLHKN HAYPVMGFONISAFHCNYCDEMFADINSLGEHIKVSHGOPHAKLHKN HAYPVMGFONISAFHCNYCDEMFADINSLGEHIKVSHGOPHAKLHKN SORNAFFCNYCDEMFADINSLGEHIKVSHGOPHAKLH SORNAFFCNYCDYCTNSPIRGSILKLIKHIKKNIKHIPLAG KASARGGSVSSDVEVSSPRKGRUSASARSISHGEYPCNYCDLK FSNFESFGYHLKLHLELLLKRQACPQCKEDPBSGESLLQHLTVH WATTSTHYVGESCOKOFSVDVD LQKINLLDMPHACTHAKKNYCK FSNFESFGYHLKLHLELLLKRQACPQCKEDPBSGESLLQHLTVH WATTSTHYVGESCOKOFSVDVDVSBPWRGGTARVDFREADLAGHALT OUTPULLAR STANDAM HAND AND AND AND AND AND AND AND AND AND			1	ADLQCIHCPEVFVDENTLLAHIHQAHANQKHKCPMCPE\QFSSV			
AVLEHILKTIHADKPQQSHTCQICLOSMPTIYNLEHURLHING HAYPVMGENISAHCHNCYDEPHADINSLGHVNGHONAP SORNAPFCNQCSMGPLTSSLTEHIQQ\AHGSVGSAKLESPV VQPTQSFMDVSCPYCTMSPTFGSILKTHRUQ\AHGSVGSAKLESPV VQPTQSFMDVSCPYCTMSPTFGSILKTHRUQ\AHGSVGSAKLESPV VQPTQSFMDVSCPYCTMSPTFGSILKTHRUQ\AHGSVGSAKLESPV VQPTQSFMDVSCPYCTMSPTFGSILKTHRUQ\AHGSVGSAKLESPV VQPTQSFMDVSSCPYCTMSPTFGSILKTHRUKHRHKHRIDLANG KKSKARGSPVSSDVEVSSPKRQRISASANSISMGEVPCHQCDLK FSNFSSGTHKLKHLELLIKRAKQAPCQKEDPSGESLQHLTVH YMTTSTHYVCSECDKQFSSVDD\LQWII\LDMPHICCTHCT\L CQEVPDS\NCVI\CQUIN\LDMPHICCTHCT\L CQEVPDS\NCVI\CQUIN\LDMPHICCTHCT\L CQEVPDS\NCVI\CQUIN\LDMPHICCTHCT\L CQEVPDS\NCVI\CQUIN\LDMPHICCTHCT\L CQEVPDS\NCVI\CQUIN\LDMPHICCTHCT\L CQEVPDS\NCVI\CQUIN\LDMPHICCTHCT\L CQEVPDS\NCVI\CQUIN\LDMPHICCTHCT\L CQEVPDS\NCVI\CQUIN\LDMPHICCTHCT\L VLLONNHELDBINI\LDMPHICCTHCT\LDMPHICCHTCH\LDMPHICC\LDMPHICA\LDMPHICC\LDMPHIC\LDMPHICC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC\LDMPHIC				\EGVYCHLDSHRQPDSSNHSVSPDPVLGSVASMSSATPDSSASV			
HAYEVMOFONISARHENYCEMPADINSLOBHIRVSHOGPNAMP SDORNAPE FORDCOSMIGHTENSLITHING) (ADSONANA FERDOCOSMIGHTENS SITERING (A) CONCOUNT OF THE STATEMENT OF THE MERIKAHI LEBIK SURVEY ON COPTOS MED VISION AND THE MERIKAHI LEBIK SURVEY PONCOUNT OF THE MERIKAHI LEBIK SURVEY PONCOUNT OF THE MERIKAHI LEBIK SURVEY PONCOUNT OF THE MERIKAHI LEBIK SURVEY PONCOUNT OF THE MERIKAHI LEBIK SURVEY PONCOUNT ON THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUNT OF THE MERIKAHI SURVEY PONCOUN	1	•		RRGSTPDSTLKPLRGQKKMRDDGQGWTKVVYSCPYCSKRDFNSL			
SDGNNAFFCNOCSMGFLTESSLTEHIO\()\AlcSUGSAKLESPV VOPTOSFREDYSCPYCTNSFJFGSILKLYHEKENKRISIPLANS KRSKARGSPVSSDVEVSSPKRQRISASANSISNGESPORODLK KRSKARGSPVSSDVEVSSPKRQRISASANSISNGESPORODLK KRSKARGSPVSSDVEVSSPKRQRISASANSISNGESPORODLK KRSKARGSPVSSDVEVSSPKRQRISASANSISNGESPORODLK COEVPDS\KVSI\QVILLAWRIKACAPOCKEDPSOSELLQHLYTH YMTTSTHYVCESCDKQFSSVDD\LQKIN\LLDMFHECTHCT\L COEVPDS\KVSI\QVILLAWRIKACAPOCKEDPSOSELLQHLYTH YMTSTHYVCSSCDKQFSSVDD\LQKIN\LLDMFHECTHCT\L COEVPDS\KVSI\QVILLAWRIKACAPOCKEDPSOSELLQHLYTH YMTSTHYVCSSCDKAPSSVDD\LQKIN\LLDMFHECTHCT\L COEVPDS\KVSI\QVILLAWRISHEKRWATCACNAMPTEKEALDO VIVKHSHLANDARAHKCIFCCGFTSTEVELQCHITTHSKYTHSK FESKAFHAI LLLEHLBREKHCFPSATRETGVUCMOTTYP  ULLONNRIKLBNINIEPGEDBESKKABFIKGSHCWVCGFTFFSEE NOLERHIOTHRGPAKHYMCPICCGFTSPLTUTTEHKVTHSKSLD TOTCRICKRYPLQSEEPF I HCCHPHDLINBETGVUCMOTTYP STLELKHGTTFHMCKLAGSSAASSPROGGLQKLYKCALCLKEFR SKODLYKLUVNGLYSCLACGCMARSANGOVGARPEPDANPCAD GREPCSVKYESAEDLSSHMQUHABLTPETGGVUCMOTTYP STLELKHGTTFHMCKLLAGSSAASSPROGGLQKLYKCALCLKEFR SKODLYKLUVNGLYSCLACGCMARSANGOVGARPEPDANPCAD GREPCSVKYESAEDLSSHMQUHABLTPETGGVUCMOTTYP STLELKHGTTFHMCKLLAGSSELLDLESHLADLEDGFR KKTYCCIKCOMPENNERS CILVANNIHI ENFECKLUCMO FISPAKLLCHLIEHISFROMGGTFKCPVCFTVFVQANKLQHTGS DISASRPNILLIAMDLGJCGCPCKFF FPOTELQMTHMSCHLALLLABSSYP VANGOEKYTLOGCOPCKF FPOTELQMTHMSCHLAFLLABDGVK LTQHISAABLCTCFFSRAPATICLLSLASPANDOHA GGLETTSTFFAKILERKGYANGLIGKNILLANCSASPHOLALLYAA CIPKINSTATITEOPMEGRATIFYVENSOMSYSTVLOMTGGS GGLETTSTFFAKILERKGYANGLIGKNILLANCSASPHOLALLYAA CIPKINSTATITEOPMEGRATIFYLLOFAUSHCHAPTLOCHAPTURCHCHPLUTLOV SPLINTITEOPMEGRATIFYLLOFAUSHCHAPTLOCHAPTURCHCHAPTLOCHAPT ALITUVAGKKTTULTPOHACHTICAPTSIADURCHAPTLOCHAPTURCHCHAPTLOCHAPT SPLINTITEOPMEGRATIFYLLOFAUSHCHAPTURCHCHAPTLOCHAPT SPLINTITEOPMEGRATICATURCHTEROPPULD COMPNIGOODLIPLLLTONGCHAPTOGORDAUCHAPTLOSPYDLO CHAMMINITITEOPMEGRATICATURCHTEROPPULD CHAMMINITITEOPMEGRATICATURCHTEROPPULD CHAMMINITITEOPMEGRATICATURCHTEROPPULD SPLINTITEOPMEGRATICATURCHTEROPPULD CHAMMINITITEOPMEGRATICATURCHTEROPPUL CHAMMINITITEOPMEGRATICATURCHTEROPPUL CHAMMINITITEOPMEGRATICATURCHTEROPPUL CHAMMINITITEOPM	İ		İ	AVLETHLKTIHADKPQQSHTCQICLDSMPTLYNLNEHVRKLHKN			
VOPTOSPMEVTSCPYCTNSPIFGSILKITKHIKENIKHILLAIN   KIKKARGGSPSSDEWSSSRAGRIASANSISHSEPPCNOCOLK   FRIFESFOTHLKILLILIKROACPOCKEDPDSGESLICHITY   YMTTSTHYVCSCCKOFFSSUDO \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \				HAIPVMQFGNISAFHCNYCPEMFADINSLQEHIRVSHCGPNANP			
KKSKAEGSPVSSDVEVSSPKRORLSASANSISNESPONGULIUTH FSNFESSPOTILLKHILELLKROACPOCKESPOSSLICHLTVH YMTTSTHYVCESCOKQFSSVDD\LQKI\LLDKMPHELCTICT\L COEVPOS\KVSI\QVHLAVKHSNEKKYMCARONDFKKEADLO VHVKHSHLGNPAKAHKCI FGGETFSTEVELQCHITTHSKYNCK FGSKAFHAI ILLEKHLEKHEKVCPDAATENGVPPMARKKAB PADLOGMILKNPEAPNSHEASEDDVDASEPMYGCDICCAAYTME ULLONHLEADHNIRGEBOKSKKAEFICAFFCVVCNOTVT GTURICKMPLOSEEFI EHCOMPDINATGFFCVVCNOTVT STLEIKIHGTFFMOKLAGSSBASSPNOGUDKINYKCALCLKEFF NGLKEHLOTHROPAKHYMCPICGEFPSLLTLTERKVTHSKSIDL TGTGRICKWPLOSEEFI EHCOMPDINATGFFCVVCNOTVT STLEIKIHGTFFMOKLAGSSBASSPNOGUDKINYKCALCLKEFF SKODLVKLUONLEYSGLGCACMARSANGGUAPPEPARPCA GLRCPECSVKFESAEDLESHMQVDHRDLTPETSGFROTTISPV PRKTYTOCI KCOMPTERERFICIHVANHHIEGOTHARCHACLKLONM FDSPAKLLCHLIEBISFBGMGGTFKCPVCFTVFVOANLOQHIFA VHGGEBKIVDCSCPCHOFFOTELONHMINGGHAP FSPAKLLCHLIEBISFBGMGGTFKCPVCFTVFVOANLOQHIFA VHGGEBKIVDCSCPCHOFFOTELONHMINGGHAO FDSPAKLLCHLIEBISFBGMGGTFKCPVCFTVFVOANLOQHIFA VHGGEBKIVDCSCPCHOFFOTELONHMINGGHAO FDSPAKLLCHLIEBISFBGMGGTFKCPVCFTVFVOANLOQHIFA UNGGEBKIVDCSCPCHOFFOTELONHMINGGHAO FDSSAKLLCHLIEBISFBGMGGTFKCPVCFTVFVOANLOQHIFA UNGGEBKIVTLSCCCPCHOFFOTELONHAUNLGLAFSASS DISASRPNILLIMADIGIGDLGCVGNNIMETPNIDELABOUK LTONIBASALCTPGRAAFTLGCKPYPTGANLAVLLSLASSASS DISASRPNILLIMADIGIGDLGCVGNNIMETPNIDELABOUK LHGGDHFYGMPFSIMGDCARMSLESKEVLKAULVLLASSASS DISASRPNILLIMADIGIGDLGCVGNNIMETPNIDELABOUK GGLFNETTFAKILEBERGYATGLIGKHHGJENCSSASHCHHEL HHGDHFYGMPFSIMGDCARMSLESKEVLKHAUFLGLASSASSCHCHHEL HHGDHFYGMPFSIMGDCARMSLESKEVLKHAUFLGLASSASCHCHHEL HHGDHFYGMPFSIMGDCARMSLESKEVLKHAUFLGLASSANCH GGLFNETTTFAKILEBERGYATGLIGKHHGJENGSASHCHUPLLARMWGDR GGLFNETTTFAKILEBERGYATGLIGKHHGJENGSBCHLIMFDFLLKV ALTURIAGKLTHILTPSSHWPVLBAGARVGCTROCKLUMFLGCUNGG GGLFNETTTFAKILEBERGYATGLIGKHHGLACSSASHCHUPLLARMWGDR GGLFNETTTFAKILDFSBCHALLANGVARMFLEKHUPLLARMWGDR GGLFNETTTFAKILDFSBCHALLANGVARMFLANGLANGLENGTHAU BCFLAMMTHTTORMCROCRTPTLLILGESCHAUPLARMWGDR BGGTRVPGIFFNBCHALLARMWGDRFTYCHALASSANCHUPLLOCH BGGLANGTLTYPTSHGGSENOLTICHKNETHFLUKALANGVARMGHAUPLANGVARMGGNUTHAURLANGVARMGHAUPLANGVARMGHAUPLANGVARMGGNUTHAURLANGVARMGHAUPLANGVARMGHAUPLANGVARMGHAUPL				VORTOGEMENT CONCERNED TERRET VIEW TO THE SAME SPO			
FENFESPOTHLILLIHELLILRIKQACPOCKEDFESDELIGILITYM YNTSTHYVCSECKOW, PSYDVD\LQNILLIDMPHELCCTICTLL CQEVFDS\KVSI\QVHLAVRHENEKMYRCTACNIDFREADLO VHVKHSHGLMPRAKHKCI FGGETFSTEVELQCHITTISKKYNCK FCSKAFHAIILLEKHLREKHCVPDATENGTANGVPPPANTKKAR PADLOGALLKNEPARNHENESEDDVDASTRATANGTANGVPPPANTKKAR PADLOGALLKNEPARNHENESEDDVDASTRATANGTOLGARYTME VLLONHELBDHAIRGEDDOSKRKAEFIKGSHKCNVCSTFFSSE NCLERHLOTHEROPAKHVMCPLGCEPFSPST NCLEKHLGTHENDKLASSEBFIENCOMHPDLRINSLICHECVUCNOTYTY STLELKTGTHMOKLASSEASSSENGOLIVEVECULCKEFF SKODLVKLDVNGLPYGLCACKARSANGQVGOLAPPEBDAIRPCA GENCPECSVKYFSARDLESHMOVDMELTTSGPRKGTGTSPV PEKTYCCIKCMTFENBEREIGIHVANHMIEGIHNECKLCKUM FDSPAKLLCHLEHSFEGMGGTFKCPVCFTVFVQANKLQOHIFA VKOOEDKIYDCSOCPAKFFSONDLESHMOVDMELTSGPRKGTGTSPV PEKTYGCIKCHLEHSFEGMGGTFKCPVCFTVFVQANKLQOHIFA VKOOEDKIYDCSOCPAKFFSONDLESHMOVDMELTSGPRKGTGTSPV PEKTYGCIKCHLEHSFEGMGGTFKCPVCFTVFVQANKLQOHIFA VKOOEDKIYDCSOCPAKFFSONDLESHMOVDMELTSGPRKGTGTSPV PEKTYGCIKCHLEHSFEGMGGTFKCPVCFTVFVQANKLQOHIFA VKOOEDKIYDCSOCPAKFFSONDLESHMOVDHAULGLOLDESPANDLOLDLAGGSVK LIQHISAASALCTPSRAAPITGTCKPVSGSMOVAGA GGLPFTSTTFAKILLEKGYATGLIGKHHJGINCESADHCHHPI HERGDHFYGMPFSIMGGCARWELEEKKVHLECKUNFLGVULALV ALTILVAGKLTHLIFVSMMPVIMSALSAVILLLASSYTYGALIVVAN DCFLMMNHTITTGPMCFGGTTTDLILQCXSFIKKNKHGPPLLFV SFLLWHIPLITMENFLCKSLHGLUNGDWVKEMBMWVGRILDTLDV EGLENNSTLIYFTSDHGGSLENQLCHTYGYAFALKNKHGPPLLFV SFLLWHIPLITMENFLCKSLHGLUNGDWVKEMBMWVGRILDTLDV EGLENNSTLIYFTSDHGGSLENQLCHTYGYRGALHGASSEYP QDRVIDGOQLUPLLLICTAGHSHEFILMFKHJKGNSTIYGGKMGMW EGGIRVPGIFRNFCVULPAGNSVEFTULLAGSSEYP QDRVIDGOQLUPLLICLTAGHSHEFILMFWHGNTISTYDFLD EGRESSTULTPGPLYDSHGGNANGVKTELLESEQGSFN VHNYPDMEAVPLLILINNKCEPPEDSLSVDHFCTGTEPVDLSINK ARTSPTAVSSFSVMTMGASSPSSTSTSSSSKLASSTVITYS VSSASSSTVLTPGPLASASSVGGOCFHILHPYSSPMLLO SKILSKVHRINE IPVVQSVPVYTAVRSSERVINTIVVPLLEDGGG GKKAGWPRGGLSRROSSSPSDDDDLPRVTLDSVRTGSTALSIA RAVGEVHEPSVSVRGNNNNNOKPPCLSFTSSTRORTULA PDDSRKTAYSTDCDP\EGGGCTLINAPAFKSKKICKGLVFGILLET LIVLFMGSKHFWPEVYRKAYDMFTFYSNGEKKKIWBIDEVTR TEIFRSGNGTDETLEWHDFKNGTTGIYFVGLOKEFITLOKVIP BESPEBELIEDBNEITTTFFFSGSVIWARARGRSS LLIUSSLODPS EEGSCLHFFSDENEITTFFFFSGSVIWARARGRSK	1	ŀ	1	KKKKAFOSDVSSDVFVSSDKDODI SASAVSTSVGBVBOVOGDI K			
WHITSTHYVCESCOKQFSSVDD\LQKIN\LDMPHLECTRICT\LCC   COEVPDS\KYSI\QVHLAVHANEKKYNTCTACNNDFRKEADLO    VHVKHSHLANPAKAHKCI PCGRIFSTEVELQCHITISKYNCK   FCSKAFHAI LLLEKHLEKEKICVPDAATENTANGVPPMARKKAB   PADLOGMILKNPRAPNSHEASEDDVDASEPMYGOLGAAYTME   VLLONNHLADHNIRGEDDOSRKKAEFIKSKIKCVCSPRIPSE   WLLERHLQTHRQPAKHYMCPICOEPPSLLTITEKKYNTKSKICO   TOTCRICKWPLOSEEPI EHCCMHPDLRNSLITGEKVYCMQNVT    STELKIHGTFHMQKLAGSSAASSPNOGGLQPEDANRCA   GLAPPECSVKPESADLDESHMQVHRDITPETSGFRKGTUTSPV   STELKIHGTFHMQKLAGSSAASSPNOGGLQPEDANRCA   GLAPPECSVKPESADLDESHMQVHRDITPETSGFRKGTUTSPV   PRKKTYQCIKCQMTFENEREIQIHVANHMIEEGINHEKLKONM    FDSPAKLLCHLIEHSFRGMGSTFKCPVCTVVVQNKLQQHIFA    VHQGBKIYDCSQCPQKFFFOTELQNITMSQHAQ    FDSPAKLLCHLIEHSFRGMGSTFKCPVCTVVQNKLQQHIFA    VHGGBKIYDCSQCPQKFFFOTELQNITMSQHAQ    FDSPAKLLCHLIEHSFRGMGSTFKCPVCTVVQNKLQQHIFA    VHSQBKIYDCSQCPQKFFFOTELQNITMSQHAQ    VHSQBKIYDCSQCPQKFFFOTELQNITMSQHAQ    VHSQBKIYDCSQCPQKFFFOTELQNITMSQHAQ    VHSQBKIYLDCSQCPQKFFFOTELQNITMSQHAQ    LTQHISAASLCTPSRASFLTGRYFVRSGMVSSIGYTLQMTGAS    STEIVMINIPLTAKILEKGKYATCLIGKHHIPLGENLEFLDRAFGKYALLIVA    ALITLYASKLITHIPVSMMPVINSALSXLIVALDSASSCHHIPL    HIGFPHFYGMFPSIMGDCARWELEERKVNLEQKLNFLFQVLLVVA    ALITLYASKLITHIPVSMMPVINSALSXLIVALSYFFQALLIVA    ALITLYASKLITHIPVSMMPVINSALSXLIVALSYFFQALLIVA    ALITLYASKLITHIPVSMGCARWELEEKKVNLEQKUNHEPQULLIVA    DCFLMRNHTITTQPMCPQTTFPLILQEVASFLKNKKIGPPLLFVA    DCFLMRNHTITTQPMCPQTTFPLVASSFVANKAGPPLLFVV    SPLINVINIPLITMEFICKSLHCLYGDBVAYQFIKLIVALDVA    DCFLMRNHTITTPPOPGCQCTTFPLVASHAGNAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNAGWAGNA	i		}				
CQEVPDS\KVSI\QVHLAVWHSNEKKYNCKACNDPKKYNCK VUNKHSHLGNPAKHAKCI FGGETFSTEVELQCHITTHSKKYNCK FGSKAFHAI ILLEKHLEKEKCVPDATENGTANGPPMATKKAR PADLOGGILLKNPPAMSHEASEDDVDASEBYMGCDICGAAYTME VULONHELDHNIRGEDDOSSKKAEFIKGSHKCVCSTFFSE NOLEHLLOTHROPAKHWED CIGGEFPSELTITTEHKVTHSKSLD TOTCRICKWPLQSEEFF EHCOMHPDLRNSLTGFFCVCVCNQTVTV STLEIKINGTFIMOKLAGSSASSSPROQUGILKYECALCKSEFF SKODLVKLDVNGLPYGLCAGCMARSANGOVGGLAPPEPADRECA GERCPEGSVKPFSABDLESHMQVDWRDLTSGPRKGTYTSPV PEKTYQCIKCOMTENBERICIHVAHMIEEDIHBCKLCNOM FDSPAKLLGHLEISSFROMGSTFKCPVCYVPVVQANKLOQNIF PENTYYCLIKCOMTENBERICIHVAHMIEEDIHBCKLCNOM FDSPAKLLGHLEISSFROMGSTFKCPVCYVPVVQANKLOQNIF VNGOBKIYDCSOCHOKPFFOTELQNITMSOHAO VNGOBKIYDCSOCHOKPFFOTELQNITMSOHAO VNGOBKIYDCSOCHOKPFFOTELQNITMSOHAO VNGOBKIYDCSOCHOKPFFOTELQNITMSOHAO VNGOBKIYDCSOCHOKPFFOTELQNITMSOHAO VNGOBKIYDCSOCHOKPFFOTELQNITMSOHAO VNGOBKIYDCSOCHOKPFFOTELQNITMSOHAO VNGOBKIYDCSOCHOKPFTOTELQNITMSOHAO VNGOBKIYDCSOCHOKPFTOTELQNITMSOHAO VNGOBKIYDCSOCHOKPFTOTELQNITMSOHAO VNGOBKIYDCSOCHOKPFTOTELQNITMSOHAO VNGOBKIYDCSOCHOKPFTOTELQNITMSOHAO VNGOBKIYDCSOCHOKPFTOTELQNITMSOHAO VNGOBKIYDCSOCHOKPFTOTELQNITMSOHAO VNGOBKIYDCSOCHOKPFTOTELQNITMSOHAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANAO VNGOKAGANA	1			YMTTSTHYVCESCDKOFSSVDD\LOKH\LLDMPHPLCCTHCT\L			
WHVRHSHLGNPARATHRC   FCGETTSTEVELQCHITTHSKKYNCK	Į.	ĺ		COEVFDS\KVSI\OVHLAVKHSNEKKMYRCTACNWDERKEADLO			
FCSKAFHAIILLEKHLREKHCVEDAATEMGTANGVPBMATKKAR  PADLOGALLKINPABANSHEASEDDVDAESPWGCDLIGAAYTME  VULOMHLRIDHNIRPGEDDGSRKARFIKGSHKKINVCSRFFFSE  NGLREHLGTHRIGALHYMCPICGERFELTLITEHKVYHSKID  TOTCRICKMPLOGEREFIEHCCHHPDLRNSITGFRCVVCMCGVVT  STLELKIHGTHIMGKLAGSBASSPNGQGLQKLYKCALCLKEFR SKODLVKLDVNGLPYGLCACCMARSANGQVGLAPPEPADRRCA GLRCPECSYKFRSARDLESHMQVDHRDLTPETSPRGTOTSFV  PRKTYGCIKCOMTEURRE EIGHTANHNIEGGNHEKCLKOM FDSPAKLLCHLIEHSFRGMGGTFKCPVCFTVYVQANKLOQHIFA  4 WGGGDRIVDCSQCPGKFFOTELGHAMNHIEGGNHEKCLKOM FDSPAKLLCHLIEHSFRGMGGTFKCPVCFTVYVQANKLOQHIFA  4 WGGGDRIVDCSQCPGKFFOTELGHAMNHOLOQHIFA FDSPAKLLCHLIEHSFRGMGGTFKCPVCFTVYVQANKLOQHIFA FDSPAKLLCHLIEHSFRGMGGTFKCPVCFTVYVQANKLOQHIFA FDSPAKLLCHLIEHSFRGMGGTFKCPVCFTVYVQANKLOQHIFA FDSPAKLLCHLIEHSFRGMGGTFKCPVCFTVYVQANKLOQHIFA FDSPAKLLCHLIEHSFRGMGGTFKCPVCFTVYVQANKLOQHTGAS DISASRNILLIMADDLGIGDIGCYGNNTMETPHIDRLAEDGVK KEPRSRSGRERDNMHLHHSCLCFRSPMLPALLAPSASS DISASRNILLIMADDLGIGDIGCYGNNTMETPHIDRLAEDGVK LIQHISAASLCTPSRSAPLTGNTRYVARMSSIGVRUCHTGAS GGLPTNETTFAKILEEKGYATGLIGKWHLGINCSSADHCHIPL HRIGPHFYGMPFSIMBOCARWELSEKHRICKONLIPCOVLLV ALITUVAGKLTHLIPVSWMPYUMSALEAVLLLASSYFYGALLVHA DCFHMRHTITTOPMCFGRTPTLLIGASSIFKENGGNFLLIPV SFLHVHIPLITMENELGKSLHGLYGDRIVKEMDWWGRILDTLDV EGLSNSTLIYFTSDHGGSLENDLGNTQYGGMNGIYKGGMGMGW BGGIRVPGIFFRHFGULFAGRVIGGFFILMOVFFTVVALAGSSVP ODRVIDGOLLELLIGTAGRISDHEFIMTYCREHPPLLPV SFLHVHIPLTARSPVFYQVMERVQCFGEKVVHHDPPLLFD LSRDPSETHILTPASEPVFYQVMERVQCFGEKVVHHDPPLLFD LSRDPSETHILTPASEPVFYQVMERVQCFGEKVVHHDPPLLFD LSRDPSETHILTPASEPVFYQVMERVQCFGEKVVHHDPPLLFD LSRDPSETHILTPASEPVFYQVMERVQCFGEKVVHHDPPLLFD SGSASSSSTVLTPGGLAASASGUGGGDTSSSPSMLASSPTVITS VSSASSSSTVLTPGGLAASASGUGGGTSSSPSMLASSPTVITS VSSASSSSTVLTPGGLAASASGUGGGTSSPSNEHLESSOGSFSRDH ARVOEVHPSPVSRVGGRRMNNOKFPGSISPFSIESTRRGFTLAM PPDSRKTARYSTCDFYLGSGFKKKIYMEIDPVTR RAYGCYCKKARABDELTRHYKHTANGYFFCACCDRSFSRSDH LALHRRHNLV  EFRARMGFBNCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFMGSKHFWBEVPKKADMEHTFYSNGEKKKIYMEIDPVTR EFFSPEEEIDENBEITTTFFEGSVIWVPAKPRIERDFILAELGPP PPDSRKTHAYSTLOFT STERSTRAGGSEELD INDYTENGIEPDPMLDERGYCIYFGROKKKIYMEIDPVTR EILLEFROBERGETHENBERGEND				VHVKHSHLGNPAKAHKCIFCGETFSTEVELOCHITTHSKKYNCK			
PADLOGNILKNIPARNSIRASEDDVDASEPMIGDICGRAYTIME VLLOMHLRDHNIR TREDEDDGSRKKA KESHKKOVCSPTFSE NGLREHLOTHREPAKHYMCPICGER PPSLLTLTEHKVTHS KSLD TOTCHICKMPLQSEEFI EHCCMHPDLRNSLTGFRCVVCMQTVT STLEKKHCTFHMQNLAGS SAASS FMGGLOGKLY KCALCKEFR SKQDLVKLDVNGLPYGLCAGGMARSANGGVOGLAPEPADARCA GLRCPECSVKFSABLDESHMQVDHRDLTPETSGPRKGTGTSPV PRKRTYCLIKCOMTFENSREIG JHVANNHMIEGEIGHECKLCNOM FDSPAKLICHLEHSFEMGGTFR CVCFTVFVQANKLOQHIFA VMGGDZHIYDCSGCPOKFF FFOTELQHHTMSQHAQ  SYETVGRIKKEVMHSQUKALCKGSLSPLPLDGENLPLLDGERPE KEPRSRGSRERDNMLHHHHSCLCFRSWLPAMLAVLISLAPSASS DISASRENTLLLMADDLIGDIGCYMTHYPHYDIRLADGVK LTQHISAASLCTPSRAAFLTGRYFVRSGMVSSIGYRVLQWTGAS GGLPNNETTFAKILEEKGYATGLIGKWHLGINCESASDHCHHPL HIGDHPYGMFPSMGDCARRELSSERULGKNIHLGKNIHLFOVLALV ALTILVAGKLTHLIPVSMMPVIMSALSAVLLLASS YFVGALIVHA DCFLMRMHTITEQPMCGPRTPLILLGCSALDKCHHPL HIGDHPYGMFPSMGDCARRELSSERULGKNIHLGKNIHLFOVLALV SFLHWHPPLITHENFLCKSLHGLYGDNVKENDMWVGRILDTLDV SFLHWHPPLITHENFLCKSLHGLYGDNVKENDMWVGRILDTLDV GGLSNSTLYFPSDNGSLENGLGNYGGNNGIYKGGMGGM BGGTRVPGIFRHPGVLPAGRVIGEPTSLMDVFPTVVRLAGSSVP ODRIVIDSOLLPLLIGTAGNIBUETHVFREPHARAHNORDR GTMKVMFVTPVQDEGGAGACYGRKVCPCFGEKVYHHDDPLLFD LSRDSETHILTPASSEPTYTOWER VOORAWHORTLSPVPLO LDLLGNINRRWLQPCCGPFPLCWCLREDDPQ  MNIHRKRKTIKNINTFERRIKHDSMAPAVRKTELLESEQGSPN VNNYDDMARAVPLLLANVGSPPEDBLSDVJHFOYQTFPVPLSLINK ARTSPTAVSSSSVSMTASASSPSSTTSSSSSSRLASSPTVITS VSSASSSSTVLTPGGLAASAGVGGOQCHLHIHPVPPSSPMILQ SNKLSHVHRIPVVQSVPVYTAVRSPGNVMNTIVVPLLEDGGG GRAQAMPBROPFRLSPRGSKSDDDDDLBTLSSVDHFOYQTSTPVDLEINK ARTSPTAVSSSPVSMTASASSPSSTTSSSSSSRLASSPTVITS VSSASSSSTVLTPGGLAASAGVGGOQCHLHIHPVPPSPFMILQ SNKLSHVHRIPVVQSVPVYTAVRSPGNVMNTIVVPLLEDGGG GRAQAMPBROPFRLSPRGSKSSDDDDDLBTLSSVDHFOYTITSERVBLG SNKLSHVHRIPVVQSVPVYTAVRSPGNVMNTIVVPLLEDGGG GRAGAMPBROFFLSTRAGSTALSIA RAVGEVHSPSVSRKGSRSDDDDDLBTHRSPFILLSECGGSPN XCTMEGCTWFFRASDELTRHYRKTGVKPFKCADCDRSFSRSDH LALHRRHHLV  1079 ETHARGGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFMPEVPKKRYDMEHTYSNGEKKKIYMELDPVTR TEIFRSGNOTDELTEVHTWN INFTLY ISGTFAKGTCRVCEPLLIGYY VYYCYQGGRVICRVIMPCNWWARMLGRV  EFSSPEEEIDENEITTTFFEGSVIWWPAKPTENEDLYKKITGLYFILLALT TEIFRSGNOTDELTEVHDF							
VULONHILDHHIR TREGEDGESKEARFIKGSHKKNVCSPTFFSE   NGLERHLOTHERGARHYMCPICGERPELITTERKYMTSKID   TOTCRICKMPLOSEREFIEHCOMPDLRNSITGFRCVVCMOGVUT   STLEIKLKHOFTHMOKLAGSSAASSPHOLOKULKCLAKER   SKODLVKLDVNGLPVGLCAGCMARSANGQVGGLAPPEPADRECA   GLRCPECSVKFESAEDLESHMQVDHDLTPSTSPRKGTQTSFV   PRKKTYQCIKCOMTENBEREIQHIVANIMIEBGINHEKCLKCMM   FISPAKLLCHLIEHSFRCMGGIFKCVCFTVYQANKLOQHIFA   PRKKTYQCIKCOMTENBEREIQHIVANIMIEBGINHEKCLKCMM   FISPAKLLCHLIEHSFRCMGGIFKCVCFTVYQANKLOQHIFA   WRGGDRIVDCSQCPQKFFYOTELGHMINGCHAG   FOSPAKLLCHLIEHSFRCMGGIFKCVCFTVYQANKLOQHIFA   WRGGDRIVDCSQCPQKFFYOTELGHMINGCHAGPLAGULSLAPSAS   DISASRNILLIMADDLGIGDIGCYGNNTMETPHIDRLAFASS   DISASRNILLIMADDLGIGDIGCYGNNTMETPHIDRLAFASS   DISASRNILLIMADDLGIGDIGCYGNNTMETPHIDRLAFASS   DISASRNILLIMADDLGIGDIGCYGNNTMETPHIDRLAFASS   DISASRNILLIMADDLGIGGIGCYGNNTMETPHIDRLAFASS   DISASRNILLIMADDLGIGGIGCYGNNTMETPHIDRLAFASS   DISASRNILLIMADDLGIGGIGCYGNNTMETPHIDRLAFASS   DISASRNILLIMADDLGIGGIGCYGNNTMETPHIDRLAFASS   DISASRNILLIMADDLGIGGIGCYGNNTMETPHIDRLAFASS   GGLPTNSTTFAKILEEKGYANGLIGKNHLGINCESASDRCHHPL   HAGDHFYGMFSMMGDCARRELSEKHNKGGNISPILLPV   SPLIVHIPLITMENDELKSHLAGINGDIKVENDEWISSIGVRUCHTABAS   GGLPTNSTTFAKILEEKGYANGLIGKNHLGINCESASDRCHHPL   HAGDHFYGMFSMMPUNFTUNGCARTHAFTUNGCNNTLFOVLLOV   SPLIVHIPLITMENTICKSLHGINGDIVKEMDMWGRILDTLDV   GGLSNSTLIYPTSDHGGSLENDLGATYGGGMNGTIKKGSKMGGMW   BGGIRVPGIFFRHPGVLPARKVICCFGEKVVHHDPPLLFD   LSRDPSSTHILITPASSEVFYQUMER\VQQAVWEHQTLSPVDLQ   GTMWKNYHVTVPFOFGGAGACYGRKVCCFGEKVVHHDPPLLFD   LSRDPSSTHILITPASSEVFYQUMER\VQQAVWEHQTLSPVDLG   GMKLGHAPAVPLLIMNVGSPPDELSCHCYCFGEKVVHHDPPLLFD   LSRDPSSTHILTPASSEVFYQUMER\VQQAVWEHQTLSPVDLG   GMKLGHAPAVPLLIMNVGSPPDELSCHCYCFGEKVVHHDPPLLFD   LSRDPSSTVLTPGDLAFASSGGGGCQFGLHIHTHPVPPSPMMLQ   SNKLSHVHIPVUQSVPVYTAVRSPGNNNTTVVPLLEGGG   HGKAQMDPAVPLLINNVGSPPDELSCHCSFSRLASSPTVITG   SCASSSSTVLTPGDLAFASSGGGGCGPLHIHTHPVPSPSPMLQ   SNKLSHVHIPVGNAVAFAVEFFCSCHCKTIKTGTALT   LIVLFNGSKHFWBEVPKKADMEHTFYSNGEKKKYMETGDPVTR   CHARKNGFPNCEDCHILNAEAFKSKKICKSLKCGLVFGILALT   LIVLFNGSKHFWBEVPKKADMEHTFYSNGEKKKYMELDDPVTR   EFFSEDEELTDNEEITTTFFEGOVIWOPAKPRICHIALT	1						
NOLREHLOTHIGPAKHIMCHIGGERPSLITHIEHKUTHISKSLD	1	1		VLLQNHRLRDHNIRPGEDDGSRKKAEFIKGSHKCNVCSRTFFSE			
TOTCRICKMPLOSEEFFIEHCMMHDLRNSLTGFRCVVCMOTVT STLELKHIGTPHNOKLAGSSASSTOGQLOKUTKCALCLKEFF SKODLVKLDVMGLPYGLCAGCWARSANGQVGGLAPPEPADRPCA GLRCPECSVKFESAEDLESHMQVDHRDLTPETSGPRKGTGTSPV PRKKTYCLKCOMTFENBERIGIHVANHMIEEGINHECKLCNOM FDSPAKLLCHLIEHSFEGNGGTFKCPVCFTVYQAMKLQOHIFA VMGGDKIYDCSQCPQKFFFOTELQUNTMSQHAQ  6060  2145  202  SYETVGKNKLEVHRSQLKALCKCSLPSRLLPLGENLPLLDGFR KPPRSRGSRERDMILHHSUCLFSWLPPMLAVLLSLAPSASS DISASRNNILLMADDLGIGDIGCYGNNTWRTPNIDRLAEDGVK LTQHISASLCTPSRAFTLTGRYPYRSGMYSSIGYRVLQWTGAS GGLPTNETTFAKILEEKGYATGLIGKWHLGIANCESASDECHHPL HRGPHHYGMFPSLMSDCARMELEEKKVNLEDKLNEFQVLALV ALTUVAKKLTHLIPVSWMPVTWASLAVLLLASSYVCALIVMA DCFLMRNHTITEQPMCFQRTTPLLIQEVASPLKENKHGPFLLFV SFLHWHIPLITHENFLGKSLHGLYGDMYKEMDMWGRLDDTLUV EGLSNSTLIYPTSDHGGSLENQLANTYQGGMNGIYKGGKGMGW BGGTRVGIFRFWGVLPAGNYLIGEFSLMOVFFTVVALAGSSVP ODRVIDGODLIPLLGTAQHSDHEFLHYCCERPLHAARWHQRDR GTMMKVHPVTPVFQPEGAGACYGKVCPCFGEKVVHHDPFLLFD LSRDPSSTHLLTPASEPVFYQVMEN\QQAVWHGRGTLSPVPLQ LDRLGNIWRRWLQPCCGFFPLSLVDMFQTVTLAGGSVP VHNYPDMEAVPLLLNNVKGEPPEDSLSVDHFTQTTPPVDLEINK ARTSPTATSSSSVSKLASSPTVTTS VSSASSSTVLTPGPLVASAGVGGQOPLHLHPVPPSSPMNLQ SNKLSHVHRIPVVQSVPVVYTAVRSPGNVNNTIVVPLLEEGGG HGKAQMDPKGLSFRQSKSDSDDDDLENVTLDSVNRTSSTALSIASPTVTTS VSSASSSSTVLTPGPLVASAGVGGQOPLHLHPVPPSSPMNLQ SNKLSHVHRIPVVQSVPVVYTAVRSPGNVNNTIVVPLLEEGGG HGKAQMDPKGLSFRQSKSDSDDDDLENVTLDSVNRTSSTALSIA RAVQEVHPSSVSRVKROMMNNQKFPCSISFSIESTRGRTVLN PPDSRKTAYSTDCDF\ECQUVYTYAVRSSPGRVVRRTTTGEKPY KCTMEGCTWKFRASDELTRHYRKHTGVKPFKCADCDRSFSRSDH LALHRRHMLV  6062  71  1079  ETMAKNGPENCEDCHILMAEAPKSKKICKSLKICGLVFGILALT LIVLFMGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNTDBTLEVHDFKNGYTGIYFVGLQKCFIKTQIKVII EFSSPEEEIDEMEELTTTFFEGGVIWVPARKITENGEKY YPYCYGGGRVICRYTMPCNWWARMLGRV  6063  71  1079  ETMAKNGPENCEDCHILMAEAFKSKKICKSLKICGLVFGILALT LIVLFMGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNTDBTLEVHDFKNGYTGIYFVGLQKCFIKTQIKVII EFSSPEEEIDEMEELTTTTFFEGGNTWARAFKISKI LFCEDNYTHYN\NFAGFELECTHTTTFFEGGNTOMEKKIYMEIDPVTR TEIFRSGNTDBTLEVHDFKNGYTGIYFVGLQKCFIKTQIKVII EFSSPEEEIDEMEELTTTTFFEGGNTOMEAKKIYMEIDPVTR TEIFRSGNTDBTLEVHDFKNGYTGIYFVGLQKCFIKTQIKVII EF				NGLREHLQTHRGPAKHYMCPICGERFPSLLTLTEHKVTHSKSLD			
SKODLVKLDVBGLPYGLCAGCMARSANGOVGLAPPEPADRECA GLRCPGCSVKPSAEDLESHINGVDHRDLTPETSEPRKGTOTSPV PRKKTYQCIKCOMTFENERSIQIHVANHHIEGGINHECKLCKOM FDSPAKLICHLI BISTBEMBGTFKCPVCPTVPVQANKLOQHIFA VHGQEDKIYDCSQCPQKFFFUTELQHITMSQHAQ VHGQEDKIYDCSQCPQKFFFUTELQHITMSQHAQ VHGQEDKIYDCSQCPQKFFFUTELQHITMSQHAQ VHGQEDKIYDCSQCPQKFFFUTELQHITMSQHAQ KEPPRSRGSRERDMALHHHSCLCFRSWLPAMLAVLLSLAPSASS DISASENTILLLMADDLGIGDIGCYGNNTMFTPHIDRLAEDGUK LTQHISAASLCTPSPAAFLIGEBKEVNLEGKANGTGRVLQWTGAS GGLPTNETTPAKILERGYATGLIGKWHLGILNCESASHCHHPL HHGPPHYGMPFSHMGDCAAPHESKEVNLEGKKNKHGPLLFV ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSIFVGALIVHA DCFLMRNHTITTEQPMCFQRTTPLILQEVASFLKRKKHGPLLFV SFLHVHIPLITMENFLGKSLHGYDNVKEMMWGRILDTLDV EGLSNSTLIVFTSDHGGSLENQUANTQYGGWNGIYKGGKMGGWV QDRVIDGGDLIPLLLGTAGHSDHEFLMHVCERPLHAARMHORDR GGTMVKUFVTPVEDPSGAGACKVCPCFGEKVVHHDPPLLFD LSRDPSETHILTPASEPVFYQWMRRVQQAVWEHQRTLSPVPLQ GTMMKVHFVTPVEDPSGAGACKVCPCFGEKVVHHDPPLLFD LDRLGNIWRFWLQPCGFFFLCWCLREDDPQ  6061 110 1330 MNIHMKRKTIKNINTFENRKLHDLCMNPAVRVKTELLESEQGSPN VHNYPDMEAVPLLLINNINGEPPEDSLSVHFQTQTEPVDLSINK ARTSPTAVSSSPVSWTASASSPSTSTSSSSSRLASSPTVITS VSSASSSTVLTTGGPLVASASGVGGQGPLHIHPVPPBSSPMNLQ SNKLSHHRI PLVVQSVPVVYLNSPSPMNTIVTVPLLEGGG GKAQMDPRGLSPRQSKSDSDDDDLPNVTLDSVNETGSTALSIA RAVGEVHPSPVSRVAGANSPSSTSTSSSSSRLASSPTVITS VSSASSSSTVLTTGGPLVASASGVGGQCPLHIHPVPPBSSPMNLQ SNKLSHHRI PLVVQSVPVVYLNSPSPMNTIVTVPLLEGGG GKAQMDPRGLSPRQSKSDSDDDDLPNVTLDSVNETGSTALSIA RAVGEVHPSPVSRVAGANSPSSTSTSSSSSRLASSPTVITS VSSASSSSTVLTTGGPLVASASGVGGQCPLHIHPVPPBSPMNLQ SNKLSHHRI PLVVGGSVFVYNGVKYRFRRTHTGKKPY KCTMEGCTWKFAASDELTRHYRKHTGVKPFKCADCDRSFRSDH LLLILMRHMLU  FESEPEEEIDENEEITTTFFEQSVLWVPAEKPIERTHTGKNY TEIFRSGNGTDETLEVHPKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVLWVPAEKPIELDGYPP EEGGLHFFANEKKGIEQNEQWVPQVVKKTRHARQASEELP INDYTENGIEFPDMLDERGYCCTIYCRGNRYCRRCPELLGYPP YPYCYQGGRVICRVINDPCHWWARMLGRV  FWYCYQGGRVICRVINDPCHWWARMLGRV TEIFRSGNGTDETLEVHPFKNGYTGIYFVGLQKCFIKTQIKVII TEIFRSGNGTDETLEVHPFKNGYTGIYFVGLQKCFIKTQIKVII TEIFRSGNGTDETLEVHPFKNGYTGIYFVGLQKCFIKTQIKVII TEIFRSGNGTDETLERTTFFFEGSVIWWPAEKPIERNFFLKNSKI				TGTCRICKMPLQSEEEFIEHCQMHPDLRNSLTGFRCVVCMQTVT			
GIRCPEGSVKFESAEDLESIMQUHRDLTFTSGPRKGTOTSPV PRKKTYQCIKCOMFFENERSINQUHRDLTFTSGPRKGTOTSPV PRKKTYQCIKCOMFFENERSINQUHRDLTFTSGPRKGTOTSPV VHGGEDKIYDCGCPGVKFFPUTELQHNITMGHAQ  6060 2145 202 SYETVGKNKLEVNISQLKALCKGLESRLLPIGEBLPLLDRGFR KEPRSRGSRERDMILHLHHSCLCFRSWLFAMLAVLLSLAPSASS DISASRPNILLHANDDLG IGIOLGYGMNTMTFPNIDRLAEDGUK LTQHISAASLCTPSRAAFLTGRYPVRSGRWSSIGYRVLQWTGAS GGLPPTETTPAK LIERGYATGLIGKWHLGINCESASDHCHHPL HGPDHFYGMPFSLMGDCARWELSERVANLEGKLMFLFQVLALV ALITUVAGKLTHLIPVSWMPVIWSALSAVILLASSYFVALLAVHAA DCFLMRHHTITEOPMCFQRTFULQEVASFLKRNKHGPFLLFV SFLHWHPLITMRNFIJGKSLIGLYGDNVKEMDWMGRILDTLDV SFLHWHPLITMRNFIJGKSLIGLYGDNVKEMDWMGRILDTLDV SFLHWHPLITMRNFIJGKSLIGLYGDNVKEMDWMGRILDTLDV GGTWKVHFVTPVFQFBGAGGCYGRVVCPCFGKVVHHDPFLLFD LSRDPSSTHILITPASSPVFYQWAER VQQAWEHQRTLSPVPLQ GDRVIDGQDLIPLLLGTAQHSDHEFLMHYCERFLHAARHWGRDR GTWKKVHFVTPVFQFBGAGGCYGRKVCPCFGKVVHHDPFLLFD LSRDPSSTHILITPASSPVFYQWAER VQQAWEHQRTLSPVPLQ LDRIGHTWRWKJFYTTVFQFBGAGGCYGRKVCPCFGKVVHHDPFLLFD LSRDPSSTHILITPASSPVFYQWAER VQQAWEHQRTLSPVPLQ WHNYPDMEAVPLLINNVKGPPEDSLSVDHFQTQTEPVDLS INK ARTSPTAVSSSVSWTASASSPSTSTSSSSSRLASSPTVITS VSSASSSTVLTTGGPLVASASGVGGQCHLHHFVPPSSPMNLQ SNKLSHWRIPVVQSVPVVYTAVRSPGNVNNTIVVPLLEGEGGFM HGKAQMDPRGLSPRQSKSDSDDDLFWTLDSVHETGSTALSIA RAVOEVHSPSVSRVGNNRMNOKPPCSIS PFSIESTRRQFRVIAN PDDSRKTAYSTDCDF\EGIQQKLYTKSSSPGRVHRRTHTGEKPY KCTWEGCTWKFARSDEDTHRYRKHTGVKFFKCADCDRSFRSDN LALHRRHMLV  6062 71 1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILAUT LIVLFMGSKHFPBEVVRKAYDMEHTFYSNGEKKIYMEIDPVTR TEIFRSGNGTDETLEVHDPKNGYTGIYFVGLQKCFILKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPICAGVYFGLAUT LIVLFMGSKHFPBEVPKKAYDMEHTFYSNGEKKIYMEIDPVTR TEIFRSGNGTDETLEVHDPKNGYTGIYFVGLQKCFILKTGIKVII  ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILAUT LIVLFMGSKHFPBEVPKKAYDMEHTFYSNGEKKIYMEIDPVTR TEIFRSGNGTDETLEVHDPKNGYTGIYFVGLQKCFILKTGIKVII  EFMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILAUT LIVLFMGSKHFPBEVPKKAYDMEHTFYSNGEKKIYMEIDPVTR TEIFRSGNGTDETLEVHDPKNGYTGIYFVGLQKCFILKTGIKVII  EFMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILAUT LIVLFMGSKHFPBEVPKKAYDMEHTFYSNGEKKIYMEIDPVTR TEIFRSGNGTDETLEVHDPKNGYTGIYFVGLQKCFILKTGIKVII				STLELKIHGTFHMQKLAGSSAASSPNGQGLQKLYKCALCLKEFR			
PRKKTYQCIKCOMTFENERGIGHVANHMIERGINHECKLCNOM FISSPAKLICHLI EISFBRMGETEKCPVCFTVFVQANKLQHI PA VHGQEDKIYDCSQCPQKFFFQTELQNHTMSQHAQ  8YEIVGNIKLEVAHRSQCKALCKCSLDSFILDIGERLPILDRGFF KEPRSRGSRERDMMLHLHSCLGFRSWLPAMLAVLISLAPSASS DISASRNILLLANDDLGIGDIGCYGNNTMFTPNIDRLAEDGVK LTQHISASSLCTPSRAPFLINGFVBSGWYSSIGVLQWTGAS GGLPTNETTPAKILEEKGYATGLIGKWHLGINCESASDHCHHPL HHGPDHFYGMFFSHMGIDCARWELSERKVNLEGKLIFLEQULALV ALITUVAGKLIHLIPVSMMPVIWSALSAVLLIASSFVCALLVHA DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRIKHGPFLLFV SFLHVHIPLITIMFNFLKSKLHGYDNVKEMBWMGYRLIDTLDV SFLHVHIPLITIMFNFLKSKLHGYDNVKEMBWMGYRLIDTLDV GURVIDGQDLLPILLGTAGHSDHEFILMHYCERFLHAARWHGRDR GTMKVHFVTPVFQPSEAGACYGRKVCFCFGEKVYHHDPFLLFD LSRDPSSTHILITASSPVFJOWHGYTLSGSEVP QDRVIDGQDLLPILLGTAGHSDHEFILMHYCERFLHAARWHGRDR GTMKVHFVTPVFQPSEAGACYGRKVCFCFGEKVYHHDPFLLFD LSRDPSSTHILITASSPVFJOWHGYVGGWMGVKFGLLESEQGSPN VHNYPDMEAVPLLLNNVKGEPPEDSLSVDHFQTQTEPVDLSINK ARTSPTAVSSSFVSMTASASSPSSTSTSSSSSRLASSPTVITS VSSASSSTVLTSPLVASASGGQGGHLHIPVPPSSPMINT ARTSPTAVSSSFVSMTASASSPSSTSTSSSSSRLASSPTVITS SSSSSSTSTSPLASSPTVITS GSSSSSTVLTSPLVASASGGGGGFHLHVPPPSSFMVL SKIKLSHYHRIPVVVQSVPVYTAVRSPGNVNNTIVPLLEDGRG HGKAQMDPRGLSPRQSKSDSDDDDDLFVTLDSVETSTSLSILA RAVOEVHPSPVSRVRGNRNNNGKPFCSISPFSIESTRRQRTVLN PPDSRKTAYSTDCDF\EGIQQKLYTTSSSPGRVHRTTHTGEKPY KCTWGGCTWFRASDELTRHYRKHTGVKPFFKCADCDRSFSRSDH LALHRRHHMLV  FISHRGGTBETLEVHDFKNGYTGIYYFGLQKCFIKTOLKVIP EFSSPEELDENER ITTTFFERGVIWVPAEKPIENRPPLKNSKI LEICDNVTMW\INPTL\ISGTFAKQLHHNPAFIILVSELQDPE EEGEDLHFANEKKGIEGNEQWVVPQUVVERCRERARGCEPLIGYY YPYCYQGGRVICRVIMPCNWWARMLGRV  FTHAKMOPPENCECHTILNAEAFKSKKICKSLKICGLVFGILALT LIVLFMGSKHFWPEVPKKAYDMEHTFYSNGEKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYYFGLQKCFIKTOLKVIP PSPEEELDENERFSKKKICKSLKICGLVFGILALT LIVLFMGSKHFWPEVPKKAYDMEHTFYSNGEKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYYFGLQKCFIKTOLKVIP TEIFRSGNGTDETLEVHDFKNGYTGIYYFGLQKCFIKTOLKVIP TEIFRSGNGTDETLEVHDFKNGYTGIYYFGLQKCFIKTOLKVIP TEIFRSGNGTDETLEVHDFKNGYTGIYYFGLQKCFIKTOLKVIP TEIFRSGNGTDETLEVHDFKNGYTGIYYFGLQKCFIKTOLKVIP TEIFRSGNGTDETLEVHDFKNGYTGIYYFGLQKCFIKTOLKVIP TEIFRSGNGTDETLEVHDFKNGYTGIYYFGLQKCFIKTOLKVIP TEIFFRS				SKODLVKLDVNGLPYGLCAGCMARSANGQVGGLAPPEPADRPCA			
FISPAKLICHLIEHSFRINGGTFKCPVCFTVFVQNKLQQHIFA VIGGDRIYIDCQCCPUKPTGLQNHTMSQHAQ  SYEYUGNKLEVNHSQLKALCKCSLPSRLLPIGENLPLLDRGFR KEPRSRSRERDNMLHLHHSCLCFRSWLPAHLAVLLSLAPSASS DISASRPNILLMADDLGIGGIGCYGNNTMTFPNIDRLABEDGVK LTQHISAASLCTPSRAFLITGRYPVRSGMVSSIGTRVLQWTGAS GGLPYNETTFAKILEEKGYAGLIGKHHLGINCESASDHCHPL HHGPHFYGMPFSLMGDCARRELSEKRVNLEQKLMFLFQVLLALV ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALTVHA DCFLMRNHTITEQPMCFQRTTPLILQEVASSLKRNKHSPPLLFV SFLHVHIFLITMENFLGKSLHGLVGGDWIGTVKGGKMGGW EGGINSVTLIYFTSDHGGSLERQLGNTQYGGMNGIYKGGKGMGGW EGGIRVPGIFRHPGVULPAGRVIGEFTSLMDVFPTVVRLAGSEVP QDRVIDGQDLIPLLIGTAGNFFLHWICKTPHARAMHORDR GTMMKVHPVTPVFQPEGAGACYGRKVCPCFGEKVVHHDPFLLFD LSRDPSETHILTPASEPVFYQVMER/VQAVWEHQRTLSPVPLQ CDRVIDGGDLIPLLIGTAGNGYGYGMYKTELLESEGGSPN WINNYDMEAVPLLINNVKGEPDSLSVSUHFQTTGFPVDLSINK ARTSPTAVSSSPVSMTASASSPSSTSTSSSSSKLASSPTVITS VSSASSSTVLTPGPLVASASGVGGQCFHIHFVPSSFMNLIG SNKLSHYHRIPVVVQSVPVVYTAVRSEGNVNNTITVVPLLEDGGG HGKAQMPRGLSPRQSKSDSDDDDLPNVTLDSVNETGSTALSIA RAVQEVHSPSVSRVGRGRMNNOKFPCSISPSISTSRSTLASSPTVITS VSSASSSTVLTPGPLVASASGVGGQCFGLSPTSTESTRRGRTVLN RAVGEVHSPSVSRVGRGRMNNOKFPCSISPSISTSTRSFTLLSIA RAVGEVHSPSVSRVGRGRMNNOKFPCSISPSISTSTRSFTLLSIA RAVGEVHSPSVSRVGRGRMNNOKFPCSISPSISTSTRSFTLLSIA RAVGEVHSPSVSRVGRGRMNNOKFPCSISPSISTSRSFTLLSIA RAVGEVHSPSVSRVGRGRMNNOKFPCSISPSISTSTRSFTLLSIA LLUHFMGSKHFWBPVFKKAVDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGITVVGLQKCFIKTQIKVIP FFSPEEEIDENEEITTTFFGGVIWVPAKKYRRVCPPLLGYY YPYCYQGGRVICRVIMPCNWWVARMLGRV  ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFMGSKHFWBPVFKKAVDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGVCPPLLGYY YPYCYQGGRVICRVIMPCNWWVARMLGRV  ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFMGSKHFWBPVFKKAVDMEHTFYSNGEKKKIMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGVCFPLLGYY YPYCYQGGRVICRVIMPCNWWARMLGRV  ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFMGSKHFWBPVFKKAVDMEHTFYSNGEKKKIMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGVCFPLLGYY YPYCYQGGRVICRVIMPCNWWARMLGRV  ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFMGSKHFBVEVFKKAVDMEHTFYSNGEKKKIMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGVVCPPLLGYVTR				GLRCPECSVKFESAEDLESHMQVDHRDLTPETSGPRKGTQTSPV			
VHGGEDKIYDCSQCPQKFFFQTELQNHTMSQHAQ				PRKKTYQCIKCQMTFENEREIQIHVANHMIEEGINHECKLCNQM			
SYETYGKKLEVNHSQLKALCKCSLPSRLLPLGENLPLLDRGFR   KEPRSRSRERDINNLHLHHSCLCTRSWLFANLAVLLSLAPSASS   DISASRPNILLIMADDLG LGGIGCYGNNTMRTPNIDRLABEGVK   LTQHISAASLCTPSRAAFLTGRYVRGMVSSIGTRVLQWTGAS   GGLPYNETTFAKILEEKGYALIGKKHKLGINCESASPHCHPL   HHGPDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLGNCESASPHCHPL   HHGPDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALVHA   ALTIVVAGKITHLIPVSMMPVIWSALSAVLLLASSYFVGALIVHA   DCFLMRNHTITEQPMCFGRTTPLILQEVASFLKRNKHSPPFLLFV   SFLWHIPLITMEMFLGKSLRGLYGDWYKEMDWWGRILDTLDV   SFLWHIPLITTEQPMCFGRTTPLILQEVASFLKRNKHSPPFLLFV   SFLWHIPLITHEQPMCFGRTTPLILQEVASFLKRNKHSPPFLLFV   SFLWHIPLITHAMFUGKSLENJCGNTYGGWNKEMDWWGRILDTLDV   SFLWHIPLITHAMFUGKSLENJCHTVGGWGWGW   EGGIRVPGIFRWPGVLPAGRVIGEPTSLMDVFPTVVLLAGSEVP   QDRVIDGQDLLPHLLGTARGRVIGEPTSLMDVFPTVVLLAGSEVP   QDRVIDGQDLLPHLLDGATGVGKVCPCFGGKVVHHPPPLLFD   LSRDPSETHILTPASEPVFYQDMER VQQAVWHHQRTLSPVPLO   LDRLGNIWRPWLQPCCGPFPLCWCLREDDPQ   MNIHWKRRTIKNINTFENRMLMLDGMPAVRWRTELLESEQGSPN   VHNYPDMEAVPLLLINNVAGEPPEDSLSVDHFOTOTEPVDLSINK   ARTSPTAVSSSPVSMTASASSPSSTSTSSSSKALSSPTVITS   VSSASSSTVITSPDPLVASASGVGQQFLHIHPVPPSSPMNLQ   SNKLSHVHRIPVVVQSVPVVTTAVRSGNVMNTIVVPLLEDGRG   HGKAQMDPRGLSPRQSKSDSDDDDLFNVTLDSVMETGSTALSIA   RAVQEVHPSPVSRVRGNRMNNQKPPCSISPFSIESTRQRTVLN   PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGRVSHRTHTGKPY   KCTWEGCTWKPARSDELTRHYRKHTGVVPFKCADCDRSFGRSDH   LALHRRHMLV   LAHRRHMLV   LAHRRHMLV   LAHRRHMLV   LAHRRHMLV   LAHRRHMLV   LEIGNDWITTFEQSVIWVPAEKPIENDRFLKNSKI   LEICDNVTMWVNINPTLV[SGTFAKQLHHNFAFIILVSELQDPF   EGGDLHFPANEKKGIEDNEEITTFFFEQSVIWVPAEKPIENDRFLKNSKI   LEICDNVTMWVNINPTLV[SGTFAKQLHHNFAFIILVSELQDPF   EGGDLHFPANEKKGIEDNEEITTFFFEQSVIWVPAEKPIENDRFLKNSKI   LEICDNVTMWVNINPTLV[SGTFAKQLHHNFAFIILVSELQDPF   EGGDLHFPANEKKGIEDNEHVPVPQVKVEKTRHARQASEEELP   INDYTEMGIEFDPMLDERGYCCTTCRRGNRYCRRVCEPLLGYYP   YPYCYQGGRVICRVIMPCNMVARMLGRV   ETMRKNGFBENEDHTITHRAFFKSKKICKSLKICGLVFGILALT   LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR   TEIFRSGNGTDETLBVHDFRKKKIYFGLQXCFIKTQIKVIF   FESPEEEIDENBEITTTFFFEQSVIWVPAEKFLKTGIKVIF   FESPEEEIDENBEITTTFFFEQSVIWVPAEKFLKDFLKNSKI							
REPRSRGSRENDMILILMADDIG LODICGYGMIYMETPHINDELAEDGYK   LTQHISAASLCTPSRAAFLTGRYPVRSGMYSSIGYRVLQWTGAS   GGLPTNETTFAKILEEKGYATGLIGKHHLGLNCESASDHCHHPL   HHGPDHFYGMPFSLMGDGYMELSEKKYNLEQKUNFLFQVLALVA   ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA   DCFLMRNHTITEQDMCGSTPTPLILQEVASFLKRKHGPPLLFV   ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA   DCFLMRNHTITEQDMCGSTPTPLILQEVASFLKRKHGPPLLFV   SFLHVHIPLITMENFLGKSLHGLYGDNYKEMDWMVGRILDTLDV   EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKEMGGW   EGGIRVPGIFRMPGVILPGAVIGEPTEHDVFFTVVLAGGSEVP    QDRVIDGODLIPLLIGTAGHSHEFIMHYCERFLHAARWHGDR   GTMMKVHFYTPVFQPEGAGACYGRKVCPCFGEKVVHHDPPLLFD   LSRDPSETHILTPASEPYTQOWMERVQOAVWEHQRTLSPVPLO    LDRIGNIWRPHLQPCCGPFPLCWCLREDDPQ   LDRIGNIWRPHLQPCCGPFPLCWCLREDDPQ   LDRIGNIWRHFYTFVFQPEGAGACYGRKVPCFTGEKVVHHDPPLLFD   LARISPTAVSSPVSNTASASSPSSTSTSSSSSLASSPTVITS   VSSASSSTVLTFGPLVASASGVGGQOFLHIHPVPPSSFMNLO    SNKLSHVHRIPVVQSVPVYTAVRSPGMVNNTIVVPLLEDGRG   HGKAQMDPRGLSPRGSKSDSDDDDLPNVTLDSVNETGSTALSIA   RAVOEVHPSPVSRVRGNRMNNQKFPCSISFSTSSTALSIASITVITS   VSSASSSTVLTFGPLVASASGVGGQOFLHIHPVPPSSFMNLO    SNKLSHVHRIPVVQSVPVYTAVRSPGMVNNTIVVPLLEDGRG   HGKAQMDPRGLSPRGSKSDSDDDDLPNVTLDSVNETGSTALSIA   RAVOEVHPSPVSRVRGNRMNNQKFPCSISFSTSLSTALSIA   RAVOEVHPSPVSRVRGNRMNNQKFPCSISFSTESTRQRTVLN   PPDSKTAYSTDCDF\STALSIA   RAVOEVHPSPVSRVRGNRMNNQKFPCSISFSRSDL   LALHRRHMLV   ETMAKNGFENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT   LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIVMEIDPVTR   TEIFRSGMGTDETLEVHDFKNGYTGIYFVGLQKCFIKTOIKVIP   EFSSPEELIDNEBITTFEGSVIWVPAEKPIPHRAQASEELP   INDYTEMGIFFDPMLDERGYCCIYCRRGMRYCRRVCEPLLGYYP   YPYCYQGGRVICRVIMPCNWWARMLGRV   YPYCYQGGRVICRVIMPCNWWARMLGRV   STAMKNGFENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT   LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIVMEIDPVTR   LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIVMEIDPVTR   ETMAKNGFENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT   LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIVMEIDPVTR   ETHRAKNGFENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT   ETHRAKNGFENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT   ETHRAKNGFENCEDCHILNAEAFKSKKICKSLKKIKGLICGLVFGILALT   LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIVMEIDPVTR   LIVL	6060	2145	202				
DISASRPNILLIMADDLG IGDIGCYGNNTWRTPNIDRLAEDGUK LDQHISAASLCTPSRAAFLTGRYFVRSGMVSSIGYRULQWTGAS GGLPTNETTFAKILEEKGYATGLIGKWHLGLNCESASDHCHHPL HHGPDHFYGMFFSLMGDCARWELSEKKVNLEQKUNFLFQVLALV ALITLVAGKLHHLIPVSWMVWSALSAVLLASSYFVGALIVHA DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPPLLFV SFLHVHIPLITMENFLGKSLHGLYGDNVKEMWDMVGRILDTLDV EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGKGKGMGW EGGINSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGKGKGMGW GGRWKVHFVTPVFQPEGAGACYGRKVCPCFGEKVVHHDPPLLFD DDRYLDGQOLDLPLLLGTANDSHEFLMHYCGRPLHAARWHQRDR GTMWKVHFVTPVFQPEGAGACYGRKVCPCFGEKVVHHDPPLLFD LSRDPSETHILTPASEPVPYQVWREN VQQAVWEHQRTLSPVPLQ LDRLGNINRPMLQPCCGPPPLCWCLREDDPQ  MNIHKKRKTIKKINTFENRMLMLDGMPAVRVKTELLESEQGSPN VHNYPDMEAVPLLLNNVKGEPPEDELSVHHFQTQTEPVDLS INK ARTSPTAVSSSFVSNTASASSPSSTSSSSRALSSPTVITS VSSASSSSTVLTPGPLVASASGVGQQFLHIHPVPPSSPMNLQ SNKLSHVHRIPVVQQSVPVVYTAVRSGRVHNTIVVPLLEDGRG HGKAQMDPRGLSPRQSKSDSDDDDLPNVTLDSVNETGSTALSIA RAVGEVHPSPVSRVRGNRNNNQKFPCSISFFSIESTRQRTVLN PPDSSKTAYSTOCPF\CQUKLYTKSSSFGNHARTHTGEKPY KCTMEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH LALHRRHMLV  5062 71 1079 ETMAKNGFENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT TEIFRSGMGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFFSPEEEIDENBEITTTFFEQSVIWVPAEKFIENDFIKNSKI LEICDNVTMWN\NPTL\ISGTFAKQLHHNFAFIILVSELQDPE EEGGLHFPANEKGSIEQNEVVPQVVVVQVKVKTRHARQASEEELP INDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP YPYCYQGGRVICRVIMPCNWWVARMLGRV 1079 ETMAKNGFENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT TEIFRSGMGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFFSPEEEIDENBEITTTFFEQSVIWVPAEKFIENDFIKNSKI LEICDNVTMWN\NPTL\ISGTFAKQLHHNFAFIILVSELQDPE EEGGLHFPANEKGSIEQNEVVPQVVVVQVVKVKTRHARQASEEELP INDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP YPYCYQGGRVICRVIMPCNWWVARMLGRV 1079 ETMAKNGFENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFMGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGMGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFFSREEEIDENBEITTTFFEGSVIWVPAEKFICHTDFIKNSKI LIVLFMGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGMGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFFSREEEIDENBEITTTFFEGSVIWVPAEKFICHTDFKNSKI	1			KEPRSRGSRERDNMLHLHHSCLCFRSWLPAMLAVILSLAPSASS			
LTQHISAASLCTBRAAFLTGRYPYRSGMVSSIGYRULQWTGAS GGLPTNETTFAKILEEKKYATGLIGKWHLGLNCESASDHCHHPL HHGPPHFYMPFSLMGDCARWELSEKKVULEQKLNFLFQVLALV ALTLVAGKLTHLIPVSMMPVIWSALSAVLLLASSYFVGALIVHA DCFLMRNHFITEQPMCRTTPLILQEVASFLKRNKHGPPLLFV SFLHVHIPLITMENFLGKSHGLVGDNYKEMBWMVGRILDTLDV EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW BGGIRVPGIFFNWFGVLAGRVIGBETSLMDVPFTVVRLAGSEVP QDRVIDGQDLLPLLGTAQHSDHEFLMHYCERFLHAARWHQRDR GTMMKVHFVTPVFQPEGAGACYGKVCPCFGEKVVHHDPPLLFD LSRDPSETHILTPASEPVFYQVMER\VQQAVWEHQRTLSPVPLQ LDRLGNINRPWLQPCCGPFPLCWCLREDDPQ  6061 110 1330 MNIHMKRKTIKNINTFENRMLMLDGMPAVRVKTELLESEQGSPN VHNYPDMEAVPILLINNVKGEPPEDSLSVDHFQTQTEPVDLSINK ARTSPTAVSSSVSMTASASSPSTSTSSSSSSRLASSPTVITS VSSASSSTVLTFGPLVASASGVGQQFLHILHPVPPSSPMNLQ SNKLSHVHRIPVVQSVPVYTAVRSFGNVNNTIVVPLLEDGRG HGKAQMDPRGLSPRQSKSDSDDDLPNVTLDSVNETGSTALSIA RAVOEVHPSPVSRVRGNRMNNQKFPCSISPFSIESTRQRTVLN PPDSRKTAYSTDCDP\GGLQQKLYTKSSSPGRVHRRTHTGEKPY KCTWEGCTWKFFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH LALHERRIMLV  6062 71 1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGGTDETLEVHDFKNGTTGIYVFUGLOKCFIKTOIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENDFLKNSKI LEICDNVTMYM\INPTL\SIGNEWVPQVVVEVETRHARQASEEELP INDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP YPYCYQGGRVLCRVIMPCNWVMARMLGRV EFSEPEEEIDENEEDTLINAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDPKNGTTGIYVFUGLOKCFIKTOIKVIP PETMAKNGFENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKYMEIDPVTR TEIFRSGNGTDETLEVHDPKNGTTGIYFVGLOKCFIKTOIKVIP TEIFRSGNGTDETLEVHDPKNGTTGIYFVGLOKCFIKTOIKVIP TEIFRSGNGTDETLEVHDPKNGTTGIYFVGLOKCFIKTOIKVIP TEIFRSGNGTDETLEVHDPKNGTTGIYFVGLOKCFIKTOIKVIP TEIFRSGNGTDETLEVHDPKNGTTGIYFVGLOKCFIKTOIKVIP TEIFRSGNGTDETLEVHDPKNGTTGIYFVGLOKCFIKTOIKVIP TEIFRSGNGTDETLEVHDPKNGTTGIYFVGLOKCFIKTOIKVIP TEIFRSGNGTDETLEVHDPKNGTTGIYFVGLOKCFIKTOIKVIP TEIFRSGNGTDETLEVHDPKNGTTGIYFVGLOKCFIKTOIKVIP TEIFRSGNGTDETLEVHDPKNGTTGIYFVGLOKCFIKTOIKVIP TEIFRSGNGTDETLEVHDPKNGTTGIYFVGLOKCFIKTOIKVIP	1						
GGLPYNETTFAKILEEKGYATGLIGKWHLGILNCESASDHCHHPL HHGPDHFYGMFPSLMGDCARWELSEKRVNLEQKLNFLFQVLALV ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPPLLFV SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDMWVGRILDTLDV GGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW EGGIRVFGIFRWFGVLPAGRVUGEFTSLMDVFPTVVRLAGGEVP ODRVIDGQDLLPLLLGTAQHSDHEFLMHYCERFLHAARWHQRDR GTMMKVHFVTPVFQPEGAGACYGRKVCFCFGEKVVHHDPPLLFD LSRDPSETHILTPASEPVFYQVMER\VQQAVWEHQRTLSPVPLQ LDRLGNINWPWLQPCCFPPLCWCLREDDPQ MNIHMKRKTIKNINTFENRMLMLDGMPAVRVKTELLESEQGSPN VHNYPDMEAVPLLLINNVKGEPPEDSLSVDHFQTQTEPVDLSINK ARTSPTAVSSSPVSMTASASSPSSTSTSSSSSRLASSPTVITS VSSASSSTVLTFGPLVASASGVGQQFLHILHPVPPSSPMNLQ SNKLSHVHRIPVVQSVPVVTAVRSGGNVNNTIVVPLLEDGRG HGKAQMDPRGLSPRQSKSDSDDDDLPNVTLDSVNETGSTALSIA RAVGEVHPSPVSRVKGNRMNNQKFPCSISPFSIESTRRQRTVLN PPDSRKTAYSTDCDF\EGLQQKLYKKSSSPGVHRRTHTGEKPY KCTMEGCYMKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH LALHRRHMLV  6062 71 1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGTTGIYVGLQKCFIKTQIKVIP EFSSPEEEIDENBEITTTFFEQSVIWVPAEKPIENDFLKNSKI LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDPE EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP INDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP YPYCYQGGRVICRVIMPCNWVARMLGRV  6063 71 1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP PFSSPEEEIDENBEITTTTFFEQSVIWVPAEKPIENDFLKNSKI							
HHGPDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV ALTLVAGKLTHLI PVSWMPVI WSALSAVLLLASSYFVGALIVHA DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPPLLFV SFLHVHIPLITMENFLGRSLHGLYGDNVKEMDWMYGRILDTLDV EGLSNSTLIYPTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW EGGIRVPGIFRWPGVLPAGRVIGEPTSLMDVFPTVVRLAGSEVP QDRVIDGQDLLPLLLGTAQHSDHEFLMHYCRRFLHAARWHQRDR GTMWKVHFVTPVPCGAGAGACYGRKVCPCFGGEKVVHHDPPLLPD LSRDPSETHILTPASEPVFYQVMER\VQQAVWEHQRTLSPVPLQ LDRLGNIWRPWLQPCCGFFPFLCWCLREDDPQ MNIHWKRTIKKINTFERNKLMLDGMPAVRVKTELLESEQSPN VHNYPDMEAVPLLLNNVKGEPPEDSLSVDHFQTQTEPVDLSINK ARTSFTAVSSSPVSMTASASSPSSTSTSSSSSSKLASSPTVITS VSSASSSSTVLTEPDLVASASGVGQQFLHIHPVPPSSPMLQ SNKLSHVHRIPVVVQSVPVYTAVRSPGNVNNTIVVPLLEDGRG HGKAQMDPRGLSFRQSKSDDDDLENVTLDSVNETGSTALSIA RAVOEVHSPSVSRVKGRNMNNQKFPCSISPFSIESTRRQRTVLN PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGNVHRTHTGEKPY KCTWEGCTWKFARSDELTRHYKKHTGVKPFKCADCDRSFSRSH LALHRRRIMLV  6062 71 1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSSPEEEIDENEEITTTFFBQSVIWVPAEKPIENRDFLKNSKI LEICDNVTMYW\INPTL\ISGTFAKQLHHRFAFIILVSELQDPE EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP INDYTENGIEFDPMLDERGYCCIYCRGRBYCRRVCEPLLGYYP YPYCYQGGRVICRVIMPCNWWARMLGRV  6063 71 1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLBVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSSPEEEIDENEEITTTFFBQSVIWVPAEKPLENDFLKNSKI LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLBVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFTSPEEEIDENEEITTTFFBQSVIWVPAEKPLENDFLKNSKI				GGLPTNETTFAKILEEKGYATGLIGKWHLGLNCESASDHCHHPL			
DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPPLLFV SFLHVHIPLITMENFLGKSLHGLYGQDNYEMDMWVGRILDTLDV EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKMGGW EGGIRVPGIFRWPGVLPAGRVIGEPTSLMDVFPTVVRLAGSEVP QDRVIDGQDLLPLLGTAQHSDHEFLMHYCERFLHAARMHQRDR GTMWKVHFVTPVPCPEGAGACYGRKVPCPGEGKVVHHDPPLLFD LSRDPSETHILTPASEPVFYQVMER\VQQAVWEHQRTLSPVPLQ LDRLGNINRPWLQPCCGPPFLCWCLREDDPQ  6061 110 1330 MNIHMKRKTIKNINTFENRMLMLDGMPAVRVKTELLESEQGSPN VHNYPDMEAVPLLLNNVKGEPPEDSLSVDHFQTQTEPVDLSINK ARTSPTAVSSSPVSMTASASSPSSTSTSSSSSRLASSPTVITS VSSASSSTVLTPGPLVASASGVGGQFLHILHPVPPSSPMNLQ SNKLSHVHRIPVVQSVPVVYTAVRSPGRVNNTIVVPLLEDGRG HGKAQMDPRGLSPRQSKSDSDDDDLPNVTLDSVNETGSTALSIA RAVGEVHPSPVSRVRGNRNNQKFPCSISFFSIESTRRQRTVLN PPDSRKTAYSTDCDF\EGLQQKLYKSSSPGVMRTHTGEKPY KCTWEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH LALHRRHHLV  6062 71 1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDPKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEITTTFFEQSVIWVPAEKPIENRDFLKNSKI LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDPE EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP INDTTENGIEFDPMLDERGYCCITCRRGNRYCRRVCEPLLGYYP YPYCYGGRVICRVIMPCNWWARMLGRV TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP ETFSEPEEEIDENEEITTTFFEGSVIWVPAEKPIENRDFLKNSKI LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEGSVIWVPAEKPIENRDFLKNSKI	1			HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV			
SFILHUHI PLITMENFICKSLINGLYGDNV KEMDWAWGRILDTLDV EGLSNSTLIYFTSDHGSLENQLGNTQYGGWNGIYKGGKGMGW EGGIRVPGIFRWPGVLPAGRVIGEFTSLMDVFPTVVRLAGSEVP QDRVIDGQDLLPLLIGTAQHSDHEFLMHYCERPLHAARWHQRDR GTMWKVHFVTPVFQPEGAGACYGRKVCPCFGEKVVHHDPFLLFD LSRDPSETHILTPASEPVFYQVMER\VQQAVWEHQRTLSPVPLQ LDRLGNIWRPWLQPCCGPFPLCWCLREDDPQ  6061 110 1330 MNIHWKRKTIKNINTFERIMLMLDGMPAVRVKTELLESEQGSPN VHNYPDMEAVPLLINNVKGEPPEDGLSVDHFQTQTEPVDLSINK ARTSPTAVSSSFVSMTASASSPSSTSTSSSSSRLASSPTVITS VSSASSSSTVLTPGPLVASASGVGGQQFLHIHPPVPPSSPPMLQ SNKLSHVHRIPVVQSVPVVYTAVRSPGNVNNTIVVPLLEDGRG HGKAQMDPRGLSPRQSKSDSDDDDLPNVTLDSVNETGSTALSIA RAVQEVHPSPVSRVVRGNRNNNQKFPCSISPFSIESTRRQRTVLN PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGRVHRRTHTGEKPY KCTWEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH LALHRRHHLV  1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI LEICDNVTMYW\INPTL\ISGTFAKQLHIMFAFTILUSELQDPE EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP INDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP YPYCYGGRVICRVIMPCNWWARMLGRV  6063 71 1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEGSVIWVPAEKPIENDFLKNSKI LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDRKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEGSVIWVPAEKPIENDFLKNSKI	1 1						
EGLSNSTLIYPTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGW EGGIRVPGIFRWPGVLPAGRYIGEPTSLMDVPFTVVRLAGSEVP QDRVIDGODLIPLLCTAQHSDHEFLMHYCERPLHAARWHQRDR GTMWKVHFVTPVFQPEGAGACYGRKVCPCFGEKVVHHDPPLLFD LSRDPSETHILTPASSPVFYQVMER\VQQAVWEHQRTLSPVPLQ LDRLGNIWRPWLQPCCGPFPLCWCLREDDPQ  6061 110 1330 MNIHWKRKTIKNINTPENRMLMLDGMPAVRVKTELLESEQGSPN VHNYPDMEAVPLLLINNVKGEPPEDSLSVDHFQTQTEPVDLSINK ARTSPTAVSSSPVSMTASASSPSSTSTSSSSSRLASSPTVITS VSSASSSTVLTFGPLVASASGVGQQFLHIHPVPPPSSPMNLQ SNKLSHVHRIPVVQSVPVVYTAVRSPGNVNNTIVVPLLEDGRG HGKAQMDPRGLSPRQSKSDSDDDDLENVTLDSVNETGSTALSIA RAVQEVHPSPVSRVRGNRMNNQKFPCSISPFSIESTRQRTVLN FPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGRVHRETHTGEKPY KCTWEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH LALHRRHMLV  6062 71 1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENDFLKNSKI LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDPE EEGGDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP INDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP YPYCYQGGRVICRVIMPCNWWARMLGRV  6063 71 1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIXMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSSPEEEIDENEEITTTFFEQSVIWVPAEKPIENDFLKNSKI							
GGGIRVPGIFRNEGVLPAGRVIGEPTSLMDVFPTVVRLAGSEVP QDRVIDGQDLLPLLLGTAQHSDHEFLMHYCERFLHAARWHQRDR GTMWKVHFVTPVFQPEGAGACYGRKVCPCFGEKVVHHDPPLLFD LSRDPSETHILTPASEPVFYQVMER\VQQAVWEHQRTLSPVPLQ LDRLGNIWRPNLQPCCGFFPLCWCLREDDPQ  6061 110 1330 MNIHMKRKTIKNINTFENRMLMLDGMPAVRVKTELLESEQGSPN VHNYPDMEAVPLLLINNVKGEPPEDSLSVDHFQTQTEPVDLSINK ARTSPTAVSSSPVSMTASASSPSSTSTSSSSSSRLASSPTVITS VSSASSSTVLTPGPLVASASGVGGQOFLHIHPVPPSSPMMLQ SNKLSHVHRIPVVVQSVPVVYTAVRSPGNVNNTIVVPLLEDGRG HGKAQMDPRGLSPRQSKSDSDDDDLPNVTLDSVNETGSTALSIA RAVQEVHPSPVSRVGNRMNNQKFPCSISFFSIESTRRQRTVLN PPDSRKTAYSTDCDF\EGLQQKLYTKSSSFGRVHRRTHTGERPY KCTWEGCTWKFASDELTRHYRKHTGVKPFKCADCDRSFSRSDH LALHRRHHMLV  6062 71 1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSSPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDFE EEGBDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP INDYTENGIEFDPMLDERGYCCIYCRGNRYCRRVCEPLLGYYP YPYCYQGGRVICRVIMPCNWWARMLGRV  6063 71 1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSSPEEEIDENEEITTTFFEQSVIWVPAEKPIENRGFKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSSPEEEIDENEETTTTFFEQSVIWVPAEKPIENRGFKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSSPEEEIDENEETTTTFFEQSVIWVPAEKPIENROFLKNSKI							
QDRVIDGQDLLPLLIGTAQHSDHEFLMHYCERFLHAARWHQRDR GTMWKVHFVTPVFQPEGAGACYGRKVCPCFGEKCVHHDPPLLFD LSRDPSETHILTPASEPVFYQVMER\VQQAWBHQRTLSPVPLQ LDRLGNIWRPWLQPCCGPFFLCWCLREDDPQ MNIHMKRKTIKNINTFENRMLMLDGMPAVRVKTELLESEQGSPN VHNYPDMEAVPLLLNNVKGEPPEDSLSVDHFQTQTEPVDLSINK ARTSPTAVSSSPVSMTASASSPSSTSTSSSSSSRLASSPTVITS VSSASSSSTVLTPGPLVASASGVGGQQFLHIHPPVPPSSPMNLQ SNKLSHVHRIPVVVQSVPVYTAVRSPGNVNNTIVVPLLEDGRG HGKAQMDPRGLSPRQSKSDSDDDDLPNVTLDSVNETGSTALSIA RAVQEVHPSPVSRVRGNRMNNQKFPCSISFFSIESTRRQRTVLN PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGRVHRRTHTGEKPY KCTWEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH LALHRRHMLV  6062 71 1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSSEPEEEIDENBEITTTFFEQSVIWVPAEKPIERRDFLKNSKI LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDFE EGGELHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP INDYTENGIEFDPMLDERGYCCIYCRGRNRYCRRVCEPLLGYYP YPYCYQGGRVICRVIMPCNWWARMLGRV  6063 71 1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSSEPEEEIDENBEITTTFFEQSVIWVPAEKPIENRDFLKNSKI LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENBEITTTFFFEQSVIWVPAEKPIENROFLKNSKI	1 :			EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW			
GTMWKVHFVTPVFQPEGAGACYGRKVCPCFGEKVVHHDPPLLFD LSRDPSETHILITASEPVFYQVMER\VQQAVWEHQRTLSPVPPLQ LDRLGNIWRPWLQPCCGPFPLCWCLREDDPQ MNIHMERKTIKETINTFENERMIMLDGMPAVRVKTELLESEQGSPN VHNYPDMEAVPLLLNNVKGEPPEDSLSVDHFQTQTEPVDLSINK ARTSPTAVSSSPVSMTASASSPSSTSTSSSSSRLASSPTVITS VSSASSSTVLTFGPLVASASGVGQQFLHIIHPVPPSSPMNLQ SNKLSHVHRIPVVVQSVPVVYTAVRSFGNVNNTITVPLLEDGRG HGKAQMDPRGLSPRQSKSDSDDDDLPNVTLDSVNETGSTALSIA RAVQEVHPSPVSRVRGNRMNNQKFPCSISPFSIESTRRQRTVLN PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGRVHRRTHTGEKPY KCTWEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH LALHRRHMLV  6062 71 1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEITTTFFEQSVIWVPAEKPIENRDFLKNSKI LEICDNVTMYW\INPTL\ISGTFAKQLHINFAFIILVSELQDPE EEGEDLHFPANEKKGIEQNGVVPQVVVEKTRHARQASEEELP INDYTENGIFFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP YPYCYQGGRVICRVIMPCNWWVARMLGRV  6063 71 1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP LIVLFWGSKHEWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI							
LSRDFSTHILTPASEPVFYQVMER\VQQAVWEHQRTLSPVPLQ LDRLGNIWRPWLQPCCGFFFLCWCLREDDPQ MNIHMKRTIKNINTFENRMLMLDGMPAVRVKTELLESEQGSPN VHNYPDMEAVPLLLNVKGEPPEDSLSVDHFQTQTEPVDLSINK ARTSPTAVSSSPVSMTASASSPSSTSTSSSSSSRLASSPTVITS VSSASSSTVLTPGPLVASASGVGGQOFLHIHPVPPSSPMNLQ SNKLSHVHRIPVVVQSVPVVYTAVRSPGNVNNTIVVPLLEDGRG HGKAQMDPRGLSPRQSKSDSDDDDLPNVTLDSVNETGSTALSIA RAVQEVHPSPVSRVRGNRMNQKFPCSISPFSIESTRRQRTVLN PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGRVHRRTHTGEKPY KCTWEGGTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH LALHRRHMLV  6062 71 1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENDFLKNSKI LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDPE EEGEDLHFPANEKKGIEQNEGWVVPQVVVETRHARQASEEELP INDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP YPYCYQGGRVICRVIMPCNWWVARMLGRV  6063 71 1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI	} I						
LDRLGNIWRPWLQPCCGPFPLCWCLREDDPQ  6061 110 1330 MNIHMRKTIKINITFENRMLDCMPAVRVKTELLESEQGSPN VHNYPDMEAVPLLLNNVKGEPPEDSLSVDHFQTQTEPVDLSINK ARTSPTAVSSSPVSMTASASSPSSTSTSSSSSRLASSPTVITS VSSASSSSTVLTPGPLVASASGVGGQFLHIIHPVPPSSPMNLQ SNKLSKYHRIPVVVQSVPVVYTAVRSPGNVNNTIVVPLLEDGRG HGKAQMDPRGLSPRQSKSDSDDDDLPNVTLDSVNETGSTALSIA RAVQEVHPSPVSRVRGNRMNNQKFPCSISPFSIESTRRQRTVLN PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGRVHRRTHTGEKPY KCTWEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH LALHRRHMLV  1079 ETMAKNGPENCEDCHILNAEAPKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI LEICDNVTMYW\INPTL\ISGTFAKQLHHHFAFIILVSELQDFE EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP INDTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP YPYCYQGGRVICRVIMPCNWWARMLGRV  6063 71 1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLBVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI	1 1			LSPDPSETHILTPASEDURYOUMED VOONUMBHORE COURT			
110   1330   MNIHMKRKTIKNINTFENRMLMLDGMPAVRVKTELLESEQGSPN VHNYPDMEAVPLLLNNVKGEPPEDSLSVDHFQTQTEPVDLSINK ARTSPTAVSSSPVSMTASASSPSSTTSSSSSSSRLASSFTVITS VSSASSSTVLTPGPLVASASGVGGQFLHIHPVPPSSPMNLQ SNKLSHVRIPVVVQSVPVVYTAVRSPGNVNNTIVVPLLEDGRG HGKAQMDPRGLSPRQSKSDSDDDDLPNVTLDSVNETGSTALSIA RAVQEVHPSPVSRVRGNRMNNQKFPCSISPFSIESTRRQRTVLN PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGNVHRRTHTGEKPY KCTWEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH LALHRRHMLV							
VHNYPDMEAVPLLINNVKGEPPEDSLSVDHFQTQTEPVDLSINK ARTSPTAVSSSPVSMTASASSPSSTTSSSSSSRIASSPTVITS VSSASSSTVLTPGPLVASASGVGGQQFLHIHPVPPSSPMNLQ SNKLSHVHRIPVVQSVPVVYTAVRSPGNVNNTIVVPLLEDGRG HGKAQMDPRGLSPRQSKSDSDDDDLPNVTLDSVNETGSTALSIA RAVQEVHPSPVSRVRGNRMNNQKFPCSISPFSIESTRRQRTVLN PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGRVHRRTHTGEKPY KCTWEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH LALHRRHMLV  6062 71 1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDPE EGGEDLHFPANEKKGIEQNEGWVVPQVKVEKTRHARQASEEELP INDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP YPYCYQGGRVICRVIMPCNWWVARMLGRV  6063 71 1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP FEFSEPEEEIDENEEITTTFFEQSVIWVPAEKFIENRDFLKNSKI	6061	110	1330				
ARTSPTAVSSSPVSMTASASSPSSTSTSSSSSRLASSPTVITS VSSASSSSTVLTPGPLVASASGVGGQQFLHIIHPVPPSSPMNLQ SNKLSHVHRIPVVVQSVPVVYTAVRSPGNVNNTITVPLLEDGRG HGKAQMDPRGLSPRQSKSDSDDDDLPNVTLDSVNETGSTALSIA RAVQEVHPSPVSRVRGNRMNNQKFPCSISPFSIESTRRQRTVLN PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGVHRRTHTGEKPY KCTWEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH LALHRRHMLV  6062 71 1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI LEICDNVTMYW\INPTL\ISGTFAKQLHINFAFIILVSELQDFE EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP INDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP YPYCYQGGRVICRVIMPCNWWVARMLGRV  6063 71 1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI							
VSSASSSTVLTPGPLVASASGVGGQQFLHIIHPVPPSSPMNLQ SNKLSHVHRIPVVVQSVPVVYTAVRSPGNVNNTIVVPLLEDGRG HGKAQMDPRGLSPRQSKSDSDDDDLPNVTLDSVNETGSTALSIA RAVQEVHPSPVSRVRGNRMNNQKFPCSISPFSIESTRQRTVLN PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGRVHRRTHTGEKPY KCTWEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH LALHRRHMLV  1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI LEICDNVTMYN\INPTL\ISGTFAKQLHHNFAFIILVSELQDFE EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP INDYTENGIEFDPMLDERGYCCIYCRGNRYCRRVCEPLLGYYP YPYCYQGGRVICRVIMPCNWWVARMLGRV  1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLBVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI				ARTSPTAVSSSPVSMTASASSPSSTSTSSSSSSRLASSPTVITS			
SNKLSHVHRIPVVVQSVPVVYTAVRSPGNVNNTIVVPLLEDGRG HGKAQMDPRGLSPRQSKSDSDDDDLPNVTLDSVNETGSTALSIA RAVGUVHPSPVSRVRGNRMNNQKFPCSISPSIESTRRQRTVLN PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGRVHRRTHTGEKPY KCTWEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH LALHRRHMLV  6062 71 1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDFE EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP INDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP YPYCYQGGRVICRVIMPCNWWVARMLGRV  6063 71 1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLBVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI				VSSASSSTVLTPGPLVASASGVGGQQFLHIIHPVPPSSPMNLQ			
RAVQEVHPSPVSRVRGNRMNNQKFPCSISPFSIESTRRQRTVLN PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGRVHRRTHTGEKPY KCTWEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH LALHRRRHMLV  6062 71 1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDFE EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP INDYTENGIEFPPMLDERGYCCIYCRGNRYCRRVCEPLLGYYP YPYCYQGGRVICRVIMPCNWWVARMLGRV  6063 71 1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLBVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI				SNKLSHVHRIPVVVQSVPVVYTAVRSPGNVNNTIVVPLLEDGRG			
PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGRVHRRTHTGEKPY KCTWEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH LALHRRHHLV  1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDFE EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP INDYTENGIEFDPMLDERGYCCIYCRGNRYCRRVCEPLLGYYP YPYCYQGGRVICRVIMPCNWWVARMLGRV  1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLBVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI							
ACTWEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH LALHRRHMLV  1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDFE EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP INDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP YPYCYQGGRVICRVIMPCNWWVARMLGRV  1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLBVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI	[ ]						
LALHRRHMLV  6062  71  1079  ETMAKNGPENCEDCHILNABAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDFE EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEBELP INDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP YPYCYQGGRVICRVIMPCNWWVARMLGRV  6063  71  1079  ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLBVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI	1 1						
6062 71 1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDFE EEGEDLHFANEKKGIEQMEQWVVPQVKVEKTRHARQASEEELP INDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP YPYCYQGGRVICRVIMPCNWWARMLGRV TPHAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLBVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI			,				
LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDFE EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP INDYTEINGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP YPYCYQGGRVICRVIMPCNWWVARMLGRV TPMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLBVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI	6062	71	1079	L			
TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDPE EEGEDLHFANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP INDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP YPYCYQGGRVICRVIMPCNWWARMLGRV 1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFMGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLBVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI		·*	1073				
EFSEPEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDPE EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP INDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP YPYCYQGGRVICRVIMPCNWWVARMLGRV  1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLBVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI	] [						
LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDFE EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP INDYTENGIEFDPMLDERGYCCIYCRGNRYCRRVCEPLLGYYP YPYCYQGGRVICRVIMPCNWWVARMLGRV  1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLBVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI							
EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP INDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP YPYCYQGGRVICRVIMPCNWWVARMLGRV  1079 ETMAKNGPENCEDCHILINAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLBVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI							
INDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP YPYCYQGGRVICRVIMPCNWWVARMLGRV  6063 71 1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLBVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI							
YPYCYQGGRVICRVIMPCNWWVARMLGRV  6063 71 1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLRVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI	1	ļ					
6063 71 1079 ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR TEIFRSGNGTDETLRVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI	<u> </u>						
LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDƏVTR TEIFRSGNGTDETLRVHDFKNGYTGIYFVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI	6063	71	1079				
EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI	[ ]			l l			
	] ]						
LBICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDFE	<u> </u>			LBICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDFE			

SEQ	Predicted	Predicted end	Design
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ĺ	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
J	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
•	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ı	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, Y=Unknown + Charles
ł	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=Possible nucleotide insertion\
			EEGEDLHFPANEKKGIEONEOWVVPOVKVEKTPHAROACERET
}			INDITENGLE POPMLDERGYCCIYCRRGNRYCRRYCHDII CVVD
6064	913		IPICYQGGRVICRVIMPCNWWVARMIGRV
""		311	NLPQSLPRPTEHSPPYSLEKMTDLVAVWDVALSDGVHKIEFEHG
1		1	TTSGKRVVYVDGKEEIRKEWMFKLVGKETFVVGAAVTVAGTNID
1			ALSGRAYEYTLEINGKSLKKYMEDRSKTTNTWVT.UMDGENEDTIV
		ł	LEKDAMDVWCNGKKLETAGEFVDDGTETHFSIGTH\ACYIKAV\
6065	1153	641	SSG \KKKEGIIHTLIVDNREIPETAS
		0 1 1	MSVRVARVAWVRGLGASYRRGASSFPVPPPGAQGVAELLRDATG
İ	1	}	AEEEAPWAATERRMPGQCSVLLFPGQGSQVVGMGRGLLNYPRVR
	J .		ELYAAARRVLGYDLLELSLHGPQETLDRTVHCQPAIFVASLAAV
6066	68	3470	EKLHHLQPSVIENCVAAAGFSVGEFAALVFAGAMEFAEG
	İ		VKENMPATRKPMRYGHTEGHTEVCFDDSGSFIVTCGSDGDVRIW
i			EDLDDDDPKFINVGEKAYSCALKSGKLVTAVSNNTIQVHTFPEG VPDGILTRFTTNANHVVFNGDGTKIAAGSSD\FLVKIVDVMDSS
1	i		QQKTFRGHDAPVLSLSFDPKDIFLASASCDGSVRVWQISDQTCA
ļ			ISWPLLQKCNDVINAKSICRLAWQPKSGKLLAIPVEKSVKLYRR
1	i !		ESWSHQFDLSDNFISQTLNIVTWSPCGOVLAAGGINGLITUWARK
			ETRICMERVEHEKGYAICGLAWHPTCGRISVTDAFGNIGII DNI
1			CDPSGKTSSSKVSSRVEKDYNDLFDGDDMSNAGDELNDNAUGTD
ļ	f		SESKGIINDDEDDEDLMMASGRPRORSHTLEDDENSUDIEMI VIII
İ	l l		GSSDDAEEEEDGOEGSIHNLPLVTSOPPEVDGDMDTDBOVDBOO
	}		GSTPLHETHREMVWNSIGIIRCYNDEODNAIDVERHOTETHIAD
	ĺ		HUSNILNYTIADLSHEAILLACESTDELASKLUCLUESCUDGOR
1	1		EWIJDLPQNEDIEAICLGQGWAAAATSALLLRLFTIGGVQKEVF
	1		SLAGPVVSMAGHGEOLFIVYHRGTGFDGDOCLGVOLLER GREEK
	i		QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSEGIVRMLNRGLG
ı İ			NTWTPICNTREHCKGKSDHYWVVGIHENPQQLRCIPCKGSRFPP
			TLPRPAVAILSFKLPYCQIATEKGQMEEQFWRSVIFHNHLDYLA
;			KNGYEYEESTKNQATKEQQELLMKMLALSCKLEREFRCVELADL
1		į	MTQNAVNLAIKYASRSRKLILAQKLSELAVEKAAELTATQVEEE EEEEDFRKKLNAGYSNTATEWSQPRFRNQVEEDAEDSGEADDEE
			KPEIHKPGQNSFSKSTNSSDVSAKSGAVTFSSQGRVNPFKVSAS
1 1	1		SKEPAMSMNSARSTNILDNMGKSSKKSTALSRTTNNEKSPIIKP
1	1		LIPKPKPKQASAASYFQKRNSQTNKTEEVKEENLKNVLSETPAI
1 1	į.		CPPQNTENQRPKTGFOMWLEENRSNILSDNPDFSDFADTIPECK
	]		TATA V LOTEBRA V WANKAKGETASEGTE A KKRKRUTTE CREMENT
6067	050		VERNARENDINUSKKOKPLDFSTNOKLSAFAFKOF
1 550, 1	858	321	LPWQRLGVLLSRGKMAVTGWLESLRTAOKTALLODGBROUNT F
i 1		ĺ	PUGKEMAKEYDEKTSELLVRKWRVKSAI.GAMGOMOT.PVGDDADA
		į	GAGNLGPELIKESNANPIFMRKDTKMSFOWDIDNIDVDKDVKK
, 1		[	SVEWCIIVRIINKKYYKKFSIPDLDRHOLPI DDALLGEN (m. )
6068	13	1730	PIAP
	==	1,30	GSKMADLANEEKPA IAPPVFVFQKDKGQKSPAEQKNLSDSGEEP
} ;	1	-	RGEAEAPHHGTGHPESAGEHALEPPAPAGASASTPPPPAPEAQL
] ]			PPFPRELAGRSAGGSSPEGGEDSDREDGNYCPPVKRERTSSLTQ
i I	<b>!</b>	ľ	FPPSQSEERSGFRLKPPTLIHGQAPSAGLPSQKPKEQQRSVLR
	i		PAVLQAPQPKALSQTVPSSGTNGVSLPADCTGAVPAASPDTAAW
1 1			RSPSEAADEVCALEEKEPQKNESSNASEBEACEKKDPATQQAFV
1 1	ļ	ĺ	FGQNLRDRVKLINESVDEADMENAGHPSADTPTATNYFLQYISS
[ ]			SLENSTNSADASSNKFVFGQNMSERVLSPPKLNEVSSDANRENA
1			AAESGSESSQEATPEKESLABSAAAYTKATARKCLLEKVEVIT
		1.	GEEAESNVLQMQCKLFVFDKTSQSWVERGRGLLRLNDMASTDDG
1 1	}	Į,	TLQSRLSDAGPRGSLR\LILNTKLWAQMQIDKASEK\SIRITAM
[ ]		1;	DNEDQGVKVFLISASSKDTGQVYAALHHRILALRSRVEQEQEAK
		;	MPAPEPGAAPSNEEDDSDDDDVLAPSGATAAGAGDEGDGQTTGS
6069	583		=
		1 '	PTRPGQAGSSSAMAAQRLGKRVLSKLQSPSRARGPGGSPGGLQK
		] :	RHARVTVKYDRRELORRLDVEKWIDGRLEELYRGMEADMPDE IN IDELLELESEEERSRKIQGLLKSCGKPVEDFIQELLAKLQGLHR

	1 D 24 3	1 8 1	
SEQ	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
		·	Q\PGLRQPSPSP\DGQPSAPFQGPGARTASPLTLLALFPGPPER
L		Ì	RPALLCVLSCI
6070	478	858	IRVTVDGEFLHY1FPLQFLDSPEW/RFTETHRGRHF\QVTLTAE
			TDCRYVSWRRKKLYLLFAQHRYISRLFSVLIGSDIADKLYALND
			RVYIGKRYHYDIRLPNFYQMSTPEIRRSPLTQHFQNSRRYW
6071	2	1654	HEARTKGNMALARP\VRLFSLVTRLLLAPRRGLTVRSPDEPLPV
			VRIPVALQRQLEQRQSRRRNLPRPVLVRPGPLLVSARRPELNQP
ŀ			ARLTLGRWERAPLASQGWKSRRARRDHFSIERAQQEAPAVRKLS
			SKGSFADLGAWKPRVLHALQE\AAPEVVQ\PTTVQSSTIPSLLR
Į.			GRHVVCAAETGSGKTLSYLLPLLQRLLG\HPSLDSLPIPAPRGL
		i	VLVPSRELAQQVRAVAQPLGRSLGLLVRDLEGGHGMRRIRLQLS
	1		ROPSADVLVATPGALWKALKSRLISLEQLSFLVLDEADTLLDES
1		}	FLELVDYILEKSHIAEGPADLEDPFNPKAQLVLVGATFPEGVGQ LLNKVASPDAVTTITSSKLHCIMPHVKQTFLRLKGADKVAELVH
1	1		ILKHRDRAERTGPSGTVLVFCNSSSTVNWLGYILDDHKIQHLRL
1			QGQMPALMRVGIFQSFQKSSRDILLCTDIASRGLDSTGVELVVN
			YDFPPTLQDY1HRAGRVGRVGSEVPGTVISFVTHPWDVSLVQKI
			ELAARRRSLPGLASSVKEPLPQAT
6072	1	742	KMERTEMMPTINSQLEFKSKPFPLVSSSRWLVKRGELTAYVEDT
			VLFSRRTSKQQVYFFLFNDVLIITKKKŞEESYNVNDYSLRDQLL
			VESCDNEELNSSPGKNSSTMLYSRQSSASHLFTLTVLSNHANEK
ì			VEMLLGAETQSERARWITALGHSSGKPPADRTSLTQVEIVRSFT
	}		AKQPDELSLQVADVVLI\YQRVSDGWYEGER\LRDGERGWFPME
			CAKEITCQATIDKNVERMGRLLGLETNV
6073	620	B60	PCRRGLARPLSRRPG/SILVHCAVGVSRSATLVLAYLMLYHHLT
<del></del>			LVEAIKKVKDHRGIIPNKGFLRQLLALDRRLRQGLEA
6074	168	1110	PGARCMATELQCPDSMPCHNQQVNSASTPSPEQLRPGDLILDHA
•	1		GGNRASRAKVILLTGYAHSSLPAELDSGACGGSSLNSEGNSGSG
1	!		DSSSYDAPAGNSFLEDCELSRQIGAQLKLLPMNDQIRELQTIIR
			DKTASRGDFMFSADRLIRLVVEEGLNQLPYKECMVTTPTGYKYE GVKFEKGNCGVSIMRSGEAMEQGLRDCCRSIRIGKILIQSDEET
1			QRAKVYYAKFPPDIYRRKVLLMYPILQTG\NTVIEAVKVLIEHG
1	!!!		VQPSVIILLSLFSTPHGAKSIIQEFPEITILTTEVHPVAPTHFG
	!		OKYFGTD
6075	320	1091	PPTCQPQEVEHH\YGYVPILGNKTLPSRCHQCVIVSSSSHLLGT
	ł i		KLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAHSSVFRV
1			LRRPQEFVNRTPETVFIFWGPPSKMQKPQGSLVRVIQRAGLVFP
			NMEAYAVSPGRMRQFDDLFRGETGKDREKSHSWLSTGWFTMVIA
1			VELCDHVHVYGMVPPNYCSQRPRLQRMPYHYYEPKGPDECVTYI
			QNEHSRKGNHHRFITEKRVFSSWAQLYGITFSHPSWT
6076	1721	107	HPSPTEAPRVQHLTMDCTWRILFLVAAATGTHAQVQLVQSGAEV
			KKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGAFDPED
			GETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCATD
			HGDYAFDIWGQGTMVTVSSAPTKAPDVFPIISGCRHPKDNSPVV
			LACLITGYHPTSV\TVTWYMGTQSQA\QRTFPEIQRRDSYYMTS
[			SQLSTPLQQWRQGEYKCVVQHTASKSKKEIFRWPESPKAQASSV
] .			PTAQPQAEGSLAKATTAPATTRNTGRGGEEKKKEKEKEEQEERE
			TKTPECPSHTQPLGVYLLTPAVQDLWLRDKATFTCFVVGSDLKD
			AHLTWEVAGKVPTGGVEEGLLERHSNGSQSQHSRLTLPRSLWNA
			GTSVTCTLNHPSLPPQRLMALREPAAQAPVKLSLNLLASSDPPE
			A\ASWLLCEVSGFSPPNILLMWLEDHGEVNTSGFAPARPLPKP\
			RSTTFWA\WSVLRVPAPPSPQPATYTCVVSHEDSRTLLNASRSL
6077	3687	1268	EVSYVTDHGPMK
````	3007	1200	LLPDMNLQPIFWIGLISSVCCVFAQTDENRCLKANAKSCGECIQ
			AGPNCGWCTNSTFLQEGMPTSARCDDLEALKKKGCPPDDIENPR
			GSKDIKKNKNVTNRSKGTAEKLKPEDITQIQPQQLVLRLRSGEP
			QTFTLKFKRAEDYPIDLYYLM\DLSYSMKDDLENVKSLGTDLMN EMRRITSDFRIGFGSFVEKTVMPYISTTPAKLRNPCTSEONCTS
			PFSYKNVLSLTNKGEVFNELVGKQRISGNLDSPEGGFDAIMOVA
	}		VCGSLIGWRWVTRLLVFSTDAGFHFAGDGKLGGIVLPNDGQCHL
			THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE S

SEC	T Description		
ID	. ,	Predicted end	
		nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:		location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	Halistiding Translatanine, Gaglycine,
ł	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
ł	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
i	amino acid	residue of	Paroline, Omegiutamine, Parainine
	residue of		S=Serine, T=Threonine, V=Valine
- 1	,	amino acid	W=Tryptophan, Y=Tvrosine v=Unknown to
- 1	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence	1	\=possible nucleotide insertion)
l l			ENNMYTMSHYVDVDCIAUTVOVICEDON
		ſ	ENNMYTMSHYYDYPSIAHLVQKLSENNIQTIFAVTEEFQPVYKE
į	J	ļ	LKNLIPKSAVGTLSANSSNVIQLIIDAYNSLSSEVILENGKLSE
	i		GVTISYQSY\CKNGVNGTGENGRKCSNISIGDEVQFEISITSNK
			CERRUSUSE KIRPLGFTEEVEVILOVICECECOCEGIDEGENESS
		1	EGNGIF ECGACKCNEGRVGRHCECSTDEVNGEDTCCETTA DECENT
- 1	l l	1	1 PARASINAGRAPSAGOCACKEDNITAETAGGEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
1	}		I NOBICGONG V CKCR V CECNPNYTGSACDCSI. DTGTCFA CNTGCTC
1	\$	1	I NGRGICECGVCKCTDPKFOGOTCEMCOTCLGVCA FUVECTO GD3
- 1	1		FNKGEKKDTCTQECSYFNITKVESRDKLPQPVQPDPVSHCKEKD
- 1	ł	1	VDDCWFYFTYSINGNMFIAGRIATING
		i	VDDCWFYFTYSVNGNNEVMVHVVENPECPTGPDIIPIVAGVVAG
- 1	İ		IVLIGLALLIWKLLMIIHDRREFAKFEKEKMNAKWDTGENPIY
6078	1426	180	KSAVITVVNPKYEGK
	1	100	ETEDVMELLEEDLTCPICCSLFDDPRVLPCSHNFCKKCLEGILE
J			1 GSVKNSLWKPVPFKCPTCRKKTFSVWFT.TDI.OUNDGT VOTI
1			I MAIAISPAMPVCKGH \ LGOPINIE\ CI.\ TDMOI DI /CGIG\
	İ		GBIT KIN F CS LEDA LAOERDAFESI FOSFF TWDD CDAL CDL DOLL
			ETSKRKSLQLLTKDSDKVKEFFEKLQHTLDQKKNEILSDFETMK
	1		LAVMQAYDPEINKLNTILQEQRMAFNIAEAFKDVSEPIVFLQQM
	i		QEFREKIKVIKETPLPPSNLPASPLMKNFDTSQWEDIKLVDVDK
1	1		LSLPQDTGTFISKIPWSFYKLFLLILLLGLVIVFGPTMFLEWSL
Į.	1		FDDLATWKCCL GNECGYL TWTA DELIGIOUT VFGPTMFLEWSL
L			FDDLATWKGCLSNFSSYLTKTADFIEQSVFYWEQVTDGFFIFNE RFKNFTLVVLNNVAEFVCKYKLL
6079	1586	141	ATARDICATARA
ſ	1		ATARDLGCARRIDRVVMESTPSRGLNRVHLQCRNLQEFLGGLSP
1			GVLDRLYGHPATCLAVFRELPSLAKNWVMRMLFLEQPLPQAAVA
1			LIVERESTANDED TO LEGEN TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE
}	) i		NURTHULGGGKAWSDDTSOLGPDKHARDVDGI.DVVAEEDWHAR
1	1		HENVESPSAAVSQDLAOLLSOAGLMKSTEDGEDDGITGAGDGT
ł	j		LEDIPAQLWYFMLOYLOTAOSRGMDIAGET CELEGI COLCEGO COM
	1		1 13 A EGINO DO DENE LO HERE EGI A FOR PROPERTIES AND A 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
	1 1		SSGVSGAGGTVHQPGFIV\VETNYRLYAYTESELQIALIALFSE
ł	1		MLYPFP\NMVV\ARVTR\ESVQQAIASGITAQQIIHFLRTRAHP
1	1 1		VMLKOTPVLPPTTTDOTPLWELEDDATASCTTAQQITHFLRTRAHP
1	1 1		VMLKQTPVLPPTITDQIRLWELERDRLRFTEGVLYNQFLSQVDF
L	1		ELL\LAHAPKLGVLVFB/NTPAKRLMVVTPAGHSDVKRFWKRQK
6080	1	1199	
1	i i		IETIDHVGEFAMAAQAAGVSRQRAATQGLGSNQNALKYLGQDFK
1	1		THRUSCHUSGVLFKDPEFPACPSALGVXDLGDGGDGGGTTTTTT
1	1 1	}	FIELCPS PQF1 VGGATRTDI COGGI,CDCWLT, N T N CT DT NTDT *
ł	1	i	TIVALEGOE OF A STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTROL OF THE STANDARD CONTRO
1	1	į	DE INTOQUEE DESEQUEENSALIERAVARING CVENTAGOGER
ĺ	1 1	ł	MOTED TIGGISEFY DLKKPPANT, YOT TOKAT, CACCET I COUTTON
i	1 1	I	SAMEABALTSQKLVKSHAYSVTGVEEVNEGGUDDVI IDI DANDA
I	1	1	DIE CONTROL DE MINISTER DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA
1.	j l		QFSRLEICNLSPDSLSSEEVHKWNLVLFNGHWTRGSTAGGCQNY
	<u>                                       </u>		PGSS
6081	3	865	
1	] [	1	EMLPLLLPLPLLWA/GALAQDARFRLEMPESVTVQEGLCIFVHC
}	1	l I	SVFYLEYGWKDSTPAYGHWFREGVSVDQETPVATNNSTQKVQKE
	1	1	TOGRIPHLIGDPSRNNCSLSIRDARRRDNGSYFFWVARGRIKFSY
	]	1	AISPESVIVIALTHRPDILIPEFI.KSCHDSMITGSVDWIGDOOD
	1		PPIPSWISAAPTSLGPRTLHSSVLTITPPPODUCTNITTCOMPRE
	, l		GAGVIIERIIQLSVSWKSGTVEEVVVI,AVCVNAVKTIIIGGGT T
6082	100		IDSTRUKKAVKAVEVEENVYAVMG
0002	283	1288	EARSPGPTQTRTAPGLAAPGLAQPAALPLILEPPPCAAMPGPGP
İ	1		PESVGQPEEASPEEOPEEASAFEFFPPFDOOFFF77777VVV I
	1		LPEPLLA/LRVLAALPRHE\LVQACR\LVCLRWKELVDGAPLWL
1	l j	] :	LKCQQEGLVPEGGVEEERDHWQQFYFLSKRRNLLRNPCGEEDL
	1	1 ;	EGWCDVEHGGDGWBVEEL DCDGGGETTE
j	}	];	EGWCDVEHGGDGWRVEELPGDSGVEFTHDESVKKYFASSFEWCR
l	]	1 '	MAY IDEQAEGIMEELLDTTOPAIVVKDWYSGDSDAGGIVER OF I
	1	4	NULSEREN VLAEFSSGOVAVPODSDGCGUMET GUMPTDVGDOVE
6083	1865	/ /	VKFERGGQDSVYWKGWFGARVTNSSVWVED
		309	KQWCAERRGLGMSLADELLADLEEAAEEEEGGSYGEEEEEPAIE

[ e=0	1 Day 34 3	<del></del>	
SEQ ID	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning	nucleotide	M=Alanine, C=CVSteine, D=Aspartic Acid p
NO:	nucleotide	location	Glutamic Acid, F=Phenylalaning C_Clossis
	location	corresponding	H=Hlstldine, I=Isoleucine K=Iveine
- 1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- 1	. amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence	İ	\=possible nucleotide insertion)
			DVQEETQLDLSGDSVKTIAKLWDSKMFAEIMMKIEEYISKQAKA
İ	1		SEVMGPVEAAPEYRVIVDANNLTVEIENELNIIHKFIRDKYSKR
	1		FPELESLVPNALDYIRTVKELGNSLDKCKNNENLQQILTNATIM
)	1		VVSVTASTTQGQQLSEEELERLEEACDMALELNASKHRIYEYVE
		ĺ	SPMSETA DNI CTITICA CTA A KINGUA COL TUNA CHARIYEYVE
ŀ	1	1	SRMSFIAPNLSIIIGASTAAKIMGVAGGLTNLSKMPACNIMLLG
	ĺ	1	AQRKTLSGFSSTSVLPHTGYIYHSDIVQSLPPIPPPFSVAP\DL
	ŀ	1	RRKAARLVAAKCTLAARVDSFHESTEGKVGYELKDEIERKFDKW
- [	· <b>[</b>		QEPPPVKQVKPLPAPLDGQRKKRGGRRYRKMKERLGLTEIR\KQ
1	1	ĺ	ANRMSFGEIEEDAYQEDLGFSLGHLGKSGSGRVRQTQVNEATKA
ł			RISKTLQRTLQKQSVVYGGKSTIRDRSSGTASSVAFTPLQGLEI
6084	1865	309	VNPQAAEKKVAEANQKYFSSMAEFLKVKGEKSGLMST
		309	KQWCAERRGLGMSLADELLADLEEAAEEEEGGSYGEEEEEPAIE
ì	1	1	DVQEETQLDLSGDSVKTIAKLWDSKMFAEIMMKIEEYISKQAKA
1	i	1	SEVMGPVEAAPEYRVIVDANNLTVEIENELNIIHKFIRDKYSKR
ļ	1		FPELESLVPNALDYIRTVKELGNSLDKCKNNENLQQILTNATIM
1	1		VVSVTASTTQGQQLSEEELERLEEACDMALELNASKHRIYEYVE
	<b>‡</b>		SRMSFIAPNLSIIIGASTAAKIMGVAGGLTNI,SKMDDCNIMIIC
	İ		AQRKTLSGFSSTSVLPHTGYIYHSDIVQSLPPIPPPFSVAP\DL
	ł		RKKAARLVAAKCTLAARVDSFHESTEGKVGYELKDETERYEDVW
	1		QEPPPVKQVKPLPAPLDGQRKKRGGRRYRKMKERI.GI.TETP\ vo
			ANKMSFGEIEEDAYQEDLGFSLGHLGKSGSGRVROTOVNFATVA
ł			RISKTLQRTLQKQSVVYGGKSTIRDRSSGTASSVAFTDLOGLET
6085	2		VNPQAAEKKVAEANQKYFSSMAEFLKVKGEKSGI.MST
""	-	1456	SGPRSFQGNRAVGRISLGGKRNPEVTLLPGVSSERVRRWRRARV
			GVARVKPGNPWKPSPATOVPR/VPAOVYT PGRGPPI PRGFPI AM
			DEEAYVLYHRAQTGAPCLSFDIVRDHLGDNRTEI.PI.TI.VI.CDCT
	-		QAESAQSNRLMMLRMHNLHGTKPPPSEGSDEEEEEEDERDERD
	i i		KPQLELAMVPHYGGINRVRVSWLGEEPVAGVWSEKGOVEVEALD
1			KLLQVVEEPQALAAFLRDEOAOMKPIFSFAGHMGFGFALDWenn
ŀ	1		VIGRLLTGDCQKNIHLWTPTDGGSWHVDORPRIGUTPSVEDIOU
1 1	i		SPIENTVFASCSADASIRIWDIRAAPSKACMI.TTATAUDGDIANI
1 1	i		I ISWSKKEPFLLSGGDDGALKIWDLROFKSGSDVATEVOUVADIM
1	[		SVEWHPQDSGVFAASGADHOITOWDLG/IVERDDEAGDURADDC
]	i		LADLPQQLLFVHQGETELKELHWHPQCPGLLVSTALSGFTIFRT
6086			ISV
6006	2419	1357	GAATQHGGAMNLLPCNPHGNGLLYAGFNQDHGCFACGMENGFRV
1 1	<u> </u>		YNTDPLKEKEKOEFLEGGVGHVEMI.FRCNVI.ALVGGGVVEVVDD
1 1	1	i	NKVMIWDDLKKKTVIEIEFSTEVKAVKLRR\DKTVAZI.DCMTVI
ł .			FTFTHNP\HQLHVFE\TCYNPKGLCVLCPNSNNSII.AEDGTHTC
1 1	1		HVQLVDLASTEKPPVDIPAHEGVLSCIALNLOGTRIATASRKCT
1 1	)	j	LIRIFDTSSGHLIQELRRGSOAANIYCINFNODASI.TCVSSDUG
1	1		TVHIFAAEDPKRNKOSSLASASFLPKYFSSKWSFSKFOUDGGED
1 1	}		CICAFGTEPNAVIAICADGSYYKFLFNPKGECIRDVYAQFLEMT
-E002		<u>.</u>	DDKL
6087	476	1877	QNSQRTGLPITIFSRSFPLLTGSDLCENMPCTCTWRNWRQWIRP
] }		]	LVAVIYLVSIVVAVPLCVWELOKLEVGIHTKAWRTAGIRIJIMT
[ [		1	PISLWVILQHLVHYTQPELQKPIIRILWMVPIYSLDSWIALKYP
1 1		1	GIAIYVDTCRECYEAYVIYNFMGFLTNYLTNRYPNLVLILEAKD
1		Í	QQKHFPPLCCCPPWAMGEVLLFRCKLGVLQYTVVRPFTTIVALI
1 1	Į.		CELLGIYDEGNFSFSNAWTYLVIINNMSQLFAMYCLLLFYKVLK
1	1		EELSPIQPVGKFLCVKLVVFVSFWQAVVIALLVKVGVISEKHTW
, ,		j	EWQTVEAVATGLQDFIICIEMFLAAIA\HHYTFSYKPYVQEABE
1 1	1		GSCFDSFLAMWDVSDIRDDISEQVRHVGRTVRGHPRKKLFPEDQ
<u> </u>	į		DQNEHTSLLSSSQDAISIASSMPPSPMGHYQGFGHTVTPQTTP
	1		TTAKISDEILSDTIGEKKEPSDKSVDS
6088	1684	689	GASGLVRLLQQGHRCLLAPVAPKLVPPVRGVKKGFRAAFRFQKE
·	İ		LEROPLIR CODDDING CENTRAL VAPRLIVE PER CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF T
	j	1	LERORLLRCPPPPVRRSEKPNWDYHAEIQAFGHRLQENFSLDLL
[	į.	1	KTAFVNSCYIKSEEAKRQQLGIEKEAVLLNLKSNQELSEQGTSF
			SQTCLTQFLEDEYPDMPTEGIKNLVDFLTGEEVVCHVARNLAVE
!		ļ	QLTLSEEFPVPPAVLQQTFFAVIGALLQSSGPERTALFIRDFLI
			TQMTGKELFEMWKIINPMGLLVEELKKRNVSAPESRLTRQSG\A

SEO	Predicted	Drods	
ID	beginning	Predicted end nuclectide	
NO:	nucleotide	location	(A=Alanine, C=CVSteine, D=Aspartic Acid p
ļ	location	corresponding	Grutamic Acid, F=Phenylalanine C-Classic
İ	corresponding	to first	Hamistidine, I=Isoloucine Kalveine
- 1	to first		L=Leucine, M=Methionine, N=Asparagine
1	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine
	residue of	residue of	S=Serine, T=Threonine, V=Valine
ŀ		amino acid	W=Tryptophan, Y=Tyrosine X-Unknown +-G
	amino acid	sequence	Codon, /=possible nucleofide deletion
ļ	sequence	1	\=possible nucleotide insertion)
ł			PTALPLYFVGLYCDKKLIAEGPGETVLVAEEEAARVALRKLYGF
			TENRRPWNYSKPKETLRAEKSITAS
6089	3	3054	TRICIDESTISSEDELONIA
			TRLGIPGSTISSRPRLCALAAEGHFLGHSWTGSRAGAHTGAPAW
1	}		PSRRLRDLPAGGMWRLRRAAVACEVCQSLVKHSSGIKGSLPLQK
ľ	1		LHLVSRSIYHSHHPTLKLQRPQLRTSFQQFSSLTNLPLRKLKFS
			PIKYGYQPKRNFWPARLATRLLKLRYT.TLGSAVGGGVTAVVIIDD
ł		1	QWKDMIPDLSEYKWIVPDIVWEIDEYTDFEKTPKALDEGEDTUK
	1	i	LAPOPOKIVESUSLLKDFFTSGSPEETAFRATDRGGEEDVIERV
1	1	]	ASDKEKIDOPOEETPHLOPKAOBILEBIEKEMARI BALATONE
	1		ROIFF LESUKKSLIDMYSEVLDVLSDYDASYNTODUL DRIVING
1		1	DQSAGK15VLEMIAQARIFPRGSGEMMTPSDWWirrt.croputura
	İ	İ	LFKDSSREFDLTKEEDLAALRHEIELRMRKNVKEGCTVSPETIS
	1		LNVKGPGLQRMVLVDLPGVINTVTSGMAPDTKETIFSISKAYMQ
1	į.	Į	DPNAILLCIQDGSVDAERSIVTDLVSQMDPHGRRTIFVLTKVDL
1			AEKNVASPSRIQQIIEGKLFPMKALGYFAVVTGKGNSSESIEAI
	1		REVEEEPFONGKI LYTCMI KALGYFAVVTGKGNSSESIEAI
1			REYEEFFONSKLLKTSMLKAFQVTTRNLSLAVSDCFWKMVRES
			VEQQADSFKATRFNLETEWKNNYPRLRELDRNELFEKAKNEILD
1	1		EVISLSQVTPKHWEEILQQSLWERVSTHVIENIYLPAAQ'IMNSG
ļ	1		TFNTTVDIKLKOWTDKQLPNKAVEVAWETLQEEFSRFMTEPKGK
f	i i		EHDDIFDKLKEAVKEESIKRHKWNDFAEDSLRVIQHNALEDRSI
			SDRQQWDAAI YFMEEALOARLKDTENAIENMYGDD\ MYYDWY YW
i	1		ANKIQEQCVHNETKNELEKMLKCNEEHPAVI.ASDETTTTUBENT E
1			SKGVEVDPSLIKDTWHOVYRRHFI,KTALNHCNI,CDDGEVYVODI
İ	1		F VDSELECNDV VLEWRIORMLAITANTI, ROOT TNTEVERS EVAN
İ	1		KEVLEDFABDGEKKIKLLTGKRVQLAEDLKKVREIQEKLDAFIE
6090			ALHQEK
6090	194	1560	PVFVPAPGAVLEQAS/ASPPLATQTVVPLQHCKIPELPVQASIL
1	1 1		FELQLFFCQLIALFVHYINIYKTVWWYPPSHPPSHTSLNFHLID
i	1		FNLLMVTTIVLGRRFIGSIVKEASQRGKVSLFRSILLFLTRFTV
	1		LTATGWSLCRSLIHLFRTYSFLNLL/FPLLSVWDVHSVPAAELR
	[		P\PKTSI.ENUMASMGPPRAYAGGT TO THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STUDIES OF THE STU
1			P\RKTSLFNHMASMGPREAVSGLAKSRDYLLTLR\RRGSSTQDS
	ļ		CMARTPCP/PHACCLSPSLIRSEVEFLKMDFNWRMKEVLVSSML
1	f f		SAYYVAFVPVWFVKNTHYYDKRWSCELFLLVSISTSVILMQHLL
	ĺ		PASYCDLLHKAAAHLGCWQKVDPALCSNVLQHPWTEECMWPQGV
	]	i	DVK.SKNVYKAVGHYNVAIPSDVSHFRFHFFFCVDIDTTNTT
	' i		LEGAVIVYQLYSLMSSEKWHOTISLALTLESNYVA FERLI BDB1
6091	3279		VLGKAYSYSASPORDLDHRFS
****	3279	412	SSRTREMEEKEILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG
i i	· • • • • • • • • • • • • • • • • • • •	l	WALL INSCRALSARY PRPSRRGYSSHHGPSWDKKYGT IND DDG
1	į.		PSDFPADHAVRPLHGARGGOPPVPOOHVI.EPOVOI.EOCOMBITIE
1 1	1		VKPPSKSGSASASGAQRGSLEEFEDTPWSDQRPREGEGEPPRGQ
1 1		ı	LQPSRPTRARGTCSVEDPLLVCQKEPGKPRMVKSVGSVGDSPRE
i i	ľ	i	PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ
1 1		]	LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR
		i	TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN
1		j	KVEKPOLIADDEDVDBVDBVDBCOVDGGG
1 1	1		KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSS
1	1	1	SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE
1 1			TPLSAYKVKSRTKIIRRRGSTSLPGDKKSGTSPAATAKSHLSLR
1 I	ļ.		RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA
1		ł	SSCHAVRTAPTSKVIKTRYRIVKKTPASPLSAPDEDT.SI.Delina
]	·	l l	RRESESRSEVENRERPVASGGGKAOPGSPWWPSKGVPCTCOUTY
}	Į		KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSDSLASDAUG
]	1	1	RSLALIRQARQRREKRKEYCMYYNRFGRCNRGFRCDYTHDDBWY
Į J	Į.	į.	AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN
	ļ	İ	CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPDFARRG
		İ	ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDATARSRVSASHG
		'	PRESASOPPTPOTICES AL MARATISPAPGPSDATARSRVSASHG
		ļ	PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSKAS
- 1		1	SSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS
6092	143		SPSPGAQPRVRAPRAPLTKDSGKPLHIKPRL
1		3190	AKAPPTGESSEPEAKVLHTKRLYRAVVEAVHRLDLILCNKTAYO
			EVFKPENISLRNKLRELCVKLMFLHPVDYGRKAEELLWRKVYYE
		·	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
]	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
{	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	1	Codon, /=possible nucleotide deletion,
Į.	1	sequence	
ļ	sequence		\=possible nucleotide insertion)
	1	ł	VIQLIKTNKKHIHSRSTLECAYRTHLVAGIGFYQHLLLYIQSHY
ĺ	ł	t	QLELQCCIDWTHVTDPLIGCKKPVSASGKEMDWAQMACHRCLVY
}	[	Į.	LGDLSRYQNELAGVDTELLAERFYYQALSVAPQIGMPFNQLGTL
}		1	AGSKYYNVEAMYCYLRCIQSEVSFEGAYGNLKRLYDKAAKMYHQ
ĺ	ļ	j	LKKCETRKLSPGKKRCKDIKRLLVNFMYLQSLLQPKSSSVDSEL
ł		ł	TSLCQSVLEDFNLCLFYLPSSPNLSLASEDEEEYESGYAFLPDL
J		1	LIFQMVIICLMCVHSLERAGSKQYSAAIAFTLALFSHLVNHVNI
1	1		RLQAELEEGENPVPAFQSDGTDEPESKEPVEKEEEPDPEPPPVT
1	1	1	PQVGEGRKSRKFSRLSCLRRRRHPPKVGDDSDLSEGFESDSSHD
}	l .	ĺ	SARASEGSDSGSDKSLEGGGTAFDAETDSEMNSQESRSDLEDME
1			EEEGTRSPTLEPPRGRSEAPDSLNGPLGPSEASIASNLQAMSTQ
1	<b>}</b>	,	MFQTKRCFRLAPTFSNLLLQPTTNPHTSASHRPCVNGDVDKPSE
ł	i		PASEEGSESEGSESSGRSCRNERSIQEKLQVLMAEGLLPAVKVF
ļ		\$	LDWLRTNPDLIIVCAQSSQSLWNRLSVLLNLLPAAGELQESGLA
ł		ł	LCPEVQDLLEGCELPDLPSSLLLPEDMALRNLPPLRAAHRRFNF
}	j	į	DTDRPLLSTLEESVVRICCIRSFGHFIARLQGSILQFNPEVGIF
1		}	VSIAQSEQESLLQQAQAQFRMAQEEARRNRLMRDMAQLRLQLEV
į		<b>{</b>	SQLEGSLQQPKAQSAMSPYLVPDTQALCHHLPVIRQLATSGRFI
1	1		VIIPRTVIDGLDLLKKEHPGARDGIRYLEAEFKKGNRYIRCOKE
1			VGKSFERHKLKRQDADAWTLYKILDSCKQLT\LAQGAGEEDPSG
j	1	f	MVTIITGLPLDNPSLLSGPMQAALQAAAHASVDIKNVLDFYKQW
ł		}	KEIG
6093	76	1002	ACGRRAMLALRVART/SRWGAL\RGAVWAPGTRPSKRRACWALL
1	1	}	PPVPCCLGCLAERWRLRPAALGLRLPGIGQRNHCSGAGKAAPR\
i	į		PAAGAGAAAEAPGGOWGPASTPSLYENPWTIPNMLSMTRIGLAP
}	}	}	VLGYLIIEEDFNIALGVFALAGLTDLLDGFIARNWANQRSALGS
Ì	Í	Ì	ALDPLADKILISILYVSLTYADLIPVPLTYMIISRDVMLIAAVF
}		1	YVRYRTLPTPRTLAKYFNPCYATARLKPTFISKVNTAVOLILVA
ł	ĺ	1	ASLAAPVFNYADSIYLQILWCFTAFTTAASAYSYYHYGRKTVOV
1	{	[	IKD
6094	23	1010	PFLRCLRGDQKAKMSERKVLNKYYPPDFDPSKIPKLKLPKDROY
0034	43	1010	· ·
}		}	VVRLMAPFNMRCKTCGEYIYKGKKFNARKETVQNEVYLGLPIFR
i		j	FYIKCTRCLAEITFKTDPENTDYTMEHGATRNFQAEKLLEEEEK
}	}		RVQKEREDEELNNPMKVLENRTKDSKLEMEVLENLQELKDLNQR
1	}		QAHVDFEAMLRQHRLSEEERRRQQQEEDEQETAALLEEARKRRL
ł			LEDSDSEDEAAPSPLQPALRPNPTAILDEAPKPKRKVEVWEQSV
}	į.	1	GSLGSRPPLSRLVVVKKAKADPDCSNGQPQA/APHPRSPAEQEG
			GQPYTPDAWRVLPEPTGCIPGQ
6095	1	1599	TRGRAAERSRGRGHGFLGGGFA\SVVDYFPSEDFYRCGYCKNES
1		[	GSRSNGMWAHSMTVQDYQDLIDRGWRRSGKYVYKPVMNQTCCPQ
}	1	}	YTIRCRPLQFQPSKSHKKVLKKMLKFLAKGEVPKGSCE\DEPMD
1	<b>}</b>	1	STMDDAVAGDFALINKLDIQCDLKTLSDDIKESLESEGKNSKKE
1	1	1	EPQELLQSQDFVGEKLGSGEPSHS
<del></del>	<del></del>	<del></del>	<del></del>

TRADOCS:1416257.1(%CSH011.DOC)

Degaming predicted and nuclotide location corresponding begaming and nuclotide location corresponding coffice and nuclotide location corresponding coffice and nuclotide location corresponding coffice and nuclotide and nuclotide and nuclotide and nuclotide location corresponding coffice and nuclotide and nuclotide and nuclotide residue of samino acid amino acid amino acid and nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotide nuclotid	SEQ	Predicted		·
Docation   Corticol   Continuation    Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continuation   Continu			Predicted end	
corresponding to first amino acid amino acid anino colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colonie, colo				I MATERIALIE, CECVSCEIDE DENGRAPHIA NELLA ME
corresponding to first amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid acid amino acid amino acid amino acid amino acid acid amino acid amino acid acid amino	1			Crucamic Acid, F=Phenvlalanine G_Cl
to first amino acid rosine, X-Unknown, *=Stop   VaryPtophan, Y-Tyrosine, X-Unknown, *=Stop   VaryPtophan, Y-Tyrosine, X-Unknown, *=Stop   VaryPtophan, Y-Tyrosine, X-Unknown, *=Stop   VaryPtophan, Y-Tyrosine, X-Unknown, *=Stop   VaryPtophan, Y-Tyrosine, X-Unknown, *=Stop   VaryPtophan, Y-Tyrosine, X-Unknown, *=Stop   VaryPtophan, Y-Tyrosine, X-Unknown, *=Stop   VaryPtophan, Y-Tyrosine, X-Unknown, *=Stop   VaryPtophan, Y-Tyrosine, X-Unknown, *=Stop   VaryPtophan, Y-Tyrosine, X-Unknown, *=Stop   VaryPtophan, Y-Tyrosine, X-Unknown, *=Stop   VaryPtophan, Y-Tyrosine, X-Unknown, *=Stop   VaryPtophan, Y-Tyrosine, X-Unknown, *=Stop   VaryPtophan, Y-Tyrosine, X-Unknown, *=Stop   VaryPtophan, Y-Tyrosine, X-Unknown, *=Stop   VaryPtophan, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Unknown, Y-Tyrosine, X-Un	- [			M-Miscialne, 1=1soleucine K-Lygine
amino acid residue of anin acid anino cquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence acquence	i			L=Leucine, M=Methionine, N=lenaragine
residue of amino acid acquence	- 1			P=Proline, Q=Glutamine, D=Arginine
amino acid sequence oquence oquence oquence oquence oquence oquence oquence  versible nucleotide disertion versible nucleotide deletion, versible nucleotide disertion versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide insertion  versible nucleotide nucleotide insertion  versible nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nu	ļ			S=Serine, T=Threonine, V-Valine
Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence	İ			W=Tryptophan, Y=Tyrosine Y-Unknown + o.
TOPOSTOLE MUCLECTED INSERTION  VENTIVERED STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE ST	- 1		sequence	Codon, /=possible nucleotide deletide
WAYNTYPROGRADLS SPECKARE I KERKELKMOON PAGEL  EGPOAGEN PSEED FOR PAKANON PSEED I TERESTREINEN PAGE  FICESPELAR TPPROPED CONTROLLES YOU KEY OWN IHMIN PEDTPEGOFTER  FICESPELAR TPPROPED CONTROLLED TY WAY LIKE YOU WE SEND THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLED THE CONTROLLE	<u> </u>	sequence	}	\=possible nucleotide incorrier\
VYRS.DPS.SIGNATILLES.YOV.YRS.YOW. IKRNPEDTPTES.GFTR FILES.SPICA.PTIPNOPPOCYGS.PHQYWLDKILIA.YOYIDLUR CVSS.YVI.YDPDYS-LIG.YOYS.NLEW.FTPGLHEKTS.GLS.YYY MGFYTHS.CPMKY.KGQYR.PSDLLCPETTWAYIF.GC.JPS.LEW.KY GYTHYS.PERVENY.KGQYR.PSDLLCPETTWAYIF.GC.JPS.LEW.KY GRENDALIS.SAMEDSEALGFEINGLDPFALGAVTDLGWSR.PLI GRAAPLALEGKOLLARARTGS.GKTAAYAI.PMLGLLIHKKAGG.P EAAAVIGYAS.LVGGKCSERRILJFRN GRUBALIS.SAMEDSEALGFEINGLDPFALGAVTDLGWSR.PLI GRAAPLALEGKOLLARARTGS.GKTAAYAI.PMLGLLIHKKAGG.P VEGAVRGIVLAVITEELE.RAGAGS.HTG.JARATAPIEVOLALIKKAGG.P VEGAVRGIVLAVITEELE.RAGAGS.HTG.JARATAPIEVOLALIKKAGG.P LILHHPYTIKLGES.GLGGPDGLGQFGVCCFTEEKKFILLIYALIK LILHHPYTIKLGES.GLGGPDGLGQFGVCCFTEEKKFILLIYALIK LILHHPYTIKLGES.GLGGPDGLGQFGVCCFTEEKKFILLIYALIK LILHHPYTIKLGES.GLGGPDGLGQFGVCCFTEEKKFILLIYALIK LILHHPYTIKLGES.GLGGPDGLGQFGVCCFTEEKKFILLIYALIK LILHHPYTIK.GGS.GLGFHVSAUNFULLIFTEGTTAN CHIMPETYKAGATARANGTARANTGTI LITHUPTGEFHLGKKEELLS.GENRGFTLLIPAYGFMEET.GGRYX CHIMPETYKGATARANGTARANTGTI LITHUPTGEFHLGKKEELLS.GENRGFTLLIPAYGFMEET.GGRYX CHIMPETYKGATARANGTARANTGTI LITHUPTGEFHLGKKEELLS.GENRGFTLLIPAYGFMEET.GGRYX CHIMPETYKGATARANTGTARANTGTARANTGTI LITHUPTGEFHLGKKEELLS.GENRGFTLLIPAYGFMEET.GTRYX CHIMPETYKGATARANTGTARATTARANGTARANTGTI LITHUPTGEFHLGKKEELS.GENRGFTLLIPAYGFMEET.GTRYX CHIMPETYKAGATARANTGTARATTARANGTARANTGTI LITHUPTGEFHLGKKES.GTRYTTDYXBGFS.GRASDFPTPGDFTGDFT CHIMPETYKAGATARANTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANTGTARANT				VKVHTVPKPGKGADI,SKPPCPKAKET PKERKET
FILESBELEAPTPNORPOGVOSHONOMISKINDEDTTESGETIR FILESBELEAPTPNORPOGVOSHONOMISKI LAVGUTDILIPN CVSSVILYOPDVSFLSLGVYSALREIAFTROLHSTIGGLSTYY MGTYTHSCPMKYKGOVTPSDLLCPSTTWVPIGCLPSLENSK YCRFRQDDEAVEDESTEDDRLOVHKRAIMPYGVYKKOOKDPS ERAAVLOVASLVGNOKSERNLIPRN GRAPALASLVGNOKSERNLIPRN GRAPALASLAVGNOKSERNLIPRN ORKAPILASKAUMENTSCHALAFTOSKITAVATHOLOLLHRKATOP VVEQAVRGLULVPTKELARQAGSMIQOLATYCARDVKYANVSAA EDSVOQRAVMEKPDVVVGTPSRLISHLOLOLLHRKATOP VVEQAVRGLULVPTKELARQAGSMIQOLATYCARDVKYANVSAA EDSVOQRAVMEKPDVVVGTPSRLISHLOLOLLHRKATOP VVEQAVRGLULVPTKELARQAGSMIQOLATYCARDVKYANVSAA EDSVOQRAVMEKPDVVGTPSRLISHLOLOLLHRKATOP VVEQAVRGLULPTKELARQAGSMIQOLATYCARDVKYANVSAA EDSVOQRAVMEKPDVVGTPSRLISHLOLOLLHRKATOP VVEQAVRGLULPTKELARQAGSMIQOLATYCARDVKYANVSAA EDSVOQRAVMENDEVVGTPSRLISHLOLOLLHRATOR VVEQAVRGLUPTKELARQAGSMIQOLATYCARDVKANVSAA ELAHIDIJEHUKLOSGLOGPOLOLOPOUVGTBKELLIVV DEADLLESGFEELKSLLCHLBRIYQAGHUROLLLANLL LELIHMIDIJEHUKLOGSGTOROLOLORUSUKANDUROLPURSE CHI ISQVINGFYLICGETUROLOPOLOLOPOUVGTBKELLIVAL LESLINGRAPTUROLOPOLOLOPOLOCHUROLPURSE CHI ISQVINGFYLICGETUROLOPOLORUSUKANDUROLPURSE CHI ISQVINGFYLICGETUROLOPOLOPOLOPOLORUSUKANDUROLPURSE CHI ISQVINGFYLICGETUROLOPOLOPOLOPOLOPOLOPOLOPOLOPOLOPOLOPOLO	1	1		EGFOAOGHPPSLEPPKAKSNORKSLEDVIDEN TOTAL DEVICE DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE LEGIS DE
CUSSYULYIPPDYSILGUYSALEATHPROLHEKTSQLSYYY MOFTHISCPIMKY KQYRPSDLLCPETTWAVEIECQLSYLEMSK YCFFKOPPEAVDEDESTEPDRICOPHKAM IMPYGYYKKOQKDPS ERAAVIQYASLVQOKCSERNILFRN ORWRALISASAMEDSEALGFEINGLDPRILQAYTDLGWSRPPLI GEKAP LALEGKULIARARTGSGKTANYAI PHOLOLLHKATGP WEGAVIRGUVIPPTELLARQASMI COLHKRATGP WEGAVIRGUVIPPTELLARQASMI COLHKRATGP WEGAVIRGUVIPPTELLARQASMI COLHKRATGP DEROLLIFRATGE FERENGLDPRILGAYTDLGWSRPPLI GEKAP LALEGKULIARARTGSGKTANYAI PHOLOLLHKRATGP WEGAVIRGUVIPPTELLARQASMI COLHKRATGE DESVSQRAVIMEKPDVVOTFSRI LISHLQODSLKIRDSLELIVV DEROLLIFSFOFFEELKSLICHIPRI YCARASTYNEOVOLKE LILHNPYTIKLQESGLOPDOLOQFOVCETTECKFILLYALLK LILHRYTIKLQESGLOPDOLOQFOVCETTECKFILLYALLK LILHRYTIKLQESGLOPDOLOQFOVCETTECKFILLYALLK LILHRYTIKLQESGLOPTOLOQFOVCETTECKFILLYALLK LILHRYTIKLQESGLOPTOLOQFOVCETTECKFILLYALLK CHI 19QNOQFYDCUIATDAEVLGAPVKKKRGKGPKGKASDP REGAVARGI DIPHVSAVINTULEPITERYIKLYTEINDRYDLISS CHI 19QNOQFYDCUIATDAEVLGAPVKKKRGKGROPKGDKASDP REGAVARGI DIPHVSAVINTULEPITERYIKLYTEINDRYDLIS LITHUPPTELAGOPTICANSTYKAN TERELIKAN TERELIK SELDISHGATTARAN TERELIK CHI 19QNOQFYDCUIATDAEVLGAPVKKKRGKGROPKGDKASDP REGAVARGI DIPHVSAVINTULEPITERYITYIKUNGETARAN TERELIK LITHUPPTIKAN TERELIKAN TERELIK TERELIKAN TERENGUN TERELIKAN TERELIK LITHUPPTIKAN TERELIKAN TERELIK TERELIKAN TERENGUN TERELIKAN TERELIK LITHUPPTIKAN TERELIKAN TERELIKAN TERENGUN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKAN TERELIKA			1	VVRSSPPSSOFKATLLEGYOUNGEROOF
MGFTHACPMKYKGYRPSDLICPETTWVPIEGCLPSLEMSK YCRFRQDPEAVEDERSTEPDRICYPHKRAIMPYGYKKGXDPS EARANUGASIAUGKCSERALLFRIM GERAPLGASIAUGKCSERALLFRIM GERAPLGASIAUGKCSERALLFRIM GERAPLGASIAUGKCSERALLFRIM GERAPLGASIAUGKCSERALLFRIM GERAPLGASIAUGKCSERALLFRIM GERAPLGASIAUGKCSERALLFRIM GERAPLGASIAUGKCSERALLFRIM GERAPLGASIAUGKCSERALLFRIM GERAPLGASIAUGKCSERALLFRIM GERAPLGASIAUGKCSERALLGEBINGLDELLLGASIAUGKCSERALLFRIM LILINIPPTIKLGESCLGPEDOLGOGPOUCATGROWATMVSAN EBSYSORAVILMSERDYVUGTERSTLSILGENGSPLALLALL LELIRGSSLFYNTLERSYRLELFLEGPSIPTCULMSELLIAVE LILINIPPTIKLGESCLGPEDOLGOGPOUCATGROWATMVSAN LILINIPPTIKLGESCLGPEDOLGOGPOUCATGROWATMVSAN LILINIPPTIKLGESCLGPEDOLGOGPOUCATGROWATMVSAN LILINIPPTIKLGESCLGPEDOLGOGPOUCATGROWATMVSALL LELIRGSSLFYNTLERSYRLELFLEGPSIPTCULMSELPLAS CHI ISGNOGPTHUSASVILMELLEGGNSGPILDGASIPTGROPPTGAP EAGWARGIDFHHUSAVILMIBLGSGNSGPILDGASPHASDE AGGARGATHARAVILMIBLGSGNSGPILDGASPHASDEPTGAP CHI ISGNOGPTHIGASTIKERSDOGPSPEVOUGHES LAGIGAPTPPSGPOHASSTIKERSDOGPSPEVOUGHES LAGIGAPTPPSGLSGCOPTSMLRIPPTGASPTGASPTGGLGO LUVPSKAKAKSSPOTTSVTTOTAGGCSGASGASIDSSLIGS FRIDENGSSPODGGKSTPRINGSPPPGAPSSRRVVLLHFIGLIGE FRIEDRICHSPRICTURY FROM PERCHANGAN PERCHAUKAG REAGENAALDENGLILALALSFEGLLGSTASTTGGLGO LUVPSKAKAKSPOTTSTGGLGOGPTSMLRIPPTGASPTGGLGO LUVPSKAKAKSPOTTSTGGLGOGPTSMLRIPPTGASPTGGLGO LUVPSKAKAKSPOTTSTGGLGOGPTSMLRIPPTGASPTGGLGO LUVPSKAKAKSPOTTSTGGLGOGPTSMLRIPPTGASPTGGLGO REAGENAALDENGLILALALSFEGLLGSTGSTGGLGOGPTGGGGG REAGENAALDENGLILALALSFEGLLGSTGSTGGLGOGPTGGGGG REAGENAALDENGLILALALSFEGLLGSTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG		1	J.	FLCSSPLEAFTPPNGPDGCCCGCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Comparison   Com	ł	ļ		CVSSVYLYYDDDVSFLGLCVVCALDDIA
6096 2277 575 QRYRAALISSAMEDSEALGFEHMOLDERLIQAVFOLGWSRPPLIT ORKAPLUSAMEDSEALGFEHMOLDERLIQAVFOLGWSRPPLIT ORKAPLUSAMEDSEALGFEHMOLDERLIQAVFOLGWSRPPLIT ORKAPLUSAMEDSEALGFEHMOLDERLIQAVFOLGWSRPPLIT ORKAPLUSAMEDSEALGFEHMOLDERLIQAVFOLGWSRPPLIT ORGANIAMEN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF THE OVER A CHILDREN OF TH	[	1		MGFYIHSCPKMKYKGOYPREDI I GRAMMETAFTROLHEKTSQLSYYY
6096  2277  575  GREATPLALESAMEDSEAGFEHMGLDPRILQAVIDLGWSRPPLI GREATPLALESKOLLARATISGKTAAVAIPMGLLLHREATGP VVEQAVEQLVLVPTEKLEARQQSSHIOLATYCARDVVANVSAA EDSVSQRAVLMEKPDVVGTTSRILSHLQODSLKLRDSLELLVV DEADLLISFGFFEELKELKLRQAGSHIOLATYCARDVANVSAA EDSVSQRAVLMEKPDVVGTTSRILSHLQODSLKLRDSLELLVV DEADLLISFGFFEELKELKLCHLBRI JODSLKLRDSLELLVV DEADLLISFGFFEELKELKLCHLBRI JODSLKLRDSLELLVV DEADLLISFGFFEELKELKLCHLBRI JODSLKLRDSLELLVX DEADLLISFGFFEELKELKLLCHLBRI JODSLKLRDSLELLVX DEADLLISFGFFEELKELLCHLBRI JODSLKRHGRGFRODMADD EAGVARGIDHHVSAVIDFLDETPETS JETVLUNGELPIRSR CHI 1SQPNQCFFDCV1ATDABVLGADVKSKRGRGFRODMADD EAGVARGIDHHVSAVIDFLDETPETS JETVLUNGELPIRSR CHI 1SQPNQCFFDCV1ATDABVLGADVKSKRGRGFRODMADD EAGVARGIDHHVSAVIDFLDETPETSLAVTFEDRFR DICT LLFULPTEQFHLGKTEELLGGERRGFILLPVQFRWEELFORFR CRIDAMSEVTOALTREARIKEIKEELHBAGKTYFEDRFR DICT LLFULPTEQFHLGKTEELLGGERRGFILLPVQFRWEELFORFR CRIDAMSEVTOALTREARIKEIKEELHBAGKTYFEDRFR DICT LLFULPTEQFHLGKTEELLSGERRGFILLPVQFRWEELFORFR DICT LLFULPTEQFHLDSLSVATENLEST LLFULPTVFDAFR DICT LLFULPTEQFHLGKTEELLSGERRGFILLSKARSTENDATSRATTLIPSL LLASLGGATTPSLSTAVTTSTEEDTSNDAPSFTCGARSTARATLIPSL LLASLGGATTPSCSFTRAGTSPTGATSCATTLIPSL RVERBAGGSGATTSPLASTAVATHLERELGAFEERMGQVPFLDS RVESPAGGSGATTSPLASTAVATHLERELGAFEERMGQVPFLDS RVESPAGGSGATTSPLASTAVATHLERELGAFEERMGQVPFLDS RVESPAGGSGATTPLASTAVATHLERELGAFEERMGQVPFLDS RVESPAGGSGATTSPLASTAVATHLERELGAFEERMGQVPFLDS RVESPAGGSGATTSPLASTAVATHLERELGAFEERMGQVPFLDS RVESPAGGSGATTSPLASTAVATHLERELGAFEERMGQVPFLDS RVESPAGGSGATTSPLASTAVATHLERELGAFEERMGQVPFLDS RVESPAGGSGATTSPLASTAVATHLERELGAFEERMGQVPFLDS RVESPAGGSGATTSPLASTAVATHLERELGAFEERMGQVPFLDS RVESPAGGSGATTSPLASTAVATHLERELGAFEERMGQVPFLDS RVESPAGGSGATTSPLASTAVATHLERELGAFEERMGQVFPLDS RVESPAGGSGATTSPLASTAVATHLERELGAFEERMGQVPFLOGGERTAGGATTSPLASTAVATHLERELGAFEERMGQVPATHLERELGAFEERMGGATTATATATATATATATATATATATATATATATATAT				YCRENODPEANDEDESTERDELCYETYVWVPIEQCLPSLENSK
QRVRAALISSAMEDSEALGFEHMOLDERILGAVTDIGMERPTLIC QRAAT PLABEROULLARRATISMCARAPISMCLALHERATOR VVEQAVRGLVLVPTKELARQAGSMICOLATY CARBY VANVESAR EDSVSQRAVIMMERPDVVGTDSRILEGOSIKLERDSILLIVV DEADLLFSFGFEELKSLLCHERIY YOAFIMSATFMEUDQLKK LILHMPYTLKLOSSOLOPPODLOGPQVVCETEERKELLIYALLK LILHMPYTLKLOSSOLOPPODLOGPQVVCETEERKELLIYALLK LILHMPYTLKLOSSOLOPPODLOGPQVVCETEERKELLIYALLK LILHMPYTLKLOSSOLOPPODLOGPQVVGSTERREGERGERGDKASDD EAGVARGIDHHVSAVURFDLPFTERSYTRIFTERGERGERGERGERGERGERGERGERGERGERGERGERGE				EEAAVI.OYASI.VCOKCEEDMI I DDV
VVEQAVRGLVLVPTRELARQASMYQCLATYCARDVANVSAS EDSVSQRAVLMEREDVVVTFSRILSHLQQDSLKLRDSLELLUV DEADLLPSFGFEEELKSLCHLPST YOAFLMSATTREDVQALKE LILHMPVILKLQESQLFGPDQLQODOVCVETEDKFLLLYALLK LSLIKGKSLFVATURESYRLEHPETYOAFLMSATTREDVGALKE LILHMPVILKLQESQLFGPDQLQODOVCVETEDKFLLLYALLK LSLIKGKSLFVATURESYRLEHPETYOAFLMSATTRARNINGTV LSPVLPTEOFHLGKIEELLSGENKGPTLDVGGRRGRGPKGDKASDP EGGVARGIDFHHVASVLNRDLDFPTPEAYIHRAGRTARANNPGIV LIFVLPTEOFHLGKIEELLSGENKGPTLDVFQFRRGETEGFRYX CRDAMRSVTKOATREARKETEELLHISEKLTYFEDDDPR\DIO LIFVLPTEOFHLGKIEELLSGENKGPTLDVFQFRRGETEGFRYX CRDAMRSVTKOATREARKETTEELLHISEKLTYFEDDDPR\DIO LIFVLPTEOFHLGKIEELLSGENKGPTLDVPQFRRGETEGDPRY LLHHDLPLHRAVVKPHLGHVDFULVPPALRGLVRPHKK\GRSCL PLVGRPREOSPRTHCASSTIGENKSDPQSPFTVVKLDHGLIGEP PRELPNGSPSRDDGGKTFRNGSPPFGADDPTFOPFTGFP FRENNGSPSRDDGGKTFRNGSPPFGAPBPTFOPFTGFP FRENNGSPSRDDGGKTFRNGSPPFGAPBPTFOPFTGFP FRENNGSPSRDDGGKTFRNGSPPFGAPBPTFOPFTGFP FRELPNGSPSRDDGGKTFRNGSPPFGAPBPTFOPFTGFP FRELPNGSPSRDGGGKTPRNGSPPFGAPBPTFOPFTGFP FRELPNGSPSRDGGGKTPRNGSPPFGAPBPTFOPFTGFP FRELPNGSPSRDGGGGTFTRNGSPPFGAPBPTFOPFTGFP FRELPNGSPSRDGGGGTFTRNGSPPFGAPBPTFOPFTGFP FRELPNGSPSRDGGGGTFTRNGSPPFGAPBPTFOPFTGFP FRELPNGSPSRDGGGGTFTRNGSPPFGAPBPTFOPFTGFP FRELPNGSPSPBGGGGTTLSHLRPPTSPTGAPATTRALSGHL DSDDDGSGGLUGIDNKIBOMBTLKSHLMFAVEREVELVLKEQI RELABRAALEDENGLGRALAN\SPFGLUGAAAMPPLEMPALIVPVFGVG VDALSNGPMSPGPLHLLITPSLLGGGGGFFTGRQCQAPFGET VOALSNGPMSPGPLHLLITPSLLGGGGGFFTGRQCQAPFGET VOALSNGPMSPGPLHLLITPSLLGGGGGFFTGRQCQAPFGET VOALSNGPMSPGPLHLLITPSLLGGGGGFFTGRQCAPFGET VOALSNGPMSPGPLHLLITPSLLGGGGGFFTGRQCAPFGET VOALSNGPMSPGPLHLLITPSLLGGGGGFTTGRQCAPFGET VOALSNGPMSPGPLHLLITPSLLGGGGGFFTGRQCAPFGET VOALSNGPMSPGPLHLLITPSLLGGGGGFTTGRQCAPFGET VOALSNGPMSPGPLHLITPSLLGGGGGFTTGRQCAPFGET VOALSNGPMSPGPLHLITPSLLGGGGGFTTGRQCAPFGET VOALSNGPMSPGPLHTGLTGATAAAMPPLATARKELD CGRIPTRANGTCHEKDTSNINROTETSVANSRSPEKAOAROK RINSAGGRSSSLPSNRKSSTPTKGLILUTPVVAYSPKRGCA VELRHSPLEKDSSPGSSTSLLIKKGRGFTSDTPIMRRLKELD CGRIPTRALKKSVSVEQCKAVYPQONDEBTAKITLAETTRFF\D \QUALFIESTYAGGGSTLLSKNESSPIRFDILLTYAATSVANSRSPGRC VOALSNAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	6096	2277	575	ORVRAALLCCAMEDCEAL CERTIFICATION
DESVSCRAVIMERDOVVOUTDSTLISHLQODSIKLINGSIELLIV DEADLLFSFGFEELKSLLCHLPRIYOAFIKASTENBUQALKE LILHMPVILKUGESGLFGPDQLOQFOVOCTSTEDKEFLLIVALKE LSLIRGKSLLFVNTLERSYRLEFLEGGSTTOVLNGELPLRSR CHI ISOPNOGPYDCVIATDAEVLGAPVKKRRGRGPKGDKASDP EAGVARGIDFHWSAVLNDLDFPTPEAYTHRAGRTRARNNGIV LIFVLJPTEOPHLGKIEELLSGENKGPTLBPYGFRWEELEGFRYR CRDAWRSVTKQAI REARLKEI KEELLISEELLSTERLTYPGREELEGFRYR CRDAWRSVTKQAI REARLKEI KEELLISEELLSTERLTYPTEOPHRY DUG LLHRIDLFLHFAVVKPHLGHVEPVILVPPALKEGLYPHKK\GRSCL PLVGRYREGSPRTYPACASSTIERKSDQOPSPPEVVGPLMS AFGTMSGGKKKSSFQITSVTTDYKSGPGSPASDPFTVOKLPHGLGEP YRRGRWTCVDVVERDLEPHSFGGLLEGIRGASGGAGGRSLDSRL LEASLGLGAPTPPSGLSGGPTSWASDPASPSPRVVKLPHGLGEP YRRGRWTCVDVVERDLEPHSFGGLLEGIRGASGGAGGRSLDSRL LEASLGLGAPTPPSGLSGGPTSWALARPPEPOPARSFTGGLO LVVDSKAKARKPPLSASSPQGRPFPETTGSAGTSRAATLPBSL RYBEAGGSGARTPPLSRRAVVMKLRMBLGAPEMGOVPPLDS RPSSPALYTHASSLVIKKSPDPFGAVAAGKESLAHSMLAISGGL DSDDDSGSGSLUGIDNXIEGAMBLUKSHDPGAVAAKKELAHSMLAISGGL VOALSMONSPSSGDLJSHLINKSDPFGAVAAKKELAHSMLAISGGL VOALSMONSPSSGDLJSHLINKSDPFGAVAAKKELAHSMLAISGGL VOALSMONSPSSGDLJSHLINGTDPTGAVAKKSUPTLAGED REALBERNALEGENGLKRALA\SPEGLGSAGPFRGQCAPFGEET OPPPSLEGTPQO  168  168  1074  NYCHRIRSDLEKGSSPGSSTSTLLIKKGRETSDTPIMRALKELD EGKIPKNWGTQTEKEDSPGSSSTSTLIKKGRETSDTPIMRALKELD EGKIPKNWGTQTEKEDTSNINPGTETSVNASSPERCAQOROK RLNSASQRSSSLPSNKKSSTPTKREIMLTYVVAYSPKSPKE NSPGFSHLLSKNESSPIRDILLDDLDTVUSTLORTHPRKOL \(\OPPLIEDDSEEK\TYSEKAT\ONI\UNHSSCPEPVPNGVKKVSVR TAMEKKKSVSVEQCKYDVSTPQGNDFSVTAKIFILAETERPP\D ETKREKQIERALSRMSSSPIRDILLDDLDTVUSTLORTHPKROL \(\OPPLIEDDSEEK\TYSEKAT\ONI\UNHSSCPEPVPNGVKKVSVR TAMEKKKSVSVEQCKYDSVTPQGNDFSVTAKIFILAETERPP\D ETKREKQIERALSRMSSSPIRDILLDDLDTVTVAYSPKSPKE  RLSPGFSHLLSKNESSPIRDILLOTTVANGRSPEKCAQOROK RLNSASGRSSSLPSNRKSSSTTKREIMLTPVVVAYSPKSPKE  RLSPGFSHLLSKNESSPIRDILLOTTVANGRSPEKCAQOROK RLNSASGRSSSSTBYSRRTDLATTVANGRSPEKCAQOROK RLNSASGRSSSSTBYSRTDLATTVANGRSPEKCAQOROK RLNSASGRSSSSSTTRAGLATTVANGRSPEKCAQOROK RLNSASGRSSSSTBYSRTDLATTRATTRETPPPDTMRALKELD EGKIPKNWGTQTEKEDTSNINPRQTETSVARSRSPEKCAQOROK RLNSAGRNSSSSTBYRSTTKREIMLTPPVVAYSPKSPSKE  TAMEKKKSVSVEQCKPVSVTPQGNDFTVAKTRITTGRPPP\	ļ	-	1	OFFAIDLALEGEN LARREDS HANGLOPRIL QAVTOLGWSRPTLI
DEADLIPSTGGEELKSLICHLPRIYOAFIMSATINEDVOALKE LILHRPVILKIQESOLPGPDOLOQFOVOCTBOKFILLIVALIK LELIKGKSLIFVITERSYRIKLFILEQFSITPTUNGELPLESSE CHIISQPNQGYDCVIATDAEVICADPVOKERGRGRGFKODKASDE EAGAVAROIDFHIVASVALWBOLDPTPEAYINEAGERRANPGIV LIFVIPTEOPHICKIEELISGENRGPILLEVQFRREEELGFRIYA CRDAMRSVIXOAIRABLAPTEARIKEILEGENRGPILLEVQFRWEEELGFRIYA CRDAMRSVIXOAIRABRAUKPELDPTPEAYINEAGERTARANNPGIV LIFVIPTEOPHICKIEELISGENRGPILLEVQFRWEEELGFRIYA CRDAMRSVIXOAIRABRAUKPELDEVDFRWEEELGFRIYA LLRHIDLPLHAAVVKPHLGHVDPILVPPALRGLVRPHKE\GRSCL LLRHIDLPLHAAVVKPHLGHVDPILVPPALRGLVRPHKE\GRSCL LLRHIDLPLHAAVVKPHLGHVDPILVPPALRGLVRPHKE\GRSCL LLRHIDLPLHAAVVKPHLGHVDPILVPPALRGLVRPHEVDDPFDPFDFP PRIPNGSPSSDPOGKGTPRNGSPPPGARSPPVWGLIGBP PRIPNGSPSSDPOGKGTPRNGSPPGARSPPVWGLIGBP PRIPNGSPSSDPOGKGTPRNGSPPGARSPRVVKLDHGLGGB PRORPAVCTUVVEREDLEPHSYSGGLISKAGSGGGGRIJDSEL ELASLGLGAPTPPSGLSGCPTSHERPPPTSPFGPPTGPFP PRIPNGSPSSLANGVORTURENBLAGAPEROMOPPLDS RYSERANIFURDASLVKSPPPGCAASPPCAMPETOPPTGPP PRIPNGSPSSLANGVORTURENBLAGAPEROMOPPLDS RYSERANIFURDASLVKSPPPGCAASPPCAMPETOPPTGPP PRIPNGSPSSLANGVORTURENBLAGAPEROMOPPLDS RYSERANIFURDASLVKSPPGCAAAAVPLEMBLAGAPEROMOPPLDS RYSERANIFURDASLVKSPPGCAAAAVPLEMBLAGAPEROMOPPLDS RYSERANIFURDASLVKSPPGCAAAAVPLEMBLAGAPEROMOPPLDS PROPPVLSLPSLTIVPLGLBCLASAAAVPLEMPETAVACSPRGSET OPPSLIPTPOQ OPPPSLPCTPOQ OPPPSLPCTPOQ OPPPSLPCTPOQ OPPPSLPCTPOQ OPPPSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPCTPOQ OPPSSLPC	1	İ		WEODURCLUTURENTARY
LILHRPYTIKUGESCLEPPOLQOFQUVCETEENFILLVALLK		ł		EDGYGORAU MEKDELERQAQSMIQQLATYCARDVRVANVSAA
LILHRPYTIKUGESCLEPPOLQOFQUVCETEENFILLVALLK	- 1	f	[	LEDS VSQRAVDMERPDVVVGTPSRTLSHLOODSLVLDDSLELLIN
LELIRGKSLLEVNTLERSYRLRFLEOFSIPTCVLNGELPLRER CHI ISOPNOGFYDCVIATDAEVLGAPVEKKREGERGDKASDE EAGWARGIDFHIVSAVLINFDLIPTPERAYHRAGERARANNPGIV LTFVLPTEOFHLGKIEELLSGERRGFILLPVOPRMEEIEGFRYR CRAMRSUTKOA REARLKEI KEELLHSGEKRGFIKOPKODKASDE LURHDLPLHPAVVKPHLGHIVPDYLLPPALRGLVSPHKK\GRSCL PLVGPREGGERKSSFOLTSVTTDYEGFGSFGASDPFTEOPPTGPF PRINGSPSPDPGGSFTRICAASSTKERNSDPOSPPEVVGPILWS APGTNISGGKKSSFOLTSVTTDYEGFGSFGASDPFTEOPPTGPF PRLENGSPSPDPGGKGTPRIGSPPCADSSPFRVVKLPHGLGEP PRLENGSPSPDPGGKGTPRIGSPPCADSSPFRVVKLPHGLGEP PRLENGSPSPDPGGKGTPWLRPPPTSPGSPGAGGRAGESLDSRL LVVSKAKAKEPLSASSPQORPPSPETGSAGTSRAATLESL LVVSKAKAKEPLSASSPQORPPSPETGSAGTSRAATLESL RVSABAGGSGARTPPLSRKAVDMKLRKELGAPEEMGOVPPLDS RPSSPALYFTHOASLVHKSPDPFGAVAAQKRSLAHSMLAISGHL JSDDDGSGSGLVGIONKIEGAMVESHLAMSVEEVEUKROI RELAERNAALEGENGLIKALA\SPSOLGSASPPROPUPPUS RPSSPALYFTHOASLVHKSPDPFGAVAAQKRSLAHSMLAISGHL SCHLERNAALEGENGLIKALA\SPSOLGSASPPROPUPPUS RPSSPALYFTHOASLVHKSPDPFGAVAAQKRSLAHSMLAISGHL VVALSNSPWSPGGPLPHLLI IPSLDGGGGGFRTGAQGAFFGET OPPPSLOFTPOG VOALSNSPWSPGPLPHLLI IPSLDGGGGFRTGAQGAFFGET OPPPSLOFTPOG VOALSNSPWSPGFLPHLLI IPSLDGGGGFRTGAQGAFFGET OPPSLOFTPOG VOALSNSPWSPGFLPHLLI IPSLDGGGGFRTGAQGAFFGET NLSPGFSHLLSKNESSPIRFDILLDLDLDTVYSTLORTNPRKQL VPLEDDSEEK_TYSERAT\DNIVNISSCPEVPNRKKVSVR NLSPGFSHLLSKNESSPIRFDILLDLDLDTVYSTLORTNPRKQL VPLEDDSEEK_TYSERAT\DNIVNISSCPEPVPNGVKKVSVR TAMEKNKSVSYEQCKPUSVTPQONDFEYTAKITILAETERFFY\D EKKENGJI EAALSMNSSSPIRFDILLDLDLDTVYSTLQRTNPRKQL VPLEDDSEEK_TYSEKAT\DNIVNISSCPEPVPNGVKKVSVR TAMEKNKSVSYEQCKPUSVTPQONDFEYTAKITILAETERFP\D ELTKEKQJI EAALSMNSSSPIRFDILLDLDLDTVYSTLQRTNPRKQL VPLENDSEEK_TYSEKAT\DNIVNISSCPEPVPNGVKKVSVR TAMEKNKSVSYEQCKPUSVTPQONDFEYTAKITILAETERFP\D ELTKEKQJI EAALSMNSSSPIRFDILLDLDLDTVPVSTLQRTNPRKQL VPLENDSEEK_TYSEKAT\DNIVNISSCPEPVPNGVKKVSVR TAMEKNKSVSYEQCKPUSVTPQONDFEYTAKITILAETERFP\D ELTKEKQJI EAALSMNSPEGGRI TLQTRILNGBAFGRSFGKD VIMLIGNKSDLESREDVKREGGAPARR\HGLI IMPETSAKTACN VEEAFINTAKEI VRKAQGLEFDVHEANGI KLQIWDTAGQBSF RSITASYVGAAGAGLLVYDITRRETFINLTISMLEDARQHSSSMM VIMLIGNKSDLESREDVKREGGAPARR\HGLI IMPETSAKTACN VEEAFINTAKEI VRKAQGLEFDVHEANGI KLGIPQOS ISTSVOP	į	1		1 DEADDIE OF GEEELKSLLCHLPRIYOAFIMSATEMEDVOAL VE
EAGVARGIF HUSAVILINE PTTEAY HIRAGRITARAMPGIV  LIFVIJETOFHIGKLEELLSCENKOP ILLPVOPFMEELEGFRYN  CRDAMRSVTKOAI RERAIKEKE KEELLHEEKKYFEDDRY DIOL  LIRHIDIELHPAVKPHIGHVEPDYLVPPALKKYFFEDDRY DIOL  LLRHIDIELHPAVKPHIGHVEPDYLVPPALKKYFFEDDRY DIOL  LLRHIDIELHPAVKPHIGHVEPDYLVPPALKGLVPPHKKKGRSCL  PLVGRPROSPETTCAASSTKERKSDPOSPEFEVOREMS  APGTMSGKKKSSFOITSVTTDVEGFGSFGASDPPTFOPDTGPP  PRIEMGERSPPDFGGKGTRRMGSPPPGADSSRFRVVKLPHGLGEP  PRIEMGERSPPDFGKGTTRMGSPPPGADSSRFRVVKLPHGLGEP  PRIEMGERSPPDGKGTTRMGSPPFGADASSFRFRVKLPHGLGEP  PRIEMGERSPPDGKGTTRMGSPPFGADASSFRFRVKLPHGLGEP  RVEAEAGGSGRTPPLSRRKAVUMRLEMBLGAPEEMGGVPPLDS  RPSSPALLYFTHDASLVHKSPDFFGAVAAOKFSLAHSMLAISGHL  LVVPSKAKALERPPLSASSFOOPPEPETGESAGTSRAATPLESL  RVEAEAGGSGRTPPLSRRKAVUMRLEMBLGAPEEMGGVPPLDS  RPSSPALLYFTHDASLVHKSPDFFGAVAAOKFSLAHSMLAISGHL  SEDDDSGSGSLVGIDMKIRDAMDLVKSHLMFAVREVEVELVKROI  RELAERNAALGORNGLURALIA\SPEGLGSAGPPRGVPRLGPPA  PROFFVLSLESLTIVPIGLGBAMPPLLVPMPGVG  VOALSNOPWSFGPLPHLLIIPSLDGGGEGFRTGRQQGAPFGEET  QPPPSLGSTDQ  168  1074  NYCLRHRSPLEKDSSPGSSSTSLLIKKORETSDTFIMRALKELD  EGKIFKNWGTGTEKEDTSNINPROTETSVNASRSPEKCAQOROK  RIMSASSORSSSLPSNKRSSTFTKREIMLTPVTVAYSPKRSPKE  MLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKGL  VOFLPLDDSEEK, VTYSEKAT\UNIVHSSCEPPVPNGVKKVSVR  TAMEKKKSVSYEQCKVSVTPQGNDFEYTAKIRTLAETERFF\D  EGKIFKNWGTGTEKEDTSNINPROTETSVNASRSPEKCAQOROK  RIMSASQRSSSIPPSNRKSSTFTKREIMLTPVTAYSPKRGL  LOFTDRAFGVYBLDTIGVEFGARMVILDDLDTVPVSTLQRTNPRKGL  VOFLDDSEEK, VTSEKAT\UNIVHSSCPEVPRNVKKVSVR  TAMEKKKSVSYEOCKPVSVTPQGNDFEYTAKIRTLAETERFF\D  EKTKENQUIEAHLSKMESSPIRFDILLDDLDTVPVSTLQRTNPRKGL  VOFLDRAFGVYBLDTIGVEFGARMVILDGGOLGKULOIMDTAGGESF  RSITASYYRGAGALLVYDTTRRTFINHLTSWLEDARGHSSMW  VIMLIGNKSDLESRRDVKREEGEAFARE\MGLIFMTSAKTACN  VEEAFINTAKEIVRKIQQGLFDVHNEANGIKIGPQOSISTSVOP  SASQRNSRIGNGCC  SASQRNSRDIGSNGCC  FREGRAWPLREVSHHLGCRRVCSWSASWGRAPALSARLSPILAER	1			LSLIBGKSLIGDEN SPRENCE STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET S
LITFULPTEOFHUGKIEELLISGENRGPILLIPVOPRMEELIGFRYR CRDAMRSVTKQAIREARLKEIKLEILHISEKLKTYFEDNPR\DLQ LERHDLPEHPAVKPHIGHVEPLISGENRGPILLIPVOPRMEELIGFRYR CRDAMRSVTKQAIREARLKEIKLEILHISEKLKTYFEDNPR\DLQ LERHDLPEHPAVKPHIGHVEPULVPPALRGLVPPIKK\GRSCL PLVGRPRGSPRTHCAASSTKERNSDPOPSPPEVUGPLMS  APGTMSGGKKKSSFQITSVTTDVEGFGSPGASDPPTPOPPTGPP PRLPNGBPSPDPGGKGTTRNGSPPGSPGASDPPTPOPPTGPP PRLPNGBPSPDPGGKGTTRNGSPPGSPGASDPPTPOPPTGPP PRLPNGBPSPDPGGKGTTRNGSPPGAPGASFRVVKLPHGLGEP YRRGRWTCVDVYERDLEPHSFGGLLEGIRGASGAGGRSLDSRL ELASLGLGAPTPPSGLAGOFFBUL RPPTSPGPQARSFTGGLGQ LVVPSKAKAEKPPLSASSPQORPPEPTETSRAGTSRAATPLESL RVEARAGGSGARTPPJSRKRAVVMRLRMELGAPEEMGQVPPLDS RPSSPALYFTHDASLVHKSPFGAVAGKTSLAHSMLAISGHL DSDDDGSGGSLVGIDNKIEGAMDLVKSHMFAVREEVEVLKRQI RELAERNAALGEORGLLERALA\SPECLGSAPERGVPR\LEPPA RPSSPALYFTHDASLVHKSPGAVAGKTSLAHSMLAISGHL DSDDDSGSGSLVGIDNKIEGAMDLVKSHMFAVREEVEVLKRQI RELAERNAALGEORGLLERALA\SPECLGSAPERGVPR\LEPPA RPSSPALYFTHDASLVHKSPGAVAGKTSLAHSMLAISGHL DSDDDSGSGSLVGIDNKIEGAMDLVKSHMFAVREEVEVLKRQI RELAERNAALGEORGLERALA\SPECLGSAPERGVPRVLKRQI RELAERNAALGEORGLERALA\SPECLGSAPERGVPRVLKRQI RELAERNAALGEORGLERALA\SPECLGGAPFGGFT QPPSLPGTPQQ PPPSLPGTPQQ PPSLPGTPQQ PPSLPGTPQQ PPSLPGTPQQ PPSLPGTPQQ PPSLPGTPQQ PPSLPGTPQQ PPSLPGTPQQ PPSLPGTPQCS RIMSASGRSSSIPPSRKSSTPIKREIMITPVTVAYSPKRSPKE NLSPGFSHLLSKNESSPIRFDILLDDLDTVVSTLQRTNPRKQL QFLPLDDSEEK\TYSEKAT\NIVNHSSCEPEVPNGVKKVSVR TAMEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\D EKIFKNWGTQTEKEDTSN INPROTETSVNASRSPEKCAQORGK RIMSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE MLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL \QFIDKRPQVHBLTIGVEFGARMVNILOGIKLQIMDTAQGBSF RSITASYYGGAGALLVYDTIRRTFFHLTSWLEADRQHSSSMM VIMLIGNKSDLESRRDVKREEGRAPARE\HGLIFMETSAKTACN VERAFINTAKEIYRKIQQGLFDVHRABAGKLICPQQSISTSWQP VERAFINTAKEIYRKIQQGLFDVHRABAGKLICPQQSISTSWQP SASQRNSDIGSNSGCC SASQRNSDIGSNSGCC SASQRNSDIGSNSGCC SASQRNSDIGSNSGCC SASQRNSDIGSNSGCC	1	i		CHILOGRACORYDONIA
CRDAMRSYTKOAIREARLEIKSELLISEKALTYFEDDRY DU  LIRHDIPLHPAVVKPHLGHVPDYLVPPALRGLVRPHKK\GRSCL  LURHDIPLHPAVVKPHLGHVPDYLVPPALRGLVRPHKK\GRSCL  PLVGRPRECSPRTHCASSTKERNSDPORSPEVVGPLMS  AFGTMSGKKKSSFQITSVTTDYEGGSGADDPTPQPPTGPP  PRLPMGERSDPDGGGTTRNGSPPPGAPSGRFTVVKLPHGLGEP  YRRGRWTCUDVYERDLEFFSGLLGEIRGAGGAGGRSLDSRL  ELASLGLGAPTPPSGLSGGPTSWLRPPTSPGPQARSFTGGLGG  LVVPSKAKALKPPLSASSPQQRPPEFTGESAGTSRAATPLJESL  RVEABAGGSGARTPPLSRKAVDMRLRWELGAPEMGQVPPLDS  RPSSPALYTTHDASLVHKSPDPFGGAVAQKFSLAHSMLAISGHL  DSDDDSGSGSSLVGIDNKLGOMDLVKSHLMFAVREEVEVLKEQI  RELAERNAALEGEMGLLEALA\SPEQLGSAGPPRKVPR\LGPPA  PNGFFVLSLPSLTIVPLCLPPLGAAMPPLEMPALIVVPYPGVG  VQALSNGPWSFGPLPHLLIIPSLAWPPLEMPALIVVPYPGVG  VQALSNGPWSFGPLPHLLIIPSLAMPPLEMPALIVVPYPGVG  CPPPSLEGTPQQ  PPSSLEGTPQQ  PPSSLEGTPQQ  RLNSASQRSSSLPPSNRKSSTPTKREIMLTVTTVAYSPKRSPKE  GEKIFKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK  RLNSASQRSSSLPPSNRKSSTPTKREIMLTVTVAYSPKRSPKE  AVENCHMERSPELBKDSSPGSSTSLLIKKQRETSDTFIMRALKELD  EGKIFKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK  RLNSASQRSSSLPPSNRKSSTPTKREIMLTVTVAYSPKRSPKE  AVENCHMERSPELBKDSSPGSSSTSLLIKKQRETSDTFIMRALKELD  ETKEKDQIEALSRMPSPGGRITLGTRLMGEAFGRSFGKD  NYCLEHRSPLEKDSSPGSSSTSLIKKQRETSDTFIMRALKELD  EKKIFKNWGTOTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK  RLNSASQRSSSLPPSNRKSSTPTKREIMLTVTVAYSPKRSPKE  AVENCHMERSPELBKDSSPGSSSTSLIKKQRETSDTFIMRALKELD  EKKIFKNWGTOTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK  RLNSASQRSSSLPPSNRKSSTPTKREIMLTVTVAYSPKRSPKE  GKKIFKNWGTOTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK  RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE  RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE  RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE  GKKIFKNWGTOTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK  RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE  AVENCHMERSPLESHBLICHDERSPGRTTTLOTTRINGEAFGRSPGKD  TAMEKKKSVSYEQCKPVSVTPQCNDPEYTAKIRTLAETERFP\D  EKKIFKNGTOTTEKEDTSNINDEGRTTLOTTRINGEAFGRSPGKD  GLTKKERQLEALSRMPSPGGRTTLOTTRINGEAFGRSPGKD  GFTGRAWFLEGEVSHULGGRRVGSWSKAWGLPALLASSRNM  VIMLIGNKSDLESRRDVKREGGAPAREVHGLIFMETSAKTACN  VEELAFINTAKET YRKIQQLSPDVHNEARGIKTGPQOSISTSVGF  SASQRNSRDIGSNSGCC  GKWYPLSCAVQOVAMKGMGSNSFVADLLASSRDIAG	1			EACUARCIDENTIAL
LLRHOLPHAPAVKPHLGHVPDYLVPPALRGLVPPHKK\GRSCL LLRHOLPHAPAVKPHLGHVPDYLVPPALRGLVPPHKK\GRSCL PLVGRPREGSPRTHCAASSTKERNSDPQSPPEVVGPLWS APGTMSGGKKSSFQTTSTTDYEGPGSPGADDPPTQPPTGPP PRLPMGEPSPDPGGKTPRNGSPPGADDPPTQPPTGPP PRLPMGEPSPDPGGKTPRNGSPPGADDPPTQPPTGPP PRLPMGEPSPDPGGKTPRNGSPPGADDPPTQPPTGPP PRLPMGEPSPDPGGKTPRNGSPPGADDPPTQPDFTGPP PRLPMGEPSPDPGGKTPRNGSPPGADDPSRFRVVKLPHGLGEP PRLPMGEPSPDPGGKTPRNGSPPGADDPSRFRVVKLPHGLGEP PRLPMGEPSPDPGGKTPRNGSPPGADDPSRFRVVKLPHGLGEP LASIGLGAPTPPGGLSGCPTSWLRPPPTSPGQARSFTGGLGG LVVPSKAKAEKPPLSASSPQGRPPETGESAGTSRAATPLPSL RVEABAGGGGATPPLSRKAVDMRLRMELGAPEMGQVPPLDG RPSSPALYFTHDASLVHKSPPPFGAVAAQKFSLAHSMLAISGHL DSDDDDGSGGSLVG LDNKLEOAMDLVKSHLMFAVKEEVEVLKEGI RELAERNAALEGENGLLRALSPEPLGASAGPPRGVPR\LGPPA PNGFFVLSLPSLTIVPLGLPGLASAAWPPLDMPALIVPVFPGVG VQALSNGPWSSGPLPFLLILDLLDLVKSHLMFAVKEEVEVLKEGI RELAERNAALEGENGLLRALSPEPLGAAWPPLDMPALIVPVFPGVG OPPPSLEGTPQQ PPPSLEGTPQQ PPPSLEGTPQQ PPPSLEGTPQQ PPPSLEGTPQQ PPPSLEGTPQQ PPPSLEGTPQQ PPPSLEGTPQQ PPPSLEGTPQQ PPPSLEGTPQQ PPPSLEGTPQQ PPPSLEGTPQQ PPPSLEGTPQQ PPPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTPQQ PPSLEGTQ	1	i		LTEVI. DTEORIG GETTER TO THE TENTH OF THE ACTION OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE TENTH OF THE T
PLVGRPREQSPRTHCARSTKERNSDPQPSPEVVGPLMS	1	]		CDDAMEGUEVOTEDESCENTERILLPYQFRMEEIEGFRYR
PLVGRPREQSPRTHCARSTKERNSDPQPSPEVVGPLMS	İ	j		LIBUDI DI UNDI DELL'ANTICO DE LA CONTRE L'ANTICE DE E L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC DE L'ANTIC
192 APGTMSGGKKKSSFOLTSVTTDVEGFGSPFEVVGPLMS APGTMSGGKKKSSFOLTSVTTDVEGFGSPGASDFPTGPFTGPF PRLPMGEPSPDPGGKGTPRNGSPPPGAPSSRFRVVKLPHGLGEP PRLPMGEPSPDPGGKGTPRNGSPPPGAPSSRFRVVKLPHGLGEP PRLPMGEPSPDPGGKGTPRNGSPPPGAPSSRFRVVKLPHGLGEP YRRGWTCVDVYERDLEPHSFGGLLEGITGASGAGGRSLDSRL ELASLGLGAPTPPSGLSQGPTSWLRPPTSGFQGARSFTGGLGQ LVVPSKAKAEKPPLSASSPQORPPEPBTGSSAGTSRAATPLPSL RVPSAGAGGGARTPPLSRRKAVDMRLRMELGAPEEMGQVPPLDS RPSSPALYFTHDASLVHKSPDFFGAVAAQKFSLAHSMLAISGHL DSDDDSGSGSLVGINKIEQAMDLVKSHLMFAVREEVEVLKEQI RELAERNAALEQENGLIRALA\SPEQLGSAGPPRGVPR\LGPPA PNGFFVLSLPSLTIVPLGLPGLASAAWPPLPMPALIVPVFPGVG VOALSNGPWSPGPLPHLLIIPSLDGGGGGFRTGRQQGAPFGEET VOALSNGPWSPGPLPHLLIIPSLDGGGGFRTGRQQGAPFGEET QPPPSLBGTPQQ  NYCLRHRSPLEKDSSPGSSSTSLLIKKQRETSDTFIMRALKELD EGKIFKNWGTOTEKEDTSNINPRQTETSVNASRSPEKCAQQROK RLNSASQRSSLPPSNRKSSTPTKEEIMITPVVVAYSPKRSPKE NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSVR TAMEKKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\D EKKIFKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQROK RLNSASQRSSSLPPSNRKSSTPTKREIMITPVVVAYSPKRSPKE NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL \QFLPLDDGEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSVR TAMEKKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\D EKKIFKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQROK RLNSASQRSSLPPSNRKSSTPTKREIMITPVVAYSPKRSPKE NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTMPRKQL \QFLDLDGEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSVR TAMEKKSVSYEQCKPVSVTPQGNDFEYTAKIRTLAETERFF\D ELTKEKDQIEAALSRMPSPGGRITLQTRINQBAFGRSFGKD  6100  2 713 FYEVSGYRSRADPEPRGRDTMTYAYLFKYIIIGDTGVGKSCLLL QFTDKRFQPVHDLTIGVEFGARMVNIDGKGIKLQIWDTAGGRSF RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDARGHSSNM VIMLIGNKSDLESRRDVKREGERAPARR\HGLIFMETSAKTACN VEEAFINTAKEITYKLEYFYNLGEFDVHREANGIKIGPQQSISTSVGP SASQRNSRDIGSNSGCC  FFGRAWPLREVSHWLGCRRVCSWSASWGRLPALSARLSPLLAFR GKMVFPLSCAQVQYAWGMSNNSEVAFLLASRDLLAFRU	<u> </u>	1 [		THE THEAVY KPHLGHVPDYINDDALDGINDDUVV CDOOK
PRLEMGEPSPDPGGKTPRMGSPPPGABSDPFTGDPTGPP PRLEMGEPSPDPGGKTPRMGSPPPGABSDFFTGDFTGE PRLEMGEPSPDPGGKTPRMGSPPPGABSGRFVKLEHGLGEP YRRGRWTCVDVVERDLEPHSFGGLLEGIRGASGAGGRSLDSRL ELASLGLGAPTPPSGLGQGPTSWLRPPPTSPGAAGSTGGLGQ LVVPSKAKAEKPPLSASSPQQRPEPETGSSAGTSRATPLPSL RVEAEAGGSGARTPPLSRRKAVDWRLEMELGAPEMGQVPPLDS RPSSPALIVFTHDASLVHKSPDPFGAVAAQKFSLAHSMLAISGHL DSDDDSGSGSLWGIDNKIEOAMDLVKSHLMFAVREEWEVLKEQI RELABRNAALEQENGLIRALASPEQLGSAGPPRGVPR\LGPPA PNGFFVLSLPSLTIVPLCLPGLASAAMPPLDMPALIVPVPGVG VQALSNGPWSPGPLPHLLIIPSLDGGGGGFRTGQQGAPPGEET VQALSNGPWSPGPLPHLLIIPSLDGGGGFRTGQQGAPPGEET UQALSNGPWSPGPLPHLLIIPSLDGGGGFRTGQQGAPPGEET PNGFFVLSLPSLTIVPLAVAYSPKRSPKE RINSASQRSSSLPPSNRKSSTPTKREIMITPVVVAYSPKRSPKE NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL \QPLPLDDSEEK\TYSEKAT\DNIVNHSSCPBPVDNGVKKVSVR TAMEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\D EKTKENQIEBALSRMPSPGGRITLQTRLNGBAFGRSFGKD NYCLRHRSPLEKDSSPGSSTSLLIKKQRETSDTPIMRALKELD EGKIFNNWGTOTEKEDTSNINPRGTETSVNASRSPEKCAQORQK RINSASQRSSSLPSNRKSSTPTKREIMITPVVVAYSPKRSPKE NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPBPVDNGVKKVSVR TANSKNKSVSYEQCKPVSVTPQGMDFEYTAKIRTLAETERFF\D EGKIFNNWGTOTEKEDTSNINPRGTETSVNASRSPEKCAQORQK RINSASQRSSSLPSNRKSSTPTREIMLTPVVVAYSPKRSPKE NLSPGFSHLLISKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPBVVNGVKKVSVR TANSKNKSVSYEQCKPVSVTPQGMDFEYTAKIRTLAETERFF\D ELTKEKQIEBALSRMPSPGGRITLQTRLNQBAFGRSFGKD  FFUKRSQVSTRGADGEFFRONTYTAYLFKYIIGDTGVGKSCLLL QFTDKRFQPVHDLTIGVEFGARMVINICKGIKLGIWDTAGGSFF RSITRSYYRGAAGALLVYDITRRETFHLITSWLEDBAGNSSSMM VIMLIGNKSDLESGRDVKREGEBAFARR\HGLIFMETSAKTACN VEEAFINTAKEITYKKEYGEFQUFDVHNEANGIKIGPQGSISTSWGP SASQRNSRDIGSNSGCC  FRGRAWPLREVSHWLGCRRVCSWSASWGRLPALSARLSPLLAFR GKMYPPLSCAVQOYAWGMGSNREVAJLASRLSPLLAFR GKMYPPLSCAVQOYAWGMGSNREVAJLASRLSPLLAFR	6097	1673	192	T DVGRFREQSPRTHCAASSTKERNSDDODGDDEINIGDI WO
TROPAGUES DE GRAGAGE STEVVKLIPHGLGEP  YRRGRWTCVDVYBERDLEPHSFGLLEG IRGASGAGGRSLDSRL ELASIGLGAPTPSGLSQPTSWLRPPPTSPGPQARSFTGGLGQ LVVPSKARAEKPPLSASSPQQRPPEDETGESAGTSRAATPLPSI RVEAEAGGSGARTPPLSRRKAVDMRIRMELGAPEEMGQVPPLDS RPSSPALYFTHDASLVHKSPDPFGAVAAQKFSLAHSMLAISGHL DSDDDSGSGSLVCINKIPDPFGAVAAQKFSLAHSMLAISGHL PRELAERNAALEQENGLIRALA\SPEQLGSAGPPRGVPR\LGOPPA PNGFFVLSLPSLTIVPLGLEGLASAAWPPLPMPALIVPVFPGVG VQALSNGFWSPGGPLBHLITPSLDGGGGFRTGRQQCAPFGEET QPPPSLPGTPQQ  NYCLRHRSPLEKDSSPGSSTSLLIKKQRETSDTPIMRALKELD EGKIFKNWGTGTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTMPRKQL \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVNGVKKVSVR TAMEKNKSVSVEQCKPVSVTPQQNDFBYTAKIRTLAETERFF\D ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  NYCLRHRSPLEKDSSPGSSTSLLIKKQRETSDTPIMRALKELD EGKIFKNWGTGTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTMPRKQL EKKIFKNWGTGTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK RLNSASGRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTMPRKQL QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSVR TAMEKNKSVSYEQCKPVSVTPOGNDFEYTAKIRTLAETERFF\D EKTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  6100 2 713 FVEVSGYRSRADPEPRGRDTMTYAYLFKYIIGFTGVGKSCLLL QFTDKRFQPVHDLTIGEFFGRMVNIDGKQIKLQINDTAGQESF RSITRSYYRGAAGALLVYDTTRRETTNHLTSWLEDARQHSSNM VIMLIGNKSDLESRRDVKREEGEAPARE\HGLIFMETSAKTACN VEEAFINTAKEIVRKJOGGEFDVHNEANGIKLGPQOSISTSVGP SASQRNSRDIGSNSGCC  5101 1 1399 FRGRAWPLREVSHWLGGGRVCSWSASWGKLPALLASRRLSPLLAFR GKMYPFLSCAVQQYAMGKMGSNSEVADLLASRRLSPLLAFR		1		PRI DNCEDGER SPORTS OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRIC
LVVBSKAKAEKPPLSASSPQORPDEPETGESSATSTRAATPLPSL RVEARAGGSGARTPPLSRRKAVDMRLRMELGAPEMGQVPPLDS RPSSPALYFTHDASLVIKSPDPFGAVAAQKFSLAHSMLAISGHL DSDDDSGSGSLVGIDNKIEQAMPLVKSHLMFAVREEVEVLKEQI RELAERNAALEQENGLIRALA\SPEQLGSAGPPRGVPR\LGPPA PNGPPVLSLPSLTIVPLGLPGLASAAWPPLPMPALIVPVPPGVG VQALSNGPWSPGPLPHLLIISLDGGGGFRTGRQQGAPFGET  OPPSLPGTPQQ  168  1074  NYCLRHRSPLEKDSSPGSSTSLLIKKQRETSDTPIMRALKELD EGKIFKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK RINSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSVR TAMEKNRSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\D ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  NYCLRHRSPLEKDSSPGSSTSLLIKKQRETSDTPIMRALKELD EGKIFKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK RINSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE RINSASQRSSSLPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE RINSASQRSSSLPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE RINSASQRSSSLPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE NLSPGFSHLLSKNESSPIRFDILLDDLDDTVPVSTLQRTNPRKQL \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSVR RINSASQRSSSLPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE RINSASQRSSSLPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE RINSASQRSSSLPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE RINSASQRSSSLPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE RINSASQRSSSLPSNTPSDLTLDDLDDTVPVSTLQRTNPRKQL \QFDKRKVSYSQCOKPVSVTPQCMDFYTAKIRTLAETERFF\D ELTKEKDQIEAALSRMPSPGGRITLQTRLNQBAFGRSFGKD TAMEKNKSVSYGCOKPVSVTPQCMDFYTAKIRTLAETERFF\D ELTKEKDQIEAALSRMPSPGGRITLQTRLNQBAFGRSFGKD GFTDKRFQPVHDLTIGVEFGARMVIDGKGQKIKUJUDTAGQESF RSITRSYYRGAAGALLVYDITRRETFHHLTSWLEDARQHSSNM VIMLIGNKSDLESRDVKREGGBAFARF\GLIFMETSAKTACN VEEAFINTAKEI VRKIQQGLFDVHNEANGIKIGPQQSISTSVGP SASQRNSRDIGSNSGCC  FRGRAWPLEVSHHLGCRRVCSWASAWGRLPALSARLSPLLAFR GKMVFPLSCAVQQVAWGKMGSNEVAJLIALSARLSPLLAFR		1		TRUPNGEPSPUPGGKGTPRNGSPPPGADGCPFPINNY DUGI COR
RVEAEAGGGGARTPILSRRKAVDMRLMELGAPEEMGQVPPLDS RPSSFALYETHDASLVHKSPDPFGAVAAQKFSLAHSMLAISGHL DSDDDSGSGSLVGIDNKIEQAMDLVKSHLMFAVREEVEVLKEQI RELAERNAALEGBNGLLRAIA\SPEQLGSAGPPRGVPR\LGPPA PNGFFVLSLPSLTIVPLGLPGLASAAWPPLPMPALIVPVPFGVG VQALSNGPWSPGPLPHHLIIPSLDGGGGFRTGRQQGAPFGEET QPPPSLPGTPQQ  QPPPSLPGTPQQ  RIMSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSVR TAWEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\D ELTKEKQQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  AVCLRHRSPLEKDSSFGSSSTSLLIKKQRETSDTPIMRALKELD EKKIFKNWGTOTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE NLSPGFSHLLSKNESSPIRFDILLDRUPTATALTERFF\D ELTKEKQQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  AVCLRHRSPLEEDSSFGSSSTSLLIKKQRETSDTPIMRALKELD ECKIFKNWGTOTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK RLNSASQRSSSLPPSNRKSSTPTRREIMLTPVTVAYSPKRSPKE RLNSASQRSSSLPPSNRKSSTPTRREIMLTPVTVAYSPKRSPKE NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSVR TANSKNKSVSYEQCKPVSVTPQGNDFEYTAKIRTLAETERFF\D ELTKEKQQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  6100  2 713 FYEVSGYRSRADPEPRGRDTMTYAYLFKYIIIGDTGVGKSCLLLL QFTDKRFQPVHDLTIGVEFGARMVNIDCKQIKJOHDTAGQESF RSITRSYYRGAAGALLVVDITRRETFNHLTSWLEDARQHSSSNM VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN VIMLIGNKSDLESRRDVSHAGCRVCSWASAWGRNEVABLIBLAFFR		1		FLACICICA CADERDEGIA SOCIETA SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS GENERAL SIGNAS
RPSSPALYFTHDASLVHKSPDPFGAVAAQKFSLAHEMIAISGHL DSDDDSGSGSLVGIDNKIEQAMDLVKSHLMFAVREEVEVLKEQI RELAERNAALEQENGLLKAILA\SPEQLGSAGPPRGVPR\LGPPA PNGFFVLSLPSLTIVPLGLGGLGAAAWPPLPMPALIVPVPFGVG VQALSNGPWSPGPLPHLLIIPSLDGGGEGFRTGRQQGAPFGEET QPPPSLPGTPQQ  168 1074 NYCLRHRSPLEKDSSPGSSTSLLIKKQRETSDTPIMRALKELD EGKIFKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK RLNSASQRSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE MLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPBPVPNGVKKVSVR TAMEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\D ELTKEKQJEAALSRNPSPGGRITLQTRLNQEAFGRSFGKD NVCLRHRSPLENDSSPGSSSTSLLIKKQRETSDTPIMRALKELD EGKIFKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE NLSPGSSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKDL GGKIFKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE NLSPGSSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSVR TAMEKNKSVSYEQCKPVSVTPQGNDFEYTAKIRTLAETERFF\D ELTKEKQQIEAALSRNPSPGGRITLQTRLNQEAFGRSFGKD FVEVSGYRRSADPEPRGRDTMTYAYLFKYIIGDTGVGKSCLLL QFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQESF RSITTSYYRGAAGALLVYDTTRRETFNHLTSWLEDARQHSSSNM VIMLIGNKSDLESRRDVKREEGEAPARE\HGLIFMETSAKTACN VEEAFINTAKEIYRKIQQGLFDVHNEANGIKIGPQQSISTSVGP SASQRNSRDIGSNSGCC FRGRAWPLREVSHWLGGCRRVCSWSASWGRLPALLASSDBLAOLINDRW	1	1		LVVPSKAKAEVERI GAGGEOGEFTSWLRPPPTSPGPQARSFTGGLGQ
DSDDDSGSGSLVGIDNKIEQAMDLVKSHLMFAVREEVEVLKEQI RELAERNAALEQENGLIRALA\SPEQLGSAGPPRGVPR\LGPPA PNGPFVLSLPSLTIVPLGLPGLASAAMPPLPMPALIVPVPPGVG VQALSNGPWSPGPLPHLLIIPSLDGGGGFRTGRQQGAPFGET QPPPSLPGTPQQ  NYCLRHRSPLEKDSSPGSSTSLLIKKQRETSDTPIMRALKELD EGKIFKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE NLSPGFSHLLSKNESSPIKFDILLDDLDTVPVSTLQRTNPRKQL \(\OPEnPLDDSEE\X\TYSEKAT\DNI\UNHSSCPEPVPNGVKKVSVR\) TAWEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\D EGKIFKWWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE NLSPGFSHLLSKNESSPIKFDILLDDLDTVPVSTLQRTNPRKQL EGKIFKWWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE GEKIFKWWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE NLSPGFSHLLSKNESSPIKFDILLDDLDTVPVSTLQRTNPRKQL \(\QFLPLDDSEE\X\TYSEKAT\DNI\UNHSSCPEPVPNGVKKVSVR\) TANEKNKSVSYEQCKPVSVTPQGNDFEYTAKIRTLAETERFF\D ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  TANEKNKSVSYEQCKPVSVTPQGNDFEYTAKIRTLAETERFF\D ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  FVEVSGYRSRADPEPRGRDTMTYAYLFKYIIIGDTGVGKSCLLL QFTDKRFQPVHDLTIGVEFGARMVNIDGKGIKLGIWDTAGQESF RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDARQHSSSNM VIMLIGNKSDLESRRDVKREEGEAFARR\HGLIFMETSAKTACN VEEAFINTAKEIYRKIQQGLFFVHNEANGIKIGFQQSISTSVGP SASQRNSRDIGSNSGCC  FRGRAWPLREVSHWLGCRRVCSWSASWGRLPALSARLSPLLAFR GKMYFPLSCAVQQYAMGKMGSNSEVAJLLASSDBLAGRLDAGARDLAFR GKMYFPLSCAVQQYAMGKMGSNSEVAJLLASSDBLAGRLDAGARDLAFR	1	1		RVEAEAGGSGAPTDDISERVALENTE
RELAERNAALDQENGLIRALA\SPEQLEGSAGPPRGVPR\LGPPA PNGPFVLSLPSLTIVPLGLPGLASAAWPPLPMPALIVPVPPGVG VQALSMGPWSPGPLPHLLIIPSLDGGGEGFRTGRQQGAPFGEET QPPPSLPGTPQQ  168 1074 NYCLRHRSPLEKDSSPGSSSTSLLIKKQRETSDTPIMRALKELD EGKIFKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE NLSPGFSHLLISKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL \QFLPLDDSEEK\TYSEKAT\DNIVMHSSCPEPVPNGVKKVSVR TAWEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\D ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD NYCLRHRSPLEKDSSPGSSTSLLIKKQRETSDTPIMRALKELD ECKIFKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE NLSPGFSHLLISKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL \QFLPLDDSEEK\TYSEKAT\DNIVMHSSCPEPVPNGVKKVSVR TAWEKNKSVSYEQCKPVSVTPQGNDFEYTAKIRTLAETERFF\D ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD VGFLPLDDSEEK\TYSEKAT\DNIVMHSSCPEPVPNGVKKVSVR TAWEKNKSVSYEQCKPVSVTPQGNDFEYTAKIRTLAETERFF\D ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD QFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQESF RSITRSYYRGAAGALLVYDITTRETFNHLTSWLEDARQHSSSNM VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN VEEAFINTAKEIYRKIQQGLFFVHNEANGIKIGFQQSISTSVGP SASQRNSRDIGSNSGCC FGRAWPLREVSHWLGCRRVCSWASSWGRLPALSSPLLAFR GKMYFPLSCAVQQYAMGKMGSNSEVAJLLASSRDAOLDERNE	1.	1		RPSSPALVETUDA SI INVORDADA DEL CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA
PNGFFVLSLPSLT1VPLICLPGLASAAWPPLPMPALIVPVFPGVG VQALSNGPWSPGPLPHLL11PSLDGGGGGFRTGRQQGAPFGEET QPPPSLPGTPQQ  NYCLRHRSPLEKDSSPGSSTSLLIKKQRETSDTF1MRALKELD EGKLFKNWGTQTEKEDTSN1NPRQTETSVNASRSPEKCAQQRQK RLNSASQRSSSLPPSNRKSSTPTKRE1MITPVTVAYSPKRSPKE NLSPGFSHLLSKNESSPIRFD1LLDDLDTVPVSTLQRTNPRKQL \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSVR TAWEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\D ELTKEKDQ1EAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  NYCLRHRSPLEKDSSPGSSTSLLIKKQRETSDTPIMRALKELD EGK1FKNWGTQTEKEDTSN1NPRQTETSVNASRSPEKCAQQRQK RLNSASQRSSSLPPSNRKSSTPTKRE1MLTPVTVAYSPKRSPKE NLSPGFSHLLSKNESSPIRFD1LLDDLDTVPVSTLQRTNPRKQL \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSVR TANSKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\D ELTKEKDQ1EAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  GLTKEKDQ1EAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  FVEVSGYRSRADPEPRGRDTMTYAYLFKY1IGDTGVGKSCLLL QFTDKRFQPVHDLTIGVEFGARMVN1DGKQ1KLQ1WDTAGQESF RSITRSYYRGAAGALLVYD1TRRETFNHLTSWLEDARQHSSSNM VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN VEEAFINTAKE1YRK1QQGLFDVINNEANGIKIGPQQSISTSVGP SASQRNSRD1GSNSGCC  FRGRAWPLREVSHWLGCRVCSWSASWGRLPALSARLSPLLAFR GKMYFPLSCAVQQYAWGKMGSNSFVARLLASSDD1AGABURDE	l i	1		DSDDDSGSGGLVGTDWVHOLKSPDPFGAVAAQKFSLAHSMLAISGHL
VOALSNSPWSPGPLPMLLITPSLDGGGEGFRTGRQQCAPFGET  VOALSNSPWSPGPLPHLLITPSLDGGGEGFRTGRQQCAPFGET  QPPPSLPGTPQQ  NYCLRHRSPLEKDSSPGSSSTSLLIKKQRETSDTPIMRALKELD EGKIFKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSVR TANEKNKSVSPQCKPVSVTPQGNDFBYTAKIRTLAETERFF\D ELTKEKDQIEAALSRMPSPGGRITLQTRLNDEAFGRSFGKD  NYCLRHRSPLEKDSSPGSSTSLLIKKQRETSDTPIMRALKELD EGKIFKNWGTQTEKEDTSNINPRGTETSVNASRSPEKCAQQRQK RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSVR TANEKNKSVSYSQCKPVSVTPQCNDFEYTAKIRTLAETERFF\D ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  TELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  FVEVSGYRSRADPEFRGDTMTYAYLFKYIIIGDTGYGKSCLLL QFTDKRRQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQESF RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDARQHSSSNM VIMLIGNKSDLESRRDVKREEGGAFARE\HGLIFMETSAKTACN VEEAFINTAKEIYRKIQQGLFDVHNEANGIKIGPQQSISTSVGP SASQRNSRDIGSNSGCC  FRGRAWPLREVSHWLGCRRVCSWSASWGRLPALSARLSPLLAFR GKMYFPLSCAVQQYAWGKMGSNSEVAFLLASSDBLAGLEDERN	1			RELAERNAALEGENGI BALA A BRANCH BALA A BRANCH BALA BALA BALA BALA BALA BALA BALA BAL
OPPSLIGSTONO  OPPSLIGSTONO  OPPSLIGSTONO  OPPSLIGSTONO  OPPSLIGSTONO  OPPSLIGSTONO  OPPSLIGSTONO  OPPSLIGSTONO  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLIGSTON  OPPSLICSTO	j i	l j		PNGPEVI.SI.BGI TIVDI GI PGI SAGPPRGVPR\LGPPA
168   1074   NYCLRHSPLEKDSPGSSSTSLLIKKQRETSDTPIMRALKELD   EGKIPKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK   RLNSASQRSSSLPPSNRKSSTPTKRE IMLTPVTVAYSPKRSPKE   NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL   \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSVR   TAMEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\D   ELTKEKDQIEAALSRMPSPGGRITLQTRINQEAFGRSFGKD   NYCLRHRSPLEKDSSPGSSTSLLIKKQRETSDTPIMRALKELD   EGKIFKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK   RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE   NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL   \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSVR   TAMEKNKSVSYEQCKPVSVTPQGNDFFYTAKIRTLAETERFF\D   ELTKEKDQIEAALSRMPSPGGRITLQTRINQEAFGRSFGKD   FVEVSGYRSRADPEPRGRDTMTYAYLFKYIIGDTGVGKSCLLL   QFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQBSF   RSITRSYTRGAAGALLVYDITRRETFNHLTSWLEDARQHSSSNM   VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN   VEEAFINTAKEIYRKIQQGLFDVHNEANGIKIGPQQSISTSVGP   SASQRNSRDIGSNSGCC   FRGRAWPLREVSHWLGCRRVCSWSASWGRLPALSARLSPLLAFR   GKWYFPLSCAVQQYAWGKMGSNSENDRIJASGDRIADALAERDHIA	1 1			VOALSNEDWEDER DUIT TERRETARIAN PRINTERS OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE
1074 NYCLRHRSPLEKDSSPGSSTSLLIKKQRETSDTFIMRALKELD EGKIFKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK RLNSASQRSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \(	L i			OPPRINCENCE
EGKIFKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK RLNSASQRSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSVR TAMEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\D ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  NYCLRHRSPLEKDSSPGSSTSLLIKKQRETSDTPIMRALKELD EGKIFKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSVR TAWEKNKSVSYEQCKPVSVTPQGNDFEYTAKIRTLAETERFF\D ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  FVEVSGYRSADPEPRGRTMTYAYLFKYIIIGDTGVGKSCLLL QFTDKRFQPVHDLTIGVEFGARMVNIDGKGIKLQIWDTAGQBSF RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDARQHSSSNM VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN VEEAFINTAKEIYRKIQQGLFDVHNEANGIKIGPQQSISTSVGP SASQRNSRDIGSNSGCC  FRGRAWPLREVSHWLGCRRVCSWSASWGRLPALSARLSPLLAFR GKMYFPLSCAVQQYAMGKMGSNSEVAZLLASSDIA ON DANNEN	6098	168	1074	MACT Bridge Co. EAND CO.
RIMSASQRSSLPPSNRKSSTPTKRE IMLTPVTVAYSPKRSPKE  RLMSASQRSSLPPSNRKSSTPTKRE IMLTPVTVAYSPKRSPKE  NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL  \[ \text{QFLPLDDSEEK\TYSEKAT\DNI\VNHSSCPBPVPNGVKKVSVR} \\ \text{TAMEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\D} \\ \text{ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD} \\  \text{MYCLRHRSPLEKDSSPGSSSTSLLIKKQRETSDTPIMRALKELD} \\ \text{EGKIFKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK} \\ \text{RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE} \\ \text{NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL} \\ \text{QFLPLDDSEEK\TYSEKAT\DNI\VNHSSCPEPVPNGVKKVSVR} \\ \text{TAMEKNKSVSYEQCKPVSVTPQGNDFEYTAKIRTLAETERFP\D} \\ \text{ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD} \\ \text{VELYGGYRSRADPEPRGRDTMTYAYLFKYIIGDTVGKSCLLL} \\ \text{QFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQESF} \\ \text{RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDARQHSSSNM} \\ \text{VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN} \\ \text{VEAFINTAKE!YRKIQQGLFDVHNEANGIKIGPQQSISTSVGP} \\ \text{SAQRNSRDIGSNSGCC} \\ \text{6101}  1  1399  \text{FRGRAWPLREVSHWLGCRRVCSWSASWGRLPALSARLSPLLAFR} \\ GKMVFPLSCAVQQYAWGKMGSNSEVARLLASSPDLAGATERPRIMEDAR AND AND AND AND AND AND AND AND AND AND	]		= - ' •	EGKTEKNWGTOTEKDSSPGSSSTSLLIKKQRETSDTPIMRALKELD
NLSASASSEPSKRSSTPTKREIMLTPVTVAYSPKRSPKE NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL \(\text{QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSVR}\) \(\text{TAWEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\D}\) \(\text{ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD}\) \(\text{DYCLRHRSPLEKDSSPGSSSTSLLIKKQRETSDTPIMRALKELD}\) \(\text{EGKIFKNWGTOTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK}\) \(\text{RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE}\) \(\text{NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL}\) \(\text{VQFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSVR}\) \(\text{TANEKNKSVSYEQCKPVSVTPQGNDFEYTAKIRTLAETERFF\D}\) \(\text{ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD}\) \(\text{ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD}\) \(\text{QFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQESF\) \(\text{RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDARQHSSSNM\) \(\text{VIMLIGNSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN\) \(\text{VEEAFINTAKEIYRKIQQGLFDVHNEANGIKIGFQQSISTSVGP\) \(\text{SASQRNSRDIGSNSGCC}\) \(\text{5ASQRNSRDIGSNSGCC}\) \(\text{6101}\) \(\text{1399}\) \(FRGRAWPLREVSHWLGCRRVCSWSASWGRLPALSSDBLAGALAERPENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAERERENSITAEREREN	1 1			RINGA SOPE CEL PROVINCIO CONTROL TELEVINAS REPEKCAQQRQK
ABJORDSEK   TABLESKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL   \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	1		ļ	KUNDASQRSSSUPPSNRKSSTPTKREIMI.TDVTTIA VCDVDCDVD
TAMEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\D  ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  NYCLRHRSPLEKDSSPGSSSTSLLIKKQRETSDTPIMRALKELD EGKIFKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSVR TAMEKNKSVSYEQCKPVSVTPQGNDFBYTAKIRTLAETERFF\D ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  G100  2  713  FVEVSGYRSRADPEPRGRDTMTYAYLFKYIIIGDTGVGKSCLLL QFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQESF RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDARQHSSSNM VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN VEEAFINTAKEIYRKIQQGLFDVHNEANGIKIGPQQSISTSVGP SASQRNSRDIGSNSGCC  6101  1  1399  FRGRAWPLREVSHWLGCRRVCSWSASWGRLPALSARLSPLLAFR GKMVFPLSCAVQQYAWGKMGSNSEVARLLASSDPLAGIND	1 1		İ	WHO F G F DRULD KNESS PIRFDII, DOT, DTVDVGTI ODTVDDVGT
ELTKEKDQI EAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  NYCLRHRSPLEKDSSPGSSSTSLLIKKQRETSDTPIMRALKELD EGKIFKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVIVAYSPKRSPKE NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSVR TANEKNKSVSYEQCKPVSVTPQGNDFEYTAXIRTLAETERFP\D ELTKEKDQI EAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  QFTDKRFQPVHDLTIGVEFGARMVN IDEKQIKLQIWDTAGQESF RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDARQHSSSNM VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN VEAFINTAKEIYRKIQQCLFDVHNEANGIKIGPQQSISTSVGP SASQRNSRDIGSNSGCC  6101 1 1399 FRGRAWPLREVSHWLGCRRVCSWSASWGRLPALSARLSPLLAFR GKMVFPLSCAVQQYAWGKMGSNSEVARLLASSDPLAGIAED	1	-		VI DEDDUSEEK TYSEKAT DNI VNIHGGODDDUDNGUUGUGUGU
168 1074 NYCLRHRSPLEKDSSPGSSTSLLIKKQRETSDTP IMRALKELD EGKIFKNWGTOTEKEDTSNINPRQTETSVNASRSPEKCAQORQK RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSVR TANEKNKSVSYEQCKPVSVTPQGNDFEYTAKIRTLAETERFF\D ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  FVEVSGYRSRADPEPRGRDTMTYAYLFKYIIIGDTGVGKSCLLL QFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQESF RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDARQHSSSNM VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN VEAFINTAKEIYRKIQQGLFDVHNEANGIKIGPQQSISTSVGP SASQRNSRDIGSNSGCC  6101 1 1399 FRGRAWPLREVSHWLGCRRVCSWSASWGRLPALSARLSPLLAFR GKMVFPLSCAVQQYAWGKMGSNSEVARLASSDPLAGIAEDEN		ł		TANEAU AS VS LEQUED VSVTPOGNDER VTA VTDTL A EMEDICAL A
RINSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKSPKE  RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKSPKE  NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL  \[ \text{QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSVR} \]  TANEKNKSVSYEQCKPVSVTPQGNDFEYTAKIRTLAETERFF\D  ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  FVEVSGYRSRADPEPRGRDTMTYAYLFKYIIIGDTGVGKSCLLL  QFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQESF  RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDARQHSSSNM  VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN  VEEAFINTAKEIYRKIQQGLFDVHNEANGIKIGPQQSISTSVGP  SASQRNSRDIGSNSGCC  FRGRAWPLREVSHWLGCRRVCSWSASWGRLPALSARLSPLLAFR  GKMVFPLSCAVQQYAWGKMGSNSEVARLLASSDPLAGIAEDEREN	6099	168	1074	POLICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE AND SERVICE
RINSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKSPKE  RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKSPKE  NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL  \[ \text{QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSVR} \]  TANEKNKSVSYEQCKPVSVTPQGNDFEYTAKIRTLAETERFF\D  ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  FVEVSGYRSRADPEPRGRDTMTYAYLFKYIIIGDTGVGKSCLLL  QFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQESF  RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDARQHSSSNM  VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN  VEEAFINTAKEIYRKIQQGLFDVHNEANGIKIGPQQSISTSVGP  SASQRNSRDIGSNSGCC  FRGRAWPLREVSHWLGCRRVCSWSASWGRLPALSARLSPLLAFR  GKMVFPLSCAVQQYAWGKMGSNSEVARLLASSDPLAGIAEDEREN	1 1	ĺ		FGK LEVANGE CONTROL OF THE
ALMOSAÇASSELPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE  NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL  \(\text{QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSVR}\)  TANEKNKSVSYEQCKPVSVTPQGNDFEYTAKIRTLAETERFF\D  ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  FVEVSGYRSRADPEPRGRDTMTYAYLFKYIIIGDTGVGKSCLLL  QFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQESF  RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDARQHSSSNM  VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN  VEEAFINTAKEIYRKIQQGLFDVHNEANGIKIGPQQSISTSVGP  SASQRNSRDIGSNSGCC  6101  1 1399  FRGRAWPLREVSHWLGCRRVCSWSASWGRLPALSARLSPLLAFR  GKMVFPLSCAVQQYAWGKMGSNSEVARLLASSDPLAGIAEDEREN	1		1	POLITI TOTAL OF PROPERTY AND A PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE
6100 2 713 FVEVSGYRSRADPEPRGRITLGTURENGESER RSITRSYNGAGAGALLVYDITRRETFHULTSWLEDARGUSER RSITRSYNGAGAGALLVYDITRRETFHULTSWLEDARGUSSF RSITRSYNGAGAGALLVYDITRRETFHULTSWLEDARGUSSF VIMLIGHTAKEINTAKEIN VERAFINTAKEIYRKIQGEFDVKREGEAFARE\HGLIFMETSAKTACN VERAFINTAKEIYRKIQQGLFDVHNEANGIKIGPQQSISTSVGP SASQRNSRDIGSNSGCC GKMVFPLSCAVQQYAWGKMGSNSEVAFLLASSDPLAGARDYS		1	1	KUNSASQKSSSIPPSNRKSSTPTKDFTMI.TDUTUAVGDVDGDVD
TAMEKNKSVSYEQCKPVSVTPQGNDFEYTAKIRTLÆTERFF\D ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD  713 FVEVSGYRSRADPEPRGRDTMTYAYLFKYIIIGDTGVGKSCLLL QFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQESF RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDARQHSSSNM VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN VEEAFINTAKEIYRKIQQGLFDVHNEANGIKIGPQQSISTSVGP SASQRNSRDIGSNSGCC  1 1399 FRGRAWPLREVSHWLGCRRVCSWSASWGRLPALSARLSPLLAFR GKMVFPLSCAVQQYAWGKMGSNSEVARLLASSDPLAGIAEDEN	1 1			MUSEGESHULSKNESSPIREDIII. ODI DEVDVOTE ODDINADATO
6100 2 713 FVEVSGYRSGERITLQTRINGEAFGRS FGKD  FVEVSGYRSRADPEPRGRITLQTRINGEAFGRS FGKD  QFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQESF RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDARQHSSSNM VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN VEEAFINTAKEIYRKIQQGLFDVHNEANGIKIGPQQSISTSVGP SASQRNSRDIGSNSGCC  1 1399 FRGRAWPLREVSHWLGCRRVCSWSASWGRLPALSARLSPLLAFR GKMVFPLSCAVQQYAWGKMGSNSEVARLLASSDPLAGIAEDEN	] ]		İ	VE DEDUSEER TYSEKAT DNI VNHSSCOFFURNOWN I
6100 2 713 FVEVSGYRSRADPEPGGRITLQTRLNQEAFGRSFGKD  FVEVSGYRSRADPEPRGRDTMTYAYLFKYIIIGDTGVGKSCLLL QFTDKRFQPVHDLTIGVEFGARMYNIDGKQIKLQIWDTAGQESF RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDARQHSSSNM VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN VEEAFINTAKEIYRKIQQGLFDVHNEANGIKIGPQQSISTSVGP SASQRNSRDIGSNSGCC  FRGRAWPLREVSHWLGCRRVCSWSASWGRLPALSARLSPLLAFR GKMVFPLSCAVQOYAWGKMGSNSEVARLASSDPLAGIAEDEN			1	TANSANAS VS YEOCKPVSVTPOCNDFEVTA V TDTL A DDDDDDD
PVEVSGIRSRADPEPRGRDIMTYAYLFKYIIIGDTGVGKSCLLL QFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQESF RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDARQHSSSNM VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN VEEAFINTAKEIYRKIQQGLFDVHNEANGIKIGPQQSISTSVGP SASQRNSRDIGSNSGCC FRGRAWPLREVSHWLGCRRVCSWSASWGRLPALSARLSPLLAFR GKMVFPLSCAVQQYAWGKMGSNSEVARLLASSDPLAGIAEDKDV	6100	2	71.7	EDIADAUQIEAALSRMPSPGGRITIOTRINOFAEGDODGED
RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDARQHSSSNM VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTACN VEEAFINTAKEIYRKIQQGLFDVHNEANGIKIGPQQSISTSVGP SASQRNSRDIGSNSGCC  1 1399 FRGRAWPLREVSHWLGCRRVCSWSASWGRLPALSARLSPLLAFR GKMVFPLSCAVQQYAWGKMGSNSEVARLLASSDPLAGIAEDKDV	]	-	,	FVEVSGIRSRADPEPRGRDTMTYAVI.FKYTITGDTCVCVCCC
VIMLIGNKSDLESRRDVKRETFNHLTSWLEDARQHSSSNM VIMLIGNKSDLESRRDVKREGEAFARE\HGLIFMETSAKTACN VEEAFINTAKEIYRKIQQGLFDVHNEANGIKIGPQQSISTSVGP SASQRNSRDIGSNSGCC  1 1399 FRGRAWPLREVSHWLGCRRVCSWSASWGRLPALSARLSPLLAFR GKMVFPLSCAVQQYAWGKMGSNSEVARLLASSDPLAGIAEDKDV	1 1		1	ALTERNATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF
6101 1 1399 FRGRAWPLREVSHWLGCRRVCSWSASWGRLPALSARLSPLLAFR GKMVFPLSCAVQQYAWGKMGSNSSCVAFLLASSDPLAGIA	]			ROLL ROLL RGAAGADLVYDITRRETENHI. TOM LEDADOUGGODIS
5101 1 1399 FRGRAWPLREVSHWLGCRRVCSWSASWGRLPALSARLSPLLAFR GKMVFPLSCAVQQYAWGKMGSNSEVARLASSDPLAGARDV				VIPLIGNASDLESKRDVKREEGEAFAPR\ HGI. TEMPERG 3 PERS CO.
6101 1 1399 FRGRAWPLREVSHWLGCRRVCSWSASWGRLPALSARLSPLLAFR GKNVFPLSCAVQQYAWGKMGSNSEVARLASSDPLAGIAEDVDV	]	ļ	1	VEENE IN TAKELYRKIOOGLEDVHNEANGIKIGDOOGIGDOOG
FRGRAWPLREVSHWLGCRRVCSWSASWGRLPALSARLSPLLAFR GKNVFPLSCAVQQYAWGKMGSNSEVARLASSDPLAGIAEDKDV	5101	1		SASQRASRDIGSNSGCC
JANIAL PROCAVOOTAMGKWGSNSEADITACTA HOWDER		-		FRGRAWPLREVSHWLGCRRVCSWSASWGRLPALSARLSPLLAFR
ALLWMGTHPRGDAKILDNRISQKTLSQWIAENQDSLGSKVKDTF			j '	GAMAL PROCESSOR AND
				ALLWING I HPRGDAKI LDNRISQKTLSQWIAENQDSLGSKVKDTF

SEQ	Predicted	Predicted end	Dmino and 2
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	amino acid	scquence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			NGNLPFLFKVLSVETPLSIQAHPNKELAEKLHLQAPQHYPDANH
	İ		KPEMAIALTPFQGLCGFRPVEEIVTFLKKVPEFQFLIGDEAATH
1			LKQTMSHDSQAVASSLQSCFSHLMKSEKKVVVEQLNLLVKRISQ
1			QAAAGNNMEDIFGELLLQLHQQYPGDIGCFAIYFLNLLTLKPGE
1			AMFLEANVPHAYLKGDCVECMACSDNTVRAGLTPKFIDVPTLCE
	i		MLSYTPSSSKDRLFLPTRSQEDPYLSIYDPPVPDFTIMKA\EVP
1			G\SVTEYKDLALDSASILLMVQGTVIASTPTTQTPIPLQRGGVL
L			FIGANESVSLKLTEPKDLLIFRACCLL
6102	70	2415	QTPQATLAANGAEDSRGGEMLPAGEIGASPAAPCCSESGDERKN
]	1		LEEKSDINVTVLIGSKQVSEGTDNGDLPSYVSAFIEKEVGNDLK
1			SLKKLDKLIEQRTVSKMQLEEQVLTISSEIPKRIRSALKNAEES
}	1		KQFLNQFLEQETHLFSAINSHLLTAQPWMDDLGTMISQIEEIER
	1		HLAYLKWISQIEELSDNIQQYLMTNNVPEAASTLVSMAELDIKL
	'		QESSCTHLLGFMRATVKFWHKILKDKLTSDFEEILAQLHWPFIA
1			PPQSQTVGLSRPASAPEIYSYLETLFCOLLKLOTSHELLTEPK\
}	<b>j</b>		HSQKNTLFLPPLLSS/WPIQVMLTPLQKRFRYHFRGNROTNVLS
1			KPEWYLAQVLMWIGNHTEFLDEKIQPILDKVGSLVNARLEFSRG
1	1		LMMLVLEKLATDIPCLLYDDNLFCHLVDEVLLFERELHSVHGYP
1			GTFASCMHILSEETCFQRWLTVERKFALOKMDSMLSSEAAWVSO
· ·			YKDITDVDEMKVPDCAETFMTLLLVITDRYKNLPTASRKLOFLE
1	1 1		LQKDLVDDFRIRLTQVMKEETRASLGFRYCAILNAVNYISTVLA
1			DWADNVFFLQLQQAALEVFAENNTLSKLQLGQLASMESSVFDDM
1			INLLERLKHDMLTRQVDHVFREVKDAAKLYKKERWLSLPSQSEQ
į.			AVMSLSSSACPLLLTLRDHLLQLEQQLCFSLFKIFWQMLVEKLD
1	·		VYIYQEIILANHFNEGGAAQLQFDMTRNLFPLFSHYCKRPENYF
6103	207	0500	KHIKEACIVLNLNVGSALTAGKDVLPVQLQGSFPAT
0.200	20,	2523	ESNSTMTTYLEFIQQNEERDGVRFSWNVWPSSRLEATRMVVPVA
1			ALFTPLKERPDLPPIQYEPVLCSRTTCRAVLNPLCQVDYRAKLW
ļ			ACNFCYQRNQFPPSYAGISELNQPAELLPQFSSIEYVVLRGPQM
			PLIFLYVVDTCMEDEDLQALKESMQMSLSLLPPTALVGLITFGR
1			MVQVHELGCEGISKSYVFRGTKDLSAKQLQEMLGLSKVPVTQAT
1			RGPQVQQPPPSNRFLQPVQKIDMNLTDLLGELQRDPWPVPQGKR
Į i			PLRSSGVALSIAVGLLECTFPNTGARIMMFIGGPATOGPGMVVG DELKTPIRSWHDIDKDNAKYVKKGTKHFEALANRAATTGHVIDI
1		I	YACALDQTGLLEMKCCPNLTGGYMVMGDSFNTSLFKQTFQRVFT
			KDMHGQFKMGFGGTLEIKTPR\EIKISGAIGPCVSLNSKGPCVS
j i			ENEIGTGGTCQWKICGLSPTTTLAIYFEVVNQHNAPIPQGG\RG
1	j		A/IQFVTQY/QHSSGQRRIRVTTIARN/WADAQTQIQNIAASFD
	j		QEAAAILMARLAIYRAETEEGPDVLRWLDRQLIRLCQKFGEYHK
1	Ī		DDPSSFRFSETFSLYPOFMFHLRRSSFLOVFNNSPDESSYVPHH
1	1		FMRQDLTQSLIMIQPILYAYSFSGPPEPVLLDSSSILADRILLM
	ł		DTFFQILIYHGETIAQWRKSGYQDMPEYENFRHLLOAPVDDAOE
. j			ILHSRFPMPRYIDTEHGGSQARFLLSKVNPSOTHNNMYAWGOES
			GAPILTDDVSLQVFMDHLKKLAVSSAA
6104	124	732	KVSEYIILSKDKILFHALAMLVLVVSPWSAARGVLRNYWERLLD
			KLPQSRPGFPSPPWGPALAVQ\AQPCLOSOOMIPVEVKRI/RST.
			LDSIFWMAAPKNRRTIEVNRCRRRNPOKLIKVKNNIDVCPECGH
į į	1	Ì	LKQKHVLCAYCYEKVCKETAEIRRQIGKQEGGPFKAPTIETVVI.
			YTGETPSEQDQGKRIIERDRKRPSWFTQN
6105	3	989	PLHGACTSLVLQRFCHRRPRPCAPARPEDMRRPAAVPLLLLLCF
1 1			GSQRAKAATACGRPRMLNRMVGGQDTQEGEWPWQVSIORNGSHF
]	J		CGGSLIAEQWVLTAAHCFRNTSETSLYQVLLGARQLVOPGPHAM
	}		YARVRQVESNPLYQGTASSADVALVELEAPVPFTNYILPVCLPD
	Ì	. 1	PSVIFETGMNCWVTGWGSPSEEDLLPEPRILQKLAVPIIDT\PR
[ [			CNLLYSKDTEFGYQPKTIKNDMLCAGFEEGKKDACKGDSAGPLV
L			CLVGQSWLQAGVISWGEGCARQNRPGVYIRVTAHHNWIHRIIPK

SEQ Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence  SEQ Predicted beginning holds beginning nucleotide location corresponding to first amino acid residue of amino acid sequence  SEQ Predicted end nucleotide (A=Alanine, C=Cysteine, D=Aspartic Ac Glutamic Acid, F=Phenylalanine, G=Gly H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, Codon, /=possible nucleotide deletion \ SEQ PRPTAPHTGRPPTANRGDPRLDLKRGCARLLTSIES  Amino acid segment containing signal (A=Alanine, C=Cysteine, D=Aspartic Ac Glutamic Acid, F=Phenylalanine, G=Gly H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine P=Proline, Q=Glutamine, R=Arginine, C=Cysteine, D=Aspartic Ac Glutamic Acid, F=Phenylalanine, G=Gly H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine P=Proline, Q=Glutamine, R=Arginine, C=Cysteine, D=Aspartic Ac Glutamic Acid, F=Phenylalanine, G=Gly H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine P=Proline, Q=Glutamine, C=Cysteine, D=Aspartic Ac Glutamic Acid, F=Phenylalanine, G=Gly H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine P=Proline, Q=Glutamic, R=Arginine, C=Cysteine, D=Aspartic Ac Glutamic Acid, F=Phenylalanine, G=Gly H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine P=Proline, Q=Glutamine, R=Arginine, C=Cysteine, D=Asparagine Acid, F=Phenylalanine, G=Gly H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine P=Proline, Q=Glutamine, C=Cysteine, D=Asparatic Acid, F=Phenylalanine, G=Gly H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine P=Proline, Q=Glutamine, R=Arginine, N=Asparagine P=Proline, Q=Glutamine, R=Arginine, N=Asparagine P=Proline, Q=Glutamine, N=Asparagine, N=Asparagine, N=Asparagine, N=Asparagine, N=Asparagine, N=Asparagine, N=Asparagine, N=Asparagine, N=Asparagine, N=	*=Stop  RGRPAAS PRACPQG RKACPQG
NO: nucleotide location corresponding to first amino acid residue of amino acid sequence  6106  NO: nucleotide location corresponding to first amino acid residue of amino acid sequence  1	*=Stop  RGRPAAS PRACPQG RKACPQG
location corresponding to first amino acid residue of amino acid sequence  6106  1	*=Stop  RGRPAAS PRACPQG RACPQG RGCQV
corresponding to first amino acid residue of amino acid sequence  6106  corresponding to first amino acid residue of amino acid sequence  corresponding to first amino acid residue of amino acid sequence  corresponding to first amino acid residue of amino acid sequence  corresponding to first amino acid residue of amino acid sequence (Codon, /=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, Codon, /=possible nucleotide deletion (Codon, /=possible nucleotide insertion)  LQVQPSEVGRPEVTPPGFGAP  GRPPTAPHTGRPPTANRGDPRLDLKRGCARLATSTEG	*=Stop , RGRPAAS PRACPQG RNGCADNO
to first amino acid residue of amino acid sequence  to first amino acid residue of amino acid sequence  to first amino acid residue of amino acid sequence  to first amino acid residue of amino acid sequence  to first amino acid residue of amino acid sequence  to first amino acid residue of amino acid sequence  to first amino acid residue of amino acid sequence  to first amino acid residue of amino acid sequence  to first amino acid residue of amino acid sequence  to first amino acid residue of amino acid sequence, T=MeMethIoline, N=Asparagine P=Proline, Q=Glutamine, N=Asparagine N=Arginine, S=Serine, T=Threonine, V=Valine, Todon, V=Tyrosine, X=Unknown, Codon, /=possible nucleotide deletion LQVQPSEVGRPEVTPPGPGAP  GRPPTAPHTGRPPTANRGDPRLDLKRGCARLATSIEG GRPPTAPHTGRPPTANRGDPRLDLKRGCARLATSIEG	*=Stop , RGRPAAS PRACPQG PRACPQV NGGAPNC
amino acid residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino acid sequence residue of amino aci	RGRPAAS PRACPOG KNGRCOV
residue of amino acid sequence S=String, Teinreonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, Codon, /=possible nucleotide deletion \ -possible nucleotide insertion)  LQVQPSEVGRPEVTPPGFGAP  6106 3 1302 GRPPTAPHTGRPPTANGGPRADLESTEE	RGRPAAS PRACPOG KNGRCOV
amino acid sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence S	RGRPAAS PRACPOG KNGRCOV
sequence   Codon, /=possible nucleotide deletion   -possible nucleotide insertion)   LQVQPSEVGRPEVTPPGPGAP   GRPPTAPHTGRPPTANRGDPRLDLKRGCARLLTSIEG	RGRPAAS PRACPOG KNGRCOV
6106 3 1302 GRPPTAPHTGRPPTANRGDPRLDLKRGCARLLTSIEG	PRACPQG KNGRCQV
3 1302 GRPPTAPHTGRPPTANRGDPRLDLKRGCARLITETEG	PRACPQG KNGRCQV
GRPFTAPHTGRPPTANRGDPRLDLKRGCARLLTSIES	PRACPQG KNGRCQV
	KNGRCQV
AGLRRDRCALRRWPLRRAPLARATRRAGSPRRCAPR	NGCADNO
WSRARHQPGGLCLLLLLCQFMEDRSAQAGNCWLRQA	VICE'S DNC
LYKTELSKEECCSTGRLSTSWTEEDVNDNTLFKWMIF	JUGAE IIC
IPCKETCENVDCGPGKKCRMNKKNKPRCVCAPDCSNI	<b>TWKGPVC</b>
GLDGKTYRNECALLKARCKEQPELEVQYQGRCKKTCRI	OVFCPGS
STCV\VDQTNNAYCVTCNRICPEPASSEQYLCGNDGV	rys\sac
HLRKATCLLGRSIGLAYEGKCIKAKSCEDIQCTGGKKK GRGRCSLCDELCPDSKSDEPVCASDNATYASECAMKEJ	CLWDFKV
I DEVKHSGSCNSTSERDEROFFORMAN AND A SECOND OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF T	ACSSGV
6107 623 168 SRCSSPRPEPGRGRGK/LSPSEHRKWVEVFKACDEDHI	1
DFKTAVVMLFGYKPSKIEVDSVMSSINPNTSGILLEGI	GYLSRE
KKEAQRYRNEVRHIFTAFDTYYRGFLTLEDFKKAFRQ\	LNIVRK
	APKLPE
6108 3 1348 GGSLRFSPPRVPSCSRVFCPVPPGGCGLPSPMSASRPC	0.000
CLPRRYMKHKRDDGPEKQEDEAVDVTPVMTCVFVVMCC	SPITPW
XYFYDLLVYVVIGIFCLASATGLYSCIADCUPPI.D\ ca	CACRON
LLAPTIPHNSLPYFHKRPOARMLLLATFCVAVSVVWCV	CONTRA
WAWVLQDALGIAFCLYMLKTIRLPTFKACTITITITIES	VDTERM
FITPLIKSGSSIMVEVATGPSDSATREKT.DMVI.KVDD	INCOR
ALCDRPFSLLGFGDILVPGLLVAYCHRFDTOVOSSPAV	EVA COST
AIGVGLLVTFVALALMORGOPALLYI,VPCTI,VTSCAVA	T.MDDDDT
GVFWTGSGFAKVLPPSPWAPAPADGPOPPKDSATDLCD	ODDeno
PAISPWPAEQSPKSRTSEEMGAGAPMREPGSPAESEGR	DQAQPS
PVTQPGASA	
I I I I I I I I I I I I I I I I I I I	RAAMLY
LEDYLEMIEQLPMDLRDRFTEMREMDLQVQNAMDQLEQ	RVSEFF
MNAKKNKPEWREEQMASIKKDYYKALEDADEKVQLANQ	I A D P A D
RHLRKLDQELAKFKMELEADNAGITEILERRSLELDTP: HHAHSHTPVEKRKYNPTSHHTTTDHIPEKKFKSEALLS	SQPVNN
SKENTLGCRNNNSTASSNNAYNVNSSQPLGSYNIGSLS:	rltsda
GI\TMAAAQAVQATAQMKEGRRTSSLKASYEAFKNNDFG	GTGAG
SMARETVGYSSSSALMTTLTQNASSSAADSRSGRKSKN	LGKEF
QQSSSSSSSSSSTVVQEISQQTTVVPESDSNS	INKSSS
YDPNEPRYCICNQVSYGEMVGCDTQDCPIEWFHYGCVGI	QVDWT
GRWYCPQCT\AAMKRRGSRHK	1
2464 ACPSAATMSDODHSMDEMTAVVKI EKGVGGNNGGNGNG	WAREO.
ARSSTGSSSTGGGGOESOPSPLALLAATTSPTES DATE	DICHDIC
QGPSQSGTGELDLTATQLSQGANGWOIISSSSGATDTC	PEOCC
SSINGSNGSESSKNRTVSGGOYVVAAA PNI, ONOOVI, TOI	DOLLAR
NIQYQVIPQFQTVDGQQLOFAATGAQVQQDGSGQTQTTp	CANOO
IIINGSGGNIIAAMPNLLOOAVPLOGLANNVI.SGOTOV	TURTUE
VALNGNITLLPVNSVSAATLTPSSOAVTISSSGSOESGS	OBUTE
GTT1SSASLVSSQASSSSFFTNANSYSTTTTTSNMGTMN	Proper
SSGTNSQGQTPQRVSGLOGSDALNIOONOTSGGSLOAGO	OVECE
\Q\NQQTQAAPKSI\SRPOLVOGG\OALO\AFOAADI.SCOT	E-T-TPC A
ISQETLQNLQLQAVPNSGPIIIRTPTVGPNGQVSWQTLQ	LQNLQ
VONPQAQTITLAPMQGVSLGQTSSSNTTLTPIASAASIP,	AGTVT
VNAAQLSSMPGLQTINLSALGTSGIQVHPIQGLPLAIAN	APGDH
GAQLGLHGAGGDG IHDDTAGGEEGENSPDAQPQAGRRTRI	REACT
CPYCKDSEGRGSGDPGKKKQHICHIQGCGKVYGKTSHLRI	AHLRW
HTGERPFMCTWSYCGKRFTRSDELQRHKRTHTGEKKFACI	PECPK
RFMRSDHLSKHIKTHONKKGGPGVALSVGTLPLDSGAGS	GSGT
ATPSALITTNMVAMEAICPEGIARLANSGINVKEGGQFCS	PINT

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	dota sequent containing signal pastial
NO:	nucleotide	1	(A=Alanine, C=CVsteine, D=Aspartic Acid p
	location	location	Giutamic Acid, F=Phenylalanine, G=Glygine
	corresponding	corresponding	H=H1Stidine, I=Isoleucine K=T.veine
	to first	to first	L=Leucine, M=Methionine, N=Asparagine
	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine
	residue of	residue of	S=Serire, T=Threonine, V=Valine
	l l	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +-c
1	amino acid	sequence	Codon, /=possible nucleotide deletion
6111	sequence		\=possible nucleotide insertion)
9111	1637	797	RVDPRVRGAMAPWGKRLAGVRGVLLDISGVLYDSGAGGGTAIAG
ŀ			SVEAVARLKRSRLKVRFCTNESQKSRAELVGQLQRLGFDISEQE
	1	ı	VTAPAPAACQILKERGLRPYLLIHDGV\ASEFDQIDTS/STPNC
	1	ľ	VVIADAGESFSYQNMNNAFQVLMELEKPVLISLGKGRYYKETSG
		1	LMLDVGPYMKALEYACGIKAEVGGKPSPEFFKSALQAIGVEAHQ
	ł	İ	AVMIGDDIVGDVGGAQRCGMRALQVRTGKFRPSDEHHPEVKADG
	1		YVDNLAEAVDLLLQHADK
6112	77	196	MSSHKSFKSKRFLAKKQKPNRPILQWIWLKTGNKIRHNWK
6113	1779	567	WEGRSWAACGVNLQGAWGERSGVRASEAESPGKRADVSWWSRQL
1			ETMVDHLANTEINSQRIAAVESCFGASGQPLALPGRVLLGEGVL
ł			TKECRKKAKPRIFFLFNDILVYGSIVLNKRKYRSQHIIPLEEVT
·	}	1	LELLPETLQAKNRWMIKTAKKSFVVSAASATERQEWISHIEECV
1	1		RRQLRATGRPA\STEHAAPWIPDKATDICMRCTQTRFSALTRRH
	1	İ	HCRKCRUNICAECCRORELL RDI CRITICIPAECTQTRESALTRRH
	1	1 .	HCRKCRVVVCAECSRQRFLLPRLSPKPVRVCSLCYRELAAQQRK
1	1		EEAEEQGAGVPRAASHLARPICGRPVEMTMTPTRTRRAAGTATG
			PAAWSSTPRGWPGLPSTADPRPAEHLSPSQLHCPGPQEGSSRSC
Į	ĺ		PGLRDPIPWWQVQRWGVALSGLPVPFCWTLCPYGFTAGNAFPFR KPONTHRSW
6114	818	246	PTSRPRPSPGSPAMSWSACVSAAPSSSWPASSSWPCGPRRCCTR
			RRCSPRCGLAAGSMCSCSPSWRCTPVPACWPSPPP\PAEQVQC
1			GHLPPHADRRALRLPVAAPARGPGPGHPAGPAGPRPARTPPASP
			HGPGRPTVPAPPCPLLAATEPTPSRPHQRWTREDRMLGRGSQVT
			GRPQWFLRGLVLFSL
6115	324	71	DVCGRVCAHPHLYTHIHMHICAHAC\IHTHAQLC/ITASHALAH
			SHLYTCMVMLTASHTPSHTHPHTAVHKEHRADVLRGTLTPLR
6116	595	1430	TGVMPPGRWHAA/ISSGPVFEGARA\LQTVKKEEEDESYTPVQ
			AARPQTLNRPGQELFRQLFRQLRYHESSGPLETLSRLRELCRWW
			LRPDVLSKAQILELLVLEQFLSILPGELRVWVQLHNPESGEE\L
J			WPCWRSCRGTLMGHPGGTRALP\EPRCALDGYRS\LRSAQIWSL
1	- 1	i	ASPLRSSSALGDHLEPPYEIEARDFLAGQSDTPAAQMPALFPRE
1 !	İ		GCPGDQVTPTRSLTAQLQETMTFKDVEVTFSQDEWGWLDSAQRN
6117			LYRDVMLENYRNMASLGK
61-/	1433	222	VGVPSPAPPCSWEVGPGGGWTPGILKEGQGGRRTPLLLLATRTR
	İ		GLLSLFPPAAMHPAAFPLPVVVAAVLWGAAPTRGLTPATSDUNA
]			SMDFADLPALFGATLSOEGLOGFLVEAHPDNACSPIADSDBADI
<b>,</b>	ļ		NGSVFIALLRRFDCNFDLKVLNAOKAGYGAAVVHNVNSNFII.NM
1 1	·	l	VWNSEKIQQQIWIPSVFIGERSSEYLRALFVYEKGAPVLLUDDW
1 1	1		TFPLGYYLIPFTGIVGLLVLAMGAVMIARCIOHRKRIODNDITTE
1			\EQUKQI\PTHDYQKGDQYDVCAICLDRYEDGDKI.PVI.DCAUAV
1			HSRCVDPWLTQTRKTCPICKQPVHRGPGDEDQEEETQGQEEGDB
1 1			GEPROHPASERTPLLGSSPTLPTSFGSLAPAPLVFPGPSTDPPL
F 6130			SPPSSPVILV
6118	1044	247	STISCRACTSGATPGAQSHRSARGHAAGGKETAALGMERGKVKK
j l	1	ļ	KEKEKETQKEKIGEKGREEKVKRKEVEQKIKQEKQEKQERRKGK
[ [	1	1	EKEEKRTKQGKETNKEKEQFKGQEEKGENKDSTLTRTPLEPLEK
1 1			NKQILVLGLDGAGKTSVLHSLASNRVQHSVAPTQGFHAVCINTE
[	Į	J	DSQMEFLEIGGSKPFRSYWEMYLSN/ADSLARSFSVGFKQDSQP
1 [			ITWKAKKYLHQLIAANPVLPLVVFANKQDLEAAYHITDIHEALA
			II
6119	1217	462	DPRFVTENTTKAPAQERTTQPRSSREGTLRSTMEYLSALNPSDL
j i		i	LRSVSNISSEFGRRVWTSAPPPQRPFRVCDHKRTIRKGLTAATR
, ,			OELLAKALETI LI NGVI TI VI EPROPRINCE DERRITARE
	f		QELLAKALETLLINGVLTLVLEEDGTAVDSEDFFQLLEDDTCLM VLOSGOSKSPTPSGULSVALGREEDWARDLANDARD
	I	1	VLQSGQSWSPTRSGVLSYGLGRERPKHSKDIARFTFDVYKQNPR DLFGSLNVKATFYGLYSMSCDFQGL\GPKKVLRELLRWTSTLLQ
		į.	GLGHMLLGISSTLRHAVEGAEQWQQKGRLHSY

SEQ	Predicted	Predicted end	Thuis and the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same	
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=	
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,	
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,	
1	corresponding	to first	L=beucine, M=Methionine, N=Asparagine,	
]	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,	
I	amino acid	residue of	S=Serine, T=Threonine, V=Valine	
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Ston	
1	amino acid	sequence	Codon, /=possible nucleotide deletion	
	sequence		\=possible nucleotide insertion)	
6120	785	179	LERAGGGGLSSRALVGSGACLSLVARANGKGLPRGRKEFVEAUR	
	1	ł	VRYVAFRYRTPRAVCLRLWSCRREVIMSGRGKOGGKVRAKAKSR	
ļ	1		SSRAGLQFPVGRVHRLLRKGNYAERVGAGAPVYLAAVLEYLTAE	
Ì			ILELAGNAARDNKKTRIIPRHLQLAIRNDEELNKIJGKVTIAGG	
6121	1612		G\VLPNIQAVLLPKKTESQKDEGANDP	
0121	1612	107	FVRAQARGSROPVRRPLLGAGSRLRCRSCGRMEPLKVEKFATAN	
1			RGNGLRAVTPLRPGELLFRSDPLAYTVCKGSRGVVCDRCLLGKE	
1			KLMRCSQCRVAKYCSAKCQKKAWPDHKRECKCLKSCKPRYPPDS	
1			VRLLGRVVFKLMDGAPSESEKLYSFYDLESNINKLTEDKKEGLR	
			QLVMTFQHFMREEIQDASQLPPAFDLFEAFAKVICNSFTICNAE	
1			MQEVGVGLYPSISLLNHSCDPNCSIVFNGPHLLLRAVRDIEVGE	
ł	İ		ELTICYLDMLMTSEERRKQLRDQYCFECD\CFRCQTQDKDADML	
į			TGDEQVWKEVQESLKKIEELKAHWKWEQVLAMCQAIISSNSERL	
į			PDINIYQLKVLDCAMDACINLGLLEEALFYGTRTMEPYRIFFPG	
			SHPVRGVQVMKVGKLQLHQGMFPQAMKNLRLAFDIMRVTHGREH	
	i		SLIEDLILLLE/AMRRQHQSILRERSQREIRRVSLLNALLRSHT LCFVSCVNLSYWKFCSVFV	
6122	2	2324	RFRKMADGGAASQDESSAAAAAAADSRMNNPSETSKPSMESGDG	
ļ	1		NTGTQTNGLDFQKQPVPVGGAISTAQAQAFLGHLHQVQLAGTSL	
İ			QAAAQSLNVQSKSNEESGDSQQPSQPSQQPSVQAAIPQTQLMLA	
1			GGQITGLTLTPAQQQLLLQQAQAQAQLLAAAVQQHSASQQHSAA	
	1		GATISASAATPMTQIPLSQPIQIAQDLQQLQQLQQQNLNLQQFV	
1	į l		LVHPTTNLQPA\QFIISQTPQGQQGLLQA\QNLLTQLPRQSQAN	
1			LLQSQPRI\TLTSQPATPTCTIAATPIQTLPQSQSTPKRIDTPS	
	į		LEEP\SDLEELEQFAKTFKQRRIKLGFT\QGDAGLAMVKLYGND	
	l l		FSPTTIFRFEALNLSFKNMCKLKPLLEKWLNDAENISSDSSISS	
	]	1	PSALNSPGIEGLSRRRKKRTSIEA\NIRVALEKSFLEN\OKPTS	
			EEITMIADQLNMEKGVIRVWFCNRROKEKRINPPSSGG\TSSSD	
			IKAIFPSPTSLVATTPSLVTSSAATTLTVSPVLPLTSAAVTNLS	
			VTGTSDTTSNNTATVISTAPPASSAVTSPSLSPSPSASASTSEA	
			SSASETSTTQTTSTPLSSPLGTSQVMVTASGLOTA/AOLLPFKG	
			AAQLPANASLAAMAAAAGLNPSLMAPSOFAAGGALLSINPCTLS	
			GALSPALMSNSTLATIQALASGGSLPITSLDATGNLVFANAGGA	
			PNIVTAPLFLNPQNLSLLTSNPVSLVSAAAASAGNSAPVASLHA	
6123	3	2944	TSTSAESIQNSLFTVASASGAASTTTTASKAQ	
		2944	HLLHRWFGTDMQMINFTTGEFQLTEACPYLGTHSEESRFGILHL	
ļ			HLQPLEMKRVGVVFTPADYGKVTSLILIRNNLTVIDMIGVEGFG	
Ī	1		ARELLKVGGRLPGAGGSLRFKVPESTLMDCRRQLKDSKQILSIT	
	i		KNFKVENIGPLPITVSSLKINGYNCQGYGFEVLDCHQFSLDPNT SRDISIVFTPDFTSSWVIRDLSLVTAADLEFRFTLNVTLPHHLL	
			PLCADVVPGPSWEESFWRLTVFFVSLSLLGVILIAFQQAQYILM	
ŀ	1		EFMKTRQRQNASSSQQNNGPMDVISPHSYKSNCKNFLDTYGPS	
	1		DKGRGKNCLPVNTPQSRIQNAAKRSPATYGHSQKKHKCSVYYSK	
!		•	HKTSTAAASSTSTTTEEKQTSPLGSSLPAAKEDICTDAMRENWI	
i	İ		SLRYASGINVNLQKNLTLPKNLLNKEENTLKNTIVFSNPSSECS	
İ			MKEGIQTCMFPKETDIKTSENTAEFKERELCPLKTSKKLPENHL	
ł			PRNSPQYHQPDLPEISRKNNGNNQQVPVKNEVDHCENLKKVDTK	
- 1		ŀ	PSSEKKIHKTSREDMFSEKQDIPFVEQEDPYRKKKLQEKREGNL	
	1		QNLNWSKSRTCRKNKKRGVAPVSRPPEQSDLKLVCSDFERSELS	
į	ļ	ļ	SDINVRSWCIQESTREVCKADAEIASSLPAAQREAEGYYQKPEK	
1	<u> </u>	ļ	KCVDKFCSDSSSDCGSSSGSVRASRGSWGSWSSTSSSDGDKKPM	
- 1			VDAQHFLPAGDSVSQNDFPSEAPISLNLSHNICNPMTGNSLPOV	
1	1		AEPSCPSLPAGPTGVEEDKGLYSPGDLWPTPPVCVTSSLNCTLE	
		- 1	NGVPCVIQESAPVHNSFIDWSATCEGQFSSAYCPLELNDYNAFP	
	]	1	EENMNYANGFPCPADVQTDFIDHNSQSTWNTPP\NMPAS\WGNA	
			QFPSSSRPYLKSTPKACLPMSGLFGPI\WAP\QSDVYENCCPIN	
450				
			450	

.:
3
÷
12
24.

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine K=Tysine
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
- 1	amino acid	residue of	S=Serine, T=Threonine, V=Valine
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +-Shan
	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
1			PTTEHSD/THMENQA\VVCKEYYPGF\NPFRAYMNLDTWTTTT\
6124	1522		NRNANFPLSRDSSYCGNV
0124	1573	236	SDEALRLAGERGMGRVQLFEISLSHGRVVYSPGEPLAGTVRVRL
		1	GAPLPFRAIRVTCIGSCGVSNKANDTAWVVEEGVENGGLGLADV
l			GSLPAGEHSFPFQFLLPATAPTSFEGPFGKIVHOVRAATHTDDE
			SKDHKCSLVFYILSPLNLNSIPDIEOPNVASATKKESVKLVKTG
			SVVLTASTDLRGYVVGOALOLHADVENOSGKDTSDVAVAGLI OVA
i	1		SYKAKRWIHDVRTIAEVEGAGVKAWRRAOWHEOILVDALDOSAL
			PGCSLIHIDYYLQVSLKAPEATVTLPVFIGNIAV/NDCDGEDDA
	1		RPGAASWGPTPGG\PSAPPQEEAEAEAAAGGPHFLDPVFLSTKS
1	İ		HSQRQPLLATLSSVPGAPEPCPQDGSPASHPLHPPLCISTGATV
			PYFAEGSGGPVPTTSTLILPPEYSSWGYPYEAPPSYEQSCGGVE
6125	<del> </del>	904	PSLTPES
-1		204	KTCPKLTCAFTVSVPDSCCRVCRGDGELSWEHSDGDIFRQPANR
1	1		EARHSYHRSHYDPPPSRQAGGLSRFFGARSHRGALMDSQQASGT
ŀ			IVQIVINNKHKHGQVCVSNGKTYSHGESWHPNLRAFGIVECVLC
1			TCNVTKQECKKIHCPNRYPCKYPQKIDGKCCKVCPG/KKAKEEL
			PGQSFDNKGYFCGEETMPVYESVFMEDGETTRKIALETERPPQV
<u>L</u> .	} i		EVHVWTIRKGILQHFHIEKISKRMFEELPHFKLVTRTTLSQWKI FTEGEAQISQMCSSRVCRTELEDLVKVLYLERSEKGHC
6126	1224	389	RLLSEAPCPRSRRRFQMNPEWGQAFVHVAVAGGLCAVAVFTGIF
Ì			DSVSVQVGYEHYAEAPVAGLPAFLAMPKNSLVNMAYTLLGLSWL
	1		HRGGAMGLGPRYLKDVFAAMALLYGPVQWLRLWTQWRRAAVLDQ
	[ [		WLTLPIFAWPVAWCLYLDRGWRP\WLFLSLECVSLASYGLALLH
ļ			PQGFEVALGAHVVPAVGQALRT\HRHYG/SATPSATYLALGVLS
İ	1		CLGFVVLKLCDHQLARWRLFQCLTGHFWSKVCDVLQFHFAFLFL
			THENTHPREHPSGGKTR
6127	1335	463	VLPRRCLVFVVNTMDSSREPTLGRLDAAGFWQVWQRFDADEKGY
ļ	l l		IEEKELDAFFLHMLMKLGTDDTVMKANLHKVKOOFMTTODASKD
			GRIRMKELAGMFLSEDENFLLLFRRENPLDSSVEFMOTWDKYDA
	i i		DSSGFISAAELRNFLRDLFLHHKKAISEAKLEEVTGTMMKIEDD
			NKDGRLDLNDLARILALOENFLLOFKMDACSTERPKGDERVIEW
			YYDVSKTGALEGP\EVDGFVKDMMELVOPSISGVDIDKEPETII.
6128	2511		RHCDVNKDGKIQKSELALCLGLKINP
0120	2511	843	TCRMSRRQLERWVWSSQQVQARGRNVRAPRLGKIAMGLEMSSKD
			SPGSLDGRAWEDAQKPQSAWCGGRKTRVYATSSRRAPDSFGTPD
1 1	ſ		GGAARPEKTAEEGPPAAPGSLRHSGPLGPHACPTALDEROUTEA
	ł		MSSQVVGIEPLYIKAEPASPDSPKGSSETETEPPVALAPG\PAP
1 1			TRCLPGHKEEEDGEGAGPGEOGGGKLVLSSIPKRICIACGDVAC
]	1		GYHYGVASCEACKAFFKRTIQGSIEYSCPASNECEITKRRRKAC
	1		QACRFTKCLRVGMLKEGVRLDRVRGGRQKYKRRPEVDPLPFPGP
1 1		İ	FPAGPLAVAGGPRKTAAPVNALVSHLLVVEPEKLYAMPDPAGPD
1 1	i		GHLPAVATLCDLFDREIVVTISWAKSIPGFSSLSLSDQMSVLQS
1 1	j	J	VWMEVLVLGVAQRSLTLQDELAFAEYLVLDEEGARPAGLGELG\
1			AALLQLVRRLQALRLEREEYVLLKALALANSDSVHIEDEPRLWS
[ ]			SCEKLLHEALLEYEAGRAGPGGGAERRRAGRLLLTLPLLRQTAG
6129	1764	771	KVLAHFYGVKLEGKVPMHKLFLEMLEAMMD
[ [	_		ARFARSAHEGKMPKKKTGARKKAENRREREKQLRASRSTIDLAK
į l			HPCNASMECDKCQRRQKNRAFCYFCNSVQKLPICAQCGKTKCMM
1			KSSDCVIKHAGVYSTGLAMVGAICDFCEAWVCHGRKCLSTHACA
		ļ	CPLTDAEC\VECERGVWDHGGRIFSCSFCHNFLCEDDQFEHQAS
ĺ	Ť	i	CQVLEAETFKCVSCNRLGQHSCLRCKACFCDDHTRSKVFKQEKG
1	1		KQPPCPKCGHETQETKDLSMSTRSLKFGRQTGGEEGDGASGYDA
	1		YWKNLSSDKYGDTSYHDEEEDEYEAEDDEEEEDEGRKDSDTESS DLFTNLNLGRTYASGYAHYEEQEN
6130	3	577	GDCCTMDEVYING CCCI CHANGE
			GRGGTMREYKVVVLGSG\GVGKSALTV\QFVTCTF1EKYDPT1E

Decining nucleotide location corresponding to first amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid ami	SEO	Predicted	1 5	
NO: nucleotide location location corresponding to first amino acid residue of amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence	1	1	Predicted end	Amino acid segment containing signal peptide
Cocresponding				(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
corresponding to first amino acid amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence				Glutamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of amino acid sequence  sequence    Perciline, O-Gluteamine, Pencipine, Sessine, Tethreonine, V-Walline, amino acid sequence   Perciline, O-Gluteamine, Pencipine, Sessine, Tethreonine, V-Walline, amino acid sequence   Perciline, O-Gluteamine, Pencipine, Sessine, Tethreonine, Coden, *-possible nucleotide insertion   Perciline, O-Gluteamine, Pencipine, Sessine, Tethreonine, Sessine, Tethreonine, Sessine, Tethreonine, Sessine, Tethreonine, Sessine, Tethreonine, Sessine, Tethreonine, Sessine, Tethreonine, Sessine, Tethreonine, Sessine, Sessine, Tethreonine, Sessine, Sessine, Tethreonine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessine, Sessi				H=Histidine, I=Isoleucine, K=Lysine,
amino acid residue of anio acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequenc				D=Leucine, M=Methionine, N=Asparagine,
maino acid maino acid sequence    Martypicophan   Yaryosine, XaUknown, *=\$top   Codon, /=possible nuclectide deletion,    -possible nuclectide deletion,     Yaryosine, ryosine, Yaryosine,     Yaryosine, Yaryosine, Yaryosine,     Yaryosine, Yaryosine, Yaryosine,     Yaryosine, Yaryosine, Yaryosine,     Yaryosine, Yaryosine, Yaryosine,     Yaryosine, Yaryosine, Yaryosine,     Yaryosine, Yaryosine, Yaryosine,     Yaryosine, Yaryosine, Yaryosine,     Yaryosine, Yaryosine,     Yaryosine, Yaryosine, Yaryosine,     Yaryosine, Yaryosine, Yaryosine,     Yaryosine, Yaryosine, Yaryosine,     Yaryosine, Yaryosine, Yaryosine,     Yaryosine, Yaryosine, Yaryosine,     Yaryosine, Yaryosine, Yaryosine,     Yaryosine, Yaryosine, Yaryosine,     Yaryosine, Yaryosine, Yaryosine,     Yaryosine, Yaryosine, Yaryosine,     Yaryosine, Yaryosine, Yaryosine,     Yaryosine, Yaryosine, Yaryosine,     Yaryosine, Yaryosine, Yaryosine,     Yaryosine, Yaryosine, Yaryosine,     Yaryosine, Yaryosine, Yaryosine,     Yaryosine, Yaryosine, Yaryosine,     Yaryosine, Yaryosine, Yaryosine,     Yaryosine, Yaryosine, Yaryosine,     Yaryosine, Yaryosine, Yaryosine,     Yaryosine, Yaryosine, Yaryosine,     Yaryosine, Yaryosine, Yaryosine,     Yaryosine, Yaryosine, Yaryosine,     Yaryosine, Yaryosine, Yaryosine,     Yaryosine, Yaryosine, Yaryosine,     Yaryosine, Yaryosine, Yaryosine,     Yaryosine, Yaryosine, Yaryosine,     Yaryosine, Yaryosine, Yaryosine,     Yaryosine, Yaryosine, Yaryosine,     Yaryosine, Yaryosine, Yaryosine,     Yaryosine, Yaryosine, Yaryosine,     Yaryosine, Yaryosine,     Yaryosine, Yaryosine,     Yaryosine, Yaryosine,     Yaryosine, Yaryosine,     Yaryosine, Yaryosine,     Yaryosine, Yaryosine,     Yaryosine, Yaryosine,     Yaryosine, Yaryosine,     Yaryosine, Yaryosine,     Yaryosine, Yaryosine	1			P=Proline, Q=Glucamine, R=Arginine,
amino acid sequence  Codom. Poposible nucleotide inaertion)  DFYRKETEV DSSPSWATE SWTQOTTSEP (TASMRDLYIKKGGG LILL) POSSBJANG STRYDOTTSEP (TASMRDLYIKKGGG LILL) POSSBJANG SWTQOTTSEP (TASMRDLYIKKGGG LILL) POSSBJANG SWTQOTTSEP (TASMRDLYIKKGGG LILL) POSSBJANG SSSGRALBERWSTGOTTSEP (TASMRDLYIKKGGG LILL) POSSBJANG SSSGRALBERWSTGOTTSEP (TASMRDLYIKKGGG LILL) POSSBJANG SSSGRALBERWSTGOTTSEP (TASMRDLYIKKGGG LILL) POSSBJANG SSSGRALBERWST PSTRYPSSBJANG SSSGRALBERWST PSTRYPSSBJANG SSSGRALBERWST PSTRYPSSBJANG SSSGRALBERWST PSTRYPSSBJANG SSSGRALBERWST PSTRYPSSBJANG SSSGRALBERWST PSTRYPSSBJANG SSSGRALBERWST PSTRYPSSBJANG SSSGRALBERWST PSTRYPSSBJANG SSSGRALBERWST PSTRYPSSBJANG SSSGRALBERWST PSTRYPSSBJANG SSSGRALBERWST PSTRYPSSBJANG SSSGRALBERWST PSTRYPSSBJANG SSSGRALBERWST PSTRYPSSBJANG SSSGRALBERWST PSTRYPSBJANG SSSGRALBER SSSGRALBERWST PSTRYPSBJANG SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGRALBER SSSGR	1			S=Serine, T=Threonine, V=Valine,
sequence    equence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence	1		i	W=Tryptopnan, Y=Tyrosine, X=Unknown, *=Stop
DPYRKETEV\DSSFSWATSWTQCTEGY-TASMRDLYIKKGGGG TLVYSUNQGSP() IKEMRDQITEVKYSKVPVI\LVGN\SVL LESEREVSSSGRALBEWGCPPMTSASKKYPVI\LVGN\SVL MYYAAQPKDDD-CSGACNIQ MYYAAQPKDDD-CSGACNIQ SPREESSBSSREPSRHGFFERLVGLSPFSYLCVPFSRPVFGG GVAAGTRRPWVLLITDQGDEVLGGMTPLKALILGEMGWTS PRSLSAMRLLDLAPGRLERGSPRHLPSCSPALLLULGGGGLGVS GVAAGTRRPWVLLITDQGDEVLGGMTPLKALIGEMGWTS SAVVPSALCCPSRASILIGKYPHNHHVNNTLECNCSSKSMGKI QENNTFPALERSKCYQTFF\AGKYLEWGAQGGLGUEVPLGA DFLDYKSNFSEPFFMTATIP\AGKYLEWGAQGGLGUEVPLGA SVYYALBENSKYYNTILSINGKARKHGENSYDVLITVLAWGL DFLDYKSNFSEPFFMTATIP\AGKYLEWGAQGGLGUEVPLGA KNFNIHGTNKHMLIRGAKTPMTNSSIGFLDNAFRKRYQTLLSVU DLUEKLVKRLEFTGELNNTI\TFYTDGMCHADQGLGUEVPLGA KNFNIHGTNKHMLIRGAKTPMTNSSIGFLDNAFRKRYQTLLSVU DLUEKLVKRLEFTGELNNTI\TFYTDGMCHADQGLGUEVPLGA KNFNIHGTNKHMLIRGAKTPMTNSSIGFLDNAFRKRYQTLLSVU DLUEKLVKRLEFTGELNNTI\TFYTDGMCHADQUSPLDIVANG KNFNIHGTNKHMLIRGAKTPMTNSSIGFLDNAFRKRYQTLLSVU DLUEKLVKRLEFTGELNNTI\TFYTDGMCHADQUSPLDIVANG KNFNIHGTNKHMLIRGAKTPMTNSSIGFLDNAFRKRYQTLLSVU DLUEKLVKRLEFTGLENDTILTSTTOLTBELLGKWURVATUTDFCDSEP FOUNDLINGTHAGNANILTSTTOLTBELLGKWURVATUTDFCCDSEP FOUNDLINGTHAGNANILTSTTOLTBELLGKWURVATUTDFCCDSEP FOUNDLINGTHAGNANILTSTTOLTBELLGKWURVATUTDFCCDSEP FOUNDLINGTHAGNANILTSTTOLTBELLGKWURVATUTDFTCCDSEP FOUNDLINGTHAGNANILTSTTOLTBELLGKWURVATUTDFTCCDSEP SGA/WESIFFROLISTHLILUALLARROUDALLLILIGGLGGFF LIHKEFTILTPNSPARMHHVYTLALELL/IGRGPAUGHFALILHIL FGRLAALKLERADIALTATSQKHLLTVULLANDRINS\CSWRGGRP SGA/WESIFFROLISTHLILUALLARROUDALLLILIGGLGGFF LIHKEFTILTPNSPARMHHVYTLALELL/IGRGPAUGHFALILHIL FGRLAALKLERADIALTATSQKHLLTVULLANDRINS\CSWRGGRPSVE VKRAIVPREVONGLENDLASVANDLATGARDURVATUTLILLIGGLGGFF LIHKEFTILTPNSPARMHHVYTLALELL/IGRGPAUGHFALILHIL FGRLAALKLERADIALTATSQKHLLTVULLANDRINS\CSWRGGRPSVE VKRAIVPREVONGLENDLASVANDLATGARDURVATULLILIGGLGGFF LIHKEFTILTPNSPARMHHVYTLALELL/IGRGPAUGHFALILINGTDVGDVIRG FUNGSSGKANGLANDRYTTSTTOLTATTOSSGAGOGGTKTSTSTTOT TVTSSGAGOGGGVANGLANDATATTOSSGAGOGGTKTSTSTTOT TVTSSGAGOGGGVANGLANDATATTOSSGAGOGGTKATTSTTOT GRAAVRANGVANGAGOTTATPHLABSFSPFPAVSISSFVT VKRRGVYTGENSENSANDATTOTTORAGETTORAGARTICHTUNGHVIRG GROGGKTAGLINTPKVANTSFRENGLGAAPLTS	İ		bequence	_possible nucleotide deletion,
6131 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 1811 3 18			<del> </del>	DEVELOR DECERTION
6131 3 1811 SSPREKTSUSSHRSKALEEMGCPMETSAKSKTMVDELFAELVR  GNAAGTRENVULLTDODEVLGSFSYLCVPSSPPVEG GVAAGTRENVULLTDODEVLGSFSYLCVPSSPPVEG GVAAGTRENVULLTDODEVLGSTPSKLCAGE GVAAGTRENVULLTDODEVLGSTPSKLTKALGEMGNTE SAVVPSALGCESRAS LICKKPRINHVUNTLEONGS SKSMOKI OENTFPAILESMGGVOTFFAGKYLINEYGAPDAGGLEIVPLGG SYMVALENKSKYNYTLSINGKARKIGSVPULTDVLAMVGI DFLDYKSNEEPFFMMTATP\APHSPMTAAPGYGKAGTOVFARN KNPINIGTNIKMILTGAKTPMINSSTOPLDGARAGTOVFARN KNPINIGTNIKMILTGAKTPMINSSTOPLDAFRENGTLLSVU DLVEKLVKRLEFTGELINNTYLFYTSINNGYHTGGFSIPLIDRAGDL EPFILKVPLLVAGGGGLINPVILFYTSINNGYHTGGFSIPLIDRAGDL EPFILKVPLLVAGGGGLINPVILFYTSINNGYHTGGFSIPLIDRAGDL EPFILKVPLLVAGGGGLINPVILFYTSINNGYHTGGFSIPLIDRAGDL EPFILKVPLLVAGGGGLINPVILFYTSINNGYHTGGFSIPLIDRAGDL EPFILKVPLLVAGGGGLINPVILFYTSINNGYHTGGFSIPLIDRAGDL EYNNLTADPDOLTIN AKTIDELLIGKRANLLANLGGGGSPTCKT PGVSDFFDLVSCHAMSNOSSUSTRRFSSKHLL FORLAALKIGAEDININTYACVTINSALMULGYGGSPTCKT PGVSDFFOLVEDPRITTINLEFTGIGGFFALSRFLFSCVESGN AMBABEPEFLYDLLGDPKGSVEPFALSRFLFSCVESGN AMBABEPEFLYDLLGDLAMSTATLEFHLYVPSLEEDMFDGLILHHL FORLAALKIGAEDIALTATSGKIKLTVVURSLEEDMFDGLILHHL FORLAALKIGAEDIALTATSGKIKLTVVURSLEEDMFDGLILHHL FORLAALKIGAEDIALTATSGKIKLTVVURSLEEDMFDGLILHHL FORLAALKIGAEDIALTATSGKIKLTVVURSLEEDMFDGLILHHL FORLSAALKIGAEDIALTATSGKIKLTVVURSLEEDMFDGLILHHL FORLSAALKIGAEDIALTATSGKIKLTVULEAVARSCCSMSGRSP SCA/MESTSFINNLLSETLELLVALAKRFDAGVILSPTNIVOREVITT ESTKSGLKSEKLVEGLTEYSTDDEPFRUVPBURDPVEVITT ESTKSGLKSEKLVEGLTEYSTDDEPFRUVPBURDPVEVITT ESTKSGLKSEKLVEGLTEYSTDDEPFRUVPBURDPVEVITT ESTKSGLKSEKLVEGCTTYSTSTDEPVRUPPBURDPVEVITTSSSGANDSSKK KTLUTLIANNAGNELVGGGGDLILTONAPAGLGHOFVLALK/ TUNNGAGSTARPTITTTTVT HAARASVGHILSTVSSGANDSSKK KTLUTLIANNAGNELVGGGGGDLILTONAPAGNGOV IVLNVQGGGTVBFTILVPARGTGFVKPTVAVDPOYSQMTDVROK KTLUTLIANNAGNELVGGGGDLILTONAPAGNAGVUT IVLNVQGGGTVBFTILVPARGTGFVKPTVAVDPOYSQMTDVROK FORWFYCTFTTTTTTTTTTTTTTTTTTTTTTTSSGGANDSSKK KTLUTLIANNAGNELVGGGGGENGTTTTSTTTTTTTTTTTTTTTTTTTTTTTTTTT	ł	1	1	DFIRALIEV \DSSPSVAGISWTQQGTEQF\ASMRDLYIKKGQGC
6131 3 1811 SSPERETSUSSERPSKEPSKEPSKEPSKEPSKEPSKEPSKEPSKEPSKEPSKE	1	1		LESEBENGSEGDALARDIGORNA SERVEVI LVGN SVD
5131 3 1811 SSPREKTSUSSIRPSKRIGELFLEVGLSFSFLLLVLIGGCLOW FRSILSAMELDLARGELDRAGS GPALLELYPESERVEG GVAAGTRENVULLITDODEVLIGHTPLKKTKALIGGMENTES GRAVESALCESRASILLUKKYEMENHVINTILERUKSKIKMEN GVAAGTRENVULLITDODEVLIGHTPLKKTKALIGGMENTES GAVPSALGCESRASILLUKKYEMENHVINTILERUKSKIKMEN GENTYEVALGKUMENSKIKMEN GOENTEPALLUKSKIKMEN GOENTEPALLUKSKIKMEN GOENTEPALLUKSKIKMEN DEPURKSKIKMEN GOENTEPALUKSKIKMEN DEPURKSKIKMEN DEPURKSKIKMEN DEPURKSKIKMEN DEPURKSKIKMEN DEPURKSKIKMEN DEPURKSKIKMEN DEPURKSKIKMEN DEPURKSKIKMEN DEPURKSKIKMEN DEPURKSKIKMEN DEPURKSKIKMEN DEPURKSKIKMEN DEPURKSKIKMEN DEPURKSKIKMEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBRAGDEN TONDOMSILDEILBR	1			MNVAAODEVDDBGGARGUE
PRSLAMMRILD-LAPGILARGS PRILESCS PALLLLVIGGCLGWY  GVAAGTRRNVULLITDODDEVLIGHTPLKTKIALIGEMGYTE  SAVPSALGCESRASILIGKY PHINHVUNTLEENCS SKSWOKI  GENTFPALLESMOGYOTFP \AGKYLINEYGAPDAGGLEVVPLOK  SYMYALEKINSKYNYNTLSINOKARKIGNAVPYDYLTDVLANVSI  DFJLDYKSNYEEFFMMTATP\APHSPATAAPGYGKAFONFAPRAN  KNENHGINIKHWILIGAKTPHYNSIS GJABAFREKWGTULSVU  DLVEKLVKRLEFTGELINNTYLFTISINGARKIGNAFREKWGTULSVU  EFPIKVPLLVAGGGIRFNGTSKHIVANDLAPTILDIAPTLINAYDLAW  TOMDGMSILPILRGASNITMRSDVLVEYGGGGNVTAPARN  TOMDGMSILPILRGASNITMRSDVLVEYGGGGNVTAPTOPTCSISL  PGYSOCFPEDCYCEDAYNITYACVCTRISAMULYCEPDOGSVP  EVYNLTADPDOLTNIAKTIDEELIKGMSKLMMLYCEPDOGSVP  EVYNLTADPDOLTNIAKTIDEELIKGMSKLMMLYCEPDOGSVP  EVYNLTADPDOLTNIAKTIDEELIKGMSKLMMLYCEPDOGSVP  EVYNLTADPDOLTNIAKTIDEELIKGMSKLKLPTSRKO  AREAMEPELYDLLQLPGVCGPPALESINGJKKKLYVVLENGKSGFTCRT  PGYFDGFKFPPPLIMIKLDFFGGGPPFALSFIJFSCVESGM  AREAMEPELYDLLQLPGVCSPPAEELIKGMSKLKLPFTSRKO  AREAMEPELYDLLQLPGVCSPPAEELIKGGKKKLPFTSRKO  AREAMEPELYDLLQLPGVCSPPAEELIKGGKKKLPFTSRKO  PKPEELQRAVLMERIHATLLEBLLYTGLESDHODGLILHHL  FGRLAALIKLEBEDLATHLVALLAKEPLJADVASLESPTIVSSGANDSTK  KGALVSKYLVGLITSYSTOKDEPFKVDFDELFLAFEKVAS  VKRALVAFVNOKLDELGISTONDEPFKTDEVPEDFYDFDELFLAFEKVAS  VKRALVAFVNOKLDELGISTONDEPFKTDEVPEDFYDVPDUFVDIFTLAFEKVAS  VKRALVAFVNOKLDELGISTONDEPFKTDEVPEDFYDVPDUFVDIFTLAFEKVAS  VKRALVAFVNOKLDELGISTONDEPFKTDEVPEDFYNDRYDNINDV  TULNNOGGGVPAPPILAHASVAGHLISTUSSGANDSSTK  KTLVLTLANNAGNDLVGGGGDELITONDEPFKTDYSSGANDSSTK  KTLVLTLANNAGNDLVGGGGDELITONDEPFKTDYSSGANDSSTK  KTLVLTLANNAGNDLVGGGGDELITONDEPFKTDYSSGANDSSTK  KTLVTLLANNAGNDLVGGGGDELITONDEPFKTDYSSGANDSSTK  KTLVTLANNAGNDLVGGGGDELITONDERSCHVYSNNNSAL  GGGRTGGPSSMKVTSSIPYFDLOGGKKICPRCAARPTYERL  POVOMONNANVTSSVASOPIFTTORPSGAGOTKSTFSTSTY  TATODTSLGGLAVOSPOGSNOTTNYKLAPSPRSPANSLSFFY  VKRROVTGENSEVAKLNVITANITYSISGAGOPTVYSNNSSAL  GGGRTGGPSSMKVTSSIPYFDLOGGKKICPRCAARPTYEAL  GGGGKVAGNOGAUNTHRYKNITANITYSISGAGOPTVYSNNSAL  GGGGKVAGNOGAUNTHRYKNITANITYSISGAGOPTVYSNNSAL  GGGGKVAGNOGAUNTHRYKNITANITANITYSISGAPPTYTENA  SKOOPTPYPSSNDTPSHALSPYTYTVRGSAGAPPTPTAL  GROGKVAGNOGAUNTHRYKNITANITANITYSISGAPPTVGLOCY  KKERTORPTONAGNATANI	6131	3	1811	CCDDRAMODOCANDON
GVAAGTRENVVLLLITDODDEVLGGMTPLKKTKALIGEMGMTE SAYVESALCCESRAS LITGKY PHINTYNTLEKNCS SKSKOKK QEENTFFAILKSMCGYQTFF/AGKKLINEYGAPDAGGLERVPLGK SYWALDKRISKYKYNYTIS. INGKRARIGYSVDYLIDVLANVGI DFLDYKSNPEPFMMTATP JAPHS PHTAADOYGKAFONVFAPRI KNININGTRKIMLING LORAKTEMTINS IQFLDNAFRKRWGTLING DLUEKLUKRLEFTGELANTYI FYTSDROYHTGGFSLPIDKROY DLUEKLUKRLEFTGELANTYI FYTSDROYHTGGFSLPIDKROY TOMDGMSLLPILRGASNLTWRSDVLVEYGGEGRNVTPTDTCPSLS PGVSQCFPDCVCEDAYNNTYACVETMSALDHILDYCEFDDOEVEV EYYNLTADPDOITINGT INGT TOHELLGEFFALLSPFILDLEGOFPODGEVEY PGWFDFGVRFPPRIMESNGSVETRESKHLL AGALLPFGLVEEDFFTRNLLEFFGLOFFALLSFFICVESGR AMEAMEPEFLYDLLQLPKGVEPPALSRFLFSCVESGR AMEAMEPEFLYDLLQLPKGVEPPALSRFLFSCVESGR AMEAMEPEFLYDLLQLPKGVEPPALSRFLFSCVESGR AMEAMEPEFLYDLLQLPKGVEPPALSRFLFSCVESGR SGA/WESTINKDLISTRILLIVALAKTYLELEDMEPGLILHHL FQRLAALKLEADIALTATSGCHKLTVVLEAVWRS\CSWRSGRP SGA/WESTINKDLISTRILLIVALAKTYLELEDMEPGLILHHL FQRLAALKLEADIALTATSGCHKLTVVLEAVWRS\CSWRSGRP SGA/WESTINKDLISTRILLIVALAKTOPLOLSLUFNOYBEVIT LITURODARSTIRNUYGLECHFOOLSPOTEDVICHTVOYBURT VKRAIVNEVNOKLDRIGLSVONLDTOSADSVLLLLLIGGEGEGL LILKEFYLTPNSPAEMLHNVTLALELL/IGROPAGLEC/LLALK TUNKDARSTIRNUYGLECHFOOKAHDETFINGAPN VKRAIVNEWOKGARDELITIONAPAGGGGTULLLLIGGEGEGE LILKEFYLITNSSAGANDSTSK KTLVTLIANNAGENPLOVGGGGGLILTONAPAGGGGNOTSTPSTSTTFT TYCSSQOPVSBAVPITAHASVAGHLSTSTTVOSGSGONGTOTTPKTSSGAGNOSDSTK KTLVTLIANNAGENPLOVGGGGGNOTTTPKTSSGAGNOSDSTK KTLVTLIANNAGENPLOVGGGGGNOTTTPKLASSPSPPALSISPVT VKRGOVTGENSNEVAKUNTLINTIPSLGGBPOVVVSINSSAH\ GSGPTSTGGLGAVOSGGSONGTTSPKTLASPSPSPALSISPVT VKRGOVTGENSNEVAKUNTLINTIPSLGGBPOVVVSINSSAH\ GSGPTSTGGESSMEVTSTPVPDLQGGGRTCTCRAAFFRYTERSTSTTP TATOPTSIGGLAVOSGGSONGTTSPKTCSTSTSTTP TATOPTSIGGLAVOSGGSONGTTSPKTCYCOVCYRSSTSYSTEV VKRGOVTGENSNEVAKUNTLINTIPSLGGBPOVVVSINSSAH\ GSGPTSTGGESSMEVTSTPVPDLQGGARTCCRAAFFRYTERSTSTTP THEADSPTPLTAMERTST PVPDLQGGARTCCRAAFFRYTERSTSTTP THEADSPTPLTAMERTST PVPDLQGGARTCCRAAFFRYTERSTSTTP THEADSPTPLTAMERTST PVPDLQGGARTCCRAAFFRYTERSTSTTP THEADSPTPLTAMERTST STATPPTPTTHRTHYTYPTSTSSTTP THEADSPTPTTAMERTST STATPPTPTTHAMERTSTS STATPPTPTTHAMERTSTS STATPPTPTTHAMERTSTS STATPPTPTTHAMERTS STA	1		1 1011	DDCLCAMBLIDE ABORD DECEMBER OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF
SAYUPSALCESRASILITGKYPHNHHVUNTILEGNCS SKSNOKL  OPENTFALLEMSCYTFF\GRKYLNEYGAPDAGGLEHVELGK SYWALEKISKYYNTISINGKARKHGENYSUPYLTDVLANVGI DFLDYKKINSPEPFFMATAT P\APHSADOYGKARONVPAPRA KNPNIKGTKKIMLIRQAKTEMTNS SIQFLDNAFKKRWQTLLSVU DLVEKLIVRLEFTGELANTYIFYTSDRGYHTGGFSLPIDKRQIX EFDIKVPLLVRGFGIKRNQTSKMLYDLGPTILDIGFDLLGHAVLL EFDIKVPLLVRGFGIKRNQTSKMLYDLGPTILDIGFDLLGYDLEN TQMDGMSILPILRGASNLIWRSDVLVEYGGGGRAVIDFTCPSLS PGWSQCFPDCVCEDANTNTACVTHWSGLWNLLYVCEFDDGEVEV EVYNLTADPDOITNIAKTIDPELLGKMNYRLMKLQSCSGPTCRT PGWFDDGYKFPPRIMFSNGSVUTRESKHLL ARGLLPPGLVPEDFRTFRILDFGIGGPFPALSRFLFSCVESGR AMEABPEFLYDLLQUFKGVEPPAELSKGKKKYLPFTSRKO PKFEELQKPA\VLMEWINATLLPFHIVVRSLEEDMFDOLILHHL FQRLAALKLEAEDIALTATSQKHKLTVVLEAVMTS\CSWRSGKP SGA\WESIFNKDLLSTLHLLVALAKRYOPDLSPTNVCVEVTIT ESTKSGLKSEKIVSQLTEYSTIKKEPPKKUTPELEKLAPEKVAR VKRALVNFVNKLKDRGLSVONLIDTPADCVILLLIGLGEFF LHIKEFYLIFNSPAEMLHNVTLALELL/IGRGPAQLPC/LALK/ TVINNANSTLRULYGLFCKHTOKAHRTPHGAPN TVISVSQCQVSAPVPLAAHASVGAHLTSTTVSSGAQNSSTK KTLVTLLANNNACNPLVQOGGGPLILTONPAPGGGTWVTQPVLR PVOVMONNANTSTSPVAGOPIFITTGGFPVNTVRPVGNAMOVG IVLNVQGGTVRPITLVFAFGTGTVKFTVGVQVFSOMTVTRFV STMPVRPTTNTFTTVIFATLTIRSTVPQSGSGOTKSTFSTSTTF TATOPTSIGGLAVGGPSSMVTTSTSTVPDLGGGRKTCPRANGFVTFAL SGMRYCPTTSTTTTTTTTTTTTTTLGFFVRTVRPVGNAMONOVG STMPVRPTTNTFTTVIFATLTIRSTVPQSGSGOTKSTFSTSTTF TATOPTSIGGLAVGGPSSMVTTSSTPVPDLQGGRKTCPRANGFVTFAL RGHMCYCCPEMYSYCKKGKSLDSEPSYPSAAYPSPERVATARS YTHESSTPIPALSPY/TXVEPSPERMYVATSPERVATARS YTHESSTPIPALSPY/TXVEPSPERMYVATSPERVATARS TATOPTSIGLAVGSGSSMVTKSTSPPPTDALGHVTVTPPVURS SRGQGRTVPVSSNDTPPSALQEAPLTSSMPPLFVTLYPVGGS GRANAHMINNHYPRKSSSILPREKKOLGGLKPGTKYTRA SRGQGRTVPVSSNDTPPSALQEAPLTSSMPPLFVTLYPVGUS CCSRAYANHMINNHYPRKSSSILPREKLGCHTSTCRTNSTFSTTF SGGGGGGGGGGGGTGTKRSSSSILPRETLGRAFTSTFPPP LASGGGGGGGGGGTGTKRSSSSILPRETLGCRTSTFT SGGGGGGGGGGGTGTKRSSSSILPRETLGCRTSTFT SGGGGGGGGGGGGTGTKRSSSSILPRETLGCRTSTFT TATOPTSICALGRAFTGTHTTHT SGRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	ļ	1 .	}	CVARCTER DANGEL LE TERRESPRIL PSCS PALLLLVLGGCLGVF
OPENTFPAILESMOGYGTEF\AGKKINEYGAPDAGGLEHVDLGA SYNYALEKNSKYKYNYLSINGKARRINSVOYLTOVLAWSI DFLDYKSNYEPFFMMTATP\APHSPMTAAPQYGKAFONVPAPEN KNYNIKGTIKKHWLIRGAKTEMINSS (DIDNAPKREWGTLLSVG DLVEKLVKRLEFTGELNNYYLYFTDNOYHTOGPSLPIDKRCKY EFDIKVPLLVRGGEGIRNOTYGHUNDLGPTILDIAGYLLKK TOMDGMSLLPILRGASNLTWRSDVLVEYGGEGRNYTDFICPSLS PGWQCGPDCVCEDAINNYTACVRTMSALBHNLQYCEFDDGEVEY TOMDGMSLLPILRGASNLTWRSDVLVEYGGEGRNYTDFICPSLS PGWGCGPDCVCEDAINNYTACVRTMSALBHNLQYCEFDDGEVEY EVYNLTAPPDQITRIAKTIDPELIGFGRYKLLMGYCEFDDGEVEY PGWFDGYRFDPRIMFSNRGSVETRRFSKHLL ARGLLPGCLVEPDFRETRRILLDFGLOFPFALSRFLFSCVESGW AMEAMEPEFLYDLLQLPKGVGKKYLPPTSRKD PFEELGKRA\VLMEWINATLIPELINGSGKKYLPPTSRKD PKFEELGKRA\VLMEWINATLIPELINGSGKKYLPPTSRKD PKFELGKRA\VLMEWINATLIPELINGSGKKYLPPTSRKD SGA\WESTINDLLSTATUSCHKKLTVVLEAVNRS\CSWRSGEP SGA\WESTINDLLSTATUSCHKKLTVVLEAVNRS\CSWRSGEP SGA\WESTINDLLSTATUSCHSCHKTVLEAVNRS\CSWRSGEP SGA\WESTINDLLSTATUSCHSCHKUTUSELEDMPGDLLIHHL FORLAALKLEEDIALTATSGKHKLTVVLEAVNRS\CSWRSGER SGALWESTINDLLSTATUSCHSCHKYLPPTSRKD VKRAIVNFVNGKLDRIGLSVONLDOFDGLEFVLLAPEKVNA VKRAIVNFVNGKLDRIGLSVONLDOFDGLEFVLLAPEKVNA VKRAIVNFVNGKLDRIGLSVONLDOFDGLEFVLLAPEKVNA VKRAIVNFVNGKLDRIGLSVONLDOFDGLEFVLLAPEKVNA VKRAIVNFVNGKLDRIGLSVONLDOFDGLEFVLLAPEKVNA VKRAIVNFVNGKLDRIGLSVONLDOFBGVUETENSVEDYNSVDKT TTVSVSQOPVSAPVPLAHASVAGHLSTSTTVSSGAONSDSTK KTLVTLLANNAGANPLVOQGGGPLILTOMPAGGLGTWYDPVLG SIMPVRPTTNTFTTVIPATLITGFPVRNVRPVONAMOVG VILNNVQGGVPRITIVTPATLITGSTVPOSQSGONSTSTPSTSTTF TATOPTSIGGLAVOSGGSONGTTNPKRTVSPVDOVSGNAMOVG SIMPVRPTTNTFTTVIPATLITTSTVPOSQSGONGTSPSTSTSTTP VKRPGVTGENSNEVAKLUNTLINTTPELGGSPOPVVVSNNSSAH\ GGORTSGDESSMKVTSSTPVPDLOGGSNOTTNPKRSTLSFPPTPAVSIASPYPAAS /*HPSSTPIPALSPPY/TVPASTSITPTC GGORTSGDESSMKVTSSTPVPDLOGGSNOTTNPKGCHCZNGKRANGFNETHALMCHWE LDQOMGSVDGHTICHCVCRVKKNGKRAFQOHYMEHGKR\NVYH\ CNKCRVGVDLFAKNKUNGHTMCHTLICHCRVST GROGGSGGGVAKKGUNGTNATHFTPTVHTSLCRVST CCSRAYANHMINNHYPRKSSSILPRENDLFUTLIYPPVOG SGORTSGDESSMATKSSSOLDKARNVILFALCCTROFAGEHFRHPQ KRIMMINGMYPPPSPTPROALLEPPTTYTHESSSILPREPPTHAGARGTRORVGH NYMMYPPPSPTNAAATVARSGGENLECKKINFRGCTRORVGH NYMMYPPSPTHORAATURATERSSSILPREPPTHYTHTYTUPSURGH STAT	1	Ì	1	CANADER GODDE OF THE TOTAL CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF T
SYWALEKNSKYYNTISINCKARKHGENYSUPYLTDULANVSI DFLDYKSNFEPPFFMTATPYAPHTADPONFAGONYPARR KNFNIHGTKKHULIRQAKTPMTNSSIQFLDNAFRKRWOTLLSVD DLVEKLVKRLEFTGELMNTY1FLONGYHTQGFSIPIDKRQLY EFDIKVPLLVRGFGIKPMQTSKMLVANIDLGFTLDIAGYDLKK TOMDGMSLLPILRGASNLTWRSDVLEYGGBGRNNTPFTCPSLS PGVSQCPPDCVCEDAYNNTYACVATNSALMNLQVGCGFDDGEVEV EVYNLTADPDQITNIAKTIDFELLGKMNYRIMMLQSCSGFTCHT PGVFDFGYKFPDFMKFNRGNSVATYMFSSKHLU AGGLEPGGLVPEDPRFTRILLPFGIQOPFALSRPLFSCVESGR AMEABPFELVDLLQLPKGVEFBELSKGGKKKVLPFTSRNC PKFEELQKRA\VLMEWINATLLEEHIVVRSLEEDMFDGLILHHL FORLAALKLEABDIALTATSOKHTAVULEAVNRS\CSMRSGKP SGA/WESIFNKDLLSTLHLLVALAKRFGPDLSLEFNUQUEVITI ESTKSGLKSKLVROLIFTYSTROEPPRVDVDELFKLAPFKVNA VKRAI VNFVNGKLDRIGLSUNGUNTOFABGVILLLIGGLEGFP LIHKEFYLIPPSPAEMHNVTLALELL/IGRPAQLFC/LALK/ TIVNNGANSTLRVLYGLFCCHTVOGFPVRVVDPUFFKLAPFKVNA VKRAI VNFVNGKLDRIGLSUNGUNTOFABGVILLLIGGLEGFP LIHKEFYLIPPSPAEMHNVTLALELL/IGRPAQLFC/LALK/ TIVNVSQCPUSAPVILAHASVGRFTFHGAPN  6133 2 4256 FVHGSMADTDLFMRCEEBELEPPGKISDVIEDSVVEDYNSVDRT TVSVSQQPVSAPVILAHASVGRNTSTTYSSSGONGDSTK KTLVTLIANNAGNPLVQGGGDLLLTONPAGGIGTMVTOPVLR POVMONANHTISSDVASOPITITOGFPVRNVRPVUNANNOVG IVLNVQGGTVRPTTTTTVPAPGTOFVKRVRPVVNRPVUNANNOVG IVLNVQGGTVRPTTTTTTVTVAPGFOTFVKRPSPSFSFRYSIAFSVT VKRRGVTGENSNEVAKLVNTLNTIDSLGQSGGVKSTPSTSTTP TATOPTSLGGLAVQSRGGNNGTNKKLAPSFSFSPAVSIAFSVT VKRRGVTGENSNEVAKLVNTLNTIDSLGQSGPVVVSNNSSAH\ GGGRTGGESSMKVTSSIVPSLOGKKICPKRNAFFVKALRAVT GRGGKVAQLINFPKVATSFRCPHCTKKLKNIRFPMHMKHNVE LDOOMGEVDGHTICHCYROFSTPNODAQVTKLILLDUDFYY GRDGGKVAQLINFPKVATSFRCPHCTKKLKNIRFPMHMKHNVE LDOOMGEVDGHTICHCHCYROFSTPOLOCHLEWNHSPYSTTKC XLCEMAFSSPLFLOHMKDTHKPRKKQLEGLKGRTVVTRA SRGQPRTVPVSSMDTPSSALORAAPLTSSNDPLPVVLYSPTVCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVGSIKLACTSCTPVT SRGQMAKHLVFNFSRFSKSSILFSRGSKILSGRGKLAGTROTROVNDR VKMMYPPSFPTNKAATVKSAGATPABPEELLTPLAPALSESPA CCSRAYANHMINNHVPRKSPKYLALFKNSVGSIKLACTSCTPVT SKGDMAKHLVFNFSRFSRSSSILPSFRTSST FRCHTTKLELGAULTUTGEGOOLP NVKMMYPPSFPTNKAATVKSAGATPABPEELLTPLAPALSESPA CCSRAYANHMINNHVPRKSPKYLALFKNSVGSIKLACTSCTPVT SKGDAMAKHLVTHSFRRSSSILSFRKSSSILPSFRTSST FRCHTLTHPHARRA VAHTLERVARRGRPGAGGGENLEGKYLSFEAREWLITTPHACO	1	]		OF DATE OF THE SALECUS RASILTIGKY PHNHHVVNNTLEGNCS SKSWOKI
DFIDYKSNEEPFFMMTATP\APHENMTARPQYCKAFONVPAPRN KNPNIHGTNKHALIRQAKTPMTAGJOFLDNAFRRWOTLLSVU DLVEKLVKRLEFTGELNNTYIFYTSONGYHTGQFSLPIDKRQLY EFDIKVPLLVRGGFQ KEMQTSKMLVANIDLGFTILDIAGYDLKK TOMDGMSLLPILRGASNLTWRSDVLVEYGGBGRNVTDFTCPSLS PGVSQCFPDCVCEDAYNNTYACVETHSALMHLQYCEFDDDGVEV EVYNLTADPDQITNIANTIDEGLIGMYNTLMALQCSGPTCRT FGVFDGYRFDFRIMFSNRGSVBTRFFSKHLL AGALLPPGLVVEDBYRFTENLLPGOPPFALSRPLFSCVESGR AMEAMEPEFLYDLLQLPKGVEPPAEBELSKGKKKYLPPTSRO PKFEELQRDA\LWHENTATLLPEHLVVRSLEEDMFDGLILHHL FQRLAALKLEAEDIALTATSQKHKLTVVLEAVNRS\CSMFSGRP SGA\WESIFNKDLLSTHHLLVALAKRFOPDLSLPTNVQVEVITI ESTKSGLKSEKLVSCLTEYSTDKPPKDVPTDEFKLAPEKVNA VKRATVNFVNGKLDRIGLSVONLDTGFABQVILLLIGGLEGFF LILKEFYLFPRSPAMEMNYTLALELL/IGROPAQLPC\LALK\ TTVNKDAKSTRVLYGLFCHTGKAHRDRTPHGAPN  6133 2 4256 FVIGSRADTDLPMECEEEELEPWGKISDVIEDSVVEDYNSVDKT TTVSVSQQPVSAPVPIAAHSVRGHLSTSTVSSSGAQNSDSTK KTLVTLIANNAGNPLVQGGGOFLILTONPAFGLGTNVTQPUR POVVNONANHTISPVASOPITTVPAGSOGOGVKSTPTSTTTP TATQTTSIGGLAVGSPGGSNQTTNPKLAPSFPSPPAVSIASFYT VRRGCVTGENSNEVALNVTLHFTVPAGSOGOGVKSTPTSTTTP TATQTTSIGGLAVGSPGGSNQTTNPKLAPSFPSPPAVSIASFYT VRRGCVTGENSNEVALNVTLHFTVPAGSOGOGVKSTPTSTSTT TATQTTSIGGLAVGSPGGSNQTTNPKLAPSFPSPPAVSIASFYT VRRGCVTGENSNEVALNVTLHFTLSGAPBPSPPAVSIASFYT TATQTTSIGGLAVGSPGGSNQTTNPKLAPSFPSPAVSIASFYT VRRGCVTGENSNEVALNVTLHFTLSGAPBPSPSPAVSIASFYT GRDGKVAQLINTPKVATSFRCPHCTKKLKNNTRFNHMKHRVE LDQONGSVOHTGHTVARAFRCPHCTKKLKNNTRFNHMKHRVE LDQONGSVOHTGHTVARAFRCPHCTKKLKNNTRFNHMKHRVE LDQONGSVOHTHEDTHALLCYPCLKVEVNGNAPQQHTWRHQKK\NVYN\ CNKCRVQPLFAKWLEHKLQHHKTFRKPKQLEGLKRGTKVTTRA SRGQFRTVPVSSRDTTPPSALGSAPLTSSNDPLPVVLYSPVQRC CCSRAYANHMINNHVPRKSPKYLALFKNSVGGKLACTSCTFVT SKGQMAKHLVFMPSRFRSSSILFPDNNFTTVVGSLGCRSTF TATPPPPTPPTHQDALAPPLATEGBELLTVPLAPALPSPA STATPPPPTPPTHPGALAPPLATEGBELLTVPLAPALPSPA STATPPPPTPPTPGALAPPLATEGBELLTVPLAPALPSPA STATPPPPTPPTPGALAPPLATEGBELLTVPLAPALPSPA STATPPPPTPPTPGALAPPLATEGBELLTVPLAPALPSPA STATPPPPTPTPGALAPPLATEGBELLTVPLAPALPSPA STATPPPPTPTPGALAPPLATEGBELLTVPLAPALPSPA STATPPPTPTPGALAPPLATEGBELLTVPLAPALPSPA STATPPPTPTPGALAPPLATEGBELLTVPLAPALPSPA STATPPPTPTPGALAPPLATEGBELLTVPLAPALPSPA STATPPPTPTPGALAPPL		i		QEPNIFPAILRSMCGYQTFF\AGKYLNEYGAPDAGGLEHVPLGW
DLUEKLUKLEFICELINTYITYITSINGHTOGESIPTUKRGUT  EFDIKUPLLURGEGILRYNJITYITSINGHTOGESIPTUKRGUT EFDIKUPLLURGEGILRYNJITYITSINGHTOGESIPTUKRGUT EFDIKUPLLURGEGILRYNJITYITSINGHTOGESIPTUKRGUT EFDIKUPLLURGEGILRYNJITYITYITYITYITYITYITYITYITYITYITYITYITYI	1		ĺ	DELDYKENEEDEEMMERGEN A DISCONSIDER OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROP
DLVEKLVRLEFTGELNNTYIFYTSDNGYHTGQFSLPIDKRQTUL  EFPIKVPLLVRGGGIRNOTDFTLDTAGYDLKK TQMDGMSLLPILRGASNLTWRSDVLVEYGGGRNVTDPTCPSLS PGVSQCPPDCVCCDAYNNTYACVRTMSALWNLQVCEPDDQEVEV EVYNLTADPOITNIAKTIDPELLGKMYRIMMLQSCSGPTCRT PGVFDPGYRFDPRIMFSNRGSVTRRFSKHLL  ARGLLPPGLVPBEPFRTRRILLDFGTGGPFFALSRPLFSCVESGW AMBAMBPEFLYDLLOLPKCVEPPABEELSKGGKKKYLPPTSRRSD PKPEELQKPA,VIMBEVINATLLPEHIVVRSLEEMPHGGLILHKL FQRLAALKLBAEDIALTATSQKHKLTVVLRAVNRS\CSWRSGRP SGA/WESIPNKDLASTLHLLVALAKRFQPBLSLFHKLAPSKVNA VKEALVNFWORLDASTLHLLVAGLBEVGNLDTGPAGVILLLLIGQLEGFF LHIKEFYLFYNSPABMLHNTYLAELLJ IGRGPAGLFC/LALK/ TIVNKDAKSTLRVLYGLFCKHTQKAHRBTFHGAPN FVEGSMAPTDLFMECEBEELBGWGKRSVLYDDYDXT TTVSVSQDPSAPVPLAAHASVAGHLSTSTTVSSSGAONSDSTK KTLVTLIANNNAGNPLVQOGGOPLILTONPAGGLGTWYTQPVLR PVOVMQNANHVTSSPVASQPIFTTIGFFVRNVRPVONNAMNOVG IVLINVQOGGTVRFITLIVBAPGTGPVKPTVGVPQVFSQMTPVRPG STMPVVPTTNTFTTVIPATLITSSTVDGSGSQCYKSTPSTSTTP TATGPTSLGGLAVQSPGGSNGTTMPKLAPSFPSPAVSLASFYT TATGPTSLGGLAVQSPGGSNGTTMPKLAPSFPSPAVSLASFYT TATQPTSLGGLAVQSPGGSNGTTMPKLAPSFPSPAVSLASFYT TATGPTSLGGLAVQSPGSNGTTMPKLAPSFPSPAVSLASFYT TATGPTSLGGLAVQSPGSNGTTMPKLAPSFPSPAVSLASFYT GRGGKVAQLTNFFVAVSLAVLTBLLGGPCKVLLMULDDFYY GRDGGKVAQLTNFFVAVSLAVLTBLLGDPCKVLLMULDDFYY GRDGGKVAQLTNFFVAVSLSFRCHCTKRKNNIRFMMHKHHVE LDQOMGEVUGHTICQCHYRGPSTPFGLQCHLENWLSPYSSTYKC KICEMAFSSPLFFQHMKDTHKPGEMPYVCOVCQVRSSLYSSVD VHFRMHHEDTRHLLCPYCLKVRGNAFQOHAMHCKKNVYHT CNKCRVOPLFAKURIERLCPALLVRGNAFQOHAMHCKKNVYHT CNKCRVOPLFAKURIERLCHAULFTFRFKQLEGLKPGTKVTIRA SRGQPTTVPVSSNDTPPSALQEAPPLTSSNDPLPVFLIVFPVQRS SGCPTTVPVSSNDTPPSALQEAPPLTTHYCSCLGTYST CCSRAYANHMNNIVPRKSSKYLALFKNSVSGIKLACTSCTFVT SGGAMAKHLYFNFSHRSSSILFGTHWATHSKGGTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPAPBEBLLTPLAALPSPA STATPPPPTPTPHPDALAPPLATARVSAGATPAPBEBLLTPLAALPSPA STATPPPPTPTHPAGLALPATVSAGATPAREELLTPLAALPSPA STATPPPPTPTHPAGLALPATVSAGATPAREELLTPLAALPSPA STATPPPPTPTHPAGLALPATVSAGATPAREELLTPLAALPSPA STATPPPPTPTHPAGLALPATVKSAGATPAREELLTPLAALPSPA STATPPPPTPTHPAGLALPATVKSAGATPAREELLTPLAALPSPA STATPPPPTTHPAGLAGRACHTGREGOLDFWHDR NVKNMYPPPSFPTNKAATVKSAGATPAREELLTPLAALPSPA STATPPPTPTTHPAGLAGRACHTUREGULDFUNGDLDESPTVTG	1	j	ļ	WHENTHOUSENE FOR WEIGHT APPROPRIATE OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PRO
EFDIKYELLVRGFGIKPNOTSKMLVANIDLGPTILDIAGYDLMA TQMDGMSLLPILERGANNITYACVETMSALWALQYCEPDQUEVE PGW3QCPPDCVCEDAYNNTYACVETMSALWALQYCEPDQUEVEV EVXNLTADPDOITNIAKTIDPELLGKMYRRMMLQSCSGPTCRT PGVFDPGYRFDPRIMFSNRGSVETRERSKHLL  6132  96  1241  ARGLLPPGLVPEDPRTENILDFGIGGPFALSRPLFSCVESON AMEABMEPELIYDLLQLPKCVEPPAEELISKGGKKYLPPTSRKD PKFEELQKPA\VLMBWINTLLPEHIVVRSLEEDMFPGLILHHL FGRLAALKLEEBLEDIALTATSQLKHTVVLBAVRRS\CSMRSGRP SGA/WESIFNKDLLSTLHLLVALAKRFOFDLSLFTNVQWEVITI ESTKSGLKSEKLVEQLTEYSTDKDEPPROVPELFKLAPEKVNA VKKALVNFVNQKIDRIGLSVONDLDTGPAGDGILLLLIGQLEGFF LIHLKEFYLIPNSPABMLHNVTLALELL/IGRGPAQLBC/LALK/ TIVNKDAKSTLEVLVSGLFCKHOKAHRDRTHFAGAPN  7UMSDAMSTLEVLVSGLFCKHOKAHRDRTHFAGAPN FVGSMADTDLFMECEEELEPWQKISDVIEDSVVEDYNSVDKT TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAQNSDSTK KTLVTLIANNANAGNELVQGGGGLILTONDAPGLGTMVTQPVLR PVQVWONANHVYSSEVASQPIFITTGGFPVRNVRPVQNAMNQVG STMPVRPTTNTFTTVIPATLTIRSTVPQSGSQQTKSTPSTSTTP TATOPPSLGQLAVOSPGGSNQTTMFLAPSFFSPPAVSTASFVT VKRPGVTGENSNEVAKLVNTLNTIPBLGGSBGGTKCPRCNAQFRVTEAL GSQRTSGPESSMKVTSSIPVPDLQDGGRKICPRCNAQFRVTEAL GRHMCYCCPEMVYQKKKKSLDSEPSVPSAKRPSFSKTSTTP TATOPPSLGQLAVGYVGKKKSLDSEPSVPSAKRPSFSTKKTAL GSQRTSGPESSMKVTSSIPVPDLQDGGRKICPRCNAQFRVTEAL KRHMCYCCPEMVYQKKKKSLDSEPSVPSAKRPSPEKLTAPUNG GRDGGKVAQLITNFFVATSFFCHCTKRLKNNIRFMNHMKHHVE LDOOMGEVOGHTICQHCYRQFSTPFQLQCHLENVHSPTSTTKC KICKWAFESPLFLQHHKDTHKPGEMPYVQVCQVRSSLYSEVD VHFRNIHEDTHLLCPYCLKFKASLDSEPSVPSAKRPSFTKYTIRA SRGQFRTVPVSSNDTPPSALGENTTSMSDLEVFLVFPVQRS SRGQPRTVPVSSNDTPPSALGARATISSMSPLEVFLVFPVQRS SRGQPRTVPVSSNDTPPSALGARATISSMSPLEVFLVFPVGRS SRGQPRTVPVSSNDTPPSALGARATISSMSPLEVFLVFPVGRS SRGQPRTVPVSSNDTPPSALGARATISSMSPLEVFLVFPVGRS CCSRAYANHMINNIVPRKSPKYLAJFKNSVGIKLACTSCTFVT SVGDAMAKHLVFNRSHRSSSILPRGLTWTHRSQCTRRVPHD NVKMYPPPSFPTNKAATVKSAGATPAPBEELLTPLAPLPSPA STATPPPTPTPTPDALAPLALFRAFQCTROPHDE NVKMYMYPPSFPTNKAATVKSAGATPAPBEELLTPLAPLPSPA STATPPPTPTTPDALAPLALFRAFLYSHGENLADDDGGSSPVTOREOLF LASGGGGGGGWKEQLSVKKLVVLFALCCNTEQAAEHFRNPQ RRIRWLRRFQASGGGNLEGKYLSFEABEKLABWVLTGREGOLF VNEETLEGAATKKIGRSLEGGFKISTEMAVPTHLKHHLTPHARA VAHTLPRUVAENAGLFITOFVQRGIINQDLIPLSMTVAIDETSLFL				DIVERSIVE FEETER DIVERSI DE LE CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA
TQMDGMSLIPILIRGASNLTWRSDULVEYQGEGRNVTDPTCPSLS PGVSQCFPDCVCEDANNITACVRIMSALMILQYCEPDDQEVEV EVNNLTADPOGTNIAKTIDPELLGKMNYRLMMLQSCSGTCRT PGVFDPGYRFDPRIMFSNRGSVRTRRFSKHLL  ARGLLPPGLVPEDPRRTRRILLDFGTQGPFFALSRPLFSCVESGW AMBAMBPEFLYDLLQLPKGVEFPABEELSKGGKKKYLPPTSRKD PKFELQKRA,VIMBENNATLLBEHLVVRSLEEDMFDGLILHHL FQRLAALKLEAEDIALTATSQKHKLTVVLEAVWRS,CSMRSGRP SGA/WESIFNKDLLSTLHHLVALAKRFOPDLS.DFTNVQVEVTIT ESTKSGLKSEKLVEQLTEYSTDKDEPPROVPGELFKLAPPKKVAA VKRATVNFVNQKLDRLGISVQNLDTOPAGVILLLLIGQLEGFF LIHKKFYLIPPASPAMHINVTLALELL/IGRGPAQLPC/LALK/ TVNKDAKSTLRVLVGLFCKHTOKAHRDRTPHGAPN  6133  Z 4256 FVHGSMADTDLFMGEEELEPWGKISDVLEDSVVEDSVVEDYNSVDKT KTLVTLIANNNAGNFLVQGGGGPLLLTONBAPGLGTMVYOPVLR PVOVMONANHYTSSPVASOPLTTIGSFPVRNVRPVQNAMNQVC SYMPVRPTTNTFTTVIPAPGTQFVKPTVGVPVSGMTPVRPG STMPVRPTTNTFTTVIPAPLTITIGSFPVRNVRPVQNAMNQVC PVVGNONANHYTSSPVASOPLTTHGGSPGVRNVPVQNFSQMTPVRPG STMPVRPTTNTFTTVIPARLTITISTSVOGSQCTKSTFSTSTTF VKRGVTGENSNEVAKLVNTLNTTTPSLGGSGCDTKSTFSTSTTF VKRGVTGENSNEVAKLVNTLNTTTPSLGGSFGFVVTSAMFY VKRGVTGENSNEVAKLVNTLNTTTPSLGGSFGFVVTSAMFY VKRGVTGENSNEVAKLVNTLNTTTPSLGGSFGFVTVSAMF GGGRTGFESSKKVTSSIPVPGLDGGRKLCPCRNAQFRVTEAL GGGRTGGPESSKKVTSSIPVPGLDGGRKLCPCRNAQFRVTEAL GGGRKVAQLITNFFVATSTFCCTKTLKNINIFRMIMKHKHVE LDQOMGEVDGHTICQHCYRGFSTPFGLQCHLENVISPYRSTTKC KLCEMAFSSEPLIFLQCHMEDTHKFQLGSGLFKGFTKVTTRA VKHMIHEDTRHLLCPYCLKVFKNGNAFQQHTMRHIGKK\NYNH\ CNKCRVQFLFAKDRIBEKLQHHHTTFKKPGLGSGLKFGTKVTTRA SRGQPRTVPVSSNTTPSSALQEAPLTSSMDPLYPFLYPPVGR SRGQPRTVPVSSNTTPSSALQEAPLTSSMDPLYPFLYPFVGR SRGQPRTVPVSSNTTPSSALGEAPLTSSMDPLYPFLYPFVGR SRGQPRTVPVSSNTTPSSALGEAPLTSSMDPLYPFLYPFYGR SRGGRKVAQLITNIVPRKSKKYLALFKNSVGIKLACTSCTFVT CKRAVRKMSVMGROTCLECSFFI PDPPMHFPTYVHCSLCRYST CCSRAYAHMMINNIVPRKSKKYLALFKNSVGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWTHARRHOOTREDCHDE NVKNMYPPPSFPTNKAATVKSAGATPABPEELLTFLAPALPSFA LASGGGSGGGKKEQLSVKKLRVVLFALCCTTEQAAEHFRNPQ RRIERWLRRFQAALGEKSLEGKVLTGRECOLFF STATTPPPTTPHPGAALAPLALGCKTTEQAAEHFRNPQ RRIERWLRRFQAALGEKSLVKKLRVVLFALCCTTEQAAEHFRNPQ RRIERWLRRFQAALGEKSLVGGFKLSVEWAURFALLTTHLAPRAR VAHTLPKUVAENAGLFI LIDFVQRQIHNQDLILSMIVALDETSLFU				FEDIKUDI UBCDCIK DNOTCKWI WINGER TO THE TRANSPORT OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPE
PGYSQCFDCVCEDAYNNTYACVRTMSALWNLQYCEPDQDEVEY EVYNLTADPOLTINIAKT IDELLIGKMYNYHAMLQSCSGPTCRT PGYFDGYRPDPRIMFSNRGSVETRRSKHLL  AAGLLPPGLVPEDPRTRNLLPFGIQGPFFALSELSRGGKKKLYPTSRKD PKFEELQKPA\VLMEWINATLIPEHIVVRSLEEDMFDGLILHHL FQRIAALKLEAEDIALTATRULYSHELDWRSACSWRSGKP SGA/WESIPNKDLLSTHHLUVALAKRPOPDLSLPTNVQVEVITI ESTKSGLKSEKLVEQUTEYSTDKDEPPKNVFDEFIKLAPEKNNA VKEAIVNFVNQKLDRIGISVQNLDTGFADGVILLLLIGGLGFF LHIKEFYLYPNSPAEMHNVTLALELL/IGRGPAQLPC/LALK/ TIVNKDAKSTRUVLYGLFGYTKOKARDRIPHGADPN  6133  2 4256 FVIGSWADTDLFWECEEELEPPQKISDVEDSVYEDYNSVDKT TIVNSOAQPYSAPVPLAHASVAGHLSTSTTVSSGAQNSDSTK KFLVTLIANNNAGNPLVQGGGPLILTOMPAGGLGTWYOPVLR PVOVMONAHVTSSPVASQPIFITTGFFVRNVRPVQNNAMNQVG STMPVRPTINTFTTVIPATLTRSTTVOSQSQOTKSTPSTSTTP TATOPTSLGGLAVQSFGGONQTTNPKLAPSFPSPPAVSIASFVT VKRPGVTGENSNEVAKLUNTLNTIPSLGQSPGPVVVSNNSSAH\ GSQRTSGPESSMKVTSSIPVFDLQDGGRICPCRAQFFKYTFAL RGHMCYCCPEMVEYCKKGKSLDSEPSVPSAARPPSPEKTAPVAS /HPSSTPIPALSPPY/TKVPPPNENVGDAVQTKLIMLUDDFYY GRDGGKVAQLITHFPKVATSFCHCHTKKLKNIRTRMIMKHYE LDQONGSVDGHTICQHCYRGFSTPPOLQCHLENVHSPYESTTKC KICEWAFESEPLFLQHMKDTRKPKQDLEGKLYGFKVTIRA SRGQPKTVPVSSNDTPFSALGPALTSKNNIRTRMIMKHYE LDQONGSVDGHTICQHCYRGFSTPPOLQCHLENVHSPYESTTKC KICEWAFESEPLFLQHKKTRKPKQLEGLKPGTKVTIRA SRGQPKTVPVSSNDTPFSALGAPALTSKRNDLPPFLYPVQSV VHFRNIHEDTRHLLCYPCLKVFKNNNAFQQHYMHQKK NVYH\ CNKCRVQFLFAKDKLEHKLQHHKKTRKPKQLEGLKPGTKVTIRA SRGGPKTVPVSSNDTPFSALGAPALTSKNDPLPPFLYPVQSV SVGDAMAKHLVFNBSHRSSS LPRGLTHIARSKGQTRRVHDR NVKMYPPPSFTTKAATVKSAGATPRSPEELLTPLAPALSPSP ATATPPPTTHQALALPPHQALALPHOQDEGSPVTOPPE LASGGGGGGGGVGKKBQLSVKKLRVVLFALCCNTEQAAEHFNNPQ RRIRRWLRRFQASQGSNLEKKLRVVLFALCCNTEQAAEHFNNPQ RRIRRWLRRFQASQGSNLEKKLRVVLFALCCNTEQAAEHFNNPQ RRIRRWLRRFQASQGSNLEKKLRVVLFALCCNTEQAAEHFNNPQ RRIRRWLRRFQASQGSNLEKKLRVVLFALCCNTEQAAEHFNNPQ RRIRRWLRRFQASQGSNLEKKLRVVLFALCCNTEQAAEHFNNPQ RRIRRWLRRFQASQGSNLEKKLLRVVLFALCCNTEQAAEHFNNPQ RRIRRWLRRFQATEGEGRENLEGKYLTHARARH VAHTLPKOVABNAGLFIDFVGQCVLHALARDCTULPTLAPEV	1			TOMDEMSTIPLINGS SNITTH PROPERTY AND AND AND AND AND AND AND AND AND AND
6132 96 1241 AGGLPPGLYPDFRIMFSNRGSVRTRPSKILL  AGGLPPGLVPEDFRTPRILLPFGIQGPFFALSRPLFSCVESGM AWEAMEPEFLYDLLQPKGVEPPAEEGLSRGGKKKYLPPTSRRD PKPEELQKPA\VLMEWINATLLPEHLVVRSLEEDMFPGILLHRL FQRLAALKLEAEDIALTATSQKKKLTVULEAVARS\CSMRSGEP SGA\WESIFNKDLLSTHALVALAKROPDLSLPTNVQVEVITI ESTKSGLKSEKLVEQLTEYSTDKDEPPKNVFDELFFLAPEKNVA VKEALVNFVNQKLDRIGISVQNLDTOFADCVILLLIGQLEGFP LHIKEFYLITPNSPAEMHNVTLALELL/IGRGPAQLPC/LALK/ TIVNKDAKSTLRVLYGLFCKHTOKARRDRTPHGAPN  4256 FVHGSMADTDLFMECEEFELEPWGKISDVIEDSVVEDYNSVDKT TTVSVSQQPVSAPVPIAHASVAGHLSTSTTVSSSGAQNSDSTK KTLVTLIANNNAGNELVQQGGQPLITONPAPGLGTMVTQPVLR FVQVMONANHVTSSPVASQPIFTTIGFFFVNRVPVONAMNQVG FVLVMONANHVTSSPVASQPIFTTIGFFFVNRVPVONAMNQVG SIMPVRPTNTFTTVIPTATISTVPQSQCQTKSTPSTSTTT TATQPTSLGQLAVQSPGQSNQTTNFKLAFSFFSPPAVSTASFYT VKRFGVTGENSNEVAKIAVNTLNTIPSLGGSPGPVVVSNNSSAH\ GSQRTSGPESSKKYTSSIPVPDLQDGGRICPRCNAQFRVTFAL RCHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS /HPSSTPIPALSPPY/TKVPEPDNENVGDAVQTKLIMLVDDFYY GRDGSKVAQLITNFPKVATSFRCPHCTKLKNNIRFMNIMKHHVE LDQONGEVDGHTICQHCXRGFSTPFQLQCHLENVHSPYESTTKC KICCEMAFSESPIFLOHMSTHERGEMPYVCOVQYNSSLYSEVD VHFRMHEDTRILLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQFLFAKUKIHNNHYPRESPELDFLOHMSTREVSTYSC CCSRAYANHMINNHYPRESPELDFLOHMSTREVSGKIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRRGQTRGDRVHDR NVKMYYPPSFPTTMAATVKSGGATPBEPELLITPLAPALDSPPA STATPPPTTPTHQALALPPLATEGRECINVDQDOGGSTVTORP STATPPPTTPTHQALALPPLATEGRECINVDQDOGGSTVTORP LASGGGGSGGVKKEOLSVKKLRVULFALCCNTEQAAEHFRNPQ RRIKRWLRFDASQGGENLEGKYLSFEABEKLAEWVLTQREQOLF VNEETLPQKATKIGRSEEGGFKISTEMAVRHHHTHHARA VAHTLPROVANNACHFILDFVGORDVOLDLESMIVATDETSLIPL	1	į		PGVSOCEPDCVCEDAVBUTVACUDDWCALLOW
6132 96 1241 AAGILPPSCIVEDEPRETNLFFGTGGPFFALSRPLFSCVESGW AWEAMEPEFLYDLLQLPKGVEPPAEELSKGKKKKYLPFTSRKD PKFELQKPA\VIMEWINATLLPEHIVVESLEEDMEDGIJHHL FQRLAALKLEAEDIALTATSQKHKLITVULEAVIRS.CSWRSGRP SGA\WESIFNKDLISTHHLUALAARFOPDLSLPTNVQVEVITI ESTKSGLKSEKLVEOLTEYSTDKDEPPKDVEDEPKLAPEKVNA VKEAIVNFVNQKLDRLGLSVQNLDTOFADGVILLLIGQLEGFF LHIKEFYLTPINSPAEMHINVTILAELL\IGRGPAQLPC/LALK\ TIVNKDAKSTRVLVSGLFCKHTOKAHRDRTPHGAPN 1 TVUSVSQEVJSASVPIAAHSVAGAHLSTSTTYSSSGAONSDSTK KTLVTLIANNNAGNPLVQGGQPFLILTONPAPGLGTMVTOPVLR PVQVMONANNIVTSSPVASQPITITOGFPVRNVRPVQNAMNQVG IVLNVQOGQTVRPITLVPAPGTQFVKPTVVPQVFSQNTPVRPG STMPVRPTTNFFTVIPATLTIRSTVPQSGSQOTKSTSTSTSTT TATQPTSLGGLAVQSPGQSNGTTINFKLAPSFPSPPAVSIASFVT VKRRGVTGERSNEVAKLNTINTTPSLGGSPGVVVSNNSSAH\ GSQRTSGPESSMEVTSSIPVFDLQDGGRKICPRCNAGFRVTFAAL RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS /THPSSTPIPALSPPY/TKVPENENVGDAYOTKLIMLJUDDFYY GRDGGKVAQLTNFPKVATSFRCHCTKRLKNNIRFMNHMKHIVE LDQONSEVJOGHTICQHCYRGFSTPFQLQCHLENVHSPYESTTKC KICEWAFESEPLFLOHMKDTHKPGLEBIKPGKVTIRA SRGQPRTVPVSSNDTPFSALQEAAPLTSSMDPLPVFLYPPVQRS SRGQPRTVPVSSNDTPFSALQEAAPLTSSMDPLPVFLYPPVQRS GRGGRTVPVSSNDTPFSALQEAAPLTSSMDPLPVFLYPPVQRS SRGQPRTVPVSSNDTPFSALQEAAPLTSSMDPLPVFLYPPVQRS SRGQPRTVPVSSNDTPFSALQEAAPLTSSMDPLPVFLYPPVQRS SRGQPRTVPVSSNDTPFSALQEAAPLTSSMDPLPVFLYPPVQRS SRGQPRTVPVSSNDTPFSALQEAAPLTSSMDPLPVFLYPPVQRS SRGQPRTVPVSSNDTPFSALQEAAPLTSSMDPLPVFLYPPVQRS SRGQPRTVPVSSNDTPFSALQEAAPLTSSMDPLPVFLYPPVQRS SRGQPRTVPVSSNDTPFSALQEAAPLTSSMDPLPVFLYPPVQRS SRGQPRTVPVSSNDTPFSALQEAAPLTSSMDPLPVFLYPPVQRS STATPPPTPTHPQALALPPLATEGBECLNVDDQDEGSPVTCEPE LASGGGGGGGVKKRVSVRGROTCLECSFIPPPNHFPTVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKRNSVGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNYPPPSFPTNKAATVKSAGATPABPEELLTPLAPALESPA STATPPPTPTHPQALALPPLATEGBECLNVDDQDEGSPVTCEPE LASGGGGGGGVKKRQLSVKKRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASGGENGKVLSVLSFLAEMVLTCREQOAEHFRNPQ VNESTLFQAATKIGRSLEGGFKISTEMAVFFMLRHHLITPHARRA VAHTLJFKDVARENAGIF IDFVQRQIHNQDLPLSNIVAIDEISLFL DTEVLSSDDRINADLYTGTBE WCDVVLAILADGTVLUPTLUEV	1	}	}	EVYNLTADPDOITMIAKTIDDELLOWNING COCCORD
AGGLIPPGLVPEDPRRTRILLPFG GGPPFALSRPLFSCVESGM AWEAMEPEF LVDLLQ LVGVEPPAEEELSKGGKKKYLPFSKOD PKFEELQKPA\VLMEWINATLLPEHIVVRSLEEDMPDGLILHLI FQRLAALKLEAED LALTATSQKHKLTVVLEAVNRS\CSWRSGRP SGG/WESIFNKDLISTILUVALAKRFOPDLSLPTNVQVEVTIT ESTKSGLKSKLLVSQLTEYSTDKDEPPKDVFDELFKLAPEKVNA VKRAIVMPVNQKLDRLGLSVQNLDTQFADGVILLLLIGGLEGFF LHLKEFYLTPNSPAEMHHNVTLALELL/IGRGPAQLPC/LALK/ TIVNKDAKSTLRVLYGLFCKHITOKAHRDRTPHGAPN  6133  2 4256 FVMGSMADTDLFMECEELEPWQKISDVIEDSVVEDYNSVDKT TVSVSQQPVSAPVPIAHASVAGHLSTSTTVSSSGAONSDSTK KTLVTLIANNNAGNPLVQGGGQPLILTONPAPGLGTMVTQPVLR PVQVMONANNVTSSPVASQPLITTONPAPGLGTMVTQPVLR PVQVMONANNVTSSPVASQPLITTONPAPGLGTMVTQPVLR GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPKCNAQFRVTFAL GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPKCNAQFRVTFAL GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPKCNAQFRVTFAL GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPKCNAQFRVTFAL RGHMCYCCPEMVSYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS /THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMHMKHHVE LDQONGEVDGHTICQHCYRGFSTPFOLQCHLENVHSPYESTTKC KICEWAFESEPJFLQHMKDTHKPGEMPFYVCQVCQYRSSLYSEVJ VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVOFLFAKDKIEHKLQHKKTFRKPRQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTFPSALQEAAPLTSSMPDLVETLYPPVQRS IQKRAVRKMSVMGRQTCLECSFFIPPPNMFFTVVHCSLCRYST CCSRAYANHMINNHVPRSKYLALEKRNSVGGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGGTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA STATFPPTPTHQALALPLAATUKSAGATPAEPEELLTPLAPALPSPA STATFPPTPTHQALALPLAATUKSAGATPAEPEELLTPLAPALPSPA STATFPPTPTHQALALPLAATUKSAGATPAEPEELLTPLAPALPSPA STATFPPTPTHQALALPLAATUKSAGATPAEPEELLTPLAPALPSPA STATFPPTPTHQALALPLAATUKSAGATPAEPEELLTPLAPALPSPA STATFPPTPTHQALALPLAATUKSAGATPAEPEELLTPLAPALPSPA STATFPPTPTHQALALPLAATUKSAGATPAEPEELLTPLAPALPSPA STATFPPTPTHQALALPLATGRAECHNDDQDGESPVTCEPE LASGGGGGGGVKKKEQLSVKKRVUFFACHTHILTPHARRA VAHTLJKKOVAENAGLFIDFOVQGIHNQDLPLSNIVATDEISLFL VNEETLFQAKATKIGRSLEGGFKISTEAWAFFMRHHILTPHARRA VAHTLJKKOVAENAGLFIDFOVQGTHNQDLPLSNIVATDEISLFL DTEVLSSDDRINGATGTGTBWCDTGRAEHFNPQ		<b>]</b>		PGVFDPGVPFDPDI.MFGNPGCVDFDPGOVFF
AWEAMEPEFTYDLLQLPKGVEPPAEELSKGGKKKXLPPTSRKD PKFEELQKFA\VLMEWINATLLPEHITVRSLEEDMFDGLILHIL FQRLAALKLEAEDIALTATSQKHKLTVVIEAVNRS\CSWRSGRP SGA\WESIFNKDLLSTHHLLVALAKRFOPDLSLPTNVQVEVTIT ESTKSGLKSKELVSOLTSTDHDEPPKDVPDELFKLAPEKVNA VKBAIVMFVNQKLDRLGLSVQNLDTOFADGVILLLLIGQLEGFP LHHKEFYLTPNSPAEMLHNVTLALELL/IGRPAQLPC/LALK/ TIVNKDAKSTLRVLYGLFCKHTQKAHRORTHGAPN  6133  2 4256 FVHGSMADTDLFMECEEELEPWQKISDVIEDSVVEDYNSVDKT TVVSVSQQVSAPVPLAHASVAGHLSTSTTVSSSGAONSDSTK KTLVTLIANNNAGNPLVQQGQQPLILTONPAPGLGTMVTQPVLR PVQVMONANNVTSSPVASQPIFITTQGFPVRNVRPVQNAMNOVG IVLNVQOGQTVRPITLVPAPGTQPVKPTVGVQPVPSQMTPVRPG STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTPSTSTTTP TATQPTSLGQLAVQSPGQSNQTTMFKLAPSFPSPAVSIASFVT VKRFGVTGENSNEVAKLVNTLNTIPSLGGSFGVVVSNNSSAH, GSQRTSGPESSMXVTSSIPVPDLQDGGRKICPRCNAQFRVTEAL RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTARDVAS /THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFFYY GRDGGKVAQLTNFPKVATSFRCHCTKRLKNNIRFMMHMKHNZ LDQONSEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYZESTKC KICEWAFESEPLFLQHMKDTHKPGLEGLKPGKVYITA GNCRVQFLFFANDKIEHKLQHHKTFRKPKQLGGLKPGTKVTIRA SRQOPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYFPVQRS SRGOPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYFPVQRS SRGOPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYFPVQRS SRGOPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYFPVQRS SRGOPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYFPVQRS SRGOPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYFPVQRS SCCSRAYAHMINNHVPRKSPKYLALFKRSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHQQTRDRVHDR NVKMYPPPSPFPTNKAATVKSAGATPBEPEELLTPLAPALESPA STATPPPTPTHPQALALPPLATEGABCLNVDDQDEGSPVTCEPE LASGGGGGGVCKKEQLSVKKRVVLFALCCNTEQAAEHFRNDPQ BRIRWLRRFQAQSGGENLSKVLSFVLJFALCCNTEQAAEHFRNDPQ RRIRWLRRFQAQSGGENLSKVLSFVLJFALCCNTEQAAEHFRNDPQ RRIRRWLRRFQAQSGGENLSKVLSFVLJFALCCNTEQAAEHFRNDPQ RRIRRWLRRFQAQSGGENLSKVLSFVLJFALCCNTEQAAEHFRNDPQ VNESTLFQAATKIGRSLEGGFKISYEWAVFFMLRHHILTPHARRA VAHTLJPKDVAENAGLFIDFDVQGTINQDLPLSSIVAIDEISLFL DTEVLSSDDRAKHALUVTGTGBPWCDVVLAALLADGTULPTLUEV	6132	96	1241	AAGIL PPGIVPEDEPETENTI DEGLOCEPENI CONTRACTOR
PRYEELOKPA/VIMEWINATLEBHIVORSLEEDMFDGLILHHL FORLAALKLEABDIALTATSOKHKLTVVLEAVNRS\CSWRSGRP SGA/WESIFNKDLLSTLHLLVALAKROPDLSLPYNVOVEVITI ESTKSGLKSEKLVEQLTEYSTDKDEPPKDVPDELFKLAPEKVNA VKRAIVMFVNKKLDRIGLSVONLDTOPADGVILLLIGQLEGFP LHLKEFYLTPNSPAEMLHNVTLALELL/IGRGPAQLPC/LALK/ TIVNKDAKSTLRVLYGLFCKHTYKAHRDRTPHGAPN 6133 2 4256 FVHGSMADTDLFMECEEELEPPKKISDVIEDSVVEDXNSVDKT TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAQNSDSTK KTLVTLIANNNAGNPLVQQGGOPLLITQNPAPGLGTMVTQPVLR PVQVMQNANNVTSSPVASQPIFITTGGFPVNNVPLYDNAMNQVG IVLNVQQGQTVRPITLVPAPGTQFVKRPVSQNGTMSPVSTSTTTP TATQPTSLGQLAVQSPGGSNQTTNFKLAPSFPSPPAVSIASFVT VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\ GSQTTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS /THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY GRDGKVAQDLTNFPKVATSFRCPHCTKRLKNNIRFMHMKHHVE LDQQNGEVDGHTICQHCYRGPSTFPQLQCHLENVHSPYESTTKC KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD VHFRMIHEDTRHLLCPVCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQFLFAKDKIEHKLQHHKTFRKFRQLEGLKFGTKVTIRA SRGQPRTVEVSSNDTPPSALQEAPLITSSMDPLPVFLYFPVGRS IQKRAVRKMSVMGRGTLECSFFEIPPDHFFTYVHCSLCRYST SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGGTRDRVHDR VKNMYPPPSFPTNKAATVKSAGATPPABPEBELLTPLAPALPSPA STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTCEPF LASGGGGGGGVKKEQLSVKKLTVLFALCCNTEQAABHFRNPQ RRIRRWLRRFQASGGENLECKYLSFEABEKLLAEWULTOREQOLD VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHITPHARRA VAHTLPKOVAERNGLTIDFVQRQTHNODLPLSMIVAIDEISLFIL DTEVLSSDDRKENALQTVGTGEPWCDVJALLAGGTVJATJUFF				AWEAMEPEEL VOLLOLD KOVERD A REEL ONGOWER TO THE
FQRLAALKLEADIALTATSQKKKLTVULEAVNRS\CSWRSGRP SGA/WESTPKKDLLSTHILLVALAKRFOPDLSLPTNVQVEVITI ESTKSGLKSEKLVEQLTEYSTDKDEPPKDVPDELFKLAPEKVNA VKEAIVMFVNGKLDRLGISVORIDTOPADGVILLLIGGLEGFF LIHLKEFTYLTPNSPABMLHNVILALELL/IGGRAQLPC/LALK/ TIVNKDAKSTLRVLYGLFCKHTOKAHRDRTPHGAPN  6133  2 4256 FVHGSMADTDLFMECEEELEPWQKISDVILDSVVEDDVNSVDKT TVVSVSQQPVSAPVPIAHASVAGHLSTSTVSSSGAONSDSTK KTLVTLIANNNAGNFLVQQGGQFLILTONPAPGLGTMVTQPVLR PVQVMQNANHVTSSPVASQPIFITTGFFVRNVRPVQNAMMQVG IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVYSQMTPVRPG STMPVRPTTNTFTTVIPATLTITSTTVPQSGQGVKSTPSTSTTP TATOPTSLGGLAVQSGOQTXTNTPSLASFVT VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGFVVVSNNSSAH\ GSQRTSGPESSMKVTSSIPVFPLQDGGRKLCPRCNAGFRVTEAL RCHMCYCCPEMVEVGKKSLDSEPSVFSAKKPSPEKTAPVAS /THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY GRDGKVAQLTNFPKVATSFRCHCTKRLKNNIRFMHMKHHVE LDQQNGEVDGHTICQHCKPGFSTPFQLQCHLENVLSPYESTTKC KICEMAFESSPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNONAFQQHVMRHQKR\NVYH\ CNKCRVQFLFFAKDKIEHKLQHKKTFRKPKQLEGLKPGTKVYIRA SRGQPRTVPVSSNDTPPSALQGAAPLTSSMDPLPVFLYPPVQRS IQKRAVRMSVMGROTCLECSFEIPDFPNHFPTYVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKKLVFNFSHRSSSILPRGLTWIAHSRHGGTRDRVHDR NVKNMYPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA STATPPPTPTPPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASGGENLEGKYLSFEABEKLAEWVLTOREQOLD VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHITPHARRA VAHTLPKOVAENGLET IDFVQRQTHNODLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGFGEPWCDVVLAILAGGFUVLDFLUGFV		l i		PKFEELOKPA\VIMEWINATI.I.DEHTIMDGI BEDWEDGI TI
SGA/WESTPKKDLISTHLLUALARREGOPLSLEPTNVQVEVITI ESTKSELKSEKLYEQLTEYSTDKDEPPKDVFDELFKLAPEKVNA VKEAIVNFVNQKLDRLGLSUQNLDTQFADGVILLLLIGQLEGFF LHIKEFYLTPNSPAEMIHNVTLALELL/TGRGPAQLPC/LALK/ TIVNKDAKSTLEVLYGLFCKHTQKAHRDRTPHGAPN  6133 2 4256 FVHGSMADTDLFMECEEEELEPWQKISDVIEDSVVEDYNSVDKT TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAQNSDSTK KTLVTLIANNNAGDLVQGGGOPLILTQNPAPGLGTMVTQPVLR PVQVMQNANHVTSSPVASQPIFITTQGFFVRNVRPVQNAMMQVG IVLNVQQGQTVRPITLVPATLTIRSTVPQSQGQCYSTPSTSTTP TATQPTSLGQLAVQSPQSNQTTNPKLAPSFPSPPAVSIASFVT VKRPGVTGEMSNEVAKLVNTLNTIPSLGQSPGFVVVSNNSSAH/ GSQRTSGPESSMKVTSSIPVPDLQDGGRKICPRCNAQFRVTEAL RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSFEKTAPVAS /THPSSTPIPALSPPY/TKVPENNENVUDAVQTKLIMLVDDFYY GRDGGKVAQLTNFPANTSFRCPHCTKRLKNIRFMNHMKHIVE LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC KICEWAFESEPLFLQHMKDTHKPGEMPYVCOVCQVRSSLYSEVD VHFRMHEDTRHLLCPYCLKVFKRGNAFQQHWRHQKG,NVYH/ CNKCRVQFLFAKDKIEHKLQHYKTFRKPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPPSALQEAPLTSSMPPLPVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIDPPNHFTYVHCSLCRYST CCSRAVANHMINNIPYPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNNYPPPSFFTNKAATVKSAGATPAEPEELLTPLAPALPSPA STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEFE LASGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASGGENLEGKYLSFEBEEKLÆEWULTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHLITPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLBLSMIVAIDEISLFIL DTEVLSSDDRKENALQTYGTGEPWCDVVLAILADGTVLETULPV		<u> </u>		FORLAALKLEAEDIALTATSOKUKI TAULEALAKSO COMPAGNI
ESTKSGLKSEKLVEOLTEYSTOKDEPPKDVFDELFKLAPEKNAA VKEAI VNEVANKURGLSVONLDTOFADGVILLLLIGGLEGFF LHLKEFYLTPNSPAEMLHNVTLALELL/IGRGPAQLPC/LALK/ TIVNKDAKSTLRVLYGLFCKHTOKAHRDRTPHGAPN  6133  2  4256  FVIGSMADTDLFMECEEELEPWQKISDVIEDSVVEDYNSVDKT TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAQNSDSTK KTLVTLIANNNAGNPLVQQGGQPLILTQNPAPGLGTMVTQPVLR PVQVMQNANHVTSSPVASQPIFITTQGFFVRNVPPVQNAMMQVG IVLINVQGQGTVRPITLVPAPGTGFVRNVPPVQNAMMQVG SYMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTPSTSTTP TATQPTSLGQLAVQSQSTTMFKLAPSFPSPPAVSIASFVT VKRPGVTGENSNEVAKLVNTLINTIPSLGSPGFVVVSNNSSAH\ GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS /THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE LDQQNGEVDGHTICQHCYKGFSTPFQLQCHLENVHSPYESTTKC KICEWAFESSPLFLQHMKDTHKPGEMPYVCQVQYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQFLFAKDKIEHKLQHKTFRRFKQLEGLKFGTKVTIRA SRGQPRTVPVSSNDTPPSALQEAPLTSSMDPLPVFLYPPVQRS IQKRAVRKMSVMGROTCLECSFEIPDPPNHPPTYVHCSLCRYST CCSRAYANHMINNIVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRGQTRDRVHOB NVKNMYPPPSFFTNKAATVKSAGATPAEPEELLTPLAPALPSPA STATPPPTPTHPQALALPPLATGGAECLNVDDQDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASGGENLEGKYLSFEABEKLAEWULTQREQOLD WNEETLFQKKTKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQQCIHDDLISMTVAIDEISLFIL DTEVLSSDDRKENAQCTVGTGEPWCDVLAILADGTVLATDEISLFIL				SGA/WESIFNKDLISTIHILIVATAK PRODDI CI DENVIOUS
VKRATVNFVNQKLDRLGISVQNIDTGFADGVILLLLIGQLEGFF LHIKEFYLTPNPAEMLHNVTLALELL/IGRGPAQLPC/LALK/ TIVNKDAKSTLRVLYGLFCKHTQKAHDRTPHGAPN  6133  2 4256  FVIGSMADTDLFMECEEEELPPVQKISDVIEDSVEDYNSVDKT TTVSVSQQPVSAPVIAAHASVAGHLSTSTTVSSSGAQNSDSTK KTLVTLIANNNAGNPLVQGGGPLILTQNPAPGLGFTWVTQPVLR PVQVMQNANHVTSSPVASQPIFITTQGFPVRNVRPVQNAMNQVG IVLNVQQGGTVPITLVPAPGTQFVKPTVGVPQVFSQMTPVRPG STMPVRPTTNTFTTVIFATLTIRSTVPQSQSQQTKSTPSTSTTP TATQPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSIASFVT VRRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\ GSQRTSGPESSMKVTSSIPVPDLQDGGRKICPRCNAQFRVTEAL RGHMCYCCPEMVEYQKGKSLDSEPSVPSAAKPPSFEKTAPVAS /THPSSTPIPPALSPY/TKVPPEPNENVGDAVQTKLIMLUDDFYY GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE LDQQNGEVGHTICQHCYRGFSTPFGLQCHLENVHSPYESTTKC KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQFLFAKDKIEHKLQHKKTFRKPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLEVFLYPFVQRS SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLEVFLYPFVQRS SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLEVFLYPFVQRS CCSRAVANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLITWIAHSRHGQTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPBAEPELLTPLLAPALPSPA STATPPPTPTPHQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGSGVGKKEQLSVKKLRVULFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQCENLEGKYLSFFALEEKLAEVALTOREQOLP VNEETLFQKATKLIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDPVQRQTHNODLPLSSNIVAIDEISLFL	[	í i		ESTKSGLKSEKLVEOLTEYSTOKDEPDKDVEDELEVT ADEKDA
LHIKEFYTPNSPAEMHNVTLALELL/IGRGPAQLPC/LALK/ TIUNKDAKSTLRULYGLFCKHTQKAHRDRTPHGAPN  FVHGSMADTDLFMECEEELEEPWQKISDVIEDSVVEDYNSVDKT TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAQNSDSTK KTLVTLIANNNAGNPLVQGGQFLILTQNPAPGLGTMVTQPVLR PVOVMQNANHVTSSPVASQPIFITTQGFPVRNVPPVQNAMNOVG IVLNVQQGGTVRPITLVPAPGTQFVKPTVGVPQVFSQMTPVRPG STMPVRPTTNTFTTVIFATLITRSTVPQSQSQQTKSTPSTTSTTP TATQPTSLGQLAVQSPGQSNQTTYPKLLAPSFPSPPAVSIASFVT VKRPGVTGENSNEVAKLVNTLNTIPSLGGSPGPVVVSNNSSAH\ GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL RCHMCYCCPEMWZQKKGKSLDSEPSVPSAAKPPSSPEKTAPVAS /THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHVE LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQVRSSLYSEVD VHFRMHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQFLFAKDKIEHKLQHKKTFKKPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPFSALQEAPLTSSNDPLPVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDPPNHFPTVHCSLCRYST CCSRAYANHMINNHYPKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKLLVFNPSHRSSSILPRGLTWIARSHGQTRQRVHDR NVKNMYPPPSFPTNKAATVKSAGATPABEPELLTPLAPALPSPA STATPPPTPTPHQALALPPLATEGABCLNVDQDDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRPQASQGENLEGKYLSFEAEEKLAEWULTQREQOLP VNEETLFQKATKLGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLJTVGTGEPWCDVULALLADGTUL JETLUEV DTEVLSSDDRKENALQTVGTGEPWCDVULALLADGTUL JETLUEV				VKEAIVNFVNQKLDRLGLSVONLDTOFADGVILLLITGOL FORB
6133 2 4256 FVHGSMADTDLFMECEEEEEPWQKISDVIEDSVVEDYNSVDKT TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSGAQNSDSTK KTLVTLIANNNAGNPLVQQGGQPLILTQNPAPGLGTMVTQPVLR PVQVMQNANHVTSSPVASQPIFITTQGFPVRNVRPVQNAMMQVG IVLNVQQGQTVRFTTLVPAPGTQFVKPTVGVPQVFSQMTPVRPG STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTPSTSTTP TATQPTSLGQLAVQSPGQSNQTTMPKLAPSFPSPPAVSIASFVT VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\ GSQRTSGPESSMKVTSSIPVFDLQDGGRRICPRCNAQFRVTEAL RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS /THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNGNAFQHYMRHQKR\NVYH\ CNKCRVQFLFANDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYFPVQRS IQKRAVRKMSVWGRQTCLECSFEIPDFPNHFPTVVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA STATPPPTTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGSGGVKKEQUSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHILTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVATUREV				LHLKEFYLTPNSPAEMLHNVTLALELL/IGRGPAOLDC/LALK/
FVIGGMADTDLFMECEEEEEFFQKISDTIEDSVVEDYNSVDKT TTVSVSQQPVSAPVPIAAHASVAGHLSTSTVSSSGANGDSTK KTLVTLIANNAGNEIVQQGGQELILTONPAPGLGTMVTQPVLR PVQWQNANHVTSSPVASQPIFITTQGFPVRNVRPVQNANNQVG IVLNVQQGTVRPITLVPAPGTQFVKPTVGVPQVFSQMTPVRPG STMPVRPTTTFTTTTPATLTIRSTVPQSQSQQTKSTPSTSTTP TATQPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSLASFVT VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\ GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS /THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY GRDGGKVAQLTNFPKVATSFPCDLCCHLENVHSPYESTTKC KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVOFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFPTYVHCSLCRYST CCSRAYANHMINNIVPRKSPKYLALFKNSVGIKLACTSCTFVT SVGDAMAKHVFFPSHRSSSILPFGLTWIAISFRGQTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA STATPPPTPTPHCQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPG RRIRWLRRFQASGGENLEGKYLSFEAEEKLAEWULTQREQOLP VNEETLFQKATKIGRSLEGGFKISFEAEEKLAEWULTQREQOLP VNEETLFQKATKIGRSLEGGFKISFEAEEKLAEWULTQREQOLP VNEETLFQKATKIGRSLEGGFKISFEAEEKLAEWULTQREQOLP DTEVLSSDDRKENALQTUGTGGEPWCDVVLAILADGTULDTILBEY				TIVNKDAKSTLRVLYGLFCKHTOKAHRDRTPHGAPN
KTLVTLIANNNAGNPIVQQGQPLILTQNPAPGLGTMVTQPVLR KTLVTLIANNNAGNPIVQQGQPLILTQNPAPGLGTMVTQPVLR PVQVMQNANHVTSSPVASQPIFITTQGFPVRNVRPVQNANMQVG IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSQMTPVRPG STMPVRPTTNTFITTVIPATLTIRSTVPQSQSQQTKSTPSTSTTP TATQPTSLGQLAVQSPGQSNQTTMPKLAPSFPSPPAVSIASFVT VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\ GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS /THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC KICEWAFESEPLFLQHMKDTHKPGEMPYVCOVCQYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQFLFAKDKIEHKLQHKKTFRKPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFPTYVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA STATPPPTTHPQALALPPLATEGAECLNVDDQDEGSPVTQEFE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWULTQREQQLP VNEETLFQKATKIGRSLESGFKISYEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQVTGTGEPWCDVVLAILADGTUJETJURFY	6133	2	4256	FVHGSMADTDLFMECEEEELEPWOKISDVIEDSVVEDYNSVDKT
RTTVTLIANNNAGNPLVQQGGQPLILTQNPAPGLGTMVTQPVLR PVQVMQNANHVTSSPVASQPIFITTQGFVRNVRPVQNMMQVG IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSQMTPVRPG STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTBSTSTTP TATQPTSLGQLAVQSPGQSNQTTMPKLAPSFPSPPAVSIASFVT VKRPGVTGENSNEVAKLVNTLNTTPSLGQSPGPVVVSNNSSAH\ GSQRTSGBPESMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS /THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMHMKHHVE LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFPTYVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPPPPSFPTNKAATVKSAGATPARPEELLTPLAPALPSPA STATPPPTPTPPPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP VNEETLFQKATKLIGKSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPKUVAENAGLFIDFVQRQIHNQDLPLSMIVATDEISLFL DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADCTVLPTLARR	1			TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAONSDSTK
POOVMQNAMHVTSSPVASQPIFITTQGFFVRNVR PVQNAMNQVG IVLINVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSQMTPVRPG STMPVRPTTNTFITVIPATLITRSTVPQSQSQQTKSTPSTSTTP TATQPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSLASFVT VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\ GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS /THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC KICEWAFESSPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQFLFAKGKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLEVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDPPNHFPTYVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA STATPPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGSGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQOLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDETSLFL DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVI.PTLMEV	1			KTLVTLIANNNAGNPLVQOGGOPLILTONPAPGI.GTMVTOPULP
IVLNVQGGTVRPITLVPAPGTGFVKPTVGVPQVFSQMTPVRPG STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQTKSTPSTSTTP TATQPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSIASFVT VKRPGVTGENSNEVAKLVNTLNTTPSLGQSPGPVVVSNNSSAH\ GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS /THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD VHFMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPPSALQEAAPLTSSMPPLPVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDPPNHFPTYVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA STATPPPTTPHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFKNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQOLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPILMEV				PVQVMQNANHVTSSPVASQPIFITTOGFPVRNVRPVONAMNOVC
STMPVRPTTNTFTTVIPATLITIRSTVPQSQSQOTKSTPSTSTTP TATQPTSLQQLAVQSPQQSNQTTNPKLAPSFFSPPAVSIASFVT VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\ GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS /THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE LDQONGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDPPNHFPTYVHCSLCRYST CCSRAYANHMINNHVPKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPABEPELLTPLAPALPSPA STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVFFMERHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLAFEV				IVLNVQQGQTVRPITLVPAPGTOFVKPTVGVPOVFSOMTDVPDC
TATQPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSIASFVT VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\ GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS /THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE LDQONGEVDGHTICQHCYROFSTPFQLQCHLENVHSPYESTTKC KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDPPNHFPTYVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDEVHDR NVKNMYPPPSFPTNKAATVKSAGATPABPEELLTPLAPALPSPA STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL	1 :			STMPVRPTTNTF1TVIPATLTIRSTVPOSOSOOTKSTPSTSTTD
VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\ GSQRTSGPSSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS /THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYFEVQRS IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFPTYVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPAEPEBLLTPLAPALPSPA STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGSGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEPWCDVVLALLADGTVI.PTLUEV		i		TATOPTSLGQLAVQSPGQSNOTTNPKLAPSFPSPPAVSTASEVT (
GSQRTSGPESMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS /THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE LDQONGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPPSALQEAAPLTSSMPPLPVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDPPNHFPTYVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPABPEELLTPLAPALPSPA STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHILTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVI.PTU.FV	'			VKRPGVTGENSNEVAKLVNTLNTIPSLGOSPGPVVVSNNSSAU\
RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS  /THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPPSALQEAAPLTSSMPPLPVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDPPNHFPTYVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVTD SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHITPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLAFEL	1 1			GSQRTSGPESSMKVTSSIPVFDLODGGRKICPRCNAOFRVTEAT
THPSSTPIPALSPY/TKVPEPNENVGDAVQTKLIMLVDDFYY GRDGGKVAQLITNFPKVATSFRCPHCTKRLKNNIRFMMHMKHHVE LDQONGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS IQKRAVKMSVMGRQTCLECSFEIPDFPNHFPTVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPABPEELLTPLAPALPSPA STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHILTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLAFEV	1 1	ł		KGHMCYCCPEMVEYOKKGKSLDSEPSVPSAAKDDSDEKTADVAS
GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE LDQONGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFPTYVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGGGGGGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLAFEV	1			/THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY
KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDPPNHFPTYVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPABPEELLTPLAPALPSPA STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGPKISYEWAVRFMLRHHILTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLAFEV	] .	1		GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHUF (
VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDPPNHFPTYVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGPKISYEWAVRFMLRHHILTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLAFEV	1 1	į.		LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC
CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA SRGQPRTVPVSSNDTPPSALQEAAPLTSSMPPLPVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDPPNHFPTVVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHILTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLAFEY				KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD
SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFPTVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPABPEELLITPLAPALPSPA STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHILTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGBFWCDVVLAILADGTVLPTLAFEY	1 1	İ	i	VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\
IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFPTYVHCSLCRYST CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA STATPPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEFWCDVVLAILADGTVLPTLAFEV	1 1			CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA
CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPABPEBLLTPLAPALPSPA STATPPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGBFWCDVVLAILADGTVLPTLAFEV				SKGQPKTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS
SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGGGGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLAFEV	1 1	}	ł	LUARAVKKMSVMGRQTCLECSFEIPDFPNHFPTYVHCSLCRYST
NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGGGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGFFWCDVVLAILADGTVLPTLAFEY		1		CUSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT
STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE LASGGGGGGGGGGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLITPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLAFEV	1			SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR
LASGGGSGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHIJTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGFPWCDVVLAILADGTVLPT	1 1			TO AND THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN A STATE OF THE PERFET IN
RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGBPWCDVVLAILADGTVLDTLUFY	[ [		•	I A SCORGE CONTROL STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE
RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGBPWCDVVLAILADGTVLDTLUFY	}		}	LASGGGGGGGGGGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ
VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLDTLUEV	]		İ	RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTOREOOLD
DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVI.PTI.VEV	1		J	VNEETLE QKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA
DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY RGOMDQPANMPDSILLEAKESGYSDDEIMFLWSTBUNGYUMAGG				VAHTLEKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL
KGOMDQPANMPDSILLEAKESGYSDDETMRI BETTERIOGUTTUR CO			• [	DIEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY
POTTONE		1	]	RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ
RSKGMLVMDCHRTHLSEEVLAMLSASSTLPAVVPAGCSSKIQPL	LL	<del></del>	<u>-</u>	RSAGHLVMDCHRTHLSEEVLAMLSASSTLPAVVPAGCSSKIQPL

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1.0.	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
. [	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	N-Truntenhan V There is a strike
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
}	sequence	2040000	\=possible nucleotide insertion)
			DVCTVDTVVNPI HVVHVEORDENA DER COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COOPERA DE COO
			DVCIKRTVKNFLHKKWKEQAREMADTACDSDVLLQLVLVWLGEV
		Î	LGVIGDCPELVQRSFLVASVLPGPDGNINSPTRNADMQEELIAS
1	J	ļ	LEEQLKLSGEHSESSTPRPRSSPEETIEPESLHQLFEGESETES FYGFEEADLDLMEI
6134	2	4256	
	_	4250	FVHGSMADTDLFMECEEEELEPWQKISDVIEDSVVEDYNSVDKT
1			TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAQNSDSTK
ļ	i e		KTLVTLIANNNAGNPLVQQGGQPLILTQNPAPGLGTMVTQPVLR
			PVQVMQNANHVTSSPVASQPIFITTQGFPVRNVRPVQNAMNQVG
i			IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSQMTPVRPG
			STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTPSTSTTP
	1		TATOPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSIASFVT
			VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\ GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL
1			RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS
[			/THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY
			GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE
f	[		LDOQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC
i			KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD
1	1 1		VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\
İ			CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA
			SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS
ĺ			IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFPTYVHCSLCRYST
			CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT
	ĺ		SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGOTRDRVHDR
	l ' l		NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA
1	}		STATPPPTPTHPQALALPPLATEGAECLNVDDODEGSPVTOEPE
1	1		LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEONAEHFRNDO
	1		RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTORROOLD
1	ĺ		VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA
i	ŀ		VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL
	-		DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY
	1		RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ
1			RSKGMLVMDCHRTHLSEEVLAMLSASSTLPAVVPAGCSSKIQPL
ŀ	ŀ		DVCIKRTVKNFLHKKWKEQAREMADTACDSDVLLQLVLVWLGEV
	<u> </u>		LGVIGDCPELVQRSFLVASVLPGPDGNINSPTRNADMQEELIAS
			LEEQLKLSGEHSESSTPRPRSSPEETIEPESLHQLFEGESETES
6135	2	4256	FYGFEEADLDLMEI
1	·	4230	FVHGSMADTDLFMECEEEELEPWQKISDVIEDSVVEDYNSVDKT
			TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAQNSDSTK KTLVTLIANNNAGNPLVQQGGQPLILTQNPAPGLGTMVTQPVLR
•			PVQVMQNANHVTSSPVASQPIFITTQGFPVRNVRPVQNAMNQVG
			IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSQMTPVRPG
			STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTPSTSTTP
	ŀ	•	TATQPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSIASPVT
			VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\
1 1		1	GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL
		İ	RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS
]			/THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY
		i	GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE
			LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC
1 1			KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD
1			VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\
1			CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA
			SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS
			IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFPTYVHCSLCRYST
[	1	1	CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT
	<del></del>		TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
Į.	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine
1	residue of	amino acid	W=Tryptophan, Y=Tvrosine Y-Unknown + Ct
	amino acid	sequence	Codon, /=possible nucleotide deletion "
<b> </b>	sequence		\=Possible rucleotide insertion\
1	Ì		SVGDAMAKHLVFNPSHRSSSILPRGLTWTAHSPHGOTPDPVHDB
			I NVKNMIPPPSEPTNKAATVKSAGATPAEPEELLTDIADALDODA
			SIATEPPTPTHPQALALPPLATEGAECLNVDDODEGGDVTOEDE
1			LASGGGGGGGKKEQLSVKKLRVVI.FAI.CCNTEGA DEUEDNIDG
1		1	RELEGIOUS DE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA CONTRE LA
			VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA
]			VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL
1			DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY
1			RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ RSKGNLVMDCHRTHLSEEVLAMLSASSTLPAVVPAGCSSKIQPL
1			DVCIKRTVKNFLHKKWKEQAREMADTACDSDVLLQLVLVWLGEV
			LGVIGDCPELVQRSFLVASVLPGPDGNINGDTDNADMORRE TAG
1			DEEQLKLSGEHSESSTPRPRSSPEETIEPESI,HOI,FEGEGETE
6136	7.504		FIGFEEADLDLMEI
1 2736	1704	539	FGVRMALEGMSKRKRKRSVOEGENPDDGVRGSPPEDVBLCOVAS
	ĺ		SHERGERISKGGTGRLASLFSSLEPOTOPVYVPVPVPVPV PGALACA
	]		DECETHORQGQKRKNSQPGVKVADRKILDDTEDTVAGODZZZA
1			1 INVESTIGATION OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE
ŀ			SLIPAEGTLSKKLAAIKRKIHPDQKNINAYVVFKEESAATQALK
			RNGAQIADGFRIRVDLASETSSRDKRSVFVGNLPYKVEESAIEK
1			HPLDCGSIMAVRIVRDKMTGIGKGFGYVLFENTDSVHLALKLNN
			SELMGRKLRVMRSVNKEKFKQQNSNPRLKNVSKPKQGLNFTSKT AEGHPKSLFIGEKAVLLKTKKKGQKKSGRPKKQRKQK
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG
1 .			MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK
1 1			I THINGG LEGITLDEAGRGHSFSFHGAALTAPKOGOELMAKALEG
1 1			LSCPRDMAPSHCAEHKDOFLOLSOYROLKTAFDVOALNEDTERO
1			LQHAGLREAGGIFYFSVPPFAYEDIARNINGCCPDGDGAWI DIW
1 1	ļ		DERPFGHUHFSAQQLATELGTFFOEEEMVRVDHVLGVOAVAOTT
1 1			PERDUNKKALDGLWNRHHVERVETIMKETUDAEGDTGEVERVOU
] [		ĺ	TREVENDED TO VAME LETT TO THE TOTAL PROPERTY OF THE TAXABLE PROPERTY OF THE TAXABLE PROPERTY OF THE TAXABLE PROPERTY OF THE TAXABLE PROPERTY OF THE TAXABLE PROPERTY OF THE TAXABLE PROPERTY OF THE TAXABLE PROPERTY OF THE TAXABLE PROPERTY OF THE TAXABLE PROPERTY OF THE TAXABLE PROPERTY OF THE TAXABLE PROPERTY OF THE TAXABLE PROPERTY OF THE TAXABLE PROPERTY OF THE TAXABLE PROPERTY OF THE TAXABLE PROPERTY OF THE TAXABLE PROPERTY OF THE TAXABLE PROPERTY OF THE TAXABLE PROPERTY OF THE TAXABLE PROPERTY OF THE TAXABLE PROPERTY OF THE TAXABLE PROPERTY OF THE TAXABLE PROPERTY OF THE TAXABLE PROPERTY OF THE TAXABLE PROPERTY OF THE TAXABLE PROPERTY OF THE TAXABLE PROPERTY OF THE TAXABLE PROPERTY OF THE TAXABLE PROPERTY OF THE TAXABLE PROPERTY OF THE TAXABLE PROPERTY OF THE TAXABLE PROPERTY OF THE TAXABLE PROPERTY OF THE TAXABLE PROPERTY OF THE TAXABLE PROPERTY OF THE TAXABLE PROPERTY OF THE TAXABLE PROPERTY OF THE TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY O
1 1			QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL
1 1			RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG
1			LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL
} [	İ		LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS
[ ]	ļ	j	QQQPEQLVPGPGPGPMPSDFOVLRAKYRESSINGAMSEST TOWN
	ļ		ANDIEM TAVRAVRREGOTHLALSGGSSPVALEOOLATAUVCEDU
	į	1	AHTHLWLVDERCVPLSDPESNFOGLOAHLLOHVRTPVVNTU\DW
1	į	f	PVHLQQRLCAEEDQGAHIYAREISALGANSSEDIATI.CMCA.DCU
			TASLEPQSPTGLDGEQLVVLTTSPSOPHRRMSI,SLDI,TMDAVVOV
		ł	AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG
6138	4587		
			EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL
J		1	TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLITTDLKTKFSVGPPLSOLORGWYDMTM
		1	TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK
			ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE
- 1		[	HLHRQWEDLCLRVAIRKQEIEDRLNTWVVFNEKNKELCAWLVQM
1			ENKVLQTADISIEEMIEKLOKDCMEEINI.FSENKT.OT.VOMODOV
İ		i	IKASNKSKAAEIDDKLNKINDRWOHLFDVIGSDVVVI VEDDA DI
}	i	1 1	QQLDKNMSNLRTWLARIESELSKPVVYDVCDDOETOKPI DECOR
	ĺ	-	LQRDIEQHSAGVESVFNICDVLLHDSDACANETECDS LOOTEDS
1		1.	LUKKWKNICAMSMERRMKIEETWRIWOKFI.DDYSDEEDWI MCAR
1	i		RTAACPNSSEVLYTSAKEELKRFEAFOROTHERT.TOT.ELTNVOV
		1	RRLARENRIDIASRLKQMVHEGNQRWDNLQRRVIAVLRRLRHFT
		-	

Deginning noticetide location corresponding to first amin acid recide some corresponding to first amin acid amin acid residue of amin acid amin acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequenc	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
No:   nuclectide   location   corresponding   to first   amino acid   residue of   residue of   residue of   amino acid   residue of   amino acid   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequ				(A=Alanine, C=Cysteine, D=Aspartic Acid, F=
Corrisponding   to first   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   am		, , ,		Glutamic Acid. F=Phenylalanine. G=Glycine
to first amino acid residue of amino acid residue of amino acid sequence  Peroline, Qegiluamine, Rahginine, S-Serine, T-Threonine, V-Valine, Meridue of amino acid sequence  Peroline, Qegiluamine, X-Duknown, *-Stop Codon, /-possible mucleotide deletion, /-possible mucleotide insertion)  NOREFRETEBILVMLTEMDLQLINVERSEDADDKURQLING POSSIBLE mucleotide deletion, /-possible mucleotide insertion)  NOREFRETEBILVMLTEMDLQLINVERSEDADDKURQLING POSSIBLE mucleotide deletion, /-possible mucleotide insertion)  NOREFRETEBILVMLTEMDLQLINVERSEDADDKURQLING POSSIBLE mucleotide deletion, /-possible mucleotide insertion)  NOREFRETEBILVMLTEMDLQLINVERSEDADDKURQLING POSSIBLE mucleotide deletion, /-possible mucleotide insertion)  NOREFRETEBILVMLTEMDLQLINVERSEDADDKURQLING POSSIBLE MERCHANGERS SAR LEEDERAQUY \California POSSIBLE MERCHANGERS SAR LEEDERAQUY \California POSSIBLE MERCHANGERS SAR LEEDERAQUY \California RECOPPLIANCE OF SAR LEEDERAQUY \California RECOPPLIANCE OF SAR LEEDERAQUY \California RECOPPLIANCE OF SAR LEEDERAQUY \California RECOPPLIANCE OF SAR LEEDERAQUY \California RECOPPLIANCE OF SAR LEEDERAQUY \California RECOPPLIANCE OF SAR LEEDERAQUY \California RECOPPLIANCE OF SAR LEEDERAQUY \California RECOPPLIANCE OF SAR LEEDERAQUY \California RECOPPLIANCE OF SAR LEEDERAQUE \California RECOPPLIANCE OF SAR LEEDERAQUE \California RECOPPLIANCE OF SAR LEEDERAQUE \California RECOPPLIANCE OF SAR LEEDERAQUE \California RECOPPLIANCE OF SAR LEEDERAQUE \California RECOPPLIANCE OF SAR LEEDERAQUE \California RECOPPLIANCE OF SAR LEEDERAQUE \California RECOPPLIANCE OF SAR LEEDERAQUE \California RECOPPLIANCE OF SAR LEEDERAQUE \California RECOPPLIANCE OF SAR LEEDERAQUE \California RECOPPLIANCE OF SAR LEEDERAQUE \California RECOPPLIANCE OF SAR LEEDERAQUE \California RECOPPLIANCE OF SAR LEEDERAQUE \California RECOPPLIANCE OF SAR LEEDERAQUE \California RECOPPLIANCE \California RECOPPLIANCE \California RECOPPLIANCE \California RECOPPLIANCE \California RECOPPLIANCE \California RECOPPLIANCE \California RECOPPLIANCE \California RECOPPLIANCE \California REC	-	location		H=Histidine, T=Tsoleucine K=Lysine
to first amino acid residue of amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid acquence  ##TYPtOplan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible mucleotide deletion,				b=Leucine M=Methionine N-Asparagine
amino acid residue of amino acid sequence saidue, yenylophan, yenyrosine, X-Juknown, *-Stop Codon, /-possible nuclectide deletion, /-possible nuclectide deletion, /-possible nuclectide insertion)  NOSEPFERIUMITERIOLOUTEVEGLIOUSEP \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \				
residue of amino acid sequence  amino acid sequence  sequence    Sequence				
amino acid sequence   Codom, /=possible nuclectide deletion,   Possible nuclectide insertion    NOREFFECTRESIL/WUITEMDLQLINVEHISSESDADEKMRQLNG   FOQETILMINKLOQLIVGEGULOKESPLOADAUIBDELEELHR   YCQEVGRVSRFHRALTSCTFGLEDEKASENETDMEDPREIGT   DSWRKGESESPSSPSGLCHUAPOHERSCETVSVDS\  THE   WOHTGRRGGPSSSH\EBDEEAQYY\SALSGKSISDGISHVPDS   PSCPEHHYKGMEDNVPPVPPASSTTYKFPYSVDS\  THE   WOHTGRRGGPSSSH\EBDEEAQYY\SALSGKSISDGISHVPDS   SCPEHHYKGMEDNVPVPVPASSTTYKFPYSVDS\  THE   KEGPRVLNGHPQQEDGGIAGITEQQSGAPDRKEMIQAQUL\HNK   LKKKONLOQLINDSISAITTHIKKTEALDEMLAMAKPPSDIQBIE   LRVKKLOSILKAFDTYXALVVSVNVSKSFFLQTS:FSSTEQSE   LRCLSLLWEAQAGVDSWRGGLRGSLMQCOPPOLOSQNILLMLA   SACNIRGOKAHVTDFKADPRALLECRERLMGLEKELVERQPQVDM   LGSINSLILKGHGSDCIEAER-KVVVI\SKLKGLEQVSQDLM   ALQGTQNPASPLPSTDEVDSGDOPFARSVPAFRAKGFRAVTTE   GEEETISSVOSTFRONGESISTRVNAPALPLGLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLL		residue of	. " "	W=Trvptophan Y=Tvrosine X=Unknown *-Stop
		I		Codon. /=possible nucleotide deletion
NOREFFECTIVES ILVAUTEMBLOUTINERSESSADEMS (AND FOOETIMENT TO COLVER SEVENDAVIS BELIEVER FOOETIMENT TO COLVER SEVENDAVIS BELIEVER YCCEVFOR VSRYHRRLITS CTPGLEDEKEASENSTDMEDDER FLOT DSWARKGES SEPS SPOSICILLY DAPORTS SCYST VSD (*) THE WONTGRAGES SPS SPS SPS SPS SPS SPS SPS SPS SPS S		1		\=possible nucleotide insertion)
FOGETINTHKIDOLIVGEOLIGKSEP LIDAVLIBELELLEH YCCEVFGRVSRFRRITSTOFLEDEREASETDMEDPREIOT DSWRKRGSEEPSSPOSICHLVAPCHERSCCETVSVSUD; IPLE WDITGRRGGSSSSH_BEDEERACTYVSALDSKSISDGIISHNYDDS PSCPEHHYKOMGODEN/WPVPPASSTTYKFYGKLLLPFGTDGG KECPFWINGRYGCOPSGALGRICOQGEL/HRNK LKKUNLOGINSDISAITTHIKKTEABLEMLMAKPSDIOGIE LKKUKNLOGINSDISAITTHIKKTEABLEMLMAKPSDIOGIE LKRUKNLOGINSDISAITTHIKKTEABLEMLMAKPSDIOGIE LRVKNLOGINSDISAITTHIKKTEABLEMLMAKPSDIOGIE LKRUKNLOGINSDISAITTHIKKTEABLEMLMAKPSDIOGIE LKRUKNLOGINSDISAITTHIKKTEABLEMLMAKPSDIOGIE LKRUKNLOGINSDISAITTHIKKTEABLEMLMAKPSDIOGIE LKRUKNLOGINSDISAITTHIKKTEABLEMLMAKPSDIOGIE LKRUKNLOGINSDISAITTHIKKTEABLEMLMAKPSDIOGIE LKRUKNLOGINSDISAITTHIKKTEABLEMLMAKPSDIOGIE LKRUKNLOGINSDISAITTHIKKTEABLEMLMAKPSDIOGIE LKRUKNLOGINSDISAITTHIKKTEABLEMLMAKPSDIOGIE LKRUKNLOGINSDISAITTHIKKTEABLEMLMAKPSDIOGIE LKRUKNLOGIENDE LKRUKNLOGIENDE LKRUKNLOGIENDE LAGUTANDE LAGUTSPETELERGE VAN STANSAITTHIKKTEABLEMLEMAKPSDIOGIE LKRUKNLOGIENDE LAGUTSPETELERGE VAN SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNCHANDE SANNIKNIKNAKAKAKELKEELFIMMLIEPKARFIELERSK AGKSGSKITCOGNATICHANSKORPTALDEBENGATORDEPKOLMIKUK SANNIKNCHANDE	NOREEFEGTRESTLVWLTEMDLOLTNVEHESESDADDVMPOLNC			
YCQEVFGRUSRFHRELTSCTPGLEDEREASINETDMEDPRELIQT DSWRKGSESPESPSSIGLICHUAPGHERSCCTEVYSUS\1PL WDHTGRRGGPSSSH\EBGERQYY\SALSGKSISDGISHWYDD PSCPEHHYKGMGDNVPVPVPASSTYYKPYGKLLLPPGTDGG KEGPRVLNGNPQQEDGGLAGITEQOSGAPDRRENIGAQGLYNK LKKKQNLQQLINSDISATTHUKKTRALDWAMMKAPPSDIGEIE LRYKRLGEILKAPDTYKALVVSYNYSKSFLGTESPSSTEELGE RCALSLIMERAGQAVDSWRGGLRGJSMCQCDPPGLSCNLLIMLA SANNRKOKAHVTDFKADPRALLECRRELMGLEKELVEROPQVDM LQBISNSLIKHGBGDLTEREKVVVI\ZKLKLEGOVGDUM ALQGTQNPASPLDSFDEVDSGDOPPATSVPAPRAKGPRAVTTE GEETERSVPGSTFRORSPISTRVARAPLQLALLLLLLLALLL PSSEEDYSCTQANNP\ARSFYPMLRYTNGPPT GEETERSVPGSTFRORSPISTRVARAPLQLALLLLLLLLALLL PSSEEDYSCTQANNP\ARSFYPMLRYTNGPPT TRRPMRASSWRTL/LAGNIGGAASVIVGHPLDTVKTRLQAGVC YGNTLSCIRVVYRRESWMGPFRASPLASTAVVEVGGVEN TORFISGURGGERASPPTLEDLLLASMVAGVVSVGLGGPVDL IKTRLQMTPPVSGROPFREVGGSGCCCDEPVHITTIV RNGGLAGLYRGASAALLRDVPGVCLYPIPVVFLSENITPEACTG PSSCAVHLAGGMAGAISWGTAPDHOVVGSRLOGVHCITTIV RNGGLAGLYRGASAALLRDVPGVCLYPIPVVFLSENITPEACTG PSSCAVHLAGGMAGAISWGTAPDHOVVGSRLOGVHCITTIV RNGGLAGLYRGASAALLRDVPGVCLYPIPVVFLSENITPEACTG PSSCAVHLAGGMAGAISWGTAPDHOVVGSRLOGVHCITTIV RNGGLAGLYRGASAALLRDVPGVCLYPIPVVFLSENITPEACTG PSSCAVHLAGGMAGAISWGTAPDHOVVGSRLOGVHCITTIV RNGGLAGLYRGASAALLRDVPGVCLYPIPVVFLSENITPEACTG PSSCAVHLAGGMAGAISWGTAPDHOVVGSRLOGVHCITTIV RNGGLAGLYRGASAALLRDVPGVCLYPIPVVFLSENITPEACTG PSSCAVHLAGGMAGAISWGTAPDHOVGSRLOGSCCCCDAPVILLERACTG PSSCAVHLAGGMAGAISWGTAPDHOVGTARAPGEPTGAGGSLA RRGHRATTOWRITG  6140 694 136 REELEIMPLESSWBPILGVPRCGTERRWEFFVRAOPESTATURAPG RCGLAEL/SPROPHLENGTRKKAKKSEFTGALUNGEPTGAGGSLA ARRIBRTDVRTTG  6141 2 984 AQVGPRSEPCHWELLBCRKKAKSEFTGALUNGEPTGAGGSLA ARRIBRTDVRTTG  6142 984 AQVGPRSEPCHWELLBCRKKAKSEFTGALUNGEPTGAGGSLA ARRIBRTDVRTTG  6143 PSELLIVITATVFLIMBELLGPQARMEEBTTARTGFCYWEEKERDLANN KSEDSIGLTTTNONGVAFTKERLEFTMALTGEFTYGAGGGSLA ARRIBRTDVRTTG  PSELLIVTLINTYCHMERLEFTARTGFCYWEEKERDALNN KSEDSIGLTTTNONGVAFTKERLEFTMALTGEFTYGAGGGSLA ARRIBRTDVRTTG  PSELLIVTLINTYCHMERLEFTARTGFCYWEEKERDALNN KSEDSIGLTTTNONGVAFTKERLEFTMALTGFCYWEEKERDALNN KSEDSIGLTTTNONGVAFTKERLEFTMATTGFCYWEEKEREPALNN KSEDSIGLTTTNONGVAFTKERLEFTMATTGFCYWEEKEREPALNN KSEDS				FOOETTINTNKTDOLTVEGEOLTOKSER\LDAVILEDELEET UP
DSMRKGESEPSSYOSLCHLVAPGHERSGCETTVSVS\SYLTER WDDTGRKGGPSSSH\EDENOYY\SALSKSIDDHSMHYPD PSCPERHYKQMEGDRVPPVPRASTPYKPPYGKLILPGTDGG KEGPRUINGHPQQEDGGLGGITEQOGGAFDREMIQAQEL\HNK LKIKQNLQQLNSDISAITTWLKHTERELEMLKWARPPSDIQEIE LRUKGLGLLKEAPDTYKALVSVMVSSKEPTGSPESTELGSE LRUKGLGLLKEAPDTYKALVSVMVSSKEPTGSPESTELGSE LRUKGLGLLKEAPDTYKALVSVMVSSKEPTGSPESTELGSE LRUKGLGLLKEAPDTYKALVSVMVSSKEPTGSPESTELGSE LRUKGLSLLKEAPDTYKALVSVMVSSKEPTGSPESTELGSE LRUKGLGLLKEAPDTYKALVSVMVSSKEPTGSPESTELGSE LRUKGLGLLKEAPDTYKALVSVMVSSKEPTGSPESTELGSE LRUKGLGLKAPDTYKALVSVMVSSKEPTGSPEGSENGURDUR ALQGTONDASDLSPPTGVENGDOPPATSPERKOPPRAVPTTE GEETTSEVPGSTR PORSPLERVVYRALPLOLLLLILLLLALL PSSSEDYSCTOANNEVARSPYPHLRVTNOPPT  6139 52 1131 LGDWVGRTCGVLETPTSVLERARAGGCPTDSKWALPRLEGGE TERRPWASSKKTL\LAGNIGGASVIVGHPLDTVKTRLOAGVU YONTLSCIRVVYRRESMFFFFKGMSPPLASIAVYNSVVFGGFS TORFISGHRCGSPRASSPRTISDLLLASMVAGVVSVGGFSVD LIKILQMOTPPVSGROPPFKGMSPPLASIAVYNSVVFGGFS TORFISGHRCGSPRASSPRTISDLLLASMVAGVVSVGGFSVD LIKILQMOTPPVSGROPPFKGMSPPLASIAVANGVVFUNGFFS PSCAVMLAGGMAGAISWFTTMDVVKSGLADGGVVILNTYKKGV LDCISGSYQKEGLKVFFFRGTVRAVNGGPPNSAAMFLGFLSLGA RREGISGYQKEGLKVFFFRGTVRAVNGGPPNSAAMFLGFLSLGA RREGISGYQREGLKVFFFRGTVRAVNGGPPNSAAMFLGFLSLGA FROLBEL/SPAPENSSNAAVPEAIPTRAMPAGPLSVTVMAP RCQRF/OPPAPEPSSNAAVPEAIPTRAMPAGPLSVTVMAP RCQRF/OPPAPEPSSNAAVPEAIPTRAMPAGPLSVTVMAP RCQRF/OPPAPEPSSNAAVPEAIPTRAMPAGPLSVTVMAP RCQRF/OPPAPEPSSNAAVPEAIPTRAMPAGPLSVTVMAP RCQRF/OPPAPEPSSNAAVPEAIPTRAMPAGPLSVTVMAP RCQRF/OPPAPEPSSNAAVPEAIPTRAMPAGPLSVTVMAP RCGRF/OPPAPEPSSNAAVPEAIPTRAMPAGPLSVTVMAP RCGRF/OPPAPEPSSNAAVPEAIPTRAMPAGPLSVTVMAP RCGRF/OPPAPEPSSNAAVPEAIPTRAMPAGPLSVTVMAP RCGRF/OPPAPEPSSNAAVPEAIPTRAMPAGPLSVTVMAP RCGRF/OPPAPEPSSNAAVPEAIPTRAMPAGPLSVTVMAP REGISTATITYPKJIMMELLGGGLGLEFTARGFORGGGSLS ASRAPARRLVFHQLAHASGGLGLEDFTAGRFORFTEGGFS NGCNIVGMYRHYDAKKLEKKEREPTFNKLJEFKKGFEIPTGAGGGSLS ASRAPARRLVFHQLAHASGGCLGEBEPGGGGSLS AGRSGECIGGAATRLRSKGGATVEBMPSETKAK\AIENID ULELMSTRANSKANTOTOTORTAKSKGATTLERKGGVLOTHHLLG LLUKRMENSKANTOTORTAKSKGATTLERKGGATUEPTGGVECHNER PROPOLICYMOIMENGAGKCODAPHVENREESTARIGFGVMENGERCH RCGLSSISLERAVSTOPPHHOHDEPC\LMP RFFO			ŀ	
MONTOGRGGPSSSH\SEDERACYY\SALSGKSISDGISHHYDDS PSCPEHHKKMKEGNDRIVPPPASSTPYKALLPGTOGG KEGPRVLNGNFQGEDGILAGITEGOGGAPRMENIOADEL\HINK LKKKONLOGINSISAITHWIKTERELBEIMKMAKPPSDIGEIE LRVKRIQBILKAPDTYKALVVSVWYSKEFLQTESPESTELGSF LRQLSLIMEADGAGAVSTRGCINGGINGCOPLISGNILLIALA SANNROKAHVTDPKADPRALLECRREIMQLEKELVEROPQVDM LQSISNSLIKHGHEDCIEREEKWILEKKUREQVSQDLM ALQCTONPASPLPSPDEVDSGDQPRATSVPAPRAKQFRAVNTTE GEBETERVPGSTRPQRSFLSRVVRARALPLQLLLILLIALLILLIAL LGHWWSRTCGVLETFTSVLERARAGGCPTDSKMAPRAKQFRAVNTTE GEBETERVPGSTRYDRSFLSRVVRARALPLQLLILLILLIALLIL CGHWWSRTCGVLETFTSVLERARAGGCPTDSKMAPRAKQFRAVNTTE GEBETERVPGSTRYDRSFLSRVVRARAGGPPTDSKMAPREGE TERRPRASSKKTL/LAGEN IGGAASVIUGHPLDTVATRIQAGVC YGNTLSCIRVVYRRESMFGFFKGMSPPLASIAVYNSVGGFSN TQRFISGNRGGEBEASPFFKSUNGSVGFTDSVGGSVGVDL IKIRLQMGTPPVSGROPFFEVQGSGCC\BPAYGGPVLICTTIV RNBGLAGLYRGASAMILLADVGVCLYLFTYPYFLSBWITPEACTG PSPCAWMLAGGMAGAISWGTATPMDVVSSLQAGGPVDL IKIRLQMGTPPVSGROPFFEVQGSGCC\BPAYGGPVLINTYKGV LDCISGSYGKGELKVFFRGITVANVAGFPMSAMMFLGVELSIQA IRGDHAVTSP SVAPQABEABRATSTGPAGSGLIGPTTGRAFFAGAGGALLS RCGRP/QPPAPEPSSRNAAVDEAIPTPRAASAALEPLIGPAPV SVAPQABEABRATSTGPAGSGLIGPTTGRAFFAGTAGGGGLIS RCGRP/QPPAPEPSSRNAAVDEAIPTPRAASAALEPLIGADVY SVAPQABEABRATSTGPAGSGLIGPTTGRAFFAGTAGGGGLIS PSFLLVCTLMTPFILDMERLLGGOLGLEDFIFAHVKGIEKEVNVY KSEDSLULTITUNGVGVAFIKRIKGGVIDSVRTICVOHHIESI NGENIVGMRHYDVAKKLELKEBLFTKLIBKKAFFIELRSK AGKSSGRTIGCGBATLRLRSKGPATVEBMPSETKAK,TIEKIDD VLELMMSIRDILATMTPBAGKOKNVNPERAVALDETLIGPFAPP DEFVDDWGVIGDAKRRGL NERNIVGMRHYDVAKKLELKEBLFTKLIBKKAFFIELRSK AGKSSGRTIGCGBATLRLRSKGPATVEBMERTGEEVKQUMEKL REKGLSHSLBAVSTDPPHHDHHBEFC\LMP LVYENKOPILGYMDIHHRIGEFQARMEENBERGEVECVEGKNRR FRVROPTLGYMDIHHRIGEFQARMEENBERGEVECVEGKNRR FRVROPTLGYMDIHHRIGEFQARMEENBERGEGEVECVEGKNRR FRVROPTLGYMDIHHRIGEFQARMEENBERGEGEVECVEGKNRR FRVROPTLGYMDIHHRIGEFQARMEENBERGEGEVECVEGKNRR FRVROPTLGYMDIHHRIGEFGARMIENBERGGEVENGUMEKL REKGLSHSLBAVSTDPHHDHHBEFC\LMP SLGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG			i .	DSWRKRGESEEDSSPOSICHIAADGHEDSGGGETDWSADC\ TOT B
PSCPEHHYKOMEGDRIVPPYPPASTTYKPPYGKLIHPGTDGG KEGPRUNINGGITSQOGGGTAGGTSQGGGTCTSFESTELOGR LKKRKORLQUINSDISAITTMLKKTERELEMLKWAKPPSJOGTIE LRVRKIGELIKEAPDTYKALVVSVMYSSKEPTSFESTELOGR LRQLSILWEAAQGAVDSWRGGLRGSIMGCODFHOLSQNILLMULA SAKNIROKAHVTDPKADPRALIEKREEMLKWAKPPSJOGTIE LRQLSILWEAAQGAVDSWRGGLRGSIMGCODFHOLSQNILLMULA ALQGTONPABALDESPEDUNGDOPPATSPOKEFULGVEROPQVDM LOSISNSLLIKGIGGDCTEAPEKVHVI\EKKLKQLEEQVSQDLM ALQGTONPABADLESPEDUNGDOPPATSPHRKOPFRAVPTTE GEETTSRVPGSTPPORSFLSRVVYRAALPLQLLLLLLLLLLACLL PSSEEDYSCTOANNPALARSPYPHLRYNTORPKOPFRAVPTTE GEETTSRVPGSTPPORSFLSRVVYRAALPLQLLLLLLLLLLLACLL PSSEEDYSCTOANNPALARSPYPHLRYNTORPLACTE GEETTSRVPGSTRYPHLRYNTORPLACTE GEETTSRVPGSTRYPHLRYNTORPLACTE GEETTSRVPGSTRYPHLRYNTORPLACTE GEETTSRVPGSTRYPHLRYNTORPLACTE GEETTSRVPGSTRYPHLRYNTORPLACTLLLACLL PSSEEDYSCTOANNPALARSPYPHLRYNTORPLACTLLLACLL PSSEEDYSCTOANNPALARSPYPHLRYNTORPLACTLLACLL PSSEEDYSCTOANNPALARSPYPHLRYNTORPLACTLLACLL PSSEEDYSCTOANNPALARSPYPHLRYNTORPLACTLLACLL IKTRLQMQTPPVSGROPFREVQGSCSCC\GPAVGCVVICITTIV REGILACLYRORPHSSKWILLAGHAGAVAGVVSVVGYGSN TOPFISGURGEBAS PPPTISDLLLASMAGAVGVVGVCHGSVDIC LKTRLQMQTPPVSGROPFREVQGSCSCC\GPAVGCVVICITTIV REGILACLYRORPHSGRAGAINSPTTYMDVVKSRLQAGDVVINKYKGV LOCISGSTQLEGENGTPFRORTRORPHSTALDAGAVC PSPCAVMLAGAMGAGATIGNETTYMDVATSRQLADAGATER FROLKEL/SPAPESSSNAAVPERITYMOKAGPENAGALSVTVANAP RCQRF/GSPAPEPSSSNAAVPERINKEPYVARADLLSVTVANAP RCQRF/GSPAPEPSSSNAAVPERINKEPYVARADLLSULGAGGEGGSLS ASRAPARRLVFHAQLAHGSATGRVEGFSSTQLFVAQLAGAFETS PSELILYCTLTYFKIDMRELLGGGLLEDFTLAFKAGITEUDO VLELYMGIRDLATTMFRAGKKVNTPERAVALDETLGGPAPF PROKOPILAGYMDVAKKLEKKEBLFTNKLIFKKKAFEIELIRGK AGKSSGEKIGCGAATRLRRSKGPATVEBMPSETKKK,IERIDO VLELYMGIRDLATTMFRAGKKVNTPERAVGENKENDEPSTALDERACL AGKSSGEKIGCGGAATRRRSKGPATVEBMPSETKKK,IERIDO VLELYMGIRDLATTMFRAGKKVNTPERATGESVAGLMEKL REKOLSISLBRAVSTOPHHOHDEDEC\LIMP FYNOPTIGDLATTMFRAGKKVNTPERATGESVAGLMEKL REKOLSISLBRAVSTOPHHOHDEDEC\LIMP FYNOPTYMBEN SVOSGDELLILLILEILGEVAGNEKILLINGSFEC COMPRETABRONNOMMENKULETSLESGKANDESTCRUMEKIL REKOLSISLBRAVSTOPHHOHDEDEC\LIMP FYNOPTYMBEN SVOSGDELLILLILLEILGEVAGNEKIL FFROPTISCH SVOSGDELLILLILLEI		ŀ		WDHTGRRGGDSSSH\FFDFFAOVV\CALCGESTFVSVDS\IPE
KEGPRVLNGNPQQEDGGLAGITEQQGGAPRMEMIQAQELYHNX LKKKQNLQUINSIDSAITHUKKTERELEMGARYPSDIQEIE LRVKRQELUKAPDTYKALVVSVMYSKEPLOTESPESTELQSE LRQLSLUKAPDTYKALVVSVMYSKEPLOTESPESTELQSE LRQLSLUKAPDTYKALVVSVMYSKEPLOTESPESTELQSE LRQLSLUKAPGOTYKALVVSVMYSKEPLOTESPESTELQSE LRQLSLUKAPGOTYKADPRALLECLKULERQUEQODUM LQSISNSLILKGHGEDCLEAPEKYMYLLKOLBEQUEQODUM ALQGTQNPASPLESPDEVDSCDQPPRTSVPAPRRKQPRAVRTTE GEBETTSSVPQSTRPQDRSPLERVVRADALPLQLLLLLLLLACLL PSSEEDYSCTQANNF\ARSPYPHLRYTRGPPT  6139  52  1131 LGDWWSRTGGVLETPTSVLERARARGFCPTDSKRAPPREGE TRRPRARASSKRTL/LAGBUGGASVTUGHPLDTVKTRLQAGVV YGNTLSCIRVVYRRESMFGFKKMSPLASIAVYMVYGGYEN TORFIGGHRGEBEASPFTKSDLLASMWAGVVSVGLGGPVDL IKIRLQMQTPPVSGRQPFFEVQGSGCC\BPAYCGPVLICTTIV RNBGLAGLYRGASAMLLRDVGVCLYFTPVYFLSENITPEACTO PSPCAVMLAGGMAGAISWGTATPMDVVKSRLQADGVTLNKYKGV LDCISGSYGKGLKVFFRGTVTVANVAGFPMSAMMFLGVELSLQA IRQDHAVTSP  6140  594  136 RFELELIKRINSSWRPLGVPRCHRRNWKEPVRAQPLSVTVWAP RCQRP/QPPAPEPSSNNAVDPAIPTPRAAASAALELPLIGPAPV SVAPQAEABARSTFGPASSKLJCFTTGRGFQFRYQDAAGFREA FRQLELL/SPRQMLRDDI\RTKRG\TVENKUGGELIAPLGAGAR ARRIRRRTDVRITG  6141 2  984 AQGPSSFPCMPLKLGKKKANSKETAGLVEGEPTGRGGGSLS PSELLYCTLNTPRILDMELLAGQLGLEDPIRAHVKGIEKEVNVY KSEDSLIGHTITOMIGVVSPIKIRIKGKGVANVETICVGDHIESI NGENIVGKRHYDVAKKLKEKKELFTMKLIEPKGAFFIELRGK ARKSPARRLVFHAQLAHGSAGGVEGFSFSTVALOETIGDFAPP DEPVEDVWGVIGDAARRGL  6142  116 602 EARGGVGGAARRGL  6143 2802 270 FRWRIFLIGHGRARKGKVANSEETARIGFGGGGSLS REKQSILGCGARRARGKUMPSEPAVALDETIGJFAPP DEPVEDVWGVIGDAARRGL  6143 2802 270 FRWRIFLIGHGRARKGKVANKGEPLADLUNVSEVCYDRGNRRR FRURGPILGYMDIHHRIGEPQARMEENMERIGEVRQUMEKL REKQLSISLEAVSTDPPHIDHIDEPC\LSGCKSTQVFHILED LLUKNBERSKCNIVCTQFRISASVLAINVGLECKGENGFGGR SLCGGGRARKSRANLETGLSECKHLISTGKLLKERQ \QKSLVETIVNSKAGGIKKYQOSTYUGHADLUNPPYQX YSSPTGHALLYMDIPKINLDLILLELLAYLDKSPOPNIEGAVLI FLEDEVHIRG SVOSDFLILILLELLGKSDLHLILMSATVDES KFSTYFTHCPILLSIGGRSYPVEVHILDLILEPGFVLKDGEYC QKKLEESEEVTINVTSKAGGIKKYQOSTYUGHADDLINPPYQX YSSPTGHALVYNDIENGLASALGRGGGAARVRGFFCFRMYTRERFEGFFOH YSVEPILRVFLEGGGGAARGRGGGFFRRYCTRERFGFFOH YSVEPILRVFLEGGELGLLHKRNGLSPBEPTGKALDPPQLQVISN ANNLERGLGGGGAGGGGGGGGFRARGCFFRMYT				PSCPEHHYKOMEGDEMUDDUDDAGGTDVKDDVGVLLI DDGTDGG
LKIKKONLOQLINSDISAITTWLKKTEAELENLKNAKPPSDIGETE LRVKRIGELILKAFDTYKALVUSVINYSELOTESPESTELGER LRVKRIGELILKAFDTYKALVUSVINYSELOTESPESTELGER LRQLSILLWEAAGGAVDSWRGGLRQSLMQCQDFFIGSQNILLWILA SANNROKAHYTDPKADPRALLECREEDQFQYDM LQSISNSLLIKGHGEDCIRAERKYNYI\EKKLKOLREGVSQDLM ALQCTONPASPLPSPDEVDGDDPATSVPAPRAKQFRANKTTE GEBETESRVPGSTRPQRSPLSRVYRAALPIQLLLLLLLLLLLLLLLLL PSSEEDYSCTQANNF\ARSFYPMLRYTNGSPPT GEBETESRVPGSTRPQRSPLSRVYRAALPIQLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLL				
LRVKRIGEILKARFITYKALVVSVNYSSKEPLOTESPESTELOSR LRGLSILWEAROGGADSWRGINGSUNGCODPHOLSONILLWIA SAKNRROKAHYTDEKADPRALLECRREIMGLEREFLYEROPOYDM LOSISMSLILWIGHEDE IRABEKYUY LYEKKIKOLBEQVSODIM ALGOTONPASPLPSPDEVDSGDQPPATSVPARRAGPRAVRTTE GEBETESRVPGSTEPGRSPLSRVVRAALPIQLILLILLLACLI PSSEEDISSTQANNFI ARSFYPMREYTVERKALPRIGEPT SSEEDISSTQANNFI ARSFYPMREYTVERKALPRIGEPT ETERRPWEASSKKTI/LAGNIGGAASVI VGPPLDTVKTELOGGVG YGNTLSCIRVVYRRESMFGFFKGMSFPLASIAVYNSVVFGFSN TORFISGRRCGEPASP PPTLISGLILAWAGVSVGUIGGFVDL IKURLOMOTPPVSGROPREFVGGSCSCC\PAPYCOPVICITTIV RNEGLAGIFKGASMAILHDDVGYCLIPVFJESHITPBEACTG PSPCAWILAGGMAGAISWFTAPPHDVVKSRLOADGVINTXYKGV LDCISGSVGXEGLKVFFRGITVNAVRGFPMSAMFLGYELSILGA IRGDHAVTSP  6140 694 136 RFFLEEMBRERSRWPLGVPRRCHRRNWKEPVRAQPLSVTVWAP RCQRF/OFPAPEPSSNNAAVPBAIPTPRAAASAALELPLGPAPV SVAPQAEAEARSTTGPAGSRLOPETFRQRFRGFRYQDAAGFREA ARRIRRTDVRITT  6141 2 984 AGVGPRSPSPCMPJKKIRGKKKAKSETAGUVEGEPTGAGGGSLS AGRAPARRLVFHAQLAHGSATGRVEGFFSIGELVAQIAGAFETS PSCILUCTLNYPKIDMERLIGGGGLEVPFAHVWGTEKEVNVY KSEDSIGLITTONOVGVAFIKRIKOGVIDSVKTTCVGDHIESI NGENIVGWRYDVAKKLKELKKEELPTMKLIBPKKAFETIELRSK AGKSSGEKIGCGRATTRRSKGPATVEEMPSSTKAK\AIEKIDD VLELMGIRDIDLATTMFPAGKOKVNPDERAVALDETLGPFAPP FRYGDVILGVRWOJIGDAKRRGL 6142 116 602 EBEGEVCGARCCGDAPHVENREEETARIGPGVWESKEERALNN LYDENVINGENDEDEEDGVANKEPLALPINNSEYCUPRGNRR FRYQDILQVRWDIMBRIGGEDGAMREEGEPRQLMEKL REKOLSHSLRAVSTOPPHDHOHDEPCLAPCHORPR FRYRQPILQVRWDIMBRIGGEDGAMREEGEPRQLMEKL REKOLSHSLRAVSTOPPHDHOHDEPCLAPTONIPREVENCHORPR FRYRQPILQVRWDIMBRIGGEPRABRETIGGEVALDERIC VLENWENSENCHIVCHORDENEDGECONFORGER FRYRGPHLAVENSONFHYBORVSKYEURDHALDHLISSTCUPGORPR FRYRGPLILAVENSDEEDTINTSECKABLISTGKLLKERIO QUEPVFWHENSONGHYBOLHLILASSTLESCKABLSTGKLLKERIO CYCLEVFWHENSONGHYBOLHLILASSTLESCKABLSTGKLLKERIO CYCLEVFWHENSONGHYBOLHLILASSTLESCKABLSTOKALLERIO TILPBRVGNENSKENITYCOORGRAGRYRDCHORPRYLENDSVC GKFLEEESEVTINTYTKAKGGIKKYGGYTPOTGAHADINSPYCK YSSRTJHALLYATURGETTIPDVVFVIDGRFKKNKNYESS OMSSLVETFVSKASALQROGGRAGRYRDGFCFRMYTRERFEGOMD YSVPEILRVELEBLCHHIKKRNICSSPORDLAKSALDPPOLICVISN ANNLLRKIGGACELNBEKLTUPLGGRHAADDSDHL				LYTYONLOOLNED ESTTTEN LYTTEN EN LYNNYDDOD TORTE
LRQLSILMEAAQGAVDSWRGGIRQSLMQCDPFDGSQMILLIMIA SANNROKAHTUPKANDFARLLECREEMQLEKELVERQPOYDM LQBISNSLLIKIGHGEDCIEAEEKVHVI\EKKLKQUREQVSQDIM ALQGTONPASDLSPSPEDVSGODQPATSPPARAGPPANTTE GEEETTSRYPGSTTPQRSPLSEVVRAALPLQLLLLLLLLLACLL PSSEEDYSCTQANNF\ARSFYPMLRYTNGFPFT  6139 52 1131 LGDWWSRTCGVLETFSVLRRARAGFDTDSKWADPRLREGE TERRPWRASSKKTL/LAGGIGGASVIVGHPLDIVKTLQAGVG VGNTLSGIRVVRRESMFFFKKMSFPJLASIAVYNSVVFGVFSN TORFISQRGGEPEASPPFLSJLLASWAGVVSVGLGGPVDL IKIRLQMOTPPVSGGOPPREVQGSSCO-BPYQGFPVGITTIV RNEGLAGLYRGASAMLLRDVRQVCLYFIPYVFLSSWTTPBACTG PSSCAWWLAGGMAGAI SWGTAPPMDVVGSRLQADGVVINKYKGV LDGISGSYQKSGLKVFFRGITVNAVRGFPMSAAMFLGYELSLQA RRGDHAVTSP 6140 694 136 RPELEWBLASSSKRVFTGITVNAVRGFPMSAAMFLGYELSLQA RCQRF/OPPAPEPSSNNAAVPRAITPTRAAASAALEDLGJADV SVAPQABEAEASTTGPAGGSRLOPETFRORFROFRYQDAAGFREA FROLREL/SPRQWBRADVBAITPTAAASAALEDLGJADV SVAPQABEAEASTTGPAGGSRLOPETFRORFROFRYQDAAGFREA FROLREL/SPRQWBRADVBAITPTAAASAALEDLGJADV SVAPQABEAEASTTGPAGGSRLOPETFRORFROFRYQDAAGFREA FROLREL/SPRQWBRDITTTNAVRGFPSSTQELVAQLAGAFEIS PSEILYCTLNTPRIDMERLLGGGLGLEDFIFAHVKGIEKEVNVY KSEDSLGITTIDNSVCYAPIKRINGGVISVKTCVGOBIESI NGENIVGGRRYDDVAKKKKKKKETAGLVSKKTETELVSKTCVGOBIESI NGENIVGGRRYDDVAKKLKELKKEELTPMKLIEPKAGTELSLRSK AGKSSGERIGTATTLRLERSKOPATVENSETSKKAPISLEKKDD VLELYMGIRDIDLATTMFPAGKDVNDEFRAVALDETLGDFAPP DEPVPDWGVIGGAKRRGL 6142 116 602 EARGEVCGARCCGDAPHVENREETTARIGFOWNSKEERALINN FRUNOPILQYRWDIMHRLGEPQARMREENMERIGEEVRQLMKL REKQLSHSLRAVSTDPPHDJHHDDFC LMP FRWRTPLIKENNOMENENDEETGRAFGGSKTOYPHFLLED LLINBWERSKCNIVCTOPRRISMSKLANNRVCDBIGCENGPGGRN SLCGYGIRMSRACCESTRLLYCTTGVLLKKLQEDGLLSNVS/HM FFUNDEV/HRRSVGOTPRRISMSCHLHILSTSCKAPTVDSE KFSTYFTHCPILLSIGGSSYPVEVHLEDILEETGRVLEKDSEYC QKFLEEBEEVTINVTKKARGIKKYMGLHKSINSINSPYVG VSSPGIRAVRNSKCNIVCTOPRRR SYNSTALNRVCDBIGCENGPGGRN SLCGYGIRMSRACCESTRLLYCTTGVLLKKLQEDGLLSNVS/HM FFUNDEV/HRRSVGOTBRRFYSERKYALHSILSTOQDAAF TLPPGVRKIVLANTNAETGITIPDVVFVIDTGRTKENKYHESS QMSSIVETFVSKASALQRGGRAGRINGGCFRMTIRRFPGGFMD SVEPEILKVGLBELCLHIKKCNIGSSPDFLIKALDSHLLILSSGLODAAP TLPPGVRKIVLANTNAETGITIPDVVFVUDTGRTKENKYHESS QMSSUTFTVSKASAGLARGGRAGRAGGCFRMTITRRFPGGFMD SVSPEILK		ł	l	
SAKNRROKAHUTDPKADPRALLECRRELMOLEKELVERQPOUMM LOSISNELLIKGHGEDCIPAEEVIJKEKULGERGVSGDIM ALQGTONPASDLDSFDEVDGSDQPPATSVPAPAKQPPANKTTE GEETTESRYGGSTPRORSPLSRVYRALPOLQLLLLLLLACLL PSSEEDYSCTQANNF\ARSPYPMLRYTNGPPPT  1098EEDYSCTQANNF\ARSPYPMLRYTNGPPPT 1098EEDYSCTQANNF\ARSPYPMLRYTNGPPPT 1098EEDYSCTQANNF\ARSPYPMLRYTNGPPPT 1098EEDYSCTQANNF\ARSPYPMLRYTNGPPPT 1098EEDYSCTQANNF\ARSPYPMLRYTNGPPPT 1098EEDYSCTQANNF\ARSPYPMLRYTNGPPPT 1098EEDYSCTQANNF\ARSPYPMLRYTNGPPPT 1098EEDYSCTQANNF\ARSPYPMLRYTNGPPPT 1098EEDYSCTQANNF\ARSPYPMLRYTNGPPPT 1098EEDYSCTQANNF\ARSPYPMLRYTNGPPPT 1098EEDYSCTQANNF\ARSPYPMLRYTNGPPPT 1098EEDYSCTQANNF\ARSPYPMLRYTNGPPPT 1098EASSWKELLYSPRGYTYNAVGRSPLASTAVYNSVYFGVFSN 1098EASSWKELKYPFRGYTVNAVGRSPLAGGGYHCETTTU 1098EAWLAGGMAGAISWGTATTMDVVKSRLQADGVYLNYKKGV 1001507QKEELKYPFRGYTVNAVGRSPMSAAMPLGYELSLQA 1001507QKEELKYPFRGYTVNAVGRSPMSAAMPLGYELSLQA 1001507QKEELKYPFRGYTVNAVGRSPMSAAMPLGYELSLQA 1001507QKEELKYPRQURAFTERWKEPPTRAASAALELPLGPAV 1001507QAFEELKERSSWRPLGVPRRCHRRIWKEPVRAQPLSVTVWAP 1001507QAFEELKERSSWRPLGVPRRCHRRIWKEPVRAQPLSVTVWAP 1001507QAFEELKERSSWRPLGVPRRCHRRIWKEPVRAQPLSVTVWAP 1001507QAFEELKERSSWRPLGVPRRCHRRIWKEPVRAQPLSVTVWAP 1001507QAFEELKERSSWRPLGVPRRCHRRIWKEPVRAQPLSVTVWAP 1001507QAFEELKERSSWRPLGVRAGGGSLS 1001507QAFEELKERSSWRPLGVRAGGGSLS 1001507QAFEELKERSSWRPLGAGGGSLS 1001507QAFEELKERSSWRPLGGGGGSLS 1001507QAFEELKERSSWRPLGGGGGSLS 1001507QAFEELKERSSWRPLGGGGGGSLS 1001507QAFEELKERSSWRPLGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG				
LOBISNSLIKGHGEDCIEREKYHVI\EKKIKGLREQUSQDIM ALGGTONPASPLBSTDEVDGGDQPSPANTTE GERETESRYPGSTPPQRSPISRVVRAADPLQLLLLLLLLLACLL PSSEEDYSCTQANNF\ARSPYPMLRYTNGPPT 6139 52 1131 LGDWWSRTCGVLETPTSVLRRRARGFCPTDSKWADPRLREGE TERRPWEASSWKTL/LAGMIGGASVIVGHDLDTVKTRLQAGVG YGNTLSCIRVVYRRESSWGFFKGWSGSGC\EPAYQGPVLCTTIV RNEGLAGLYRGORSAMLLRDVPGYCLYPIPVYFLSEWITPEACTG PSPCAVWLAGGMAGAI SWGTATTMUXSRLQADGVYLNKYKGV LDCISQSYQKEGLKVFFRGITVNAVRGFPMSAAWITGYBLISLQA 136 RFELEWALGSRWAGI SWGTATTMUXSRLQADGVYLNKYKGV LDCISQSYQKEGLKVFFRGITVNAVRGFPMSAAWITGYBLISLQA RGCRP/QPPAPEPSSPMAAVPEAIPTPRAAASALELPLGPAPV SVAPQABABARSTEPAGSSKIGPTFRQRFRQFRYQDAGSPTRA FRQLREL/SPRQWLRPDI\RTKEQ\IVEMLVQEQLLAILPEARA ARIKRRTIVRITG ARRIBRTIVRITG ARRAPARRIVFHAQLANGSATGRVEGFSIGLEVAQTAGGGSLS ASRAPARRIVFHAQLANGSATGRVEGFSIGLEVAQTAGGGSLS ASRAPARRIVFHAQLANGSATGRVEGFSIGLEVAQTAGGGSLS ASRAPARRIVFHAQLANGSATGRVEGFSIGLEVAQTAGGFSIG FSGLIL/SPRQWLRPDI\RTKRCGGVIDSVKTICVGOHIESI NGENIVGKRHDVDAKKLKELKKELFTHKLIEPKKAFEIELRSK AGKSSGEKIGGGRATLLRSKGGATVEEMPSETAK\AISKIDD USLEYMGIRDIDLATTHFPEAGKKAHLEPKKAFEIELRSK AGKSSGEKIGGGRATLLRSKGGATVEEMPSETAK\AISKIDD USLEYMGIRDIDLATTHFPEAGKAHLEIGKLAGFLEGFFIGHFG BEPVEDVNGVIGOAKRRGL LIVERVNQENDEKDEVANGEPLALPLNVSEYCVPRONRRR FRVRQPILQYRWDIMHRLGEFQARMEENMERIGEEVRQLMERL REKQLSHGLARVSTOPHHDHDIDEPC\LMP FRWRIFTHCPILRISGGSYPVEVFHLEDIIETGFVLEKRRQ SLGYQIRMESRAGESTRLLYCTTGVLRKLOEDGCLENGFGGRN SLCGYGIRMESRAGESTRLLYCTTGVLRKLOEDGLLSCTNGFGGRN SLCGYGIRMESRAGESTRLLYCTTGVLRKLOEDGLLSCTNGFGGRN SLCGYGIRMESRAGESTRLLYCTTGVLRKLOEDGLLSCTNGFGGRN SLCGYGIRMESRAGESTRLLYCTTGVLRKLOEDGLLSCTNGFGGRN SLCGYGIRMESRAGESTRLLYCTTGVLRKLOEDGLLSCTNGFGGRN SLCGYGIRMESRAGESTRLLYCTTGVLRKLOEDGLLSCTNGFGGRN SLCGYGIRMESRAGESTRLLYCTTGVLRKLOEDGLLENGFGRN FFVDEVYHRESVOGSFTLLITKERRVVVVAGGFY\GSGKSTOPPHSTLESSYC QKFLEESEEVTINVTEKAGGIKKYGEYTPVGTGAHADLNFYQK YSSRTQHAILYMNPHKUNLDLILLLALLDKSPQFRNIBGAVLI FFLOGLANLAGGRAGALAGGAAGAPGADAGAPGCOFGCPGFTMTTRRRFEGFMO YSVPEILRVPLEELCCHIMKCRLGSPEDFLSKALDDPQLQVISN ANNLRKUGAGLAGAAADGSALAGAAADASDHL GGCLDDVATLAAVWTEKSEPTTTJGCALAAADASDAL				
ALGOTONPASPLASTDEVDASDQPPATSVPARNKQPPANKTTE GEBETESRVPGSTPROPRSPISTURVARALPIQLILLILLILACIL PSSEEDYSCTQANNF\ARSPYPMLRYTNGPPPT  LGGWVWSRTGVLETPTSVLRRARARGFCPTDSKWALDFLREGE TERRPWEASSWETL\LAGNIGGASVIVCHPLDTVKRTLQAGVG YGNTLSCIRVVYRRESMEGFFKGMSPPLASIAVYNSVVFGVFSN TQRILSGURCGEPFRSASPPRITSDLLAWNAGVVSVGLGGPVDL IKKRLQMCTPPVSGRQPRFEVQGSGSC\DEPAYGCPVHCITTIV RNSGLGLGLYGRASMALDVUSGVCLYFIPYVFLSWITTPEACTG PSPCAWHLAGGMAGAISWGTATPMDVVKSRLQADGVVLNYKGV LDCISGSYQKBGLKVFFRGITVNAVNGFFMSAMFLCYELSLQA IRGDHAVTSP  6140 694 136 RFPLELWRLRSRSWRPLGVPRCHRRNWEBPVRAQPLSVTVWAP RCORP/OPPAPEPSSPANAUPEAIPTPRAASAMELPLGPEDV SVAPOAEAEARSTPCDPASSRLGPETPGRPRQFRYQDAAGPRRA FROLRELS/SPRQWLRPDI\RTKEQ\IVENUVQEQLLAILPEAAR ARRIRRTDVRITG  6141 2 984 AQGGPSRFCKMPLKLEGKKKAKSKETAGLVEGEFTGAGGGSLS ASRAPARRIVFHAGLAMGSATGRVEGFSSIGELVAQIAGAFEIS FSEILYCTINTPKIDMRRLLGGGLGLEDFIFAHVKGIEKEVNVY KSEDSLGLTITDNGVAFAFKTKLGGVLDSVKTICQDHIESI NGENIVGGRHVDVAKKLKELKKEELFTMKLIEPKKAPEIELRSK AGKSSGEKIGCGRATLRLRSKGPATVEEMPSETKAK\AIEKIDD VLELYMGIRDIDLATTMFEAGGKKVNPDEFAVALDETLGDFAPP DEPVPDWGVJGDAKRRGL  6142 116 602 EARGBUCGAKCCGDAPHVENREEETARIGFGVMESKEERALNN LIVENVNQENDEKDEKBOVANKGEPLALDLAVSSYCVPRGNRRR FRUROPILQYRRDIMBLGEPOARMEIGEVRQLMEKL REKQLSHSLRAVSTDPPHHDHHDEPC\LMP FRUROPILQYRRDIMBLETSDLESKKAHLSIQKLKERVQ VSEVERSNSVGSPRLILIKERLSGGGGGRN SLCGVGIMESFACESTRLLYCTIVAKGEGVGGGKSKSTOVPHFILLED LLLINBMEASKCNIVCTOPRRISAVSLAMRVCDBLGCENGFGGRN SLCGVGIMESFACESTRLLYCTIVAKGGGGGSKSTOVPHFILLED LLLINBMEASKCNIVCTOPRRISAVSLAMRVCDBLGCENGFGGRN SLCGVGIMESFACESTRLLYCTIVAKIAGET\GSGKSTOVPHFILED LLLINBMEASKCNIVCTOPRRISAVSLAMRVCDBLGCENGFGGRN SLCGVGIMESFACESTRLLYCTIVAKIALDETGLIELSVNS/HM FTVDEV\HERNSVGSPPLILIKELLGLGKRLDEDGLISNNS/HM FTVDEV\HERNSVGSSPPLILIKELLGLGKRLDEDGLISNNS/HM FTVDEV\HERNSVGSSPPLILIKELGDCFRYSTERFGFMM SCGCGVILEBEBEVTINNTSKAGGIKKYGEYIPVGTGAHADLNFFYQK VSSRTQHAILYMNPHKINLDLILELLALVKSPOFRNIBGAVLI FLEGLAHALQUVDLLGBNGRFYSSRYVIAHABSLLSTOQQAAAF TLPPGVKKIVLANTIAETGITIPDVVFVIAHABSLETGOQAAF TLPPGVKKIVLANTIAETGITIPDVVFVIAHABLETGOQAAF TLPPGVKKIVLANTIAETGITIPGOVFFVTTRKKSNYHESS OMSSLVETTFVSKASALDGRGGAGRAVFOFFCFMYTTE				
GEEETESRYPGSTRORSPLSRVYRALPLOLLLLLLLLACLL PSSEEDYSCTOANNY NASSTPHAYTNORPPT  131  LGDWVWSRTCGVLETFTSVLRRARARGFCPTDSKWALPRLREGE TERRPWEASSWKTL/LAGWIGGAASVIVQPLDIVTKTRLQAGVG YONTLSCIRVVYRRESMFGFFKGWSFPLASIAVYNSVVFGVFN TORFLSQHRCGEPRASPPRTLSDLLLASWAGVVSVGLGGPVDL IKIRLQMOTPPDVSGROPFFFGGGSGCC\PEPATGGPVGCPVHCITTIV RNEGLAGLYRGASANLLRDVPGYCLYFIPYVFLSENITPEACTG PSPCAWWLAGGMAGAISWNTATDVVKSKLQAGVYLNKYKGV LDCISGSYQKEGLKVFFRGITVNAVRGFPMSAAMFLGYELSLQA IRODHAVTSP  6140  694  136  RFELELWRLRSRSWRPLGVPRRCHRRNWKEPVRAQPLSVTVWAP RCQRF/QPFAPEPSSDNAAVPEATPTRAARSAALBLDLGAPLV SVAPQAAEARASTFGAGSGLFFKGRFRGYRGFYGDAASPREA FRQLREL/SPRGWLRPDI\RTKEQ\IVEMLVQEGLLAILPEAAR ARRIRRTDVRITG  6141  2  984  AQVGPRSRPSCWPLKLBGKKKAKSKETAGLVEGEPTGAGGGSLS ARRARRLVFRAGLAHGSAGTGVEGFSTIGLIYAQIAGAFEIS AGRAPARRLVFRAGLAHGSAGTGVEGFSTIGLIYAQIAGAFEIS NGENIVGWRHYDVAKKLKELKKEKSFTSTLGVKGGTGAGGSLS AGRSSGEKIGCGRATLRLRSKGPATVEEMPSTKAK\AIEKIDG VLELWGGRDIJDATTHPEAKGKKVNPDEFSVALDETLGDFAPP DEFVPDVWGVIGDAKRGGL  6142  116  602  EREGEVCGAKCCGAPHVERREBETARIGFGWMESKERFALNN LIVENVNQENDEKCGAPHVERREBETARIGFGWMESKERFALNN LIVENVNQENDEKCGAPHVERREBETARIGFGWMESKERFALNN LIVENVNQENDEKCAPATURERWERTGGEVRCJMBKL LIVENVNQENDEKCAPATURERWERTGGEVRCJMBKL LIVENVNQENDEKCHGVERTSSTGVPHFLLED LLINEWASKCNIVCTOPRRISAVSLANKCOBLIGGENGPGGN SLCGYGIRMESRACESTRLLVCTIVLLRKLDEGGLISNVS/HM FIVDEV\HRR\SVQSDFLLILKEILQKGGLISNVS/HM FIVDEV\HRR\SVQSDFLLILKEILQKGGLISNVS/HM FIVDEV\HRR\SVQSDFLLILKEILQKSCPFNIERGAVIL SKRTYFTRCFILRIGRSYPVEVHHEBILSTOQDAAAF TLPPGVRKIVLANNIABTGITTPDVDTGATKENKYHESS OMSSLVETTVSKASALDKOGRAGVROGPCFRNYTERREGWD VSVPEILRVPLEELCHIMKCNLGSPEDPLSKALDPPQLQVISN ANNILERKIGACELBEPKLITPLGQHLAALDVNKIGKMLIFGGNIF VSVPEILRVPLEELCHIMKCNLGSPEDPLSKALDPPQLQVISN ANNILERKIGACELBEPKLITPLGQHLAALDVNKIGKMLIFGGNIF CGCLDDVATLAAVWTEKSEPTTPTGGRADADABALAMADSDHL	•			
PSSEEDYSCTQANNF\ARSFYPMLRYTNGPPT   LGWWWSRTGGULEFTSTSULRARGEPCPDSKWALDFILREGE   TERRPWEASSWKTL/LAGWIGGASVIVGHPLDTVKTRLQAGVG   YGNTLSCIRVVYRRSSMFGFFKGMSFPLASIAVYNSVVFGVFSN   TORFISQHRCGEFFASPPRTLSAIAVYNSVVFGVFSN   TORFISQHRCGEFFASPPRTLSDLLLASMVAGVVSVGLGGPVDL   IKIRLQMQTPPVSGRQPRFEVQGSGSCC\PPAYQGPVHCLITTIV   REGLAGLINGRAGAAILRDVPCVLIFIPVYFLSEBHITPBACTG   PSPCAVWLAGGMAGAISWGTATPMDVVKSRLQADGVYLNKYKGV   LDCISGYQKEGLKVFFRGITVNAVRGFPMSAMFLGYELSLQA   IRGDHAVTSP     G140   694   136   RFELELWRLRSRSWRPLGVPRRCHRRNWKEPVRAQPLSVTVWAP   RCQRP/QPPAPEPSSPNAAVPEATPTRAAASAALEIPLGPAPV   SVAPQAEAEARSTEGPAGSRLGPETFRQRFRQFRYQDAAGPREA   FROLERL/SPRQWLRPDI\RTKEQ\IVEMLUGEQLLAILPEARA   ARRIRRTDVRITG     AQVGPRSPCKMFLKLRKKKKAKSKETAGLVEGEPTGAGGGSLS     ASRAPARRLVFHAQLAHGSATGRVEGFSSIQLIYAGIAGAFEIS     FSELLYCTLNTPKLDMRELLGQLGLEDFJFAHVKGIEKEVNVY     KSEDSLGJTITONGGVAFIKRINGGVIDSVKTICVGGHIESI     NGENTUGRRHYDVAKKLKELKKEELFTMKLIEPKKAFEIELRSK     AKKSGEKIGCGRATLRLRSRGATLLRSKGVIDSVTEMPEFFERAK\ATEKIDD     VLELYMGIRDIDLATTMFEAGKDKVNPDEFAVALDETLGDFAFP     DEPYDDWGVJGDAKRRGL     LIVENVNQENDEKBGVANKGEPLALPLNVSEYCVPRGNRRR     FPURGYILQYRWINFILGEFORAMREENDERIGEEVRQLMEKL     REKQLSHSLRAVSTDPPHHDHHDEPC\LMP     FPURGYILQYRWRINNLETISEGKRYDVPHFLLED     LLLNEWEASKCNIVCTOPRRISAVSLANRVODELGEENOPGGRN     SLGGYGIRMESRAGESTRLLVTGULLKRLEGEGLISNVS/HM     FTUDEV\HER\SVQSDFLLILKELDGGLGLISNVS/HM     FTUDEV\HER\SVQSDFLLILLKELDGGLGLISNVS/HM     FTUDEV\HER\SVQSDFLLILLKELDGGLGLISNVS/HM     FTUDEV\HER\SVQSDFLLILLKELDGGLGLISNVS/HM     FTUDEV\HER\SVGSDFLUILINDRFTYFUXLBRAULTHEAVTUDE     KFSTYFHCPILLR ISGRSYPVPUTULRRLLGBGGLLSNVS/HM     FTUDEV\HER\SVGSDFLUILIKLBETLDGGLANAFTUDE     KFSTYFHCPILLR ISGRSYPVPUTULRRLLGBGGLLSNVS/HM     FTUDEV\HER\SVGSDFLUILIKLBETLDGGLLSNVS/HM     FTUDEV\HER\SVGSDFLUILIKNDRFYFSKVVLALHSILSTGQAVLA     TLPPFGVKKIVLATNIABTGITTPDVYTYTRERFEGFMD     YSVPEILRVPLEELCLHIMKCNLGSPEPLSKALDPPQLVVISN     ANNILERLIGACELBEPKLITPLGQHLABLDVNKIKMLIFGAIF     GCLDPVATLAAVWTRKSSFTTJGRADEADLABLANADSDHL			!	
Communication				PSSEEDVSCTOANNE/ ADSEVDMI DVTMCDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
TERRPWEASSWKTL/LAGWIGGASVIVGIPLDTVKTRIQAGVG YGNTLSCIRVVYRRESMEGFFKGMSFPLASIAVYNSVVEGVESN TORFISQHRCGEPEASPPRTLSAIAVYNSVVEGVESN TORFISQHRCGEPEASPPRTLSAIAVYNSVVEGUEGPUL IKIRLQMQTPPVSGROPRFEVQGSCSCC\EPAYQGEVHCLTTIV REGLAGLYRGASANLLRDVPGYCLYFIPVYFLSEMITPEACTG PSPCAVWLAGGMAGAISWGTATPMDVVKSRLQADGYYLNKYKGV LDCISGSYQKEGLKVFFRGITVNAVRGFPMSAMMFLGYELSLQA IRODHAVTSP 6140 694 136 RFELELWRIRSSSWRPLGVPRCHRRNWKEPVRAQPLSVTVWAP RCORP/OPPAPPSSPNAAVPEAIPTPRAAASAALELPLGPAPV SVAPQAEAEARSTFOPAGSRLGPETFRGRRGPRYQDAAGPREA FRQLREL/SPRQWLRPDI\RTKEQ\IVEMUQEQLLAILPEAAR ARRIRRTDVRITU 6141 2 984 AQVGPRSRPSWAPLAHGSATGRVEGFSSIQELYAQIAGAFEIS SEELLYCTINTPKIDMRELLGGQLGLEDFIFAHVGGIGGSLS ASRAPARRLVFHAQLAHGSATGRVEGFSSIQELYAQIAGAFEIS PSELLYCTINTPKIDMRELLGGQLGLEDFIFAHVGGIEKEVMVY KSEDSLGITITDNGVGYAFIKRIKDGGUIDSVKTICVGGHIESI NGENIVGRHYDVANKKLKELKEHFFMKLIEPKKHFEIELRSK AGKSSGEKIGCGRAPILRIRSKGPATVEEMPSETKAK\AIEKIDD VLELYMGIRDIDLATTMFEAGKDKVNPDEFAVALDETLGDFAFP DEPYPDWGVIGDAKRRGL 6142 116 602 EAEGEQVCGAKCCGGAPHVERREEETARIGPGVMESKEERALNN LIVEMVNQENDENDEKEQVANKGEPLALPLNVSEYCVPPGNRRR FRVQOPILGYRRDIMHRLGEPQARMREEMERIGEEVRQLMEKL LLVEWNQENDENDEKEQVANKGEPLALPLNVSEYCVPPGNRRR FRVQOPILGYRRDIMHRLGEPQARMREENMERIGEEVRQLMEKL REKQLSSLRAVSTDPPHHDHHDEPC\LWG  6143 2802 270 FMRITFLGPHNQQMWKIWMLLETSLESCKAHLSIQKLLKER\Q QLPVFKHRBGIVETLKRRRVVVVAGET\SGKSTQVPHFLLED LLLMEMEASKCHIVCTOPRRISALANRVCDELGECNDGFGGN SLCGYQIRMESRACESTRLLYCTTGVLLRKLQEDGLLSNVS/HM FIVDEV\HERS\SVGSDFLLIILKEILQENGDLHSNVS/HM FIVDEV\HERS\SVGSDFLLIILKEILQENGDLHSNVS/HM FIVDEV\HERS\SVGSDFLLIILKEILQENGDHLSNVS/HM FIVDEV\HERS\SVGSDFLLIILKEILQENGDHLSNVS/HM FIVDEV\HERS\SVGSDFLLIILKEILGRSYPVUPTVLEKDSEYC QKFLEEESEVTINVTSKAGGIKKYQEYIPVQTGAHADLNPFYQK YSSRTQHAILYMNPHKINLDLILELLAYLDKSPOPPNIEGAVLI TLPPPGVKKIVLANINIAETGITIPDVVFVUTGARTADHAPFYQK YSSRTQHAILYMNPHKINLDLILELLAYLDKSPOPPNIEGAVLI TLPPPGVKKIVLANINIAETGITIPDVVFVUTGARTADHAPFYGK YSVPEILBEVPLEEELCLHHMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRKIGACELNEPKLTPLQGHLAALPVNVKIGKMLIFGAIF AMNLLRKIGACELNEPKLTPLQGHLAALPVNVKIGKMLIFGAIF	6139	52	1121	
YGNTLSCIRVVYRRESMFGFFKGMSPPLASIAVYNSVUFGUFEN TORFLSOHRGERPEAS PPRIDLILASMYAGVVSVGLGGPVDL IKIRLQMQTPPVSGRQPRFEVQGSCSCC\EPAYQGFVHCITTIV RNEGLAGLYRGASAMLLRDVGYCLYF1PVFLSEMITEACTG FSPCAWLLAGGMAGAISMGTATMDVVKSRLQADGYYLMKYKGV LDCISGSYQKEGLKVFFRGITVNAVRGFFMSAMFLGYELSLQA IRODHAVTSP RCQRF/QPPAPESSBNAAVBGAIPTRAAASAALELPLGPAPV SVAPQAEAEARSTFCPGAGSKLGPETTRQRFRGPRYQDAAGPRIA FRQLREL/SPRQMLRPDI\RTKEQ\IVEMLVQEQLLAILPEAAR ARRIRRTDVITIG  6141 2 984 AQVGPRSRPCKMFLKLRGKKKAKSKETAGLVEGEPTGAGGGSLS ASRAPARRLVFHAQLAHGSATGRVEGFSIQELYAQIAGAFEIS FSEILYCTLNTFKIDMERLLGGQLGLEDFIFAHVKGISEKVMYV KSEDSIGLITITNIGVSYAFIKRIKDGGVLGEVBIFAVKGISEKVMYV KSEDSIGLITITNIGVSYAFIKRIKDGGVLGEVBIFAKKALEKIDD VLELYMGIRDIDLATTMFEAGKDKVNPDDEFAVALDETLGDFAFP DEFYEDVWGVIGDAKRGL LIVENVOQENDE BEDEELDETMALIEFTGLENK AGKSSGEKIGCGRATLRLRSKGPATVEEMPSETKAK\AIEKIDD VLELYMGRIDDEAKRGL LIVENVOQENDE BEDEELDEVALDLENVESYCVPRGNRRR FRVRQPILQYRWDIMHRLGEPQARMREENMERIGEEVRQLMEKL REKQLSHSLRAVSTDPPHHDHIDERC\LMP 6142 116 602 EAEGGOVCGKCCGDAPHVENREESTARIGFGVMESKEERALINN LIVENVOQENDE BEDEELDEVALDLENVESYCVPRGNRRR FRVRQPILQYRWDIMHRLGEPQARMREENMERIGEEVRQLMEKL REKQLSHSLRAVSTDPPHHDHIDERC\LMP 6143 2802 270 FRMRTIPLHGPWRQOMKIKULLETSLESCKAHLSIQKLLKER\Q QLFVFKHRDSIVETIKKRRVVVVAGET\GSGKSTQVPHFLLED LLLNEWEASKCNIVCTOPRRISAVSLANRVCDELGCENGPGGRN SLCGYQIRMESRACESTELLIYCTTISVLEKLQEDGLLSNVS/HM FIVDEV\HER\SVQSDFILIILKEILQKRSDLHLILMSATUDSE KSSTYFTHCPILRISGRSSYPEVFHLEDIIEFGFVLKSDESYC QKFLEEEERVTINVTSKAGGIKKYQEYIPVQTGAHADLMPPYQK YSSRTQHAILYMNPHKINLDLILLELLAYLDKSPQFRNIEGAVLI FLPGGLAHQQLVDLLSNDRRFYSERYKVIALHSILSTQCQAAF TLPPGVRRIVLATHIAETGITIPDVVVIDTGRTKENKYHESS OMSSLVETTVSKASAALQRGGRGRGRVRDGFCFRWTTRERFEGFMD YSVPEILRWPLEELCLHMKCRLGSPEDFLSKALDPPQLQVISN AMNLLKKIGACELNEPKLIPLGQHLAALPVWVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGKKDESALALANADSDHL	0133	) 22	1131	
TORFISOHRGEPEAS PPRTLSDLLLASWAGGVESUGGPUDL  IKIRLQMQTPPVSGRQPRFEVQGSCSCC\PPAYQGPUTCITTIV  RNEGLAGLYRGASAMLLRDVPGYCLYFIPYVFLSEWITEACTG  PSPCAWWLAGGMAGAISWGTATTMDVVKSRLQADGYYLNKYKGV  LDCISGSYQKEGLKVFFRGITVNAVRGFFMSAAMFLGYELSLQA  IRODHAVTSP  6140 694 136 RPELELWRLRSRSWRPLGVPRRCHRRNWKEPVRAQPLSVTVWAP  RCQRP/QPPAPEPSSDNAAVPEAIPTPRAAASAALELPLGPAPV  SVAPQAEAEARSTPGFAGSRLGPETTROKFRGPKYGDAAGPREA  ARRIRRTDVRITG  4 AQVGPRSRPCKMPLKLRGKKKAKKETAGLVEGEPTGAGGGSLS ASRAPARRLVFHAQLAHGSATGRVEGFSSIQELYAQIAGAFEIS PSEILYCTLNTPKIDMERLLGGQLGLEDFIPAHVKGIEKEVNVY  KSEDSLGLTITDNUGGYAFIKRIKDGGVIDSVKTICVGDHIESI  NOENIVGWRHYDVAKKLKELKKEBLFTMKLIEFKKAFEIELRSK AGKSSGEKIGCGRATLRLRSKGPATVEEMPSSTKAK\AIEKIDD  ULELWAGIRDIDLATTMFEAGKVANDEFAVALDETLGDFAFP DEPVFDVWGVIGDAKRRGL  6142 116 602 REGEGVCGAKCCGDAPHVENREESTARIGPGVMESKEERALNN LIVENVNOENDEKDEKEVANKGEPLALPLNVSEXCVPRGNRRR FRVRGPILGYRMDIMHRLGEPQARMEENMERIGEEVRQLMEKL REKQLSHSLRAVSTDPPHHDEDFC\LMP  6143 2802 270 FRMRIFLHCPWNQOMKIWNLLETSLESCKAHLSIQKLLKER\Q V\LPVFKHRDSIVETLKRRRVVVVAGET\GSGKSTQVPHFLLED LLINEMPASKGNIVCTOPRRISAVSLANRVCDEGGGRN SLCGYQIRMESRACESTRLLYCTTGVLLRKLQEDGLLSNVS/HM FIVDEV\HER\SVQSDFLLILLKELLQKRSDLHLILMSATVDSE KSTYFTHCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC QKFLEEESEVTINVTSKAGGIKKYQEYIPVQTGAHADLNPFYQK YSSRTOHALLYNDHKINLDLILLLALDLSOPPRNIEGRAVI.I FLPGLAHIQQLYDLLSNDRRFYSERYKVIALHSILSTQDQAAAF TLPPGVRKIVLATNIAETGITIPDVVFUTDTGRKEKMKYHESS GMSSLVETFVSKASALQRGGRGRRVRDGFCFMYTTREFEGFMD TSVPBILRVPLEELCLHMKCNLGSPEDFLEKALDPDQLQUISN AMNLLKKIGACELNEPKLTPLGQALAALANVTSKSALANRVCDGVAIF				
IKIRLOMOTPPVSGROPRFEVOGSSCC\EPAYOGPVHCITTIV RNEGLAGLYRGASAMLLRDVPGYCLYFIPYVFLSEWITPEACTG PSPCAWLAGGMAGAISWGTATPMDVVKSRLQADGVILNKYKGV LDCISGSYQKEGLKVFFRGITVNAVRGFPMSAAMFLGYELSLQA IRGDHAVTSI  6140 694 136 RPELELWRLRSRSWRPLGVPRRCHRRWKEPVRAQPLSVTVWAP RCQRP/QPPAPEPSSDNAAVPEAITPTRAAASAALELLIGPAPV SVAPQAEAEARSTGPASGRIGPETFRGYRQFKYQDAAGPREA ARRIRRTDVRITG  6141 2 984 AQVGPRSRPCKMPLKURGKKKAKSKETAGLVEGEPTGAGGGSLS ASRAPARRLVPHAQLAHGSATGRVEGFSIQELVAQIAGAFEIS PSEILVCTLNTPRIDMERLIGQQLGLEDFIPAHVKGIEKEVNVY KSEDSLGLTITDNGVGYAFIKRIKDGGVIDSVKTICVGDHIESI NOENIVGWRRYDVAKKLKELKKEELFTMKLIEPKKAFFIELRSK AGKSGEKIGGGATLALRGKGPATVEEMPSETKAK,AIEKIDD ULELYMGIRDIDLATTMPEAGKDKVNPDEFAVALDETLGDFAFP DEPVFDVWGVIGDAKRRGL  6142 116 602 EAEGEQVCAKCGGDAPHVENREEETARIGFGVMESKEERALNN LIVENNORENDEKDEKEQVANKGEPLALPLNVSSPCVPRGNERR FRVRQPILQYRWDIMHRLGEPQARMREENMERIGEEVQLMEKL REKQLSHSLRAVSTDPPHHDHHDEFC\LMP FRWIFIHOPWNQQMKKINLLETSLESCKHALSIQKLLKER\Q VLPVFKRDSIVETLKRHRVVVVAGET\GSGKSTQVPHFILED LLINEWASKCNIVCTQPRISAVSLANRVCDBLGCEMGPGGRN SLCGYQIRMESRACESTRLLYCTTGVLLKKLQEDGLLSNVS/HM FIVDEV\HRK\SVGSDFLILKELIKLIKLICKESCHHLIGHANTVDSE KFSTYFTHCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC QKFLEEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNPFYQK YSSGRTQHAILYMPHKINILLIKLILKENDKSPGFRIEGAVLI FLPGLAHIQQLYDLLSNDRFFYSERXVIALHSILSTQDQAAAF TLPPPGVKKIVLANNAERSPTSPTSPTKVIALHSILSTQDQAAAF TLPPPGVKKIVLANNAERSPTSPTSPTKENTKENSEGFMF YSVPBILRVPLEELCLHIMKCNLGSPBDFLSKALDPPQLQVISN AMNLLKKIGACELNEPKITPLGGNLARAALPANVKIGKMLIFGAJIF GCLDPVATLAAVWTEKSPFTTPIGRKDEADLAKSALAMADSDHL				
RREGLAGLYRCASAMLLRDVPGYCLYTPYVYFLSEWITPEACTG PSPCAWWLASGMAGAI SWGTATPMDVVKSRLQADGYLINKYKGV LDCISQSYQKEGLKVFFRGITVNAVRGFPMSAAMFLGYELSLQA IRGDHAVTSP FPELEUMRLRSRSWRPLGVPRRCHRRNWKEPVRAQPLSVTVWAP RCQRP/QPPAPEPSSDNAAVPEATPTPRAASAALELPLGPAPV SVAPQAEAEARSTPGPAGSRLGPETFRGRFRGFRYGPAGPLSVTVWAP FRQLREL/SPRQWLRPDI\RTKEG\IVEMLVQEQLLAILPEAAR ARRIRRTDVRITG AQVGPRSRPCKMPLKLRGKKKAKSKETAGLVEGEPTGAGGGSLE ASRAPARRLVFHAQLAHGSATGRVEGFSSIQELVAQIAGAFEIS PSEILVCTLNTPKIDMERLLGGQLGLEDFIFAHVWGIEKEVMVY KSEDSIGLTITDNSVGYBAFKRINDGGVIDSVKTICVGDHIESI NGENIUGWRHYDVAKKLKELKKEELFTMKLIEPKKAFPIELRSK AGKSSGEKIGCGRATLRLRSKGPATVEEMPSETKAK\AIEKLDD VLELYMGIRDIDLATTMFEAGKDKVNNPDEFAVALDETLGDFAFP DEPVPDVWGVIGDAKRRGL BEBGEQVGGAKCCGDAPHVENREEETTARIGPGVMESKEERALNN LIVENVNQENDEKDEKEQVANKEFPLALPLNVSEYCVPRGRRR FRVRQPILQYRWDIMHRLGEPQARMREENMREENERIEEEVQLMEKL REKGLSHSLRAUSTDPPHDHHDEPC\LMB BLLLNEMASKCRIVCTOPRRISAVSLAURVCDELGCERGPGGRN SLCGYGIRMESRACESTRLLYCTIGVLLRKLOEDGLLSNVS/HM FIVDEV\HER\SVGSDFLLIKELICKRSDLHLILMSATVDSE KFSTYFTHCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC QKFLEEEEEVTINVTSKAGGIKKYQEXIPVQTGAHADLNPFYQK YSSRTQHAILYMPHKINDLILLELLALDKSPGPFRNTTERFEGFMD YSVPBILRVPLEBELCHIMKCNLGSPBDFLSKALDPPQLQVISN AMNLLRKIGACEINEPKLTPLGRULALPVNVKIGKMLIFGAIF GGLDPVATLAAVWTEKSBFTTPIGRROEADLAKSALAMADSDHL				
PSPCAWILAGGMAGAISWGTATPMDVVKSRLQADGVYLNKYKGV LDCISQSYQKEGLKVFFRGITVNAVRGFPMSAAMFLGYELSIQA IRGDHAVTSP  6140 694 136 RPELELWRLRSRSWRPLGVPRRCHKRRWKEPVRAQPLSVTVMAP RCQRP/QPPAPEPSSPNAAVPEAIPTPRAAASALELPLGPAPV SVAPQAEAEARSTECPAGSRLGPETFRQRFRGFRYQDAAGPREA FRQLRRI/SPRQWLRPDI\RTKEQ\IVEMLVQEQLLAILPEAAR ARRIRRITOWRITG  6141 2 984 AQVGPRSRPCKMPLKLRGKKKAKSKETAGLVEGEPTGAGGGSLS ASRAPARRLVFHAQLAHGSATGVEGFSSIGELYAQIAGAFEIS PSEILVCTLNTPKIIDMERLLGGQLGLEDFIFAHVKGIEKEVNVY KSEDSIGLITITDNGVGYAFIKRIKDGGVIDSVKTICVGDHIESI NGENIVGWRHYDVAKKLKELKEBLFTMKLIEPKKAFEIELRSK AGKSSEGKIGCGRATLRLRSKGPATVEEMPSETKAK\AIEKIDD ULELYMGIRDIDLATTMFEAGKDKVNPDEFAVALDETLGDFAFP DEFYFDWGGVIGDAKRRGL LIVENVNQENDEKDEKEQVANKEETARIGPGVMESKEERALNN LIVENVNQENDEKDEKEQVANKEETARIGPGVMESKEERALNN LIVENVNQENDEKDEKEQVANKEETARIGPGVMESKEERALNN LIVENVNQENDEKDEKEQVANKEETARIGPGVMESKEERALNN REKQLSHSLRAVSTDPPHDHDHDEPC\LMP FFMRFIFLHCPWNQQMKKWNLLETSLESCKAHLSIQKLLKER\Q VQLFVFKHRBIVETLKRHRVVVVAGET\GSGKSTQVPHFLLED LLLNEWEASKCNIVCTQPRRISAVSLANRVCDELGCENGPGGRN SLCGYQIRMESRACESTRLLYCTTGVLLKKLQEGLLSNVS/HM FIVDEV\HREK\SVQSDFLLITLKEILGVRSDLHILLMSATVDSE KFSTYFTHCPILRISGRSYPVEVFHLEDIIETGFVLEKDSEYC QKFLEEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNFPYQK YSSRTQHAILYMMFHKINDLDILELLAYLDKSPGFRNIEGAVLI FLPPLAHIQQLYDLLSNDRRFYSERYKVIALHSILSTQDQAAAF TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS QMSSLVETFVSKASALQROGGRAGRVRDGFCFRNYTRERFECFMD YSVPEILRVPLEELCLHIMKCNLGSBEDFLSKALDPPQLQVISN AMNLLKKIGACELNEPKLTPIGGKLBALALAKALAMADSDHL			İ	
LDCISGSYQKEGLKVFFRGITVNAVRGFPMSAAMFLGYELSLQA IRGDHAVTSP  6140 694 136 RFELEUMRLESRSWRPLGVPRRCHRRNWKEPVRAQPLSVTVWAP RCQRP/QPPAPEPSSPNAAVPEAIPTPRAAASAALBI,DLGPAPV SVAPQABAEARSTPGPAGSRLGPETFRQRPRQFRYQDAAGPREA FRQLREL/SPRQWLRPDI\RTKEQ\IVEMLVQEQLLAILPEAAR ARRIRRSTDVRITG  6141 2 984 AQVGPRSRPCKMPLKLRGKKKAKSKETAGLVEGEPTGAGGGSLS ASRAPARRLVFHAQLAHGSATGRVEGFSSIQELYAQIAGAFEIS PSEILVCTLNTPKIDMERLLGGQLGLEDFIFAHVKGIEKEVNVY KSEDSLGITTTDNGVGYAFIKRIKDGGVIDSVKTICVGDHIESI NGENIVGWRRYDVAKKLKELKKEBLFTMKLIEPKKAFEIELRSK AGKSSGEKIGCGRATLRLRSKGPATVEEMPSETKAK\AIEKIDD ULELYMGIRDILATTMPEAGKDKVNPDEFAVALDETLGDFAFP DEPVFDVWGVIGDAKRGL  6142 116 602 EBAEGEQVCGAKCCGDAPHVENREEETTARIGPGVMESKEERALNN LIVENNVQBENDEKDEVANKGEPLALPLNVSEYCVPRGNRR PRVRQPILQYRWDIMHRLGEPQARNREEMMERIGEEVRQLMEKL REKQLSHSLRAVSTDPPHHDHIDEPC\LMP FRYRQPILQYRWDIMHRLGEPGARNREEMMERIGEEVRQLMEKL REKGLSHSLRAVSTDPPHDHHDEPC\LMP CLLVPKYRHDSIVETLKRHRVVVVAGET\GSGKSTQVPHFLLED LLLNEWEASKCNIVCTQPRISAVSLANRVCDELGCENGPGGRN SLGGYQIRMESRACESTRLLYCTTGVLLKRLQEDGLLSNVS/HM FIVDEV\HER\SVQSDFLIILKEILQKRSDLHLILMSATVDSE KFSTYFTHCPILRISGRSYPVEFHLEDILEFTGFVLEKDEYC QKFLEEEEEVTINVTSKAGGIKKYQGYIPVQTGAHADLNPFYQK YSSRTQHAILYMNPHKINLDLILELLAYLDKSPGFRNIEGAVLI FLPPGAHTQQLYDLLSNDRFFYSERYKVILAHSILSTODGAAF TLPPPGVRKRIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS QMSSLVETFVSKASALQRGGRAGRVROFCFFRMYTRERFEGFMD YSVPBILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN ANNLLKKIGACELNEPKLTPIGQKLDALALPVNVKIGKMLIFGAIF GCLDPVATLAAVNTEKSPFTTPIGRKDEADLAKSALAMADSDHL				
1 IRODHAVTSP  RPELELWRLRSRSWRPLGVPRRCHRRNWKEPVRAQPLSVTVWAP RCQRP/QPPAPEPSSPNAAVPEA1PTPRAAASAALELPLGPAPV SVAPQAEAEARSTFGPAGSRLGPETFRGRFROFRYQDAAGFREA FRQLREL/SPRQWLRPDI\RTKBQ\IVEMLVQEQLLAILPEAAR ARRIRRTDVRITG ARGIRRTDVRITG PSEILVCTLNTPKIDMERLLGGQLGLEDFIFAHVKGLEKEVNVY KSEDSLGLTITDNGUGYAFIKRIKOGGVIDSVKTICUGDHIESI NGENIUWARHVDVAKKLKELKKEELFTMKLIEPKKAFEIELRSK AGKSSGEKIGCGRATLRLRSKGPATVEEMPSETKAK\AIEKIDD VLELYMGIRDIDLATTMFEAGKKKNAKPETALDETLGDFAFP DEPVFDVWGVIGDAKRRGL  6142 116 602 EARGEQVCGAKCCGDAPHVENREEETARIGPGVMESKEERALNN LIVENNNQENDEKDEKEQVANKEPLLAIDLAVSEYCVPRGNRRR PFRRQPILQYRWDIMHRLGEPQARMREENMERIGEEVRQLMEKL REKQLSHSLRAVSTDPPHHDHHDEPC\LMP 6143 2802 270 FRMRIPLHGPWNQQMWKIWNLETSLESCKAHLSIQKLLKER\Q CQLPVFKHRDSIVETLKRRRVVVVAGET\GSGKSTQVPHFILED LLLNEWASKCNIVCTQPRRISAVSLANRVCDELGCENGPGGRN SLCGYQIRMESRACESTRLLYCTTGVLLKKLQEDGLLSNVS/HM FIVDEV\HER\SVQSDFLLIILKEILQKRSDLHLLIMSATVDSE KFSTYFTHCPILRISGRSYPVEVFHLEDIIETGFVLEKDSEYC QKFLEEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNPFYQK YSSRTQHAILYMNPHKINDLILELLAYDKSPQFRNIEGAVLI FLPGLAHIQQLYDLLSNDRRFYSERYKVIAHSILSTODQAAAF TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS QMSSLVETFVSKASSALQRGGRAGRVRNGFCFRMYTRERFEGFMD YSVPBILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPTTTIGGKDEADLAKSALAMADSDHL				
6140 694 136 RPELELWRLRSRSWRPLGVPRRCHRRNWKEPVRAQPLSVTVWAP RCQRP/QPPAPEPSSDNAAVPEATPTPRAAASAALELPLGPAPV SVAPQABEARSTFGPGAGSRLGPETFRQRFRGFRYGPROGRERA FRQLREL/SPRQWLRPDI\RTKEQ\IVEMLVQEQLLAILPEAAR ARRIRRTDVRITG AQVGPRSPCKMPLKLIRGKKKAKSKETAGLVEGEPTGAGGGSLS ASRAPARRLVFHAQLAHGSATGRVEGFSSIQELYAQIAGAFEIS PSEILVCTLNTPKIDMERLLGGGLGLEDFIFAHVKGIEKEVNVY KSEDSIGLITITDNGGYAFIKRIKOGGVIDSVKTLCVGDHIESI NGENIVGWRHYDVAKKLKELKKEELFTMKLIEPKKAFEIELRSK AGKSSGEKIGGGRATTLRIESKGPATVEEMPBETKAK\AIEKIDD VLELYMGIRDIDLATTMFEAGKDKNVNPDEFAVALDETLGDFAFP DEFVFDVWGVIGDAKRRGL 6142 116 602 EAEGEQVCGAKCCGDAPHVENREEETARIGFGVMESKEERALNN LIVENNVAGENDEKDEKEQVANKGEPLALPLNVSEYCVPRGNRRR PRVRQPILQYRWDIMHRLGEPQARMREENMERIGEEVRQLMEKL REKQLSHSLRAVSTDPPHHDHHDEFC\LMP 6143 2802 270 FRMRIFIHGPWNQOWKIWNLLETSLESCKAPLSIQKLLKER\Q \QLPVFKHRDSIVETLKRHRVVVVAGET\GSGKSTQVPHFLLED LLLNEWEASKCNIVCTQPRRISAVSLANRVCDELGCENGPGGRN SLCGYQIRMESRACESTRLLYCTTGVLLRKLQEDGLLSNVS/HM FIVDEV\HER\SVQSDFLLILKELQEDGLLSNVS/HM FIVDEV\HER\SVQSDFLLILKELQEGLGLLSNVS/HM FIVDEV\HER\SVQSDFLLILKELQEGLGLLSNVS/HM FIVDEV\HER\SVQSDFLLILKELQEGLGLLSNVS/HM FIVDEV\HER\SVQSDFLLILKELDEGLGLLSNVS/HM FIVDEV\HER\SVQSDFLLILKELDEGLLSLNSAVIDPPYQK YSSRTQHAILYMNPHKINLDLILELAYLDKSPQFRNIEGAVLI FLPGLAHIQQLYDLLSNDRRFYSERYKVIALHSILSTQDQAAAF TLPPPGVRKIVLATNIAETGITTPDVVVVIDTGTKENKYHESS QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTRERFEGFMD YSVPBILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRKIGACELNEPKLTPLGQHLAALPVWVKIGKMLIFGALIF GCLDPVATLAAVWTEKSPFTTPIGRKDEADLAKSALAMADSDHL				
RCQRP/QPPAPEPSSPNAAVPEAIPTPRAASAALELPLGPAPV SVAPQAEAEARSTFGPAGSRLGFBTFRGRFRGFRYCDAAGPREA FRQLREL/SPRQWLRPDI\RTKBQ\IVEMLVQEQLLAILPEAAR ARRIRRTDVRITG ARGIRRTDVRITG  8141 2 984 AQVGPRSRPCKMPLKLRGKKKAKSKETAGLVEGEPTGAGGGGLS ASRAPARRLVFHAQLAHGSATGRVEGFSSIGELYAQIAGAFEIS PSEILVCTLNTPKIDMERLLGGQLGLEDFIFAHVKGIEKEVNVY KSEDSLGLTITDNGUGYAFIKRIKDGGVIDSVKTICVGDHIESI NGENIVGWRHYDVAKKLKELKKELFTMKLIEPKKAFEIELRSK AGKSSGEKIGGGRATLRLRSKGPATVEEMPSSTKAR\AIERIDD ULELYMGIRDIDLATTMFEAGKDKVNPDEFAVALDETLGDFAFP DEFVFDVWGVIGDAKRRGL LIVENVNQENDEKDEKEQVANKGEPLALPLNVSEYCVPRGNRR FRVRQPILQVRWDIMHRLGEPQARMREENMERIGEEVRQLMEKL REKQLSHSLRAVSTDPHDHHDEPC\LMP 6143 2802 270 FRMRIFLHGPWNQQMWKIWNLETSLESCKAHLSIQKLLKER\Q VQLPVFKHRDSIVETLKRRRVVVVAGGT\GSGKSTQVPHFILLED LLLNEWEASKCNIVCTQPRRISAVSLANKVCDELGCENGPGGRN SLCGYQIRMESRACESTRLLYCTTGVLLRKLQEDGLLSNVS/HM FIVDEV\HER\SVQSDFLLIILKEILQKRSDLHLILMSATVDSE KFSTYFTHCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC QKFLEEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNPFYQK YSSRTQHAILYMNPHKINLDLILELLAYLDKSPQFRNIEGAVLI FLEGLAHIQQLYDLLSNDRRFYSERXIVALHSILSTQDQAAAF TLPPPGWRKTVLATNIAETGITIPDVVFVIDTGTKENKYHESS QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTRERFEGFMD YSVPEILRVELEELCLHIMKCNLGSBEDFLSKALDPPQLQVISN AMNLLRKIGACELMERLTPLGQHLAALPVWKIGKMLIFGALIF GCLDPVATLAAVWTEKSPFTTDIGKDEADLAKSALAMADSDHL	6140	594	136	
SVAPQABABARSTPGPAGSRLGPETFRQRFRQFRYQDAAGPREA FRQLREL/SPRQWLRPDI\RTKEQ\IVEMLVQEQLLAILPEAAR ARRIRRTDVRITG  6141 2 984 AQVGPRSRPCKMPLKLRGKKKAKSKETAGLVEGEPTGAGGGSLS ASRAPARRLVFHAQLAHGSATGRVEGFSSIQELYAQIAGAFEIS PSEILYCTLNTPKIDMERLLGGQLGLEDFIFAHVKGIEKEVNVY KSEDSLGLTITDNGVGYAFIKRIKDGGVIDSVKTICVGDHIESI NGENIVGWRHYDVAKKLKELKKEBLFTMKLIEPKKAFEIELRSK AGKSSGEKIGCGRAFLELRSKGBATVEEMPSETKAK\AIEKIDD VLELYMGIRDIDLATTMFEAGKDKVNPDEFAVALDETLGDFAFP DEFVFDVWGVIGDAKRRGL  6142 116 602 EABGEQVCAAKCCBAPHVENREEETARIGFGVMESKEERALNN LIVENNNQENDEKDEKEQVANKGEPLALPLNVSEYCVPRGNRRR FRVRQPILQYRWDIMHRLGFPQARMREENMERIGEEVRQLMEKL REKQLSHSLRAVSTDPPHHDHDEPC\LMP 6143 2802 270 FRMRIFLHGDWNGWMKIWNLLETSLESCKAHLSIQKLLKER\Q \QLPVFKHRDSIVETLKRHRVVVVAGET\GSGKSTQVPHFLLED LLLNEWEASKCNIVCTQPRRISAVSLANRVCDELGCENGPGGRN SLCGYQIRMESRACESTRLLYCTTGVLLRKLQEDGLLSNVS/HM FIVDEV\HER\SVQSDFLLIILKEILQKRSDLHLILMSATVDSE KFSTYFTHCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC QKFLEEEEEVTINVTSKAGGIKKYQBYIPVGGAHADLMPFYQK YSSRTQHAILYMNPHKINLDLILELLAYLDKSPQFRNIEGAVLI FLPGLAHIQQLYDLLSNDRFYSERYKVIALHSILSTQDQAAAF TLPPPGVRKIVLAINIAETGITIPDVFYIJDTGRTKENKYHESS QMSSLVETFVSKASALQRGRAGRVRDGFCFRMYTRERFEGFMD YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRKIGACELBPEKLTPLQQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL	0110	054	150	· .
FRQLREI/SPRQWLRPDI\RTKEQ\IVEMLVQEQLLAILPEARR ARRIRRTDVRITG ARRIRRTDVRITG AQVGPRSRCKMPLKLRGKKKAKSKETAGLVEGEPTGAGGGSLS ASRAPARRLVFHAQLAHGSATGRVEGFSIQELYAQIAGAFEIS PSEILYCTLNTPKIDMERLLGGQLGLEDFIFAHVKGIEKEVNVY KSEDSLGLTITDNGVGYAFIKRIKDGGVIDSVKTICVGDHIESI NGENIVGWRHYDVAKKLKELKKEELFTMKLIEPKKAFEIELRSK AGKSSGEKIGCGRATLRLRSKGPATVEEMPSETKAK\AIEKIDD VLELYMGIRDIDLATTMFEAGKDKVNPDEFAVALDETLGDFAFP DEFVFDWGVIGDAKRRGL LIVENVNQENDEKDEKEBQVANKGEPLALPLNVSEYCVPRGNRRR FVRQPILQYRMDIMHRLGEPQARMREEMMERIGEEVRQLMEKL REKQLSHSLRAVSTDPPHHDHDEFC\LMP FRMRIFLHCPWNQQMWKIWNLETSLESCKAHLSIQKLLKER\Q \QLPVFKMESIVETLKRRKVVVVAGET\GSGKSTQVPHFLLED LLLNEWBASKCNIVCTQPRRISAVSLANRVCDELGCENGPGGRN SLCGYQIRMESRACESTRLLYCTTGVLLRKLQEDGLLSNVS/HM FIVDEV\HER\SVQSDFLLIILKEILQKRSDLHLILMSATVDSE KFSTYFTHCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC QKFLEEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNFFYQK YSSRTQHAILYNNPHKINLDLILELLAVLDKSFQFRNIEGAVLI FLPPGVKIVLLATNIAETGITIPDVVFVIDTGRTKENKYHESS QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTRERFEGFMD YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRKIGACELIDEPKLTPLGGHLAALDVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTIGGRKDEADLAKSALAMADSDHL				
ARRIRRETDVRITG  AQVGPRSRPCKMPLKLRGKKKAKSKETAGLVEGEPTGAGGGSLS  AGRAPARRLVFHAQLAHGSATGRVEGFSSIQELYAQIAGAFEIS PSEILYCTLNTPKIDMERLLGGQLGLEDFIFAHVKGIEKEVNVY KSEDSLGLTITDNGVGYAFIKRIKDGGVIDSVKTICVGDHIESI NGENIVGWRHYDVAKKLKELKEELFTMKLIEPKKAFEIELRSK AGKSSGEKIGCGRATLRLRSKGPATVEEMPSETKAK\AIEKIDD VLELYMGIRDIDLATTMFEAGKDKVNPDEFAVALDETLGDFAFP DEFVFDVWGVIGDAKRRGL  6142  116  602  EAEGEQVCGAKCCGDAPHVENREEETARIGPGVMESKEERALNN LIVENVNQENDEKDEKEQVANKGEPLALPLNVSEYCVPRGNRRR FRVRQPILQYRWDIMHRLGEPQARMREENMERIGEEVRQLMEKL REKQLSHSLRAVSTDPPHDHHDEFC\LMP  6143  2802  270  FRMRIFTDVRITG FRMRIFLHCPWNQQMWKIWNLLETSLESCKAHLSIQKLLKER\Q \QLPVFKHRDSIVETLKRHRVVVVAGET\GSGKSTQVPHFLLED LLLNEWEASKCNIVCTQPRRISAVSLANRVCDBLGCENGPGGRN SLCGYQIRMESRACESTRLLYCTTGVLLRKLQEDGLLSNVS/HM FIVDEV\HER\SVQSDFLLIILKBILQKRSDLHLILMSATVDSE KFSTYFTHCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC QKFLEEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNPFYQK YSSRTQHAILYMNPHKINLDLILLELLAYLDKSPGFNIEGAVLI FLPGLAHIQQLVDLLSNDRRFYSERYKULAHBILSTODQAAAF TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS QMSSLVETFVSKASALQRGGRAGRVRDGFCFRNYTRERFEGFMD YSVPEILKVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN AMNLLKKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL				FROLDET / SDROWLDDDI / DTKRO / TVENT VOROLLATI DENAD
AQVGPRSRPCKMPLKLRGKKKAKSKETAGLVEGEPTGAGGGSLS ASRAPARRLVFHAQLAHGSATGRVEGFSSIGELYAQIAGAFEIS PSEILYCTINTPKIDMERLLGGQLGLEDFIFAHVKGIEKEVNVY KSEDSLGLTITDNOVGYAFIKRIKDGSVIDSVKTICVGDHIESI NGENIVGWRHYDVAKKLKELKKEBLFTMKLIEPKKAFEIELRSK AGKSSGEKIGCGRATLRLRSKGPATVEEMPSETKAK\AIEKIDD VLELYMGIRDIDLATTMFEAGKDKVNPDEFAVALDETLGDFAFP DEFVFDVWGVIGDAKRRGL  6142 116 602 EAEGGQVCGAKCCGDAPHVENREETARIGFGVMESKEERALNN LIVENVNQENDEKDEKEQVANKGEPLALPLNVSEYCVPRGNRRR FRVRQPILGYRWDIMHRLGEPQARMREENMERIGEEVRQLMEKL REKQLSHSLRAVSTDPPHHDHDEFC\LMP FRMRIFLHCPWNQQWMKIWNLLETSLESCKAHLSIQKILKER\Q QLPVFKHRDSIVETLKRHRVVVVAGET\GSGKSTQVPHFLLED LLLNEWEASKCNIVCTQPRRISAVSLANRVCDELGCENGPGGRN SLCGYQIRMESRACESTRLLYCTTGVLLRKLQEDGLLSNVS/HM FIVDEV\HER\SVQSDFLLIILKEILQKRSDLHLILMSATVDSE KFSTYFTHCPILKISGRSYPVEVFHLEDIIEETGFVLEKDSEYC QKFLEEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNPFYQK YSSRTQHAILYMNPHKINLDLILELLAYLDKSPQFRNIEGAVLI FLPPGAKHIQQLYDLSNDRRFYSERYKVIALHSILSTQDQAAAF TLPPPGVRKIVAATNIAETGITIPDVVFVIDTGRTKENKYHESS QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTRERFEGFMD YSVPELIRVPLEELCHIMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRKIGAGCELNEPKLTPLGQHLAALPVMVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL				
ASRAPARRLVFHAQLAHGSATGRVEGFSSIQELYAQIAGAFEIS PSEILYCTINTPKIDMERLIGGQLGLEDFIFAHVKGIEKEVNVY KSEDSLGLTITDNGVGYAFIKRIKDGGVIDSVKTICVGDHIESI NGENIVGWRHYDVAKKLKELKKEBEFTMKLIEPKKAFEIELRSK AGKSSGEKIGCGRATLRLRSKGPATVEEMPSETKAK\AIEKIDD VLELYMGIRDIDLATTMFEAGKDKVNPDEFAVALDETLGDFAFP DEPVFDVWGVIGDAKRGL  6142 116 602 EAEGEQVCGAKCCGDAPHVENREEETARIGPGVMESKEERALNN LIVENVNQENDEKDEKEQVANKGEPLALPLNVSEYCVPRGNRRR FRVRQPILQYRWDIMHRLGEPQARMREEMBRIGEEVRQLMEKL REKQLSHSLRAVSTDPPHDHDHDEPC\LMP  6143 2802 270 FRMRIFHLGPWNQQMWKIWNLLETSLESCKAHLSIQKLLKER\Q \QLPVFKHRDSIVETLKRHRVVVVAGET\GSGKSTQVPHFLLED LLLNEWEASKCNIVCTQPRRISAVSLANRVCDBLGCENGPGGRN SLCGYQIRMESRACESTRLLYCTTGVLLKKLQEDGLLSNVS/HM FIVDEV\HER,SVQSDFLLIILKEILQKRSDLHLILMSATVDSE KFSTYFTTCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC QKFLEEESEVTINVTSKAGGIKKYQBYIPVQTGAHADLNPFYQK YSSRTQHAILYMNPHKINLDLILELLAYLDKSPQFRNIEGAVLI FLPGLAHIQQUYDLLSNDRRFYSERKVIALHSILSTQDQAAAF TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS QMSSLVETFVSKASALQRGGRAGRVRDGFCFRMYTRERFEGFMD YSVPEILRVPLEELCHHMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRKIGACELNEPKLTPLGQHLAALPVMVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL	6141	2	984	
PSEILYCTLNTPKIDMERLLGGQLGLEDFIFAHVKGIEKEVNVY KSEDSLGLTITDNGGYAFIKRIKDGGVIDSVKTICVGDHIESI NGENIVGWRHYDVAKKLKELKKEELFTMKLIEPKKAFEIELRSK AGKSSGEKIGGRATLRLRSKGFATVEEMPSETKAK\AIEKIDD VLELYMGIRDIDLATTMFEAGKDKVNPDEFAVALDETLGDFAFP DEFVFDWGVIGDAKRGL  6142  116  602  EAEGEQVCGAKCCGAPHVEREETARIGFGVMESKEERALNN LIVENVNQENDEKDEKEQVANKGEPLALPLNVSEYCVPRGNRRR FRVRQPILGYRWDIMHRLGEPQARMREEMMERIGEEVRQLMEKL REKQLSHSLRAVSTDPPHHDHHDEFC\LMP  6143  2802  270  FRMRIFLHGPWNQQWKIWNLLETSLESCKAHLSIQKLLKER\Q \QLPVFKHRDSIVETLKRHRVVVVAGET\GSGKSTQVPHFLLED LLLNEWEASKCNIVCTQPRRISAVSLANRVCDELGCENGPGGRN SLCGYQIRMESRACESTRLLYCTTGVLLRKLQEDGLLSNVS/HM FIVDEV\HER\SVQSDFLLIILKEILQKRSDLHLILMSATVDSE KFSTYFTHCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC QKFLEEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNPFYQK YSSRTQHAILYMNPHKINLDLILELLAYLDKSPQFRNIEGAVLI FLPGLAHIQQLYDLLSNDRRFYSERYKVIALHSILSTQDQAAAF TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS QMSSLVETFVSKASALQROGRAGRVRDGFCFRMYTRERFEGFMD YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL		1 -	]	
KSEDSLGLTITDNGVGYAFIKRIKDGGVIDSVKTICVGDHIESI NGENIVGMRHYDVAKKLKELKKEBLFTMKLIEPKKAFEIELRSK AGKSSGEKIGCGRATLRLRSKGPATVEEMPSETKAK\AIEKIDD VLELYMGIRDIDLATTMFEAGKDKVNPDEFAVALDETLGDFAFP DEFVFDVWGVIGDAKRGL  116 602 EAEGEQVCGAKCCGDAPHVENREEETARIGPGVMESKEERALNN LIVENVNQENDEKDEKQVANKGEPLALPLNVESYCVPRGNRRR FRVRQPILQYRWDIMHRIGEPQARMREENMERIGEEVRQLMEKL REKQLSHSLRAVSTDPPHHDHHDEFC\LMP  6143 2802 270 FRMRIFLHCPWNQQMWKIWNLLETSLESCKAHLSIQKLLKER\Q \QLPVFKHRDSIVETLKRHRVVVVAGET\GSGKSTQVPHFLLED LLLNEWEASKCNIVCTQPRISAVSLANRVCDBLGCENGPGGRN SLCGYQIRMESRACESTRLLYCTTGVLLRKLQEDGLLSNVS/HM FIVDEV\HER\SVQSDFLLIILKEILQKRSDLHLILMSATVDSE KFSTYFTHCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC QKFLEEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNFFYQK YSSRTQHALTYMNPHKINLDLILELLAYLDKSPQFRNIEGAVLI FLPGLAHLQQLYDLLSNDRRFYSERYKVIALHSILSTQDQAAAF TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTRERFEGFMD YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRRIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL		<u> </u>		
NGENIVGWRHYDVAKKLKELKKEELFTMKLIEPKKAFEIELRSK AGKSSGEKIGCGRATLRLRSKGPATVEEMPSETKAK\AIEKIDD VLELYMGIDIDLATTMFEAGKDKVNPDEFAVALDETLGDFAFP DEFVFDVWGVIGDAKRRGL  116 602 EAEGEQVCGAKCCGDAPHVENREEETARIGFGVMESKEERALNN LIVENVNQENDEKDEKEQVANKGEPLALPLNVSEYCVPRGNRRR FRVRQPILQYRWDIMHRLGEPQARMREENMERIGEEVRQLMEKL REKQLSHSLRAVSTDPPHHDHHDEFC\LMP FRMRIFLHCPWNQQMWKIWNLLETSLESCKAHLSIQKLLKER\Q \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \\ \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\		1		
AGKSSGEKIGCGRATLRLRSKGPATVEEMPSETKAK\AIEKIDD VLELYMGIRDIDLATTMFEAGKDKVNPDEFAVALDETLGDFAFP DEFVFDVWGVIGDAKRRGL  6142  116  602  EAEGEQVCGAKCCGDAPHVENREEETARIGPGVMESKEERALNN LIVENVNQENDEKDEKEQVANKGEPLALPLNVSEYCVPRGNRRR FRVRQPILQYRWDIMHRLGEPQARMREENMERIGEEVRQLMEKL REKQLSHSLRAVSTDPPHHDHHDEFC\LMP  6143  2802  270  FRMRIFLHGPWNQQMWKIWNLLETSLESCKAHLSIQKLLKER\Q \QLPVFKHRDSIVETLKRHRVVVVAGET\GSGKSTQVPHFLLED LLLNEWEASKCNIVCTQPRRISAVSLANRVCDELGCENGFGGRN SLCGYQIRMESRACESTRLLYCTTGVLLRKLQEDGLLSNVS/HM FIVDEV\HER\SVQSDFLLIILKEILQKRSDLHLILMSATVDSE KFSTYFTHCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC QKFLEEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNPFYQK YSSRTQHAILYMNPHKINLDLILEILAYLDKSPQFRNIEGAVLI FLPGLAHIQQLYDLLSNDRRFYSERYKVIALHSILSTQDQAAAF TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTRERFEGFMD YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRKIGACELNEPKLTPLGGHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL				
VLELYMGIRDIDLATTMFEAGKDKVNPDEFAVALDETLGDFAFP DEFVFDVWGVIGDAKRRGL  6142  116  602  EAEGEQVCGAKCCGDAPHVENREEETARIGFGVMESKEERALNN LIVENVNQENDEKDEKEQVANKGEPLALPLNVSEYCVPRGNRRR FRVRQPILQYRWDIMHRLGEPQARMREENMERIGEEVRQLMEKL REKQLSHSLRAVSTDPPHHDHHDEFC\LMP  6143  2802  270  FRMRIFLHGPWNQQMWKIWNLLETSLESCKAHLSIQKLLKER\Q \QLPVFKHRDSIVETLKRHRVVVVAGET\GSGKSTQVPHFLLED LLLNEWEASKCNIVCTQPRRISAVSLANRVCDELGCENGPGGRN SLCGYQIRMESRACESTRLLYCTTGVLLRKLQEEDGLLSNVS/HM FIVDEV\HER\SVQSDFLLILKEILQKRSDLHLILMSATVDSE KFSTYFTHCPILRISGRSYPVEVFHLEDIIETGFVLEKDSEYC QKFLEEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNPFYQK YSSRTQHAILYMNPHKINLDLILELLAYLDKSPQFRNIEGAVLI FLPGLAHIQQLYDLLSNDRRFYSERYKVIALHSILSTQDQAAAF TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTRERFEGFMD YSVPEILRVPLEELCHHIMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL				
DEFVFDVWGVIGDAKRRGL  6142  116  602  EAEGEQVCGAKCCGDAPHVENREEETARIGPGVMESKEERALNN LIVENVNQENDEKDEKEQVANKGEPLALPLNVSEYCVPRGNRRR FRVRQPILQYRWDIMHRLGEPQARMREENMERIGEEVRQLMEKL REKQLSHSLRAVSTDPPHHDHDEPC\LMP 6143  2802  270  FRMRIFLHCPWNQQMWKIWNLLETSLESCKAHLSIQKLLKER\Q \QLPVFKHRDSIVETLKRHRVVVVAGET\GSGKSTQVPHFLLED LLLNEWEASKCNIVCTQPRRISAVSLANRVCDELGCENGPGGRN SLCGYQIRMESRACESTRLLYCTTGVLLRKLQEDGLLSNVS/HM FIVDEV\HER\SVQSDFLLIILKEILQKRSDLHLILMSATVDSE KFSTYFTHCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC QKFLEEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNPFYQK YSSRTQHAILYMNPHKINLDLILELLAYLDKSPQFRNIEGAVLII FLPGLAHIQQLYDLLSNDRRFYSERYKVIALHSILSTQDQAAAF TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTRERFEGFMD YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL		1		
6142  116  602  EAEGEQVCGAKCCGDAPHVENREEETARIGPGVMESKEERALNN LIVENVNQENDEKDEKEQVANKGEPLALPLNVSEYCVPRGNRRR FRVRQPILQYRWDIMHRLGEPQARMREENMERIGEEVRQLMEKL REKQLSHSLRAVSTDPPHHDHHDEFC\LMP  6143  2802  270  FRMRIFLHCPWNQQMWKIWNLLETSLESCKAHLSIQKILKER\Q \QLPVFKHRDSIVETLKRHRVVVVAGET\GSGKSTQVPHFLLED LLLNEWEASKCNIVCTQPRRISAVSLANRVCDBLGCENGPGGRN SLCGYQIRMESRACESTRLLYCTIGVLLRKLQEDGLLSNVS\HM FIVDEV\HER\SVQSDFLLIILKEILQKRSDLHLILMSATVDSE KFSTYFTHCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC QKFLEEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNPFYQK YSSRTQHAILYMPPHKINLDLILEILAYLDKSPQFRNIEGAVLI FLPGLAHIQQLYDLLSNDRRFYSERYKVIALHSILSTQDQAAAF TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTRERFEGFMD YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL				
LIVENVNQENDEKDEKEQVANKGEPLALPLNVSEYCVPRGNRRR FRVRQPILQYRWDIMHRLGEPQARMREENMERIGEEVRQLMEKL REKQLSHSLRAVSTDPPHHDHHDEPC\LMP  6143  2802  270  FRMRIFLHCPWNQQMWKIWNLLETSLESCKAHLSIQKLLKER\Q \QLPVFKHRDSIVETLKRHRVVVVAGET\GSGKSTQVPHFLLED LLLNEWEASKCNIVCTQPRRISAVSLANRVCDELGCENGPGGRN SLCGYQIRMESRACESTRLLYCTTGVLLRKLQEDGLLSNVS\/HM FIVDEV\HER\SVQSDFLLIILKEILQKRSDLHLILMSATVDSE KFSTYFTHCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC QKFLEEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNPFYQK YSSRTQHAILYMNPHKINLDLILELLAYLDKSPQFRNIEGAVLI FLPGLAHIQQLYDLLSNDRRFYSERYKVIALHSILSTQDQAAAF TLPPPGVKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTRERFEGFMD YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL	6142	116	602	L
FRVRQPILQYRWDIMHRLGEPQARMREENMERIGEEVRQLMEKL REKQLSHSLRAVSTDPPHHDHDEFC\LMP  FRMRIFLHCPWNQQMWKIWNLLETSLESCKAHLSIQKLLKER\Q \QLPVFKHRDSIVETLKRHRVVVVAGET\GSGKSTQVPHFLLED LLLNEWEASKCNIVCTQPRRISAVSLANRVCDELGCENGEPGGRN SLCGYQIRMESRACESTRLLYCTTGVLLRKLQEDGLLSNVS\HM FIVDEV\HER\SVQSDFLLIILKEILQKRSDLHLILMSATVDSE KFSTYFTHCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC QKFLEEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNPFYQK YSSRTQHAILYMNPHKINLDLILELLAYLDKSPQFRNIEGAVLI FLPGLAHIQQLYDLLSNDRRFYSERYKVIALHSILSTQDQAAAF TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTRERFEGFMD YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL		1	1	
REKQLSHSLRAVSTDPPHHDHDEFC\LMP  6143  2802  270  FRMRIFLHCPWNQQMWKIWNLLETSLESCKAHLSIQKLLKER\Q \QLPVFKHRDSIVETLKRHRVVVVAGET\GSGKSTQVPHFLLED LLLNEWEASKCNIVCTQPREISAVSLANRVCDBLGCENGPGGRN SLCGYQIRMESRACESTRLLYCTTGVLLRKLQEDGLLSNVS/HM FIVDEV\HER\SVQSDFLLIILKEILQKRSDLHLILMSATVDSE KFSTYFTHCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC QKFLEEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNPFYQK YSSRTQHAILYMNPHKINLDLILELLAYLDKSPQFRNIEGAVLI FLPGLAHIQQLYDLLSNDRRFYSERYKVIALHSILSTQDQAAAF TLPPPGVKIVLATNIAETGITIPDVVPVIDTGRTKENKYHESS QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTRERFEGFMD YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL				
FRMRIFLHCPWNQQMWKIWNLLETSLESCKAHLSIQKILKER\Q \QLPVFKHRDSIVETLKRHRVVVVAGET\GSGKSTQVPHFLLED LLLNEWEASKCNIVCTQPRRISAVSLANRVCDELGCENGPGGRN SLCGYQIRMESRACESTRLLYCTTGVLLRKLQEDGLLSNVS/HM FIVDEV\HER\SVQSDFLLIILKEILQKRSDLHLILMSATVDSE KFSTYFTHCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC QKFLEEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNPFYQK YSSRTQHAILYMNPHKINLDLILELLAYLDKSPQFRNIEGAVLI FLPGLAHIQQLYDLLSNDRRFYSERYKVIALHSILSTQDQAAAF TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTRERFEGFMD YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL				
\QLPVFKHRDSIVETLKRHRVVVVAGET\GSGKSTQVPHFLLED LLLNEWEASKCNIVCTQPRRISAVSLANRVCDBLGCENGPGGRN SLCGYQIRMESRACESTRLLYCTTGVLLRKLQEDGLLSNVS/HM FIVDEV\HER\SVQSDFLLIILKEILQKRSDLHLILMSATVDSE KFSTYFTHCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC QKFLEEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNPFYQK YSSRTQHAILYMNPHKINLDLILELLAYLDKSPQFRNIEGAVLI FLPGLAHIQQLYDLLSNDRRFYSERYKVIALHSILSTQDQAAAF TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGTKENKYHESS QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTRERFEGFMD YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL	6143	2802	270	
LLLNEWEASKCNIVCTQPRRISAVSLANRVCDELGCENGPGGRN SLCGYQIRMESRACESTRLLYCTTGVLLRKLQEDGLLSNVS/HM FIVDEV\HER\SVQSDFLLIILKEILQKRSDLHLILMSATVDSE KFSTYFTHCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC QKFLEEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNPFYQK YSSRTQHAILYMNPHKINLDLILELLAYLDKSPQFRNIEGAVLI FLPGLAHIQQLYDLLSNDRRFYSERYKVIALHSILSTQDQAAAF TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTRERFEGFMD YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL			2,0	1 · · · · · · · · · · · · · · · · · · ·
SLCGYQIRMESRACESTRLLYCTTGVLLRKLQEDGLLSNVS/HM FIVDEV\HER\SVQSDFLLIILKEILQKRSDLHLILMSATVDSE KFSTYFTHCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC QKFLEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNPFYQK YSSRTQHAILYMNPHKINLDLILELLAYLDKSPQFRNIEGAVLI FLPGLAHIQQLYDLLSNDRRFYSERYKVIALHSILSTQDQAAAF TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTRERFEGFMD YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL		1		
FIVDEV\HER\SVQSDFLLIILKEILQKRSDLHLILMSATVDSE KFSTYFTHCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC QKFLEEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNPFYQK YSSRTQHAILYMPHKINLDLILEILLAYLDKSPQFRNIEGAVLI FLPGLAHIQQLYDLLSNDRRFYSERYKVIALHSILSTQDQAAAF TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTRERFEGFMD YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL				
KFSTYFTHCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC QKFLEEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNPFYQK YSSRTQHAILYMNPHKINLDLILELLAYLDKSPQFRNIEGAVLI FLPGLAHIQQLYDLLSNDRRFYSERYKVIALHSILSTQDQAAAF TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTRERFEGFMD YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL				
QKFLEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNPFYQK YSSRTQHAILYMNPHKINLDLILELLAYLDKSPQFRNIEGAVLI FLPGLAHIQQLYDLLSNDRRFYSBRYKVIALHSILSTQDQAAAF TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTRERFEGFMD YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL				1
YSSRTQHAILYMNPHKINLDLILELLAYLDKSPQFRNIEGAVLI FLPGLAHIQQLYDLLSNDRRFYSERYKVIALHSILSTQDQAAAF TLPPPGVRKIVLATNIAETGITIFDVVFVIDTGRTKENKYHESS QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTRERFEGFMD YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL				
FLPGLAHIQQLYDLLSNDRRFYSERYKVIALHSILSTQDQAAAF TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTRERFEGFMD YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL				QAFLEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNPFYQK
TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTRERFEGFMD YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL		1		
QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTRERFEGFMD YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL				,
YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL				
AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL		1		
GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL		]		
		1		
TIYNAYLGWKKARQEGGYRSEITYCRRNFLNRTSLLTLEDVKQE				
		1		TIYNAYLGWKKARQEGGYRSEITYCRRNFLNRTSLLTLEDVKQE

Deginning   cortesponding   contesponding   cortesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding   contesponding	SEQ	Predicted	Predicted end	Dmino agid
NO: nucleotide corresponding to first amino acid residue of amino acid residue of amino acid sequence corresponding to first amino acid residue of amino acid sequence corresponding to first amino acid sequence corresponding to first amino acid sequence corresponding to first the ce corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence corresponding to the sequence				Amino acid segment containing signal peptide
Cocation   Corresponding	NO:			Glutamic Acid E Phanual Lair Acid, E=
corresponding to first amino acid senino acid senino acid senino acid senino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence se				Graduite Acid, F=Pnenylalanine, G=Glycine,
to first a maino acid araid creidue of samino acid amino acid anino acid anino acid sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control of the sequence control o	1			n=nistidine, l=isoleucine, K=Lysine,
amino acid residue of amino acid sequence ence amino acid acid sequence amino acid sequence amino acid acid sequence amino acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence a				L=Leucine, M=Methionine, N=Asparagine,
residue of amino acid asquence    M*Tryptophan, Y=Tyrosine, X=Dukhom, *=Stop codon, /=possible nucleotide insertion.  \[ \begin{array}{cccccccccccccccccccccccccccccccccccc	- I			Parrollne, QaGlutamine, RaArginine,
amino acid sequence    Sequence	j .		1	S=Serine, T=Threonine, V=Valine,
Sequence    A-phose ib	1		i e	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
LIKUVKARGPSSTTTSTSWERNRASUTISPGEIALLKAVLVAGI.  IDRAITSKAVTIATET. STORTTSKARCHENSTTISPGEIALLKAVLVAGI.  FONLYGEKITTKSUDVTTSKARCIVETRQCKAQVHPSSVARDLOTH GONLYGEKITTKSUDVTTSKARCIVETRQCKAQVHPSSVARDLOTH GONLYGEKITTKSVAVILETTIT. TPPPVLLEGODIEVQHRERLIS- IDGAIT PROAPVKIAUT FKQLKVILIDSVLRKKLEMPKMSLEMDKI LIDGAIT PROAPVKIAUT FKQLKVILIDSVLRKKLEMPKMSLEMDKI VASAGGARIGGROGGPVICTYGPDLFPLWAYTIGAAFVAKWAS VASAGGARIGGROGGPVICTYGPDLFPLWAYTIGAAFVAKWAS VASAGGARIGGROGGPVICTYGPDLFPLWAYTIGAAFVAKWAS VASAGGARIGGROGGROGFVICTGGTBLEDEGRORRADTVOKAAP OUYADMIRAQLFETSSKTGGSVDELFGKVAEDTVAVAAPQWATE KORVIDIGVTUGHTETVGARKSCHENSERVYAGAAATVCVDLTDSS FERRAKWYKELERLEEGGGIYLGGTKSDLEDEGRORRAPVIL GDWAJAICYCLPRIADLEARVADSKTILESERGELFAKWEDT DFVOMALDVLSPRLISTSMLGRKKYNINSISSDTWTGLIOVALD GOWNTOWFVTUGMPETYGARLOGSPFGETVAKADALTYV VASAASICAKVARDQAVKKWQFVERLODLDTDYG\SSYMPDOD /TXAMIKENTEVPTGMPTOKERSPRVAHORSTALLESERGELFAKWEDT  FORMVAICYCLPRIADLEARHOOSCHOPKFSIKKYFLERGLESTTS LIKKKGKEKRAEQOVEALFGFSLUDMHRRAGGEEGGFVLITDEOKS R/YGGIEARDGGCNDAROSITRKVVDPETGRETALLKGGSVLG BIVKKRIREINKQATRODCLAPGWRRAGLIP  LIKKKGKEKRAEQOVEALFGFSLUDMHRRAGGEEGGFVLITDEOKS R/YGGIEARDGGCNDAROSITRKVVDPETGRKLIKGGSVLG BIVTKRIREINKQATRODCLAPGWRRAGLIP  LIKKGLEKRAEQOVEALFGFSLUDMHRRAGGEEGGFVLITDEOKS R/YGGLEARDFACHDPLDTDLINGAHFDFSVYLDKLRECCPLAQLIMDS BIVTKRIREINKQATRODCLAPGWRRAGLIP  LIKKGLEKRAEQOVEALFGFSLUDMHRRAGGEEGGFVLITALGERA EIVERKARAGEGGGROSSITENKALGHUKLIVYGISE GEAAGRAGPDPLDDTDLINGAHFDFSVYLDKLRECCPLAQLIMDS ETUMNAQIRALDSDMCTILVSKALGEELGSPSPRAKHOMIKLIVYGISE GEAAGRAGDPLDDTDLINGAHFDFSVYLDKLRECCPLAQLIMDS BEDERLATMANITTSFARISTATLQDHRRITIKLAGVHALLIKL QFIFEDPSRITKKVSULGANGAVKYOGRAQAVKYOGRAQAVKYOGRAQAVKYOGRAQAVKYOGRAQAVKYOGRAQAVKYOGRAQAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAVKYOGRAGAV	1		sequence	Codon, /=possible nucleotide deletion,
A SOFT STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF TH	<u> </u>	sequence		\=possible nucleotide insertion)
### STANUGKTITTKSUDVTSKLAGUVETNOGKAQHEPS\NABDLOTH   GRILAYDEKTRAWNYLERTILTPFPVLLEGGISTEVGHERILS    LIDGHIYPQAPWKIAVIFRQURVILISVERVYHDERUNGFYON    SGFGSMSGGRUDWKVWILIKSYVGKTSLVERVYHDERUNGFYON    VASAGGARIGGRISGGFUCTYGPDLFPLUNTGAFVAKWA   VODRTVTLGINDTAGSENTEMBRITYMGAKAAIVCVDLTDSS    FERRAWNYLERLSLEGCQITYLGGYKSDLLEGAFVAKWA   VODRTVTLGINDTAGSENTEMBRITYMGAKAAIVCVDLTDSS    FERRAWNYLERLSLEGCQITYLGGYKSDLLEGAFVAKWA   VODRTVTLGINDTAGSENTEMBRITYMGAKAAIVCVDLTDSS    FERRAWNYLERLSLEGCQITYLGGYKSDLLEGAFVAKWA   ODYADNIKAQLFSTSSKTGGSVDELFGKVAEDYVSVAAFQWMTE    DKWYDLGGKPHPYFYSCH    GMMDLGELERDNTGRGRUSSFVFAVCREFCVLGVUDAGGGFUL   GMMDLGELERDNTGRGRUSSFVFAVCREFCVLGVUDAGGFUL   OGWNTOVFVUTVGMFETYGARLQGSPFGIETVKAKADANLTYP   VASAASICAKVABDQAVKKMQFVERLQDLDTDYG\SGYPNDFOQ    /TKAMIKENUPPVGPF\GPF\GPF\SWRTAGTLEREADEVIT   DEDSASSROQEGLRKITSYLLMEGSQARFRSSHRYFLERGLESTTS    LKKKGKERERAQQVEALFGFSLDQWHRSAGEEGGFUTDBGKS    R/YGGERHDGG\NDAGG\NDAGGSPFGTSSHRYFLERGLESTTS    LKKKGKERERAQQVEALFGFSLDQWHRSAGEEGGFUTDBGKS    R/YGGERHDGG\NDAGG\NDAGGSPGTGSFEGGFTBLIKGDGSVLE    EIVYKERHREINKQATRGDCLAFQMRAGLLP    TILDEALSTANDLAGAGARAGAAIACHARACHARACHARACHARACHARACHARACHARAC	1	1		LIKLVKAAGFSSSTTSTSWEGNRASQTLSFQEIALLKAVLVAGL
GRLLYORKIRYARYTLRETTLITPFPVLLREGGLEVCHREBLLS IDGNIYPQAPVKIAVIRGKEVUGKKILENPKMSLENDKI LOHITPLIKTENN SOFSMSGORDVKVVVMLGKEVVGKTSLVERYVMDRFLUGPYON VSASGGARHGGRGSGGVTUTTGFDLFPLVA\TIGASFVAVMS VSASGGARHGGRGSGGVTUTTGFDLFPLVA\TIGASFVAVMS VSASGGARHGGRGSGGVTUTTGFDLFPLVA\TIGASFVAVMS VSASGGARHGGRGSGGVTUTTGFDLFPLVA\TIGASFVAVMS VSASGGARHGGRGSGGVTUTTGFDLFPLVA\TIGASFVAVMS VSASGGARHGGRGSGGVTUTTGFDLFPLVA\TIGASFVAVMS VSASGGARHGGRGSGGVTUTTGFDLFPLVA\TIGASFVAVMS PFERAKFWVELRSLESGCQIVLCGTKSDLLEEDRRERRYDFHDV ODYADNIKAQLFETSSKTOGSVBLFFGKVABDVVAVAAFQVMTE DKGVDLGQKPNPYFYSCCHH GPWVAICVCPLPRLADLEALKVADGKTLLISSREBLFAMSDT DFVGMALDULSPNLISTSHLGRVXYANLEDPAGVICHEAMSDT DFVGMALDULSPNLISTSHLGRVXYANLEDPAGVICHAMSDT OPWOMALDULSPNLISTSHLGRVXYANLEDPAGVICHAMSDT VXAASICAKARDQAVKAMGPUAKLODHVO\SCYPUDOOL /TKAMLKEHVZPUV-GFP\QFVQR-ISKPTAOTI\LEKEAEDVIR GDVSASSINQGGLRKITSYFLNEGSQARPRSHRYTAOTI\LEKEAEDVIR EDSASSNQGGRKKITSYFLNEGSQARPRSHRYTADOKS R/YFGHEAHDQGG-MDAROSIIRKVDPPTGETTLIKGDGEVLE EJYTKERHEE INKQARRGDLAPPMODID FVVILKEREGFLESTTS L KKKGKGKAEAQQVEALPGPSDLOWHRSAGGEEAGFVLAGMSS R/YFGHEAHDQGG-MDAROSIIRKVDPPTGETTLIKGGEVLE EINYKGURALDSDMTLNCHHPDSVYLDKLRERGFLAGLHSTYGLSE GEAGGRPAADPDLDPTINGAPFAGGAVLQOYOHLSFFAA LOPDOVITABLAQGLAPPLADPTINGARPAGVALQOYOHLSFFAA LOPDOVITABLAQGLARGFREGGGAPEGAVLUCYOHLSFFAA LOPDOVITABLAQGLARGRFEGGGAPEGAVLUCYOHLSFFAA LOPDOVITABLAQGLARGFREGGGAPEGAVLUCHLALGGEPA EELCEFFLANRAGRLEKELARGEGGAPEGAVLUCHLALGGEPA EELCEFFLANRAGRLEKELARGEGGAPEGAVLUCHLALGGEPA EELCEFFLANRAGREEAGLARGHEAGLARAGLAAAACLAAAACHAAACHAAACHAAACHAAACHAAACH	İ	į	1	YDNVGKIIYTKSVDVTEKLACIVETAOGKAOVHPSSVNPDLOTH
106HYPQAPVKIAVIFKQLRVLIDSVLKKKLENPKMSLENDKI 11189 568 SGPSSMSGORUDVKYWILKERVUKTSLVERYWIDRFLUGEPQM VASSGGARIGKGSGGGVUTVKTMIGKERVUKTSLVERYWIDRFLUGEPQM VASSGGARIGKGSGGGVUTVKTMIGKERVUKTSLVERYWIDRFLUGEPQM VASSGGARIGKGSGGGVUTVKTMIGKERURATIVGAAFVAKVMS VODRIVILGIMDTAGSEKVEAMSRIYYRGAKAATVCVDLTDSSS FERAKWIKVERISLEBGCUTVLGTKSDLEPRRRRVDFDHDV ODYADNIKAQLEETSSKTGGSVDELFQKVAEDYVSVAAFQVMTE MKGULIGQVRPYPYSCUTH ODYADANIKAQLEETSSKTGGSVDELFQKVAEDYVSVAAFQVMTE DKGULIGQVRPYPYSCUTH ODYADANIKAQLEETSSKTGGSVDELFQKVAEDYVSVAAFQVMTE DFVGMALDVLSPRULISTSMLGRVKTMIANSLSHDTATGLIQVALL OGWNTOVSVDTVCMPETYQARLQGSFCIEVTVKAKADALYEV VSAASICAKVARDQAVKKGYPEKLQULDTDKS\GSPPNDPOD /TXAMILKENVEPPYGFP\QFVRF\SMRTAGTI\LEKEAEDVTR EDSASENGEGLRKITSYTHANGSGGARPRSKRYFLERGLEETIT I LKKKGKEKAEAQQVEALFGFSLDQWHRSAGEEDGFVLTDECKS R/FRGIERHDOGG WDARGSTIRKVTDETTETLIKGGGEVLE ETYMKRIBERINKQATREGDLAPQMAGGLY  GTRGLEPPSPGSGGGSSPEGEGEAERRRRAIGMIKLYYGLSE ETYMKRIBERINKQATREGDLAPQMAGGLY DEMDRIATIMAVTDPSAR ISATLQDRIBERGEPIAQLMDS ETYMKQTRALDSDMGTLVYENYNKFISATDTTTRMKKDPRKME DEMDRIATIMAVTDPSAR ISATLQDRIBERGEPIAQLMDS ETYMKQTRALDSDMGTLVYENYNKFISATDTTTRMKKDPRKME DEMDRIATIMAVTOPSAR ISATLQDRIBERGELILLAIGEPA ETHELPSRLTKCUELGBYGGAVXOGRAQAVLOOYOGHISFFA IQDDCQVTTAALQOLORGFREGGGSAPPADLILLILLGEPA ETHELPSRLTKCUELGBYGGAVXOGRAQAVLOOYOGHISFFA IQDDCQVTTAALQOLORGFREGGGSAPPADLILLILLGEPA ETHELPSRLTKCUELGBYGGAVXOGRAQAVLOYOGHISFFA IQDDCQVTTAALQOLORGFREGGGSAPPADLILLLLGEPA ETHELPSRLTKCUELGBYGGAVXOGRAQAVLOOYOGHISFFA IQDCQVTTAALQOLORGFREGGGSAPPADLILLLILGEPA ETHELPSRLTKCUELGBYGGAVXOGRAQAVLOOYOGHISFFA IQDCQVTTAALQOLORGFREGGGSAPPADLILLLS ETHELARGREGGHAVCHUALAPRVACKEEP GCGGVEGISLUVALDGFHREGGGAPPADLILLLS RLLLDYETATTSTILTITURGFLVOQOPPVTPYSTLCGRREFT RRLITHYKVKGJUFSOLORGFGGAPPADLILLIS RLLLDYETATSTISTITUTURGFTCOLORGFTPADLICLIS SGSVGGLIVAGGASSVARSEVEPOONNSPTREGGGAPPADLICLIS SKASSGONGGASSSAVARSEDDALAPRVACKEEP CKSKAVLEDDHALFGGLYGGVAVATTHOVYGGGGAPPADLICLIS SKASSTENDANIENIKASTERGESSPONAKRANKAV VEDTTAIDVOULBRLAGGATVPAGGATTATIONDALTTKTROKTYAVAR SYASSTENDANIENIKASTERGGANAVUNDULITHRISTUR UKRSGTRAKALTARGRGANAVUNDULITHRISTUR DLPGGAK		İ		GWLLYQEKIRYARVYLRETTLITPFPVLLFGGDIEVOHRERLLS
6144  1289  568  SOFGSMSGORIDVRVVMIAKEVVGKTSLVERYVHDRFLVGPVON VSASGORINGGRGSGGVTUTTGFDLFPLVA\TIGAAFVAVMS VSDRITVLIGHDTAGSERVERMSRITYRGKARAIVCVDLTDGSS FERRKFWVRELESLEGCCIVLCGTKSDLLEEDGRFRRVDFHDV ODYADNIKAOLPETSSKTCSVDELFQKVARDYVVVAAFQVMTE DKGVDLGOKDNFYFYSCCHH GEMDLSEELEGCCIVLCGTKSDLLEEDGRFRRVDFHDV DKGVDLGOKDNFYFYSCCHH GEMDLSEELEGCTVLCGTKSDLLEEDGRFRRVDFHDV DKGVDLGOKDNFYFYSCCHH OPWYAICVCPLFRLADLEALKVADGKTLLESEREKLFAKWEDT DFVGRALDVLSFNLISTSNLGRVKYMINSLSHDTARGLIOVALD OGWNTYOVYDTVOMMETTYARLOGSFFGIEVVKAKADALYPV VSAASICAKVARDQAVKKMOFVEKLQDLDTDVG\SGYNDPOD /TXAMLKEURYPPV\GFP\QFVPR\SMRTYLLEGEGVLTDEKS FIRKKEURYPPV\GFP\QFVPR\SMRTYLLEGEGVTTDEKS RYFGIELAHDGGG\WADAGATIKKVDFBTGTRTLIKGGEVLE EDSASENQEGLRKITSYFLNGGSGAPRRSHKYFLERGLESTTS L LKKKGEKAEAQOVEALFGFSLDWHRSAGEELDGFVLTDEKS RYFGIELAHDGGG\WADAGATIKKVDEGSTIKKVDEFBTGTRTLIKGGEVLE EIVYKRRHREINKQATRGDCLAPQMRAGLLD GEARGRPAGPDPLDPTDLNGAHEDDFVYLDKLERGCPLADLMDG ETDMVRGITADLEGGG\WADAGATIKKVDEGSFEGEFBEFBREAGMKLIVYGLSE GEARGRPAGPDPLDPTDLNGAHEDDFVYLDKLERGCPLADLMDG ETDMVRGITALDSDMTILVYNNNKFISHTRIKMGVHLEITEN OFFFELDFRIKKVELGIAVGOWFYGGRAQAVLOGHESFFRA LQDDCQVTTARLAQOLRORFBEGGGAPEQARCVELLIALIGERA EELCESFLAHARGRLEKELRNLEBALGFSPPAPDULEFTHIGS SGFVGGLCOVAAAYGELFAAQGFAGAELLAAARGLADAAT EIVEVARERLGHHLQGLAAAFIGCLTDVGHLESFFRA GRALLAWASSILSHIKASLAAVHLFTAKSVSFSNKFYSRGF CSGVWRGLIAVGVSTVGGSGGGAPPALLLLLS RLLLDYBTATISVILTILTDRQFILVQDOFPTIVSTLGARRTTA RRLLTHTWYKQGLVSGUKRSVETROHLAAARAGGGAPPALLLLLS RLLLDYBTATISVILTILTDRQFILVQDOFPTIVSTLGARRTTA RRLLTHTAVKVGGLVSGUKRSVETROHLAAARAGCLCPRS CSFSAQDYDTPAFILIPVEKGRLSVTTGWFRAGGCLCPRS CSFSAQDYDTPAFILIPVEKGRLSVTTGWFRAGGCLCPRS CSFSAQDYDTPAFILIPVEKGRLSVTTGWFRAGGCLCPRS CSFSAQDYDTPAFILIPVEKGRLSVTTGWFRAGGCLCPRS CSFSAQDYDTPAFILIPVEKGRLSVTTGWFRAGGCLCPRS CSFSAQDYDTPAFILIPVEKGRLSVTTGWFRAGGCLCPRS CSFSAQDYDTPAFILIPVEKGRLSVTTGWFRAGGCLCPRS CSFSAQDYDTPAFILIPVEKGRLSVTTGWFRAGGCLCPRS CSFSAQDYDTPAFILIPVEKGRLSVTFFRAGGSHDLKLBPRTCSBELLDFRG VKRSSINFSKINSTNSTYTK VKRSSINFSKINSTNSTYTK PVGGGGGGGMFAGABERFFTTYSCSHDLKFTFFTGRGSILDREG VKRSSINFSKINSTNSTYTK LQCARGATAAARAGCLAAARAGCLAAARAGCLAARAGCLAARAGCLAARAG		1	l	IDGWIYFQAPVKIAVIFKQLRVLIDSVLRKKLENPKMSLENDKI
SOFOSSINGURI/VAVMILIKER/VORTSIL/DETYORA VASAGGARRIGGROSGG/SYLVA(TIGALPAKVMS VODRIVITLGINDTAGSER/EMSRIYYRGAKAAIVCUDLTDSSS FERAKFWIKERSLESECJIVLCCTKSDLEEDRRRRUPHDW ODYADNIKAQLFETSSKTGQSVDELFQKVABDYVSVAARQVMTE DKGVDLGQVPDPYPYSCCHH  6145 1109 196 GGMDLSELERDNTGRCRLSSPVPAVCRKEPCVLGVDEARGPVL  GGMVJAICVCPLPRIADLEALKVADKSKTLSSEREBLPAKWEDT DPVGWALDVLSPNLISTSNLGRVKYNINSLSHDTAGILOVALD OGVAVTOVYDVTOVMPETYDARLQOSPEVTVAKADAJIPV VASAASICAKVARDOAVKKWOFVEKLODLDTDVG\SGVPNDPDD / TKAMLKERVEPVVGPPQFVPR\SKRTVILESEREBLPAKWEDT DPVGWALDVLSPNLISTSNLGRVKYNINSLSHDTAGILOVALD OGVAVTOVYDVTOVMPETYDARLQOSPEVTVAKADAJIPV VASAASICAKVARDOAVKKWOFVEKLODLDTDVG\SGVPNDPDD / TKAMLKERVEPVVGPVGPVPR\SWRTVILESEREBLPAKWEDT DPVGWALDVLSPVNLISTSNLGRVKYNINSLSHDTAGILOVALD OGVAVTOVYDVOVMPETYDARLQOSPEVTVAKADAJIPV VASAASICAKVARDOAVKKWOFVEKLODLDTDVG\SGVPNDPDD / TKAMLKERVEPVVGTARLQOSPEVTVAKADAJIPV VASAASICAKVARDOAVKWOFVEKLODLDTDVG\SGVPNDPDD / TKAMLKERVEPVVGTARLQOSPEVTVAKADAJIPV VASAASICAKVARDOAVKWOFVEKLODLDTDVG\SGVPNDPDD / TKAMLKERVEPVVGTARLQOSPETYTAL KEGREDVUT LEKEREDVD / TKAMLKERVEPVVGTARLGOSPETYTAL KEGREDVIT LEKEREDVD / TKAMLKERVEPV OF TOR THE STANLONGARGAN I KRAMLTONGAR KEGREDVIT DE GRAGRPAG TIRVETYDE TOR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE STANLONGAR THE S				LQIITELIKTENN
SASGGRHGGRSGGPVICTYGPDLFPLWA\TIGGAFYAKUNS VODRYLIGINDTAGSERYAMBRITYCHDV ODYADNIKAQIETETSKTEGSVDELFGRKARAIAUVCYDTESS FERAKFWYKELBEGCQIYLGTKSDLLEEDRRRRRYDFHDV DYADNIKAQIETETSKTEGSVDELFGKABOLLEEDRRRRRYDFHDV DYADNIKAQIETETSKTEGSVDELFGKABOLVEEDRRRRRYDFHDV DRGWDLGQKPNPYFYSCCHH GGMDLSELEDBTTGGKELSSPVPAVCRKEPCULGVDEAGRGFVL OPWYAALCYCPLPRIADLEALKYADSKTLLESERELFAKMEDT DFVGRADULSENLISTSMLGRYKYNINASIETAGGIYGAGAPOL OGVANTOVFYDTYGRPETYQARLQQSFPGIEVTVKAKADALIYV VSANSICANARDQAVKKWQRVEKLQDLDTDYGSGYPNDPQD /TKAWIKEHVEPVV\GPPT\QFFPETYQRRLQQSFPGIEVTVKAKADALIYV VSANSICANARDQAVKKWQRVEKLQDLDTDYGSGYPNDPQD /TKAWIKEHVEPVV\GPP\QFFPETYQRRLQSFPGIEVTVKAKADALIYV VSANSICANARDQAVKKWQRVEKLQDLDTDYGSGYPNDPQD /TKAWIKEHVEPVV\GPP\QFFPETYQRGSGAPPDFUTDEGKS R/YSGHEAHDQGG\WADROSIIRKVVDPTGRTRLIKGDGEVLE BIVYKERHBEINKQATGDCLAFQMRAGLLF GTRQLPFPFPGSGGGDSPEFPGEAPERPRRKAHGMIKLYYGLSE GEAAGRPAGPDPLDPTDLMCAHFDPEVYLDKLRRECPLAQLMDS GTRULPFPFPGSGGGDSPEFPGEAPERPRRKAHGMIKLYYGLSE GEAAGRPAGPDPLDPTDLMCAHFDPEVYLDKLRRECPLAQLMDS ETDMVRQIRALDSMOTLVYENYKRIFTDTITLRKMYNDEFROM DEMBRIATIMAVITDFSARISATLQDRHBEITKLAGWALLRRL QFLFELEFFLHARGGLEERGRAFDAGAVLQOYCHLSPFRAM DEMBRIATIMAVITDFSARISATLQDRHBEITKLAGWALLRRL QFLFELEFFLHARGGLEERGRAFDAGAVLQOYCHLSPFRAM GEALCEPLAHARGGLEERGRAFDAGAVLQOYCHLSPFRAM GEALCEPLAHARGGLEERGRAFDAGAVLQOYCHLSPFRAM GEALCEPLAHARGGLEERGRAFDAGAVLQOYCHLSPFRAM GUARALLANGARGGGGGNSLLAVARAVGLFAAQCDPAGABKLAAFAQCLGSRYFALV ERILAGGCGGONSLLVARADLAFAGCLGAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAGACAAAAGACAAAGACAAAAGACAAAGACAAAAGACAAAGACAAAAGACAAAGACAAAAGACAAAGACAAAAGACAAAGACAAAAGACAAAAGACAAAAGACAAAAGACAAAAGACAAAAGACAAAAGACAAAAGACAAAAGACAAAAGACAAAAGACAAAAAA	6144	1289	568	SGPGSMSGQRVDVKVVMLGKEYVGKTSLVERYVHDRFLVGPYON
SOUND TO THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE	1	1	ł	VSASGGARHGGRGSGGPVICTYGPDLFPLVA\TIGAAFVAKIMS
FERRKFWYKELBEEGCQIYLCGTKSDLLEEDRRRRRVDFHDV DYDYADNIKQQLETISSTSTGSVDEEDGVAEDVSVAAFQWTE DKGWDLGQKPNPYFYSCCHH GGMDLSELERDNTGREKISSFVPAVCRKEPCVLGVUEAGRGFDVL GGMDLSELERDNTGREKISSFVPAVCRKEPCVLGVUEAGRGFDVL GGWDLGSLERDNTGREKISSFVPAVCRKEPCVLGVUEAGRGFDVL GGWDLSELERDNTGREKISSFVPAVCRKEPCVLGVUEAGRGFDVL GGWDLSELERDNTGREKISSFVPAVCRKEPCVLGVUEAGRGFDVL GDPVQMALDVLSPNLISTMLGRWKXNINSLEHDTATGLIQVALD GGWATOVFVDTVGMPETYORALQOSPFGIEVTVKAKADALYPV VSAASICAKANDROAVKROGVEKLQDLIVYGSGYPNDFQD /TKAMILKEHVEBVPVGPFVQFVRLQDLIVYGSGYPNDFQD /TKAMILKEHVEBVPVGPFVLGVEKLQDLIVYGSGYPNDFQD /TKAMILKEHVEBVPVGPFSLQWHRSAGEEDGPVLTDEQKS ESSASENQEGLRKTSYTLNEGSGARPRSSHKYFLERGLESITS  6146 428 781 LRKKGKEKAEAQCVEALPGPSLDQWHRSAGEEDGPVLTDEQKS R/YFGHEAHDQGGVWARGSIIRKVVDFTGTSTRLIKGDGEVLE EIVYKERHEINKQATAGDCLAFQMRAGLLP GTRGLPFSFGSGGGSPEFSPEGEAPERPRKRAHGMLKLYYGLSE GEAAGRPAGPDPLDPTDLNGAHFDPEVLDKLRRECPLAQLMDS ETDMVRQIFALDSDWOTLVYENVKRIFADTILGRUFALLGRUF GEAAGRPAGPDPLDPTDLNGAHFDPEVRLDKLRRECPLAQLMDS ETDMVRQIFALDSDWOTLVYENVKRIFADTILGRUFARKAG DEMBRIATIMAVITDFSARISATLQDRHERITKLAGVHALLRRL QFFFELFERFLHARGGLEKERLRELEELGANALOGVANLOGYCHLSFFRA IQDDCQVITARLAQOLROFFREGGGAPEGARLCVELLLALGEPA EELCEEPFLAHARGGLEKERLRELEELGANALOGANLOGYCHLSFFRA IQDDCQVITARLAQOLROFFREGGGAPEGARLCVELLLALGEPA EELCEEPFLAHARGGLEKERLRELEELGERGATPPADLLISFE CSGVGGLCQVAAAYGELFAAQCDPAGAKKLAAFARQLGSRYFALV ERRLAGGCGGONSLLVARADDFIFRAGVENGATHACHGSRYFALV ERRLAGGCGGGONSLLVARADDFIFRAGVENGATHACHGSRYFALV VERTITATIOVOVLRALAGRIVARDDFIFRAGVENGAFTETDHGVS GGFGGGANGTANASSILSHIKASLAAVHLFTAREVSSNRFYFRGGF CSGSMCINASSINASSIVERGGMRSVENTUGAGEARETA RRLLTHTVAVQGLVI LGGMLRKSVETRUBUSTLEFRAVNAMIKN VEDTTATIOVOVLRALGGGROWELGVENTSCHAGAGEERFTA SYKAKJESTRNNNENLLLEVKYPDLPRNAQVALITIBDYGGGRAV VENSINFNYLGGFRCVUCODERSGIYTYCQMFASGMCLLCPS SYKAKJESTRNNNENLLLEVKYPDLPRNAQVALITIBDYGGGRAV VENSINFNYLGGFRCVUCODERSGIYTYCROMORHYTHOCT SYKARSTRNNNENLLLEVKYPDLFRNAQVALITIBDYGGGRAV VENSINFNYLGGFRCVUCODERSGIYTYCROMORHYTHOCT SYKARSTRNNNENLLLEVKYPDLFRNAQVALITIBDYGGGRAV VENSINGNYLMGGFRCVUCODERSGIYTYCROMORHYLITIFICE LVKNSDFROMSHLEDGEARGEARCHAUSDUELLSSHYTNPTVRRYAVAR LKQADDEDLLM				VGDRTVTLGIWDTAGSERYEAMSRIYYRGAKAAIVCVDLTDGGG
6145  1109  196  GOMPLISELERDNIGKRILSSEVPAVCRKEPCVLGVDERGRGFFVL GOMPVART CYCPLERIADLEALKAVADSKILLESERERLERACMEDT DFVGMALDVLSPNLISTSMLGRVKYNLNSLSHDTATGLIGYALD OGNAVOTOVFDTVGWBFTVQARLQGSFFOLGVGFRENDET DFVGMALDVLSPNLISTSMLGRVKYNLNSLSHDTATGLIGYALD OGNAVOTOVFDTVGWBFTVQARLQGSFFOLGVGFPNDFQD /TXANLKEHVZEVFGFF\GFF\GFVEF\SMFTAGTI\LEERAGDEDT PVGMALDVLSPNLISTSMLGRVKYNLNSLSHDTATGLIGYALD OGNAVOTOVFDTVGWBFTVQARLQGSFFOTI\LEERAGDUTPV VSAASICAKVARDQAVKKMGFVEKLQDLDTDYG\SGYPMPDGD /TXANLKEHVZEVF\GFF\GFVEF\SMFTAGTI\LEERAEDUTR EDSASERQEGLEKITSYTLNEGGGRTGT\LEERAEDUTR EDSASERQEGLEKITSYTLNEGGGRTGT\LEERAEDUTR EDSASERQEGLEKITSYTLNEGGGRTGLETUT\LEERAEDUTR EDSASERQEGLEKITSYTLNEGGEEDGFVLTDEOKS R/YPGHEAHDQGG\NDAROSIIRKVVDPETGRTKLIKGDGEVLE EIVTKRERREINKOATRGCLLAPPGRSHRYFLKEGLESTTS LKKKKGKEKAEAQQVEALFGFSLDWHRSAGEEEDGFVLTDEOKS R/YPGHEAHDQGG\NDAROSIIRKVVDPETGRTKLIKGDGEVLE EIVTKRERREINKOATRGCLLAPPUTLDKLHERECLAQLMES ETMAVRGIRALDSDMOTLVVENVNKFISATDTIRKMNDFRKME DEMDRIATMANAVIDFSARISATLQDRHERITKLAGVHALLKRL OFLFEUFSKLITKVELGAYOQAVAYGGRAQAVLOOYGHDFSFRA IQDDCQVITARLAQQLRQRRREGGGAPPOLAGVCHLUFRIC DEMDRIATMANAVIDFSARISATLAQDRHERITKLAGVHALLKRL OFLFEUFSKLITKVELGAYOQAVAYGGRAQAVLOOYGHDFSFRA IQDDCQVITARLAQQLRQRRREGGGAPPOLAGVCHLUFRIC SGFVGGLGCVAAAYQERFAQGBGAGEKLAAFRQLGSRYFALV ERRLAQGGGGGNSLLAAFRQCGSRYFTHOLSTTLLAGREVAGKEGP GLAELLANVASSILSHKASLAAVHIFTAKEVGFSNKPYFRGEF CSQAVREGLIVGFVHSNCQTAGGFCDSPGEKGGATPPALLLLLS RRLLDTYLTTDFOOLPHOOPPVTPVSTLCAERAETA RRLLTHYVKVQGLVISOMLRKSVETRDBLSTLERRNVRAMKNV VEDTTALTDVOLPPLAGVALTOAGGFVPSRGAGAAEDHWGLDP GGMCTWASHGASSVARASVEFPQCNKSPRNYTTAGGECLCPRS CSFSAQDYDIPAPILDEVAGRLVTQDFPRSGAGAAEDHWGLDP GGMCTWASHGASSVARASVEFPQCNKSPRNYTTAGGECLCPRS CSFSAQDYDIPAPILDEVAGRLVTQDFVRAGLIVVLKIRPGTNS CLIPPHSTGSINSDHVPYK SYKAFSTRNNNENLKLEVKYPDLEFRAQMATIMDVYGPGGAV PVGGTTVSLEFKYMERGQAHLDKYVPCOVFAEGRFLALPVTT SYKAFSTRNNNENLKLEVKYPDLEFRAQMATIMDVYGPGGAV PVGGTTVSLEFKYMERGQCHNLEVYTCOVFAEGRFLALPVTT SYKAFSTRNNNENLKLEVALYPBCDLAVVERSQMPTTFORTS STLSEDOMSBLANGSHALTKAHRQCHMVKDMLGRATIKLITSVI W DLPGGAKOALALLGKMYMFTSGALLKGMSVYPSKPPDLSKTKFWPDG ENLEGDLCTFLISRASKNSTLANLYVYVIVECDOD	1	1		FERAKFWVKELRSLEEGCOIYLCGTKSDLLFFDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
6145 1109 196 GGMDLSELERDNINGERCHLSSPVPAVCRKEPCVLGVDEAGRGPVL GPMVYAICYCPLFRLADLEALKAVADSKTLLESERSELPAKGEDT DFVGMALDVLSPRLISTSMLGRYKAVADSKTLLESERSELPAKGEDT DFVGMALDVLSPRLISTSMLGRYKAVADSKTLLESERSELPAKGEDT DFVGMALDVLSPRLISTSMLGRYKAVADSKTLLESERSELPAKGEDT DFVGMALDVLSPRLISTSMLGRYKAVADSKTLLESERSELPAKGEDT DFVGMALDVLSPRLISTSMLGRYKAVADSKTLLESERSELPAKGEDT VYSAASICAVARDQAVKKWOFVEKLQDLIDTIG GSTPADPOD ATKAMLKEHVEPVF GFF\QFVERY-SWRTAQTILLEKRAEDVIR EDSASENQEGLERITSYFLEBGSQARPRSSHRYFLERGLESTTS L KKKKGKEKABAQOVEALFGPSLOWHRSAGEEEDGFVLTDEOKS R/YGGHEAHDOGG \( VARKING MARGSLIF KY LERGLESTTS L LEGGLESTTS L LEKKKGKEKABAQOVEALFGPSLOWHRSAGEEEDGFVLTDEOKS R/YGGHEAHDOGG \( \text{VARKING MARGSLIF KY LERGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L LEGGLEST L L LEGGLE	Ī	1		QDYADNIKAQLFETSSKTGOSVDELFOKVAEDVIGVAAROVMTE
6145 1109 196 GGMDLSELERDNTGRCRLSSEVPAVCRKESCULGVDEAGRGFVL GPMYVALCYCPLERILADLEALKVADSKTLLESSERERLFAKMEDT DFVGMALDVLSPNLISTSMLGRVKTVILNSLSDTATCLICYALD OGVNVTOVTDTVGMETYGARLQGSFPGIETVVKAKADALIYV VVSAASICAKVARDQAVKKMOFVEKLQDLDTDYG\SGYPMDPQD /TKAMLKEHVEPVP\GFF\OFVRF\SMRTAQTI\LEKKAEDALIYV VSAASICAKVARDQAVKKMOFVEKLQDLDTDYG\SGYPMDPQD /TKAMLKEHVEPVP\GFF\OFVRF\SMRTAQTI\LEKKAEDALIYV VSAASICAKVARDQAVKKMOFVEKLQDLDTDYG\SGYPMDPQD /TKAMLKEHVEPVP\GFF\OFVRF\SMRTAQTI\LEKKAEDALIYV VSAASICAKVARDQAVKAMOFVEKLQDLDTDYG\SGYPMDPQD /TKAMLKEHVEPVP\GFF\OFVRF\SMRTAQTI\LEKKAEDALIYV LEKKAESANQCELKITSYYSLMEGSQANFYSSHRYFLERGLESTTS L KKKKGKEKAEAQQVEALFGSELDQWIRSAGEEEDGPVLTDEQKS R\YFGHEAHDOGG\NDARGSIIRKVVDPETGKTELIKGGEVLE EIVYKERHREINKQATARGCLAPQMRAGLID EIVYKERHREINKQATARGCLAPQMRAGLID GTRCLPFSFGSGFQFDSFGFEGEAPERRKKAHMLKLYYGISE GEAAGRPAGFDDLDTDLNGAHPDDEVYLDKIRECCPLAQLMOS ETDWYRQIALADMOGTULVYENINKFISATIOIRKRMDFRKME DEMDRLATMMAVITDFSARISATLOPRHERITIKLAGUHALLKIL QFIFEPSSIITKCVELGAYQGAVPGRAQAVLOOYDHLPSFRA IQDDCQVITARIAQOLQRORTREGGSGAPEQAECVELLLALIGEP EELCESPLAHARGRLEKELRNLEAELIGSPSPAPADVLEFTDHG\S SGFVGGLQVAAAVQELFPAAQGFAGAGALAAAFGLADAAT EIVERVARRRICHHLQCLRAPFIGCTLTDVRQALAAPRVAGKEGP GLAELLANVASSILSHIKASLAAVHLFTTAKEVSFSINKPYFRGEF CSQVVERGELTVGFYHSKOCTAQSFCDEKGGATPPALLLLIS RLCLDVETATISYILTITDEQFLVXDQPFPYTYSTLCAEARETA RRLLTHYVKVQGULVSMCKSVETDMUSTREGECLCPRS CSGVSGCGIVGTHAAGVAATGGGTVPSRGAGAAEDHGSLPG GGDMCIMASHGASVARASVREPQGNKSFRMYTRAGECLCPRS CSFSAQDVDIPAPILDVEKQTLAVTQVEVRAGLVLVKIRPQTNS CLIPPHSTGSINSDHYPTK SYKASTSTRNNNEBLKLUPKYPDLDFRAQVALTIMVTYPYTKARVAMKV VEDTTALDVOVLPRLAGVALTQVEVRAGLVLVKIRPQTNS SYKASTSTRNNNEBLKLUPKYPDLDFRAQVALTIMVTYPYTKRYAVA VEDTTALDVOVLPRLAGVATYTYSCROMESPLLTPFE LVKVPDPGMSLEMLVESKHHNLPRSLRSGSGDDLKPYFSPRDQ LKNIVSTYPSKPPTYPERQOLLWERTYYPTVRRYAVAR LKQADDEBCLMYLLGUVQALKYENDDLKYPTSPRDQ LKNIVSTYPSKPTYPTYRRYDPVRRYAVAR LKQADDEBCLMYLLGUVQALKYENDIJKRILTSVIW DLPGGAKQALALIGKWRPMDVBDSLELLSSHYTNPTVRRYAVAR LKQADDEBCLLMYLLGUVQALKYMBSLLAAQQIFTVDRLHHM KAVQRESGNRKKNEBLQALLIGDMEKWNLDRULIPLPLEPOVK IRGITIPETATLFKSALMPAQLFFRIEGGRYPTYFKHODLROD				DKGVDLGQKPNPYFYSCCHH
GPMYYAICYCPLPRIADLEALKVADSKTLIESERERLFAKMEDT DPVGMALDULSPRILSTSMLGRYKYNINSLISHDTATGLIOYALLO GGVNVTOYFUDTUGMETYOARLOGSPGIETTVKAKADALYDV \VSAASICAKVARDOAVKKMOPEVLODLTDYGYGSGYPMDPDD /TKAMLKEHUEPUF\GFP\QFVRF\SWRTAGTI\LEKEABDVIR EDSASENGEGIRKITSYFLWEGSQARPRSSHKYLEKGLESTTS L  6146 428 781 LKKKGKEKAEAQOVEALFGPSLDQWHRSAGEEEDGPVLTDEOKS R/YPGHEAHDQGG\NDAROSIIKKVYDPETGRTRLIKGDGEVLE EIVYKGRHERINKQATRGDCLAPQMRAGGLIP GTRQLPPSFGSGFGDSSEGFGEFBRRKAHGMLKLYYGLEE GEAAGRPAGPDLDPTDLNGAHFDPSVYLDKLURRECPLAQLMDS ETDWNGIRALSDWOTLVYRUNKFISATDTIRKMENDFRKWE DBMDRLATNMAVITDFSARISATLORHERITKLAGHALLAKL QFLFELPSRLITKCVSLGAYGQAVRYQGRQAVLQOYCHLPSFFA LQDCQVITARLAQOLKQRFREGSGAPFQAECVELLLALGEPA EELCESFLAHAAGRLEKSLENLEAGLGPSPPAPDVLEFTDHG\S SGFVGGICVAAAVQGLFAAQGGAGKLAAFRGGLEAGHAVAGKSGP GLAELLANVASSILSHIKASLAAVHLFTAKSVSSNKPYFRGEF CSGVVSGCLIVGAVYQGLFAAQGGAGKLAAFRGGLAGKFYFALV ERRLAQCGGGGNSLLVRALDFHRRLRAGALLAAAGLADAAT EIVERVARRELGHHLGGLRAFHGCTUVQQLAFFACGGAGATPALLLLLS RLLHYVYKGGLVISGMIRKSVETROMLSTLERRWRAVMKRV VEDTTAIDVQUIPRLAGVALTONGGTVPSRGGAAEDHQSLPG GGMCIWASHGASSVARASVREPQCNKSPRINTRAGECLCPRS CSGSVAGDVIPAPILDVEKGRLTVQCVAGGAVVLVKIRPQTNS CLIPLPHSTGSINDHPYTK  6148 3056 353 VPAGGTTPADGAMGEARKFFYTYSCDLDINVQLKIGSLEGKREQ KSYKAVLBDPHLKPSGLYODTCSDLYVTCQVFAGGVLLVKIRPQTNS SYKAFSTRNNNNEWLKLPVYPDLPRINAQVALITINDVYGPGKAV PVGGTTVSLFGKYGMFRQCMHDLKWPNCRSQMDQKPTTPGRT SSTLSEDQMSRLAKLTKAHRQCHMVKVDWLDRLTRETEIMINES VKRSSNFYLMGGFRCKCDDKEGYTYPKROGSSVS ENVSNSGINSAEIDSSQITT/SAPPSVSSPP\ASKTYPSPRDQ LKNIVSYPSPSPPTYERQOLLWERPTYNDDLIKKLTSTVM DLPGGKKQALALLGKWRPMOVEDSLELLSSHYTNPTVRRYAVAR LKQDDEDLMYLLOLVQALKYENFODI KNGLEPTKNDGSSVS ENVSNSGINSAEIDSSQITT/SAPPSVSSPP\ASKTKEVPDG ENLEQDLCTFLISRASKNSTLANLYWYVUEEDQDTQQDDP THEMILANWRRFSGALLKGMSVENSSLLAAQQTFVDRUPLHLM KAVQRESGNRKKNERELQALLGDMEKWNLEDVELIPLELEDOVK INGSINNAKKNERLQALLGDMEKWNLEDVELIPLELEDOVK INGSINNAKKNERLQALLGDMEKWNLEDVELIPLELEDOVK INGSINNAKKNERLGALLGDMEKWNLEDVELIPLELEDOVK INGSINNAKKNERLGALLGDMEKWNLEDVELIPLELEDOVK INGSINNAKKNERGLALLGDMEKWNLEDVELIPLELEDOVK	6145	1109	196	GGMDLSELERDNTGRCRLSSPVPAVCRKBDCVICUDEACECTE
DEVGMADDUSPRILISTSINLGRYKTINISLEHDTATGLIQYALD QGVMYTOVFDTUGMETYQARIQGSFGIEVTVKAKADALIYDV \VSAASICAKVARDQAVKMQPVELLQDITDVG\SGYPNDPQD \TXAMIKEHTEPPVF\GFP\GFP\SWRTAQTI\LEKEAEDVIR EDSASENQEGLRKITSYFLNEGSQARPRSSHRYFLERGLESTTS L  6146 428 781 LKKKGKEKAEAQQVEALFGFSLDQWHRSAGEEEDGFVLTDEQKS R/YPGHEAHDQGG\WDARGSIIRKVVDPETGRTRLIKGDGEVLE EIVYKERHRBINKQATRGCLAFQWRAGLLP 6147 1 2304 GTRQLPPFSGSGGUSPBGPBGEAPERRKAHGMLKLYYGLSE GEAAGRAGDPLDJDTDLNGAHFDDEVYLDKLRRECFLAQLMDS ETDMVRQIRALDSDMYTLVYENYKFISATDITKKKNDFRKME DEWDRLATMANITDFSARISATLQDRHERITKLAGVHALLKKL QFLFEDSRITKCVELGBYGQAVEYQGRAQAVLOQVOHLPSFRA IQDDCQVITARLAQQLROFFREGGSGAPEQACCVELLLALGEPA EELCEFPLHAHRGRIEKELRIKELGFSPAPADVLEFTDHG\S SGFVGGLCQVAAAYQBLFAAQGPAGAKLAAFARQLGSRYFALV ERKLAQDGGGGINSLLVRALDRFHRRLAPGAGLALAAFARQLGSRYFALV ERKLAQDGGGGINSLLVRALDRFHRRLAPGAGLALAAFARQLGSRYFALV ERKLAQDGGGGNSLLVRALDRFHRRLAPGAGLALAAFARQLGSRYFALV ERVARERLGHHLQGLRAAFIGCLTDVRQALAAPRVAGKEGP GLAELLANNASSILSHIKASLAAVHETTAKEVFSRKVFRGEF CSGGVRGGLIVOFVISMCQTAGSEDSPGKGGATPPALLLLLS RLCLDVETATISYLITLTDEGFLVQDGFFTPVFSTLGABRETA RRLLTHYVKVGGUYLSQMLRKSVETROWLSTLEFRVRVRAVMKV VEDITAIDVQULPRLAGVALTQAGGTVPSRGAGAABDHHQSLPG GGMCIMASHGASVARSVETROWLSTLEFRVRVRAVMKV VEDITAIDVQULPRLAGVALTQAGGTVPSRGAGAABDHHQSLPG GGMCIMASHGASVARSVETROWLSTLEFRVVRVMKV VEDITAIDVQULPRLAGVALTQAGGTVPSRGAGAABDHHQSLPG GGMCIMASHGASVARASVETROWLSTLEFRVVRVMKV VEDITAIDVQULPRLAGVALTQAGGTVPSRGAGAABDHHQSLPG GGMCIMASHGASVARASVETROWLSTLEFRVVRVMKV VEDITAIDVQULPRLAGVALTQAGGTVPSRGAGAABDHHQSLPG SYKAFSTRNNNEWHIKLPVXYPDLPNAQVALTIDDVGGKAV PVGGTTVSLFGKYGMFRQGHDLKVWPDCRSQMDQKPTKTPGT SYKAFSTRNNNEWHIKLPVXYPDLPNAQVALTIDDVGGKAV PVGGTTVSLFGKYGMFRQGHDLKVWPDCRSQMDQKPTKTPGT SYSTAFSTRNNEWHIKLLPXYPTYPLYDLPNAQVALTIDDVGGKAV PVGGTTVSLFGKYGMFRQGHDLKVWPDCRSSSPILDSFE LWKVPDPQMSLENLVESKHINLPRSLESGGSPHDLKPYFSPRDQ LKNIVSYPPSKPPTYPEQDLUWEFYLYTVINQOKALTKILTSVI W DLPQGAKQALALLGKMKYMPSLLAAQTYVLKOGEGOTOQRDFK THEMYLNVWRFSGALLKGDKSVVWRSLLAAQTFVURCEQDOTOQRDFK THEMYLNVWRFSGALLKGDKSVVWRSLLAAQTFVURCEQDOTOQRDFK THEMYLNVWRFSGALLKGDLKSVVWRSLLAAQTFVDRLINGK	]			GPMVYAICYCPLPRLADLEALKVADSKTLLEGEDEDLEA KMEDON
OGWNTOVFORTUGNETTYCALGOSPEIEVTWARGADLTYPU VSAASICAKWARQAVKKOOPVEKLODLDTDVG/SGYPNDPOD /TKAWILKEHVEPUP\GFP\QFVGFV,SWRTAQTI\LEKEAEDVIR EDSASENQEGLRKITSYFLNEGSQARPRSSHRYFLERGLESTTS L LKKKGKEKAEAQQVEALFGFSLDQWHRSAGEEDGFVLITDEOKS R/YPGHEAHDQGG\WDARGSIIRKVVDPETGRTRLIGGDGEVLE EIVTKERHREINKQATRGDCLAFQMRAGLLP 6147 1 2304 GTRQLPPPSPGSEGFDSPEGFEGEAPERRRKAHGMLKLYYGLSE GEAAGRPAGPDPLDPTDLNGAHFDDEVYLDKLRECCPLAQLMDS ETDWINGIRALDSDMGTLVYENYNKF1SATDTIRKMKNDFRKME DEMBRLATMNAVITDFSARISATDTIRKMKNDFRKME DEMBRLATMNAVITDFSARISATDTIRKMKNDFRKME DEMBRLATMNAVITDFSARISATDTIRKMKNDFRKME OFFIFELPSRITKCVELGAYGQAVRYGGRAQAVLQOYGHLPSFFA IQDDCQVITARLAGOLORGFREGGAPEQABECVELLLALGEPA EELCEEFLAHARGRLEKELRNLEAELGPSPPAPDVLEFTDHG\S SGFVGGLCQVAAAYQELFAAGGPAGAKKLAGRAGLADAAT EIVERVARRELGHHLQGLRAAFLGCLTDVRQALAAPGLADAAT EIVERVARRELGHHLQGLRAAFLGCLTDVRQALAAPGRAGREG GLAELLANVASSILSHIKASLAAHLFTAKEVSFSKKPYFRGEF CSQSVREGLIVGFVISMCQTAQSFCDSFGRGGATPALLLLLS RLCLDVETATISYILTITDEOFLVQDQFPVTPVSTILCAERETA RRLLTHYVKVQGLVISMALRKSVETRDMLSTLEPRRVRAVMKRV VEDTTAIDVOUPRLAGGAAFLGCLTDVRGALAAPGRAGHGG GGMCTMASHGASSVARSVETRPONSPRAGAAAEDHHQSLPG GGMCTMASHGASSVARSVETRPONSPRAGAAAEDHHQSLPG GGMCTMASHGASSVARSVETRDDLSTLEPRRVRAVMKRV VEDTTAIDVOUPRLAGGATPSRGAGAAEDHHQSLPG GGMCTMASHGASSVARSVETPDLFRAGQALVLVLKIRPQTNS CSFSAQDYDIFAPILIPVEKQRLRVTQEVRAGLVLVLKIRPQTNS CSFSAQDYDIFAPILIPVEKQRLRVTQEVRAGLVLVLKIRPQTNS SYKASFSTRNNNNEWHLKLPVXFYDLPRAQVALITUDVGGKAV PVGGTTVSLFGKYGMFRQGMDLKVWFNCCSMDQKPYKTFGRT SYKASFSTRNNNEWHLKLPVXFYDLPRAQVALITUDVGGKAV PVGGTTVSLFGKYGMFRQGMDLKVWFNCCSMDQKPYKTFGRT SSTLSEDQMSRLAKLTKAHRQGTVYYLNDQKALTKLTESTIM LKXVPPPSKPPTYERQLLVWFRCSGSPHDLKPYFSPRDQ LKNIVSYPPSKPPTYERQLLVKFNFDDIRNGVALTKLTESTIM DLPQGAKQALALLGKMKRMDVEDSLELLSHTNFTVRRAVAR LRQADDEDLLMYLLQLVALKYRPFDDIRNGVALTKLTESTIM DLPQGAKQALALLGKMKRMDVEDSLELLSHTNFTVRRAVAVA ENVSSGINSAEIDSSGITT/SAPPPSVSSPPP\ASKTKEVPDG ENLEGOLCTFILISRASKNSTLANULYVYVIVECEDQDTQGNDFK THEMILNVARPFSQALLKGDKSVRWRSLLAAQQTFVDRLVHLM KAVQRESGNRKKKRELQALLGDLGDGROMSLADAGOTFUDRLUHLM KAVQRESGNRKKKRELQALLGGLGGGRAFHGGGLFYPTFGHDDL	ļ			DFVGWALDVLSPNLISTSMLGRVKYNINSISHDTATCI TOVALD
VSAASICAKVARDQAVKKMQRVEKIQLDITDYG\SGYPNDPQD   TKAMIKEHUEPV\GF\QF\QFVER\SMRTAGTI\LEKEAEDVIR   EDSASENQEGIRKITSYFLNEGSQARPRSSHRYFLERGLESTTS L   LKKKGKEKAEAQQVEALFGPSLDQMHRSAGEEEDGFVLTDEOKS   R/YPGHEAHDQGG\MDARGSIIRKVVDPETGRTKLIKGDGEVLE   EIVYKERHREINKOATRGDCLAFQMRAGLLE   GETAGRAFAPQGG\MDARGSIIRKVVDPETGRTKLIKGDGEVLE   EIVYKERHREINKOATRGDCLAFQMRAGLLE   GEAAGRPAGPDFLDETDLNGAHFDPEVYLDKLRRECFLAQLMDS   GEAAGRPAGPDFLDETDLNGAHFDPEVYLDKLRRECFLAQLMDS   ETDMVRQIRALDSDMGTLVYENYNKFISATDTIKKVNDPFKME   DEMDRLATHNAVITDFSARISATLQDHERITKLAGVHALLKKL   QFIFELPSRLIKKVCUELGAYGQAVLQOYQHLDPSKA   LQDDCQVITARLAQQLRQRFREGGSGAPEAGEVELLLALGEPA   ELCEEFLAHARGRLEKELRRLEEBLGPSPPAPDVLEFTDHG\S   SGFVGGLCQVAAAYGELPAAQGARKLAAFRAGLSNAFALV   ERRLAQEQGGGNSLLVRALDRFHRRLRAPGLLAAAGLADAAT   EIVERVARRELGHHLQGLRAFLGTDVQDGFPYFVSTLCAEARBTA   RLLTHYVKVQGLVISQMLRSVETRDWLATABPVARKEP   GLAELLANVASSILSHIKASLAAVHLFTAKEVSFSNKPYFRGEF   CSQSVREGLIVGFHIRKQTAQSFCDSFGGKGGATPPALLLLLS   RCLDPTATISYILTLTDEGFINQDGFPYFTVSTLCAEARBTA   RRLLTHYVKVQGLVISQMLRSVETRDWLSTLEPRNVRAVMKKV   VEDITALDVOVLPRLAGVALIOAGGTVPSGRGGAADDHAOSLPG   GGMCTWASHGASSVARASVREPQGNKSPRWNTKRAGECLCPRS   CSFSAQDYDIPAPILPVEKQRLZVTGEVRAGLVILVLKTRPQTNS   CLIPPHSTGSINSDHYPTK   CLIPPHSTGSINSDHYPTK   SYKASTSTRNNMEWLKLPVKYPDLPRNAQVALITIMDVSGPGKAV   PVGGTTVSLFGKYGMFRQGHDLKVWPNGCKSMDQKPTKTFGRT   SYTLSEDGMSRLAKLTKAHRQGMVKVDMLDRLTFREIEMINES   VKRSSNFMYLMGGFRCVKCDDLFSGLFSSFILTSFE   LKVPDPOMSLEINLSKHNLYSKLTSLRSGPSDHDLKPYPSPRQ   LKNIVSYPPSKPPTYEEQDLVWEFRYYLTNDRALTKLTSTVI W   DLPQGAKQALALLGKWKPMDVEDSLELSSHTNPTVRRAVAR   LKQADDEDLLMYLLQLVALKYRPDDI KNGLEFTKKDSOSSVS   ENVSNGINSAEIDSSGITT/SAPPPSVSSPPP\ASKYKEVPDG   ENLEGDLCTFFILISASKNSTLANYLYWYVIVECEDQDTQQRDPK   THEMYLNVMRRFSQALLKGDKSVRWRSLLAAQGTFVDRLHMM   KAVQRESGNRKKKRELQALLGDNEMMLSDVELIPLPLEEQUVK				QGVNVTQVFVDTVGMPETYOARLOOSEPGTEVTVKAKADAT VDV
6146 6146 6146 6146 6146 6146 6147 6146 6147 6147	1	į į		\VSAASICAKVARDOAVKKWOFVEKLODI.DTDVC\ CCVDVDDOD
6146 428 781 LKKKGKEKAEAQQVEALPGPSLDQWHRSAGEEDGPVLTDEQKS R/YPGHEAHDQGG\WDARGSIIKVVDPETGRTRLIKGDGEVLE EIVTKERHREINKQATKGDCLAFQMRAGLIP 6147 1 2304 GTRQLPPPSPGSGFGDPEGEGEAPERRKAAGMKLYYGLSE GEAAGRPAGPDPLDPTDLAGHDEVDLAKKRECPLAQLMDS ETDWYRQIRALDSDMQTLVYENYNKFISATDTIRKMKNDFRKME DEMDRLATNNAVITDFSARISATLQNHERITKLAGVHALLKRL QFIFELPSRITKCVELGAVQAVRYQGRAQAVLQOYGHLPSFRA IQDDCQVITARLAQOLRQFFREGSGAPEGAECVELLLALGEPA EELCEFELAHAGRGEKEKELNEAEIGPSPPAPDVLEFTDHG\S SGFYGGLCQVAAAYQELFAAQGPAGAEKLAAFARQLGSRYFALV ERRLAGGGGGONSLLVRALDRFHRRITRAFGALLAAAGLADAAT EIVERVARERLGHHLQGLRAAFIGCLTDVRQALAAPRVAGKEGP GLAELLANVASSILSHIKASLAAVHLFTAKEVSFSNKPYFRGEF CSQSVREGLIVGFVHSMCOTAQSFCDSPGEKGGATPPALLLLIS RLCLDYETATISYILTTDEQFIVQDQFPVTVSTLCAEARETA RRLLTHYVKVQGLVISQMLKSVETRDWISTLEPRNVRAVMKRV VEDTTAIDVOVLPRLAGVALTOGGTVPSRGGAAEDHWGSLPG GGMCIWASHGASSVARASVRSPQGNKSSPMNTKRAGECLCPRS CSSAQDYDIFJAPILDVERVGRVTVQEVRAGLAUVLKIRPQTNS CLIPPHSTGSINSDHVPTK 6148 3056 353 VPAVGGTFADGAMGEAEKFHYIYSCDLDINVQLKIGSLEGKREQ KSYKAVLEDPMLKFSGLVQGTCSDLYVTCQVPAGGKPLALPVRT SYKAFSTRNWMEWLKLPVKYPDLPRNAQVALTIWDVYGPGKAV PVGGTTVSLIFGKYGMFRGGMDLLKWPRCRSOMQKPKTFGRT SYKAFSTRNWMEWLKLPVKYPDLPRNAQVALTIWDVYGPGKAV PVGGTTVSLIFGKYGMFRGGMDLLKWLTFRSIEMINES VKRSSNFWLMGGFRCVKCDDKPGIVYYEKGGDESSFILTSFE LKVVPPPQMSLENLVESKHHNLPRSLRSGSFDDLLKPYPSPRDQ LKNIVSYPPSKPPTVEEQDLVWFRYYLTNQDKALTKILTSVIW DLPQGAKQALALLGKWRMDVEDSLELLSSHYTMFTVRRYAVAR LRQADDEDLLMYLLQLVQALKYENPDDIKNGLEFTKKDSGSVS ENVSNSGINSABIDSSGIIT/SAPPSVSSPPP\ASKTKEVPPDG ENLEDDLCTFTLISRASKNSTLANVLYWYVIVECEDQDTQQDPK THEMYLNVMRRFSQALLKGLKSVVMSLLAAQQTFVDRLVHLM KAVQRESGNRKKKWERLQALLGDMEKNISDELIPLPLEPQUK THEMYLNVMRRFSQALLGDLEFKHOLSSVTJFHURDL	Į.			/TKAWLKEHVEPVF\GFP\OFVFF\SWPTAOTI\IEVEAEDUZE
6146 428 781 LKKKGKEKABAQQVEALFGPSLDQWHRSAGEEEDGPVLTDEQKS R/YPGHEAHDQGG\WDAROSIIRKVVDPETGRTLLKGDGEVLE EIVTKERHREINKQATRGDCLAFQMRAGLLP GTRQLPPFSPGSGPGD5EPGERPERRKAHGMLKLYYGLSE GEAAGRPAGPDPLDDTDLNGAHFDDEVYLDKLRRECPLAQLMDS ETDMVRQIRALDSDMQTLVYBYNKFISATDTIRMKNDFRRME DEMDRLATNMAVITDFSARISATLQDRHERITKLAGVHALLRKL QFIFELPSRITKCVELGAYGQAVFYOGRAQAVLQQYCHLPSFRA IQDDCQVITTARLAQOLKGYFGEGGGAPEQDAEVUELLLALGEPA EELCEBFLAHARGRLEKELRNLEAELGPSPPPAPDVLEFTDHG\S SGFVGGLCQVAAAYQELFAAQGPAGAKLAAFARQLGSRYFALV ERRLAGRGGGGDNSLLVARADDFHRRIRAFGALLAAAFARQLGSRYFALV ERRLAGRGGGGDNSLLVARADDFHRRIRAFGALLAAAFARQLGSRYFALV ERRLAGRGGGGDNSLLVARADDFHRRIRAFGALLAAAFARGLEGPA GLAELLANVASSILSHLKASLAAVHLFTAKEVSFSNKPYFRGEF CSQGVREGLIVGFVHSNCCTAQGFCDSFGEKGGATPPALLLLLS RLCLDVETATISVILTITDEDGFLVQDOFPVTPVSTLCAEARETA RRLLITHYKVGGLVISGMURKSVETRDNLSTLEPRNVRAMKRV VEDTTATDVQVLPRLAGVALTQAGGTVPSRGGAAEDHWQSLPG GGDMCIWASHGASSVARASVREDGGNKSPRWNTKRAGECLCPRS CSFSAQDYDIFAPILLEVEKQRLEVTQEVRAGQLVLVLKIRPQTNS CSFSAQDYDIFAPILLEVEKQRLEVTQEVRAGQLVLVLKIRPQTNS CLIPJEPHSTGSINSDHVPTK  6148 3056 353 VPAVGGTFFADCAMGEAEKFHYIYSCDLDINVQLKIGSLEKKREQ KSYKAVLEDPMLKFSGLYQETCSDLVYTCQVFAEGKPLALPVRT SYKAFSTRNNWEBULKLPVKYPDLPRNAQVALITUDVYGGGKAV PVGGTTVSLEGKYGMFRGCMHDLKVWPNCRSQMDQKBTKTFGRT SSTLSEDQMSRLAKLTKAHRQGHMVKVDWLDRLTFREIEMINES VKRSSNFMYLMGFKSKYGMFRGCMHDLKVWPNCRSQMDQKBTKTFGRT SSTLSEDQMSRLAKLTKAHRQGHMVKVDWLDRLTFREIEMINES VKRSSNFMYLMGFRCVKCDDKEYGITYYSKDGDESSPILTSFF LVKVPDPQMSLENLVESKHHNLPRSLRSGFSUDBLKBYPSPRDQ LKNIVSYPPSKPPTYBEQDLVWEFRYYLTMODKALTKILTSVIW DLPQGAKQALALLGKWKPMDVEDSLELLSSHYTNPTVRRXVAVR LRQADDEDLIMYLLQLVQALKYENFDDI KNGLEFTKKNSQSSVS ENVSNSG INSAEIDSSQIIT/SSPPPVSSPPPVASRPPDG ENLECDLCTFLISRASKNSTLANYLWWYLVVECEDQDTQQRDPK THEMYLNVMRRFSQALLKGDKSVVMRSLLAAQQTFVDRLVHIM KAVQRESGMRKKKNERLQALLGKMYPLTVRECDDDTQQRDPK THEMYLNVMRRFSQALLKGDKSVVPFKTEDDLGDLGDLFDLFLDEPQVK IRGGIPFETTERSALMPAQLFFKTEDDERMOLDDLFUPLEPQVK IRGGIPFETTERSALMPAQLFFKTEDDLGARGDLFUPLEPDLOVK	}	1		EDSASENOEGI.RKITSVFI.NEGSOAPPREGURVELERGI ROTTO
6146  6147  1 2304    LKKKGKEKAEAQQVEALFGFSLDQWHRSAGEEEDGFVLTDEQKS R/YFGHEAHDQGG WDAROSIIRKVUPETGRTRLIKGGEVLE EIVYKEHRIERIKGATROCLAFQMRAGLIP  6147  1 2304   GTRQLPPSPGSGFDGSFGDESEAPERRRKAHGMLKLYYGLSE GEAAGRPAGPAPPLOPTDLINGAHFDPEVYLDKLREECFLAQLWDS ETDMVRQIRALDSDWQTLVYSNYNKFISATDTIRKMKDFRKME DEMDRLATNWAVITDFSARISATLQRHERITKLAGVHALLKKL QFIFELPSRITKCVELGAYGQAVKYQGRAQAVLQOYGHLSFRA LODDCQVITARLAQOLRORFFEGGSGAPEQABCVELLLALGEPA EELCEBFLAHARGKLEKELRUKALGAYAGAVKYQGRAQAVLQOYGHLSFRA LODDCQVITARLAQOLRORFFEGGSGAPEQABCVELLLALGEPA EELCEBFLAHARGKLEKELRUKALGAHAFARQLGSRYFALV ERRLAGEQGGGDNSLUVRALDRFHRRIRAPGALLAAAGLADAAT EIVERVARERIGHHLQCLRAAFLGCLTDVRQALAPRVAGKEGP GLAELLANVASSILSHIKASLAAVHLFTAKEVSFSNKPYFRGEF CSQAVERGLIVGFHSMCQTAQGFCDSPGKKGGATPFALLLLS RLCLDYETATISVILTITDEGFLVQDGFPVTPVSTLCAERRETA RRILIHHVKVQGLVISGMLRKSVETRDWLSTLEFRNVRAMKRV VEDTTAIDVOLVPRLAGVATQAGGTVPSGAGAAAEHMOSLDG GGMCTWASSIGASSVARASVREPQGNKSPRMYTKRAGECLCPRS CSFSAQDYDIPAPILPVEKQRLRVTQVFRAGCVLVLKIRRQTINS CLIPLPHSTGSINSDHVPTK  6148  3056  353  VPAVGGTTALGAGGTVPSKAGGAVACVHKIGRGEKREQ KSYKAVLEDPMLKFSGLYQDTCSDLYVTCOVFRAGKCLALDVRT SYKAPSTRNNMNENLKLPVKYPDLFNNAQVALTIMDVYGFGKAV PVGGTTVSLFGKYGMFRQGMHDLKKVPNCRSQMDQKPTKTPGRT SYTASFTRNNMNENLKLPVKYPDLFNNAQVALTIMDVYGFGKAV PVGGTTVSLFGKYGMFRQGMHDLKVVPNCRSQMDQKPTKTPGRT SYTLSEDQMSRLAKLTKAHRQGMVKVDMLRITFREIEMINES VKRSSFMYLMGGFRCVKCDDKEYGTVYYEKDGDESPILTSFF LVKVPDPOMSLENLVSSKHNLPSRLSRSGSDHILKPYPPRDQ LKNYJYPPSPRDQ LKNYJYPPSPRDQ LKNYJYPPSPRDQ LKNYJYPPSPRDQ LKNYJYPPSPRDQ LKNYJYPPSPRDQ LKNYJYPPSPRDQ LKNYJYPPSPRDAKTKEVPDG ENLSCHLSSHYTNPTVRRYAVAR LRQADDEDLLMVLLLOLVQALKYENFDDI KNGLEPTKKRSQGSVS ENVSNSGINSAEIDSSUTT/SAPPPSVSSPPP\ASKTKEVPDG ENLSCDLCDLCTFLISPASKNTNPDURKNJLBAQQTTVVDRLIVHLM KAVQRESGRRKKKNERLQALLKGDKKVPTVERLDAAQQTFVDRLIVHLM KAVQRESGRRKKKNERLQALLKGDLKKYPTFITEDLEPQVK THEMYLNVMRRFSQALLKGDLKKYPTFITEDLEPQVK THEMYLNVMRRFSQALLKGDLALLCDLARGNTJEPTRLEPGPCK				L
6147 1 2304 GTRQLFPSFGSGNDARGSI IRKVVDPETGRTRLIKGDGEVLE EIYYKERIRE INKOATRGDCLAPQMRAGLLD GTRQLFPSFGSGFGDSPEGFEGAPERRKAHGMLKLYYGLSE GEAAGRARAGPDPLDFTDLINGAHFDPEVYLDKLRECCPLAQLMDS ETDMVRQITALDSDMQTLVYENYNKT ISATDTIR KURKDDFRKME DEMDRLATNMAU ITDFSAR ISATLQDRHERITKLAGVHALLRKL QFLFELPSRLTKCVELGAYGQAVYGGRAQAULQQYGHLPSFRAR IQDDCQVITARLAQDLAGRFREGSGAPEQAECVELLLALGEPA EELCEEFLAHARGRLEKELINLEAELGPSPPAPDVLEFTDHG\S SGFYGGLCQVAAAYQELAAQFAGAEKLAAFARQLGSRYFALV ERRLAQEQGGGDNSLLVRALDRFHRRLRAGCALAAAAGLADAAT EIVERVARERIGHHLQGLRAAFLGCLTDVRQALAAPRVAGKEGP GLAELLANVASSILSHIKASLAAVHLFTAKEVSFSNKPYFRGEF CSQSVREGLIVGFVHSMCQTAQSFCDSPGEKGGATPPALLLLS RLCLDYETATISYILTLTDEGFLOVQDFFPVTVSTLCAEARETA RRILTHYVKVQGLVISQMLRXSVETRDWLSTLEPRNYRAMKRV VEDTTATDVOVLPRLAGVALTQAGGTVPSRGAGAADHWQSLPG GGMCIWASHGASS VARASVEPQGNKS PRMNTKRAGECLCPRS CSFSAQDYDIPAPILPVEKQRLRVTQEVRAGLVLVLKIRRQTNS CILPLPHSTGSINSDHVPTK CSCSCAVALEDPMLKFSGLYQETCSDLYVTCQVFAEGKFLALPVRT SYKAFSTRNWMNENBULKLPVKYPDLFRNAQVALTIMDVYGGFKAV PVGGTTVSLEGKYGMFRGGMHDLKVWPNCRSOMDOKPTKTPGRT SSTLSEDQMSRLAKLTKAHRGGHMVKVDWLDRLTFREIEMINES VKRSSNFMYLMGGFRCVKCDDKEYGIVYYEKDGDESPILTSFE LVKVPDPQMSLENLVESKHNNLPSLRSGFSDHDLKPYPSPRDQ LKNIVSYPPSKPPTYEEDDLWERFYYLTNODKATKILTSVIW DLPGGAKQALALIGKWRMDVEDSLELLSSHYTNPTVRRYAVAR LRQADDEDLMYLLGKWRMDVEDSLELLSSHYTNPTVRRYAVAR LRQADDEDLLMYLLGKWRMDVEDSLELLSSHYTNPTVRRYAVAR LRQADDEDLLMYLLGKWRMPDVEDSLELLSSHYTNPTVRRYAVAR LRQADDEDLLMYLLGKWRSPDDLKKGLEDQATGVOTQDFPK THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQQTFVURCIVLHLM KAVQRESGNRKKKNERLQALLGDNEKMLSDVELIPLPLEFPQVK IRGIIPETATLFKSALMPALIFFCIEGKYPUFFKKDSGSSVS ENVSNSGINSAEIDSSQIIT/SAFPSVSSPPP\ASKTKEVPDG ENLECDLCTFLISRASKNSTLANNLYWVYUVECEDDOTQORDPK THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQQTFVURCIVLHLM KAVQRESGNRKKKNERLQALLGDNEKMILSDVELIPLPLEFPQVK IRGIIPETATLFKSALMPALIFFTEDGGKYPVIFKHGDDLROD	6146	428	781	LKKKGKEKAEAOOVEAT.PGPST.DOWHPSAGEREDCDUT TDROVG
6147 1 2304 GTRQLPPSPGSGGDSPEGBEAPERRKAHGMLKLYYGLSE GEAAGRPAGPDPLDPTDLMGAHFDPBVYLDKLRRECPLAQLMDS ETDWVRQTRALDSDWQTLVYEBVNKFISATDTIKKMKNDFRKME DEMPRIATMANITDFSARISATLQDRHERITKLAGVHALIRKL QFFELPSRLTKCVELGAYGQAVRYQGRAQAVLQYOHLPSFRA IQDDCQVITARIAQQLRQFFREGSGSAPEQAECVELLIALGEPA EELCEBFLAHARGRILEKBLRNLEAELGPSPPAPDVLEFTDHG\S SGFVGGLCQVAAAYQELFAAQGPAGAEKLAAFARQLGSRYFALV ERRLAQEQGGDNSLLVRALDFHRRLRAPGALAAAGLADAAT EIVERVARERIGHHIQGLRAAFIGGLTDVRQALAAPAPVAGKEGP GLAELLANVASSILSHIKASLAAVHLFTAKEVSFSNKPYFRGEF CSQGVREGLIVGFVHSWCQTAQSFCDSPGEKGGATPPALLLLS RRLLTHYVKVQGLVISQMLRKSVETRDWLSTLEBPRNVRAVMKRV VEDTTATIOVQUIPRLAGVALTQAGGTVPSRGGAAEDHWQSLPG GGDMCIWASHGASSVARASVEFPQONKSPRWNYKRAGEGLCPRS CGFSAQDYDIFAPILPVEKQRLRVTQEVRAGLVIVLKIRFQTNS CLIPLPHSTGSINSDHVPTK  6148 3056 353 VPAVGGTFADGAMGEAEKFHYIYSCDLDINVQLKIGSLEGKREQ KSYKAVLEDPMLKFSGLYQETCSDLYVTCQVFAEGKPLALPVRT SYKAPSTRNWNEWLKLEVYXYPDLPRNAQVALTIWDVYGPGKAV PVGGTTVSLFGKYGMFRQGMHDLKVWPNCRSGMDQKPTKTPGRT SSTLSEDQMSRLAKLTKAHRGGHWVKUDMLDRLTFREIEMINES VKRSSNFWYLMGGFRCVKCDDKEYGIVYYEKDGDESSPILTSFE LVKVPDPQMSLENLVESKHNLPSSLRSGPSDHDLKPYFSPRDQ LKNIVSYPPSKPDTYEGQDLVWERTYYLTNOQKATKILITSVIW DLPQGAKQALALLGKWKPMDVEDSLELLSSHYNTPTVRYAVAR LRQADDEDLLMYLLQLVQALKYENFDDIKMGLEPTKKDSQSSVS ENVSNSGINSABIDSSQIIT/SAPFPSVSSPP)ASKTKEVPDG ENLEQDLCTFLIFRASKNSTLANVLYWVIVECEDDDTQQDRDK THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQQTFVDRLVHLM KAVQRESGMRKKKNERLQALLGDKSVPVMRSLLAAQQTFVDRLVHLM KAVQRESGMRKKKNERLQALLGDKSVPVMRSLLAAQQTFVDRLVHLM KAVQRESGMRKKKNERLQALLGDKSVPVFRISDLFRDEDOT		]		R/YPGHEAHDOGG\WDAROSTIRKYDDDETCETTEL LYCDGELT E
GTRQLPPSPGSGFGDSPEGFEGEAPERRRAHGMLKLTYGLSE GEAAGRPAGPDPLDPTLINGAHFDPEVYLDKLRRECPLAQLMDS ETDMVRQIRALDSDMQTLVYENYNKFISATDITKMKNDFRKME DEMDRLATINMAVITDFSARISATIQDRHERITKLAGWHALLIKKL QFFFELSFRITKVEVELGAYGQAVRYGGRAQAVLOOYOHLPSFRA IQDDCQVITARLAQQLRQRFREGGSGAPEQACVELLLALGEPA EELCEEFLAHARGRLEKELRNLEALGPSPPADPULEFTDHG\S SGFVGGLCQVAAAYQELFAQQPAGAEKLAAFAQCLSGRYPALV ERRLAQRQGGGDNSLLVRALDRFHRRLRACGALLAAAGLADAAT EIVERVARERIGHHLQGLRAAFIGCLTDVRQALAARVAGKEGP GLAELLANVASSILSHIKASLAAVHIFTAKEVSFSNRPYFRGEF CSGGVREGLIVGFVHSMCQTAQSFCDSPGEKGGATPPALLLLLS RLCLDYETATISYILTDEQFLVQDQFPVTPVSTLCAEARETA RRLLTHYVKVQGLVISQMLRKSVETRDWLSTLEFRNVRAVMKRV VEDTTAIDVOVLPRLAGVALTQAGGTVPSRGAGAADHWGSLPG GGGMCINASHGASSVARXVERPQGNKSPRMYKRAGECLCPRS CSFSAQDYDIFAPILPVEKQRLRVTQEVRAGLVLVLKIRPQTMS CILPLPHSTGSINSDHVPTK SYKAFSTRWNNEWLKLPVKYDEVTSDLAITINDVYGGKAV PVGGTTVSLFGKYGMFRQGMBDLKVWPNCRSQMDQKPTKTPGRT SSTLSEDQMSRLAKLTKAHRGGMUVLDWLITGREIBNINES VKRSSNFMYLMGGFRCVKCDDKEYGIVYYKDGDESPILTSFE LVKVPDPQMSLENLVESKHNLPRSLRSGFSHDLKKPYFSPRDQ LKNIVSYPPSKPPTYERQDLVWERRYYTINODKALTKILTSVIW DLAPGAKQALALLGKWADVDUDLELLSSHTINPTVRRYAVAR LRQADDEDLLMYLLQLVQALKYENFDDI KNGLEPTKKDSQSSVS ENVSNSGINSAEIDSSQIIT/SAPFPSVSSPP)ASKTKEVPDG ENLEQDLCTFLISRASKNSTLANVLYWVIVECEDQDTQQRDPK THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQQTFVDRLVHLM KAVQRESGNRKKKNERLQALLGDKKPVLIFRLEDGOKVPUIFRKHGDDLROD	L .	1		EIVTKERHREINKOATRODCIAROMPACIAR
GEAAGRPAGPPLDPTLINGAHFDPEVYLDKLRRECPLAQLMDS ETDMYRQIRALDSDMQTLVYENYNKFISATDTIRKMKNDFRKME DEMDRIATNMAVITDFSARISATLQDRHERITKLAGVHALLRKL QFLFELPSRLTKCVELGAYGQAVRYQGRAQAVLQQQHLPSFRA IQDDCQVITARLAQCHQRFREGGSAPEQAECVELLLALGEPA EELCEEFLAHARGRLEKELRNLEAELGFSPPAPDVLEFTDHG\S SGFVGGLCQVAAAYQELFAAQGPAGAEKLAAFARQLGSRYFALV ERRLAQEGGGGDNIVARALDRFHRRIRAPGALLAAAGLADAAT EIVERVARERLGHHLQGLRAAFLGCLTDVRQALAAPRVAGKEGF GLAELLANVASSILSHIKASLAAVHLFTAKEVSFSNKPYRRGEF CSQGVREGLIVGFVHACQTAQSFCDSFGEKGGATPPALLLLS RLCLDYETATISYILTLTDEQFLVQDQFFVTVSTLCAEARETA RRLLTHYVKVQGLVISQMERKSVETRDWLSTLEPRNVRAWMKRV VEDTTALTDVOVLPRLAGVALTQAGGTVPSRGAGAEDHWGSLPG GGDMCIWASHGASSVARASVREPQGNKSPRMNTKRAGECLCPRS CSFSAQDYDIPAPILPVEKQRIRVTQEVRACLVLVLKIRPQTNS CLLPLPHSTGSINSDHVPTK  6148 3056 353 VPAVGGTFADGAMGEAEKFHYIYSCDLDINVQLKIGSLEGKREQ KSYKAVLEDPMLKFSGLVQETCSDLYVTCQVFAEGKPLALPVST SYKAFSTRWNNEWLKLPVKYPDLFRNAQVALITIMDVYGGFKAV PVGGTTVSLFGKYGMFRQGMHDLKVWPNCRSQMDQKPTKTPGRT SSTLSEDQMSRLAKLTKAHRQGHMVKTVMLDRLTFREIEMINES VKRSSFMYLMGGFRCVKCDDKEYGIVYYEKOBESSPILTSFE LVKNYPDPQMSLENLVESKHHNLPRSLRSGPSDHDLKPYPSPRDQ LKNIVSYPPSKPTYEEGDLWFFRYYLTMQDKALTKLITSVIW DLPQGAKQALALLGKWKPMDVEDSLELLSSHYTMPTVRRYAVAR LRQADDEDLLMYLLQLVQALKYENFDDIKNGLEPTKKDSQSSVS ENVSNSGINSAEIDSSQITT/SAPFPSVSSPPP\ASKTKEVPDG ENLEQDLCTTLISRASKNSTLANYLLWYVIVECEDQDTYQGNPK THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQQTFVDRLVHLM KAVQRESGNRKKNERRQALLFGDEKWNLSDVFKHGDGKPVTVFKHDDDLKDRD	6147	1	2304	GTROLPPPSPGSGPGDSDFGDFGFADEDDERAUGMI VI VVOI GD
ETDWYRQIRALDSDMOTLVYENYKFISATDTIRKMKNDFRKME DEMDRLATMMAVITDFSARISATLQDRHERITKLAGVHALLRKL QFLFELPSRLTKCVELGAYQQAVRYQGRAQAVLQQYQHLPSFRA IQDDCQVITARLAQOLRQRFREGGSGAPBQAECVELLLALGEPA EELCEEFLAHARGRLEKELRNLEAELGPSPPAPDVLEFTDHG\S SGFVGGLCQVAAAYQELFAAQGRAGAEKLAAFARQLGSRYFALV ERRLAQEGGGGNSLLVRALDRFHRRLRAPCALLAAAGLADAAT EIVERVARERLGHHLQGLRAAFLGCLTDVRQALAAPRVAGKEGP GLAELLANVASSILSHIKASLAAVHLFTAKEVSFSNKPYFRGEF CSQQVREGLIVGFVHSMCQTAQSFCDSFDEKGGATPPALLLLS RLCLDYFTATISYILTLTDEQFLVQDQFPVTPVSTLCAEARETA RRLLTHYVKVQGLVISQMLRKSVETRDWLSTLEPRNVRAWKRV VEDTTATDVOVLPRLAGVALTQAGGTVPSRGAGAAEDHWQSLPG GGDMCIWASHGASSVARFAVTGPEVRAGAGVLVLKIRPQTNS CSFSAQDYDIPAPILPVEKQRLRVTQEVRAGGLVLVKKRPQTNS CLUPLPHSTGSINSDHVPTK 6148 3056 353 VPAVGGTFADGAMGEAEKFHYIYSCDLDINVQLKIGSLEGKREQ KSYKAVLEDPMLKFSGLYQETCSDLYVTCQVFAEGKPLALPVRT SYKAFSTRWWMEWLKLPVKYPDLPRNAQVALTIWDVYGFGKAV PVGGTTVSLFGKYGMFRGCMHUKVDWLDRLTFREIEMINES VKRSSNFMYLMGGFRCVKCDDKEYGIVYYEKDGDESSPILTSFE LVKVPDPQMSLENLVESKHHNLPRSLRSGFSDHDLKPYFSPRDQ LKNIVSYPSKPPTYEEQDLVWEFRYYLTNQDKALTKLITSVIW DLPQGAKQALALIGKWKPMDVEDSLELLSSHYTNPTVRRYAVAR LRQADDEDLLMYLLQLVQALKYENFDDIKNGLEPTKKDSQSSVS ENVSNG INSAEIDSSQIIT/SAPFPSVSSPPP\ASKTKEVPDG ENLEQDLCTFLISRASKNSTLANYLWYVIVECEDQDTQQRPPK THEMYLNVMRRFSQALLKGDKSVRVRSLLAAQQTFVDRLVHLM KAVQRESGNRKKKNERLQALLGDDEKMILDSUELIPLPLEPQVK IRGIIPETATLFKSALMPAQLFFKYEDGGGKYPVTKHODDLROD	į			GEAAGRPAGPDPLDPTDLNGAHEDPEVVLDVLBPEGRLAGI MOD
DEMDRIATIMAVITDESARISATLQDRHERITKLAGUHALLRKL QFIFELPSRLIKKUELGAYGQAVRYQGRAQAVUQQYQHIPSFRA IQDDCQVITARIAQQLRQRFREGGSGAPEQAECUPLILLAIGEPA EELCEEFLAHARGRLEKELRNLEAELGPSPPAPDVLEFTDHG\S SGFVGGLCQVAAAVQLFAAQQBAGAKLAAFARQLGSRYFALV ERRLAQEGGGDNSLLVRALDRFHRRLRAPGALLAAAGLADAAT EIVERVARERIGHHLQGLRAAFIGCLTDVRQALAAPRVAGKEGP GLAELLANVASSILSHIKASLAAVHLFTAKEVSFSNKPYFRGEF CSQGVREGLIVGFVHSNCQTAQSFCDSPGEKGGATPPALLILLS RLCLDYETATISYILTITDEOFLVQDOFFVTPVSTLCAEARETA RRLLTYVKVQGLVISQMLRKSVETRDWLSTLEPRNVRAVMKRV VEDTTAIDVOVLPRLAGVALTQAGGTVPSRGAGAAEDHWQSLPG GGMCIWASHGASSVARASVEPQCNKSPRNTTRAGEGLCPRS CSFSAQDYDIPAPLIVEKQRLRVTQEVRAGLVLVLKIRPQTNS CILPLPHSTGSINSDHVPTK  6148 3056 353 VPAVGGTFADGAMGEAEKFHYIYSCDLDINVQLKIGSLEGKREQ KSYKAVLEDPMLKFSGLYQETCSDLYVTCQVFAEGKPLALPVXT SYKAFSTRWNNNEWLKLPVKYPDLPRNAQVALTIMDVYGDFGKAV PVGGTTYSLFGKYGMFRQGMUKVDWLDRLTFREIEMINES SYKAFSTRWNNNEWLKLPVKYPDLPRNAQVALTIMDVYGDFGKAV PVGGTTYSLFGKYGMFRQGMUKVDWLDRLTFREIEMINES STLSEDQMSRLAKLTKAHRQGHMVKVDWLDRLTFREIEMINES VKRSSMFMYLMGGFRCVKCDDKEYGIVYYEKDGDESSFILTSFE LVKVPPPGMSLENLVESKHHNLPRSLRSGFSDHDLKPYPSPRDQ LKNIVSYPPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSVIW DLPQGAKQALALLGKWKPMDVEDSLELLSSHYNNPTVRRYAVAR LRQADDEDLLMYLLQLVQALKYEMFDDI KNGLEPTKKDSQSSVS ENVSNSGINSAEIDSSQIIT/SAPFPSVSSPPP\ASKTKEVPDG ENLEQDLCTFLISRASKNSTLANVLYWYVIVECEDQDTOQRPDK THEMYLNVMRFSQALLKGDKSVRVMRSLLAAQQTFVDRLVHLM KAVQRESGNRKKNERLQALLGDNEKNALSDVELIFLPLEEQVK	l	ì		ETDMVROIRALDSDMOTLIVENVNKET CATOTI DVMVATO DDVM
QFFELPSRITKCVELGAYGGRAQAVEYGGRAQAVEQYQHLPSFRA IQDDCQVITARLAQQLRQRFREGGSAPEQAECVELLLAGEPA EELCEEFLAHARGRLEKELRNLEAELGGSPPAPDVLEFTDHG\S SGFYGGLCQVAAAYQELFAAQGRAGAEKLAAFARQLGSRYFALV ERRLAQEQGGGDNSLLVRALDRFHRRLRAPGALLAAAGLADAAT EIVERVARERLEGHHLQGLRAAFLGCLTDVRQALAAPRVAGKEGP GLAELLANVASSILSHIKASLAAVHLFTAKEVSFSNKPYFRGEF CSQGVREGLIVGFVHSMCQTAQSFCDSFGEKGGATPPALLLLLS RLCLDYETATISVILTLTDEQFLVQDQFPPTPVSTLCAEARETA RRLLTHYVKVQGLVISQMLRKSVETRDWLSTLEPRNVRAVMKRV VEDTTAIDVOVLPRLAGVALTQAGGTVPSRGAGAAEDHWOSLPG GGMCIWASHGASVARASVREPQONKSPRMTKRAGECLCPRS CSFSAQDYDIPAPILPVEKQRLRVTQEVRAGLVIVLKIRPQTINS CILPLPHSTGSINSDHVPTK CILPLPHSTGSINSDHVPTK SYKAYLEDPMLKFSGLYQETCSDLYVTCQVFAEGKPLALPVRT SYKAYESTRWNWEWLKLPVKYPDLPRNAQVALTIWDVYGPGKAV PVGGTTVSLFGKYGMFRQGMHDLKVWPNCRSGMDQKPTKTFGRT SSTLSEDQMSRLAKLTKAHRQGHMVKVDWLDRLTFREIEMINES VKRSSNFWLMGGFRCVKCDDKEYGIVYYEKDGDESSPILTSFE LVKVPDPQMSLENLVESKHHNLPRSLRSGPSDHDLKPYPSPRDQ LKNIVSYPPSKPPTYEEDDLWWEFRYYLTNQDKALTKILTSVIW DLPQGAKQALALLGKWKPMDVEDSLELLSSHYTNFTVRRYAVAR LRQADDEDLLMYLLQLVQALKYENFDDIKNGLEFTKKDSQSSVS ENVSNSGINSAEIDSSQIIT/SAPFPSVSSPPP\ASKTKEVPDG ENLEQDLCTFLISRASKNSTLANYLYWVIVECEDQDTQQRDPK THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQQTFVDRLVHLM KAVQRESGNRKKKNERLQALLGDNEKMNLSDVELIPLPLEFQVK IRGIIFETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLROD		l		DEMORLATIONAVITOESARISATIOOPHEPITYIAGINALIDIT
IQDDCQVTTARLAQQLRQRFREGGSGAPEQAECVELLLALGEPA EELCEFLAHARGRLEKELRNLEAELGPSPPAPDVLEFTDHG\S SGFVGGLCQVAAAYQELFAAQGPAGAEKLAAFARQLGSRYFALV ERRLAQEGGGDNSLLVRALDRFHRRLRAPGALLAAAGLADAAT EIVERVARERLGHHLQGLRAAFIGCLTDVRQALAAPRVAGKEGP GLAELLANVASSILSHIKASLAAVHLFTAKEVSFSNKPYFRGEF CSQGVREGLIVGFVHSMCQTAQSFCDSPGEKGGATPPALLLLLS RLCLDYETATISVILTLTDEQFLVQDQFPVTPVSTLCAEARETA RRLLTHYVKVQGLVISQMLRKSVETRDWLSTLEPRNVRAVMKRV VEDTTAIDVOVLPRLAGVALTQAGGTVPSRGAGAAEDHWOSLDC GGMCIWASHGASSVARASVREPQGNKSPRMTKRAGECLCPRS CSFSAQDYDIFAPILPVEKQRLRVTQEVRAGLVLVLKIRPQTNS CILPLPHSTGSINSDHVPTK SYKAFSTRWMSHWLKLPVKYPDLPRNAQVALTIWDVYGPGKAV PVGGTTASLFGKYGMFRQGMHDLKVWPNCRSGMDQKPTKTPGRT SYKAFSTRWMNEWLKLPVKYPDLPRNAQVALTIWDVYGPGKAV PVGGTTVSLFGKYGMFRQGMHDLKVWPNCRSGMDQKPTKTPGRT SSTLSEDQMSRLAKLTKAHRQGHMVKVDWLDRLTFREIEMINES VKRSSNFMYLMGGFRCVKCDDKEYGIVYYEKDGDESSPILTSFE LVKVPDPQMSLENLVESKHNLPRSLRSGPSDHDLKPYPSPRDQ LKNIVSYPPSKPPTYEEQDLWEFRYYLTNQDKALTKILTSVIW DLPQGAKQALALLGKMXPMDVEDSLELLSSHYTNPTVRRYAVAR LRQADDEDLMYLLQLVQALKYENFDDIKNGLEPTKKDSQSSVS ENVSNGGINSAEIDSSQITT/SAPPSVSSPPP\ASKTKEVPDG ENLEQDLCTFLISRASKNSTLANYLYWYVIVECEDQDTQQRDPK THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQQTFVDRLVHLM KAVQRESGNRKKKNERLQALLGDNEWMLSVVIFKHGDDLROD	}	]		OFLFELPSRLTKCVELGAYGOAVRYOGRAGAYI GOYOU BEERR
SGFVGGLCQVAAAYQBLFAAQGPAGAEKLAAFARQLGSRYFALV ERRLAQEQGGGDNSLLVRALDRFHRRLRAPGALLAAAGLADAAT EIVERVARERLGHHLQGLRAAFLGCLTDVRQALAAPRVAGKEGP GLAELLANVASSILSHIKASLAAVHFTAKEVSFSNRPYFRGEF CSQQVREGLIVGFVHSMCQTAQSFCDS PGEKGGATPPALLLLS RLCLDYETATISYILTLTDEQFLVQDQFPVTPVSTLCAEARETA RRLLTHYVVQQLVISQMLRKSVETRDWLSTLEPRNVRAVMKRV VEDTTAIDVOVPLALAGVALTQAGGTVPSRGAGAAEDHWQSLPG GGDMCIWASHGASSVARASVREPQCNKSPRWNTKRAGECLCPRS CSFSAQDVDIFAPILDVEKQRLRVTQEVRAGLVLVLKIRPQTNS CILPLPHSTGSINSDHVPTK CILPLPHSTGSINSDHVPTK SYKAYLEDPMLKFSGLYQETCSDLYVTCQVFAEGKPLALPVRT SYKAFSTRWNWNEWLKLEVKYPDLDFNNAQVALITIWDVYGPGKAV PVGGTTYSLFGKYGMFRQCMHDLKVWPNCRSQMDQKPTKTPGRT SSTLSEDQMSRLAKLTKAHRQGHVKVDWLDRLTFREIEMINES VKRSSNFWYLMGGFRCVKCDDKEGIVYYEKDGDESSPILTSFE LVKVPDPQMSLENLVESKHHNLPRSLRSGFSDHDLKPYPSFRDQ LKNIVSYPPSKPPTYEEQDLVWEFRYYLTMQDKAHTKLITSVIW DLPQGAKQALALLGKWKPMDVEDSLELLSSHYTNPTVRRYAVAR LRQADDEDLLMYLLLQLVQALKYENFDDIKNGLEPTKKDSQSSVS ENVSNGSINSAEIDSSQIIT/SAPFPSVSSPPPV\ASKTKEVPDG ENLEQDLCTFLISRASKNSTLANYLYWYVIVECEDQDTQQRDPK THEMYLNVMRRFSQALLKGDKEKMLSAQQTFVDRLVHLM KAVQRESGNRKKKNERLQALLGDNEKMNLSAQQTFVDRLVHLM KAVQRESGNRKKKNERLQALLGDNEKMNLSAQCTFVDRLVHLM KAVQRESGNRKKKNERLQALLGDNEKMNLSAQCTFVDRLVHLM	1			IODDCOVITARIAOOI.RORFREGGGGAPEOARGURI I ALGROA
SGFVGGLCQVAAAYQELFAAQGPAGAEKLAAFARQLGGRYFALV ERRLAQEQGGGDNSLLVRALDRFHRRLRAPGALLAAAGLADAAT EIVERVARERLGHHLQGLRAAFLGCLTDVRQALAAAPRVAGKEGP GLAELLANVASSILSHIKASLAAVHLFTAKEVSFSNKPYFRGEF CSQGVREGLIVGFVHSMCQTAQSFCDS PGEKGGATPPALLLLIS RLCLDYETATISYILTLTDEQFLVQDQFPVTPVSTLCAEARETA RRLLTHYVKVQGLVISQMLRKSVETRDWLSTLEPRNVRAVMKRV VEDTTAIDVQVLPRLAGVALTQAGGTVPSRGAGAAEDHWQSLPG GGDMCIWASHGASSVARASVREPQCNKSPRINTKRAGEGLCPRS CSFSAQDVDIFAPFLDVEKGRLRVTQEVRAGLVLVLKIRPQTNS CILPLPHSTGSINSDHVPTK  6148 3056 353 VPAVGGTFADGAMGEAEKFHYIYSCDLDINVQLKIGSLEGKREQ KSYKAVLEDPMLKFSGLYQETCSDLYVTCQVFAEGKPLALPVRT SYKAFSTRNNWNEWLKLPVKYPDLPRNAQVALTIMDVYGPGKAV PVGGTTVSLFGKYGMFRQGMHDLKVWPNCRSQMDQKPTKTFGRT SSTLSEDQMSRLAKLTKAHRQGHMVKVDMLDRLTFREIEMINES VKRSSNFMYLMGGFRCVKCDDKEYGIVYYEKDGDESSPILTSFE LVKVPDPQMSLENLVESKHHNLPRSLRSGFSDHDLKFYPSPRDQ LKNIVSYPPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSVIW DLPQGAKQALALLGKWKPMDVEDSLELLSSHYTPFTVRRYAVAR LRQADDEDLLMYLLQLVQALKYENFDDIKGLEPTKKDSQSSVS ENVSNSGINSABIDSSQIIT/SAPFPSVSSPPP\ASKTKEVPDG ENLEQDLCTFLISRASKNSTLANYLYWYVIVECEDQDTQQRDPK THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQQTFVDRLVHLM KAVQRESGNRKKNERLQALLGDNEKMNLSDVELIPLPLPEPQVK IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLROD				EELCEFLAHARGRIEKEIRNI.EARI.GDSBDADDU BERDUGA
ERRIAGEGEGINSLLVRALDEFHERLRAPGALLAAAGLADAAT EIVERVARERIGHHLQGLRAAFIGCLTDVRQALAAPRVAGKEEG GLAELLANVASSILSHIKASLAAVHLFTAKEVSFSNKPYFRGEF CSQGVREGLIVGFVHSMCQTAQSFCDSPGEKGGATPPALLLLIS RLCLDYETATISYILTLTDEQFLVQDQFPVTPVSTLCAEARETA RRLLTHYVKVQGLVISQMLRKSVETRDWLSTLERRNVRAVMKRV VEDTTAIDVQVLPRLAGVALTQAGGTVPSRGAGAAEDHWQSLPG GGDMCIWASHGASSVARASVREPQGNKSPRMTKRAGECLCPRS CSFSAQDYDIFAPILDVEKQRLRVTQEVRAGLVLVLKIRPQTNS CILPLPHSTGSINSDHVPTK CILPLPHSTGSINSDHVPTK SYRAVLEDPMLKFSGLYQETCSDLYVTCQVFAEGKPLALPVRT SYKAFSTRWNWNEWLKLPVKYPDLPRNAQVALTIWDVYGPGKAV PVGGTTVSLFGKYGMFRQGMHDLKVWPNCRSQMDQKPTKTPGRT SSTLSEDQMSRLAKLTKAHRQGHMVKVDWLDRLTFREIEMINES VKRSNFWYLMGGFRCVKCDDKEYGIVYYEKDGDESSPILTSFE LVKVPDPQMSLENLVESKHHNLPRSLRSGPSDHDLKPYPSPRDQ LKNIVSYPPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSVIW DLPQGAKQALALLGKWKPPDUVEDSLELLSSHYTNPTVRRYAVAR LRQADDEDLLMYLLQLVQALKYENFDDIKNGLEPTKKDSQSSVS ENVSNSGINSAEIDSSQITT/SAPFPSVSSPPP\ASKTKEVPDG ENLEQDLCTFLISRASKNSTLANYLYWYVIVECEDQDTQQRDPK THEMYLNVMRRFSQALKGDKSVRVMRSLLAAQQTFVDRLVHLM KAVQRESGNRKKKNERLQALLGDNEKMNLSDVELIPLPPQVK IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVJFKHGDDLROD				SGFVGGLCOVAAAYOELFAAOGPAGAFKI.AAFAROI GGRUFAII
EIVERVARERIGHHLQGLRAAFIGCLTDVRQALAAPRVAGKEGP GLAELLANVASSILSHIKASLAAVHLFTAKEVSFSNKPYFRGEF CSQQVREGLIVGFVHSMCQTAQSFCDS PGEKGATPPALLLLIS RLCLDYETATISYILTLTDEQFLVQDQFPVTPVSTLCAEARETA RRILITHYVKVQGLVISOMIRKSVETRDWLSTLEPRNVRAVMKRV VEDTTAIDVQVLPRLAGVALTQAGGTVPSRGAGAAEDHWQSLPG GGDMCIWASHGASSVARASVREPQOMKSPRMNTKRAGECLCPRS CSFSAQDYDIFAPILPVEKQRLRVTQEVRAGLVLVLKIRFQTNS CTLPLPHSTGSINSDHVPTK  OPAVGGTFADGAMGEAEKFHYIYSCDLDINVQLKIGSLEGKREQ KSYKAVLEDPMLKFSGLYQETCSDLYVTCQVFAEGKPLALPVRT SYKAFSTRWWNEWLKLFVKYPDLPRNAQVALTIWDVYGFGKAV PVGGTTVSLFGKYGMFRQGMHDLKVWPDCRSQMDQKPTKTPGRT SSTLSEDQMSRLAKLTKAHRQGHMVKVDWLDRLTFREIEMINES VKRSNFMYLMGGFRCVKCDDKEYGIVYYEKDGDESSPILTSFE LVKVPDPQMSLENLVESKHHNLPRSLRSGFSDHDLKFYFSFRDQ LKNIVSYPPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSVIW DLPQGAKQALALLGKWKPMDVEDSLELLSSHYTNPTVRRYAVAR LRQADDEDLMYLLQLVQALKYENFDDIKNGLEPTKKDSQSSVS ENVSNSGINSAEIDSSQIIT/SAPFPSVSSPPP\ASKTKEVPDG ENLEQDLCTFLISRASKNSTLANYLYWYVIVECEDQDTQQRDPK THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQQTFVDRLVHLM KAVQRESGNRKKKNERLQALLGDNEKMNLSDVELIPLPLEPQVK IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLROD	1			ERRLAGEOGGGDNSLI.VRALDREHDRI.RADCATIANACIARAM
GLAELLANVASSILSHIKASLAAVHLFTAKEVSFSNKPYFRGEF CSQGVREGLIVGFVHSMCQTAQSFCDS FGEKGGATPPALLILLIS RRLCLDYETATISYILTLTDEQFLVQDQFPVTPVSTLCAEARETA RRLLTHYVKVQGLVISQMLRKSVETRDWLSTLEPRNVRAWMKRV VEDTTAIDVOVLPRLAGVALTQAGGTVPSRGAGAAEDHWQSLPG GGDMCIWASHGASSVARASVREPQGNKSPRNNTKRAGECLCPRS CSFSAQDYDIFAPILPVEKQRLRVTQEVRAGLVLVLKIRPQTNS CTLPLPHSTGSINSDHVPTK CTLPLHSTGSINSDHVPTK SYKAVLEDPMLKFSGLYQETCSDLYVTCQVFAEGKPLALPVRT SYKAFSTRWNWHEWLKLPVKYPDLPRNAQVALITWDVYGPGKAV PVGGTTVSLFGKYGMFRQGMHDLKVWPNCRSQMDQKPTKTPGRT SSTLSEDQMSRLAKLTKAHRQGHMVKVDWLDRLTFREIEMINES VKRSSNFMYLMGGFRCVKCDDKEYGIVYYEKDGDESSPILTSFE LVKVPDPQMSLENLVESKHHNLPRSLRSGPSDHDLKPYPSPRDQ LKNIVSYPPSKPPTYEEQDLVWEFRYYITNQDKALTKILTSVIW DLPQGAKQALALLGKWKPMDVEDSLELLSSHYTNPTVRRYAVAR LRQADDEDLLMYLLQLVQALKYENFDDIKNGLEPTKKDSQSSVS ENVSNSGINSAEIDSSQIIT/SAPFPSVSSPPP\ASKTKEVPDG ENLEQDLCTFLISRASKNSTLANYLYWYVIVECEDQDTQQRDPK THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQQTFVDRLVHLM KAVQRESGNRKKKNERLQALLGDNEKMLSDVELIPLPPLEPQVK IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLROD				EIVERVARERIGHHIOGIRAAFI GCLTDVDONI ANDRUNGUNGO
CSGQVREGLIVGFVHSMCQTAQSFCDSPGEKGGATPPALLLLLS RLCLDYETATISYLLTLTDEQFLVQDQFPVTPVSTLCAEARETA RRLLTHYVKVQGLVISQMLRKSVETRDWLSTLEPRNVRAVMKRV VEDTTAIDVQVLPRLAGVALTQAGGTVPSRGAGAAEDHWQSLPG GGDMCIWASHGASSVARASVREPQGNKSPRMTKRAGECLCPRS CSFSAQDYDIFAPILPVEKQRLRVTQEVRAGLVLVLKIRPQTNS CILPLPHSTGSINSDHVPTK  OPAVGGTFADGAMGEAEKFHYIYSCDLDINVQLKIGSLEGKREQ KSYKAVLEDPMLKFSGLYQETCSDLYVTCQVFAEGKPLALPVRT SYKAFSTRWNNEWLKLPVKYPDLPRNAQVALTIMDVYGPGKAV PVGGTTVSLFGKYGMFRQGMHDLKVWPNCRSQMDQKPTKTPGRT SSTLSEDQMSRLAKLTKAHRQGHMVKVDWLDRLTFREIEMINES VKRSSNFMYLMGGFRCVKCDDKEYGIVYYEKDGDESSPILTSFE LVKVPDPQMSLENLVESKHHNLPRSLRSGPSDHDLKPYPSPRDQ LKNIVSYPPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSVIW DLPQGAKQALALLGKWKPMDVEDSLELLSSHYINPTVRRYAVAR LRQADDEDLLMYLLQLVQALKYENFDDIKNGLEPTKKDSQSSVS ENVSNSGINSAEIDSSQIIT/SAPFPSVSSPPP\ASKTKEVPDG ENLEQDLCTFLISRASKNSTLANYLYWYVIVECEDQDTQQRDPK THEMYLNVMRRFSQALLKGDKSVVMRSLLAAQQTFVDRLVHLM KAVQRESGNRKKKNERLQALLGDNEKMNLSDVELIPPLEPQVK IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVJFKHGDDLROD		į		GLAELLANVASSTI SHIKASI AAVUI ETAVEVERONVENDER
RLCLDYETATISYILTLTDEQFLVQDQFPVTPVSTLCAEARETA RRLLTHYVKVQGLVISQMLRKSVETRDWLSTLEPRNVRAVMKRV VEDTTAIDVOVLPRLAGVALTQAGGTVPSRGAGAAEDHWQSLPG GGDMCIWASHGASSVARASVREPQGNKSPRMTKRAGECLCPRS CSFSAQDYDIFAPILPVEKQRLRVTQEVRAGLVLVLKIRPQTNS CILPLPHSTGSINSDHVPTK  6148 3056 353 VPAVGGTFADGAMGEAEKFHYIYSCDLDINVQLKIGSLEGKREQ KSYKAVLEDPMLKFSGLYQETCSDLYVTCQVFAEGKPLALPVRT SYKAFSTRWNWNEWLKLPVKYPDLPRNAQVALTIWDVYGPGKAV PVGGTTVSLFGKYGMFRQGMHDLKVWPNCRSQMDQKPTKTPGRT SSTLSEDQMSRLAKLTKAHRQGHMVKVDWLDRLTFREIEMINES VKRSSNFMYLMGGFRCVKCDDKEYGIVYYEKDGDESSPILTSFE LVKVPDPQMSLENLVESKHHNLPRSLRSGFSDHDLKPYPPSPRDQ LKNIVSYPPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSVIW DLPQGAKQALALIGKWKPMDVEDSLELLSSHYTNPTVRRYAVAR LRQADDEDLLMYLLQLVQALKYENFDDIKNGLEPTKKDSQSSVS ENVSNSGINSAEIDSSQIIT/SAPFPSVSSPPP\ASKTKEVPDG ENLEQDLCTFLISRASKNSTLANYLYWYVIVECEDQDTQQRDPK THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQQTFVDRLVHLM KAVQRESGNRKKNERLQALLGDNEKMNLSDVELIPLPLEPQVK IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLROD	1	i		CSOGVREGLIVGFVHSMCOTAOSECDSDGBVCCAEDDALLIAG
RRLTHYVKVQGLVISQMLRKSVETRDWLSTLEPRNVRAVMKRV VEDTTAIDVQVLPRLAGVALTQAGGTVPSRGAGAAEDHWQSLPG GGDMCIWASHGASSVARASVREPQGNKSPRMNTKRAGECLCPRS CSFSAQDYDIFAPILPVEKQRLRVTQEVRAGLVLVLKIRPQTNS CILPLPHSTGSINSDHVPTK  VPAVGGTFADGAMGEAEKFHYIYSCDLDINVQLKIGSLEGKREQ KSYKAVLEDPMLKFSGLYQETCSDLYVTCQVFAEGKPLALPVRT SYKAFSTRWNWNEWLKLPVKYPDLPRNAQVALTIWDVYGPGKAV PVGGTTVSLFGKYGMFRQGMHDLKVWPNCRSQMDQKPTKTPGRT SSTLSEDQMSRLAKLTKAHRQGHMVKVDWLDRLTFREIEMINES VKRSSNFMYLMGGFRCVKCDDKEYGIVYYEKDGDESSPILTSFE LVKVPDPQMSLENLVESKHINLPRSLRSGPSDHDLKPYPPSPRDQ LKNIVSYPPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSVIW DLPQGAKQALALLGKWKPMDVEDSLELLSSHYTNPTVRRYAVAR LRQADDEDLLMYLLQLVQALKYENFDDIKNGLEPTKKDSQSSVS ENVSNSGINSAEIDSSGIIT/SAPFPSVSSPPP\ASKTKEVPDG ENLEQDLCTFLISRASKNSTLANYLYWYVIVECEDQDTQQRDPK THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQQTFVDRLVHLM KAVQRESGNRKKKNERLQALLGDNEKMNLSDVELIPLPLEPQVK IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLROD	1 1	I		RLCLDYETATISYILTITDEOFLUODOEDURDURT CARA-
VEDTTAIDVOVLPRLAGVALTQAGGTVPSRGAGAAEDHWQSLPG GGDMCIWASHGASSVARASVAREPQCHKSPRMNTKRAGECLCPRS CSFSAQDYDIPAPILPVEKQRLRVTQEVRAGLVLVLKIRPQTNS CILPLPHSTGSINSDHVPTK  6148 3056 353 VPAVGGTFADGAMGEAEKFHYIYSCDLDINVQLKIGSLEGKREQ KSYKAVLEDPMLKFSGLYQETCSDLYVTCQVFAEGKPLALPVRT SYKAFSTRWNWNEWLKLPVKYPDLPRNAQVALTIWDVYGPGKAV PVGGTTVSLFGKYGMFRQGMHDLKVWPNCRSQMDQKPTKTPGRT SSTLSEDQMSRLAKLTKAHRQGHMVKVDWLDRLTFREIEMINES VKRSSNFMYLMGGFRCVKCDDKEYGIVYYEKDGDESSPILTSFE LVKVPDPPQMSLENLVESKHHNLPRSLRSGPSDHDLKPYPSPRDQ LKNIVSYPPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSVIW DLPQGAKQALALLGKWKPMDVEDSLELLSSHYTNPTVRRYAVAR LRQADDEDLLMYLLQLVQALKYENFDDIKNGLEPTKKDSQSSVS ENVSNSGINSAEIDSSQIIT/SAPFPSVSSPPP\ASKTKEVPDG ENLEQDLCTFLISRASKNSTLANYLYWYVIVECEDQDTQQRDPK THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQQTFVDRLVHLM KAVQRESGNRKKKNERLQALLGDNEKMNLSDVELIPLPLEPQVK IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLROD	1			RRLLTHYVKVOGLVISOMI.PKSUFTPDWY.COT. PD77777
GGDMCIWASHGASSVARASVREPQGNKSPRMNTKRAGECLCPRS CSFSAQDYDIPAPILPVEKQRLRVTQEVRAGLVLVLKIRPQTNS CILPLPHSTGSINSDHVPTK  6148 3056 353 VPAVGGTFADGAMGEAEKFHYIYSCDLDINVQLKIGSLEGKREQ KSYKAVLEDPMLKFSGLYQETCSDLYVTCQVFAEGKPLALPVRT SYKAFSTRWNWNEWLKLPVKYPDLPRNAQVALITIWDVYGPGKAV PVGGTTVSLFGKYGMFRQGMHDLKVWPNCRSQMDQKPTKTPGRT SSTLSEDQMSRLAKLTKAHRQGHMVKVDWLDRLTFREIEMINES VKRSSNFMYLMGGFRCVKCDDKEYGIVYYEKDGDESSPILTSFE LVKVPDPPQMSLENLVESKHHNLPRSLRSGPSDHDLKPYPSPRDQ LKNIVSYPPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSVIW DLPQGAKQALALLGKWKPMDVEDSLELLSSHYTNPTVRRYAVAR LRQADDEDLLMYLLQLVQALKYENFDDIKNGLEPTKKDSQSSVS ENVSNSGINSAEIDSSQIIT/SAPFPSVSSPPP\ASKTKEVPDG ENLEQDLCTFLISRASKNSTLANYLYWYVIVECEDQDTQQRDPK THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQQTFVDRLVHLM KAVQRESGNRKKKNERLQALLGDNEKMNLSDVELIPLEPQVK IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLROD	1 1			VEDTTAIDVOVI.PRIAGVAI.TOAGGTUBERGAGAARRIVAGA
CSFSAQPYDIFAPILPVEKQRLRVTQEVRAGLVLVLKIRPQTNS C11PLPHSTGSINSDHVPTK  6148 3056 353 VPAVGGTFADGAMGEAEKFHYIYSCDLDINVQLKIGSLEGKREQ KSYKAVLEDPMLKFSGLYQETCSDLYVTCQVFAEGKPLALPVRT SYKAFSTRWNWNEWLKLPVKYPDLPRNAQVALTIWDVYGPGKAV PVGGTTVSLFGKYGMFRQGMHDLKVWPNCRSQMDQKPTKTPGRT SSTLSEDQMSRLAKLTKAHRQGHMVKVDWLDRLTFREIEMINES VKRSSNFMYLMGGFRCVKCDDKEYGIVYYEKDGDESSPILTSFE LVKVPDPQMSLENLVESKHHNLPRSLRSGPSDHDLKPYPSPRDQ LKNIVSYPPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSVIW DLPQGAKQALALLGKWKPMDVEDSLELLSSHYTNPTVRRYAVAR LRQADDEDLLMYLLQLVQALKYENFDDIKMGLEPTKKDSQSSVS ENVSNSGINSAEIDSSQIIT/SAPFPSVSSPPP\ASKTKEVPDG ENLEQDLCTFLISRASKNSTLANYLYWYVIVECEDQDTQQRDPK THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQQTFVDRLVHLM KAVQRESGNRKKKNERLQALLGDNEKMNLSDVELIPLPLEPQVK IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLROD	}			GGDMCIWASHGASSVARASVREPOGNIKEDDMITTERAGECT
CILPLPHSTGSINSDHVPTK  OPAVGGTFADGAMGEAEKFHYIYSCDLDINVQLKIGSLEGKREQ KSYKAVLEDPMLKFSGLYQETCSDLYVTCQVFAEGKPLALPVRT SYKAFSTRWNWNEWLKLPVKYPDLPRNAQVALITIWDVYGPGKAV PVGGTTVSLFGKYGMFRQGMHDLKVWPNCRSQMDQKPTKTPGRT SSTLSEDQMSRLAKLTKAHRQGHMVKVDWLDRLTFREIEMINES VKRSNFMYLMGGFRCVKCDDKEYGIVYYEKDGDESSPILTSFE LVKVPDPQMSLENLVESKHHNLPRSLRSGPSDHDLKPYPSPRDQ LKNIVSYPPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSVIW DLPQGAKQALALLGKWKPMDVEDSLELLSSHYTNPTVRRYAVAR LRQADDEDLLMYLLQLVQALKYENFDDIKNGLEPTKKDSQSSVS ENVSNSGINSAEIDSSQIIT/SAPFPSVSSPPP\ASKTKEVPDG ENLEQDLCTFLISRASKNSTLANYLYWYVIVECEDQDTQQRDPK THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQQTFVDRLVHLM KAVQRESGNRKKKNERLQALLGDNEKMNLSDVELIPLPLEPQVK IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLROD	[ ]	[	ĺ	CSFSAODYDTRAPTI.DVEKOPI.DVECOPVDAGTITATITATE
VPAVGGTFADGAMGEAEKFHYIYSCDLDINVQLKIGSLEGKREQ KSYKAVLEDPMLKFSGLYQETCSDLYVTCQVFAEGKPLALPVRT SYKAFSTRWNWNEWLKLPVKYPDLPRNAQVALTIWDVYGPGKAV PVGGTTVSLFGKYGMFRQCMHDLKVWPNCRSQMDQKPTKTPGRT SSTLSEDQMSRLAKLTKAHRQGHMVKVDWLDRLTFREIEMINES VKRSSNFMYLMGGFRCVKCDDKEYGIVYYEKDGDESSPILTSFE LVKVPDPQMSLENLVESKHINLPRSLRSGPSDHDLKPYPSPRDQ LKNIVSYPPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSVIW DLPQGAKQALALLGKWKPMDVEDSLELLSSHYTNPTVRRYAVAR LRQADDEDLLMYLLQLVQALKYENFDDIKNGLEPTKKDSQSSVS ENVSNSGINSAEIDSSGIIT/SAPFPSVSSPPP\ASKTKEVPDG ENLEQDLCTFLISRASKNSTLANYLYWYVIVECEDQDTQQRDPK THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQQTFVDRLVHLM KAVQRESGNRKKNERLQALLGDNEKMNLSDVELIPLPLEPQVK IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLROD			[	CILPLPHSTGSINSDHUDTK
KSYKAVLEDPMLKFSGLYQETCSDLYVTCQVFAEGKPLALPVRT SYKAFSTRWNWNEWLKLPVKYPDLPRNAQVALITIMDVYGPGKAV PVGGTTVSLFGKYGMFRQGMHDLKVWPNCRSQMDQKPTKTPGRT SSTLSEDQMSRLAKLTKAHRQGHMVKVDWLDRLTFREIEMINES VKRSSNFMYLMGGFRCVKCDDKEYGIVYYEKDGDESSPILTSFE LVKVPDPQMSLENLVESKHHNLPRSLRSGPSDHDLKPYPSPRDQ LKNIVSYPPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSVIW DLPQGAKQALALLGKWKPMDVEDSLELLSSHYTNPTVRRYAVAR LRQADDEDLLMYLLQLVQALKYENFDDIKNGLEPTKKDSQSSVS ENVSNSGINSAEIDSSQIIT/SAPFPSVSSPPP\ASKTKEVPDG ENLEQDLCTFLISRASKNSTLANYLYWYVIVECEDQDTQQRDPK THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQQTFVDRLVHLM KAVQRESGNRKKNERLQALLGDNEKMNLSDVELIPLPLEPQVK IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLROD	6148	3056	353	
SYKAFSTRWNWNEWLKLPVKYPDLPRNAQVALTIWDVYGPGKAV PVGGTTVSLFGKYGMFRQCMHDLKVWPNCRSQMDQKPTKTPGRT SSTLSEDQMSRLAKLTKAHRQGHMVKVDWLDRLTFREIEMINES VKRSSNFMYLMGGFRCVKCDDKEYGIVYYEKDGDESSPILTSFE LVKVPDPQMSLENLVESKHINLPRSLRSGPSDHDLKPYPSPRDQ LKNIVSYPPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSVIW DLPQGAKQALALLGKWKPMDVEDSLELLSSHYTNPTVRRYAVAR LRQADDEDLLMYLLQLVQALKYENFDDIKNGLEPTKKDSQSSVS ENVSNSGINSAEIDSSGIIT/SAPFPSVSSPPP\ASKTKEVPDG ENLEQDLCTFLISRASKNSTLANYLYWYVIVECEDQDTQQRDPK THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQQTFVDRLVHLM KAVQRESGNRKKNERLQALLGDNEKMNLSDVELIPLPLEPQVK IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLROD	1			KSYKAVLEDPMI.KFSGI.VOETCSDI.VUTCOVER BOURT ET
PVGGTTVSLFGKYGMFRQGMHDLKVWPNCRSQMDQKPTKTPGRT SSTLSEDQMSRLAKLTKAHRQGHMVKVDWLDRLTFREIEMINES VKRSSNFMYLMGGFRCVKCDDKEYGIVYYEKDGDESSPILTSFE LVKVPDPQMSLENLVESKHHNLPRSLRSGPSDHDLKPYPSPRDQ LKNIVSYPPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSVIW DLPQGAKQALALLGKWKPMDVEDSLELLSSHYTNPTVRRYAVAR LRQADDEDLLMYLLQLVQALKYENFDDIKNGLEPTKKDSQSSVS ENVSNSGINSAEIDSSQIIT/SAPFPSVSSPPP\ASKTKEVPDG ENLEQDLCTFLISRASKNSTLANYLYWYVIVECEDQDTQQRDPK THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQQTFVDRLVHLM KAVQRESGNRKKKNERLQALLGDNEKMNLSDVELIPLPLEPQVK IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLROD				SYKAFSTRWNWNEWI,KI,DVKVDDI,DDNIA OVAT TITUDING
SSTLSEDQMSRLAKLTKAHRQGHMVKVDWLDRLTFREIEMINES VKRSSNFMYLMGGFRCVKCDDKEYGIVYYEKDGDESSPILTSFE LVKVVPDPQMSLENLVESKHHNLPRSLRSGPSDHDLKPYFSPRDQ LKNIVSYPPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSVIW DLPQGAKQALALLGKWKPMDVEDSLELLSSHYTNPTVRRYAVAR LRQADDEDLLMYLLQLVQALKYENFDDIKMGLEPTKKDSQSSVS ENVSNSGINSAEIDSSQIIT/SAPFPSVSSPPP\ASKTKEVPDG ENLEQDLCTFLISRASKNSTLANYLYWYVIVECEDQDTQQRDPK THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQQTFVDRLVHLM KAVQRESGNRKKKNERLQALLGDNEKMNLSDVELIPLPLEPQVK IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLROD		ļ		PVGGTTVSLFGXYGMFPOGMUDLVINIONGOROUSONS
VKRSSNFMYLMGGFRCVKCDDKEYGIVYYEKDGDESSPILTSFE LVKVPDPQMSLENLVESKHHNLPRSLRSGPSDHDLKPYPSPRDQ LKNIVSYPPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSVIW DLPQGAKQALALLGKWKPMDVEDSLELLSSHYTNPTVRRYAVAR LRQADDEDLLMYLLQLVQALKYENFDDIKNGLEPTKKDSQSSVS ENVSNSGINSAEIDSSQIIT/SAPFPSVSSPPP\ASKTKEVPDG ENLEQDLCTFLISRASKNSTLANYLYWYVIVECEDQDTQQRDPK THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQQTFVDRLVHLM KAVQRESGNRKKNERLQALLGDNEKMNLSDVELIPLPLEPQVK IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLROD	1	ł		SSTI-SEDOMSRI.AKI.TKAUDOCUMUKATUKI DD. MODOS
LVKVPDPQMSLENLVESKHHNLPRSLRSGPSDHDLKPYPSPRDQ LKNIVSYPPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSVIW DLPQGAKQALALLGKWKPMDVEDSLELLSSHYTNPTVRRYAVAR LRQADDEDLLMYLLQLVQALKYENFDDI KNGLEPTKKDSQSSVS ENVSNSGINSAEIDSSQIIT/SAPFPSVSSPPP\ASKTKEVPDG ENLEQDLCTFLISRASKNSTLANYLYWYVIVECEDQDTQQRDPK THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQQTFVDRLVHLM KAVQRESGNRKKNERLQALLGDNEKMNLSDVELIPLPLEPQVK IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLROD				VKRSSNEMVIMCGEPCUVCDDVEVGTTVVDVDGDDGGGGGGGGGGGGGGGGGGGGGGGG
LKNTVSYPPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSVIW DLPQGAKQALALLGKWKPMDVEDSLELLSSHYTNPTVRRYAVAR LRQADDEDLLMYLLQLVQALKYENFDDIKNGLEPTKKDSQSSVS ENVSNSGINSAEIDSSQIIT/SAPFPSVSSPPP\ASKTKEVPDG ENLEQDLCTFLISRASKNSTLANYLYWYVIVECEDQDTQQRDPK THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQQTFVDRLVHLM KAVQRESGNRKKNERLQALLGDNEKMNLSDVELIPLPLEPQVK IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLROD	1 1		1	LVKUPDPOMCI PNI UPCVUUNI PROTECCIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERVICIO SERV
DLPQGAKQALALLGKWKPMDVEDSLELLSSHYTNPTVRRYAVAR LRQADDEDLLMYLLQLVQALKYENFDDIKNGLEPTKKDSQSSVS ENVSNSGINSAEIDSSQIIT/SAPFPSVSSPPP\ASKTKEVPDG ENLEQDLCTFLISRASKNSTLANYLYWYVIVECEDQDTQQRDPK THEMYLNVMRFSQALLKGDKSVRVMRSLLAAQQTFVDRLVHLM KAVQRESGNRKKNERLQALLGDNEKMNLSDVELIPLPLEPQVK IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLROD	1 1		!	LKNTVCYDDCKDDTVDDODI INIDANIA TO TO THE TOTAL TO THE TOTAL TO THE TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL
LRQADDEDLIMYLLQLVQALKYENFDDIKNGLEPTKKDSQSSVS ENVSNSGINSAEIDSSQIIT/SAPFPSVSSPPP\ASKTKEVPDG ENLEQDLCTFLISRASKNSTLANYLYWYVIVECEDQDTQQRDPK THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQQTFVDRLVHLM KAVQRESGNRKKNERLQALLGDNEKMNLSDVELIPLPLEPQVK IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLROD	1			DI DOGA YOA I ALL CHURCHER WEEKYYL TNODKALTKILTSVIW
ENVSNSGINSAEIDSSQIIT/SAPFPSVSSPPP\ASKTKEVPDG ENLEQDLCTFLISRASKNSTLANYLYWYVIVECEDQDTQQRDPK THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQQTFVDRLVHLM KAVQRESGNRKKKNERLQALLGDNEKMNLSDVELIPLPFQVK IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLROD	]		l	LPOADDEDLIMAT OF HOLDSTELLSSHYTNPTVRRYAVAR
ENLEQDLCTFLISRASKNSTLANYLYWYVIVECEDQDTQQRDPK THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQQTFVDRLVHLM KAVQRESGNRKKKNERLQALLGDNEKMNLSDVELIPLPLEPQVK IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLROD				ENVENIORING PETERSON AND THE PROPERTY OF THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND THE PETERSON AND
THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQQTFVDRLVHLM KAVQRESGNRKKKNERLQALLGDNEKMNLSDVELIPLPLEPQVK IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLROD	] [			ENVSNSGINSAEIDSSQIIT/SAPFPSVSSPPP\ASKTKEVPDG
KAVQRESGNRKKKNERLQALLGDNEKMNLSDVELIPLPLEPQVK IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLROD	Į l		1	ENDEQUECTFLISRASKNSTLANYLYWYVIVECEDQDTQQRDPK
KAVQRESGNRKKKNERLQALLGDNEKMNLSDVELIPLPLEPQVK IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLROD	i I	Į		THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQQTFVDRLVHLM
IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLROD	]	1		KAVQRESGNRKKKNERLQALLGDNEKMNLSDVELIPLPLEPOVK
QLILQIISLMDKLLRKENLDLKLTPYKVLATSTKHGFMOFIOSV	j		!	IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLROD
	LL			QLILQIISLMDKLLRKENLDLKLTPYKVLATSTKHGFMQFIQSV

Predicted

beginning

location

to first

nucleotide

corresponding

Predicted end

corresponding

nucleotide

location

to first

amino acid

SEO

ID

NO:

Amino acid segment containing signal peptide

(A=Alanine, C=Cysteine, D=Aspartic Acid, E=

Glutamic Acid, F=Phenylalanine, G=Glycine,

SASIVKGQHEMSEMDGRWEEHRSLLSGRATQFTGATGAI\MTTE TTITARATGASRDVAGAQAAAVALNEEFLKNYFTDKAASYTEED ENHTAKDCLLVYSQEETESLNASIGCCSFIEGELDDRFLDDLGL kfktlaevclgqkidinkeieqrqkpatetsmntashslceqtm VNSENTYSSGSSFPVPKSLQEANAEKVTQEIVTERSVSSRQAQK VATPLPDPMASRNVIATETSYVTGSTMPPTTVILGPSQPQSLIV TERVYAPASTLVDQPYANEGTVVVTERVIQPHGGGSNPLEGTQH

H=Histidine, I=Isoleucine, K=Lysine,

P=Proline, Q=Glutamine, R=Arginine,

L=Leucine, M=Methionine, N=Asparagine,

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
}	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			LQDVPYVMVRERESFLAPSSGVQPTLAMPNIAVGQNVTVTERVL
			APASTLQSSYQIPTENSMTARNTTVSGAGVPGPLPDFGLEESGH
			SNSTITTSSTRVTKHSTVQHSYS
6154	3660	2146	KKKTKMKNTLQKTVNFGAWPKPTISDKSHLLQMVSKLDLTDAKN
1			SDTAHIKSIEITSILNGLQASESSAEDSEOEDERGAODMDNNGK
			EESKIDHLTNNRNDLISKEEQNSSSLLEENKVHADINTSKRUSK
1			SPERLRKDIEVLSEDTDYEEDEVTKKRKDVKKDTTDKSSKPOTK
ł	1		RGKRRYCNTEECLKTGSPGKKEEKAKNKESLCMENSSNSSSDED
			EEETKAKMTPTKKYNGLEEKRKSLRTTGFYSGFSEVARKRIKTI.
1			NNSDERLQNSRAKDRKDVWSSIQGQWPKKTLKELFSDSDTEAAA
1	į –		SPPHPAPEEGVAEESLQTVAEEESCSPSVELEKPPPVNVDSKPT
	1		EEKTVEVNDRKAEFPSSGSNFSA*IPLPYLHLNRLHQSL*QKGS
1			RQQSSVTVSEPLAPNQEEVRSIKSETDSTIEVDSVAGELQDLQS
i			ERE*LASRF*CQCELEQ**SARTRTS*KSLYRSEKSERCSGRRK
6155	869		FIKKAEKKP*SNSGKQQKEGK
"""	""	121	HLLPELRGKSWITMKYVFYLGVLAGTFFFADSSVQKEDPAPYLV
	i i		YLKSHFNPCVGVLIKPSWVLAPAHCYLPNLKVMLGNFKSRVRDG
1	i i		TEQTINPIQIVRYWNYSHSAPQDDLMLIKLAKPAMLNPKVQALN
l	! !		P\PTTNVRPGTVCLLSGLDWSQENSGRHPDLRQNLEAPVMSDRE
1	}		CQKTEQGKSHRNSLCVKFVKVFSRIFGEVAVATVICKDKLQGIE VGHFMGGDVGIYTNVYKYVSWIENTAKDK
6156	5725	3984	GTSTVTMATKKHFSIILNLLGMLLKKDNQDTRKLLMTWALEVAV
ļ	j i		VMKKSETYAPLFCLPSFHKFCKGLLADTLVEDVNICLQACSSLH
			ALSSSLPDDLLQRCVDVCRVQLVHRGTCIRQAFGKLLKSIPLGV
	·		FLSNNNHTEIQEISLALRSHMSKAPSNTFHPQDFSD/VISFILY
}			GNSHRTGKDNWLERLFYSCQRLDKRDOSTIPRNLLKTDAVLWOW
			AIWEAAQFTVLSKLRTPLGRAODTFOTIEGIIRSLAGUTLNDDO
			DVSQWTTADNDEGHGNNQLRLVLLLQYLENLEKLMYNAYEGCAN
	]		ALTSPPKVIRTFLYTNRQTCQDWLTRIRLSIMRVGLLAGOPAVT
			VRHGFDLLTEMKTTSLSQGNELEVSIMMVVEALCELHCPEATOG
			IAVWSSSIVGKHLLWINSVAQQAEGRFEKASVEYOEHT:CAMTGV
1	1		DCCISSFDKSVLTLASAGCKSASLKHCLNGESRKSVLSKPTDSS
	1		PEVINYLGNKACECYISTADWAAVQEWQNAIHDLKKSTSSTSLN
			LKADFNYIKSLSSFESGKFVECTEQLELLPGENINLLAGGSKEK
6157	946	220	IDMKKLLRNM
	2 20	329	MANRGPSYGLSREVQEKIEQKYDADLENKLVDWIILQCAEDIEH
	ĺ	ľ	PPPGRAHFQKWLMDGTVLCKLINSLYPPGQEPIPKISESKMAFK
		İ	OMEQISQFLKAAETYGVRTTDIFQTVDLWEGKDMAAVQRTLMAL
; l			GSVAVTKDDGCYRGEPSWFHRKAQQNRRGFSEEQLRQGQNVIGL QMGSNKGASQAGMTGYGMPRQIM*DAASCP
6158	441	1482	LGSLIVLSLHCKVIFSSQSLERAMKEKAVDLVPILAQNPGLAQN
			PILEGKDHNQNTGVDPIIDHVQDRKTD/SRSKSPHKKRSKSRER
			RKSRSRSHSRDKRKDTREKIKEKERVKEKDREKEREREKEREKE
]			KERGKNKDRDKBREKDREKDKEKDREREKEHEKDRDKEKEKE
(		İ	QDKEKEREKDRSKEIDEKRKKDKKSRTPPRSYNASRRSRSSSRE
			RRRRRSRSSRSPRTSKTIKRKSSRSPSPRSRNKKDKKREKERD
			HISERRERESTSMRKSSNDRDGKEKLEKNSTSLKEKEHNKEPD
L l			SSVSKEVDDKDAPRTEENKIQHNGNCQLNEENLSTKTEAV
6159	53	84	AVIAPLHISLGDRARPYLKNTEKSSTTCSRRRNOSFPPVMSLTH
	ļ		RLHLCKYWGCAVSNVCRFWEGRPLPLMIVVPYTLPVSLPVGSCV
	<b>}</b>		IITGTPILTFVKDPQLEVNFYTGMDEDSDIAFOFRLHFGHPAIM
	1	. [	NSCVFGIWRYEEKCYYLPFEDGKPFELCIYVRHKEYKVMVNGOR
		`	IYNFAHRFPPASVKMLQVFRDISLTRVLISD*GRCVRITAVOEF
6160	1555		DVSVSCDCTTAYQPG
9790	1626	1790	AGAKFFP*F*KVADAQPTESEKEIYNQVNVVLKDAEGILEDLQS
L		<u> </u>	YRGAGHEIREAIQHPADEKLQEKAWGAVVPLVGKLKKFYEFSQR

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	Amitho acid segment containing signal peptide
NO:	nucleotide	l.	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
I NO:	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence	1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -	\=possible nucleotide insertion)
		<del>                                     </del>	TENAL POLL CAL MCMP V CPMCVV PROCESSION
			LEAALRGLLGALTSTPYSPTQHLEREQALAKQFAEILHFTLRFD
}	1	ì	ELKMTNPAIQNDFSYYRRTLSRMRINNVPAEGENEVNNELANRM
i	1	1	SLFYAEATPMLKTLSDATTKFVSENKNLPIENTTDCLSTMASVC
	}		RVMLETPEYRSRFTNEETVSFCLRVMVGVIILYDHVHPVGAFAK
J	1	1	TSKIDMKGCIKVLKDQPPNSVEGLLNALRYTTKHLNDETTSKQI
L	1	1	KSMLQ*QLLTLVNKG
6161	455	1569	PVSGSESSLRRAWASILRLMLGPRVAVSILCEDGISH*LLEKH*
ļ	1		KSHVLEPLSSLALEEQCLALSLDWSTGKTGRAGDQPLKIISSDS
	}	1	TGQLHLLMVNETRPRLQKVASWQAHQFEAWIAAFNYWHPEIVYS
		1	GGDDGLLRGWDTRVPGKFLFTSKRHTMGVCSIQSSPHREHILAT
	1	1	
i	ł		GSYDEHILLWDTRNMKQPLADTPVQGGVWRIKWHPFHHHLLLAA
	ĺ		CMHSGFKILNCQKAMEERQEATVLTSHTLPDSLVYGADWSWLLF
	<u> </u>	Į.	RSLQRAPSWSFPSNLGTKTADLKGASELPTPCHECREDNDGEGH
		1	ARPQSGMKPLTEGMRKNGTWLQATAATTRDCGVNPEEADSAFSL
		<u></u>	LATCSFYDHALHLWEWEGN
6162	1	586	RTIHATGRAGASPMHRLIVWRLAEANKOHVRCOKCLEFGHWTYE
1			CTGKRKYLHRPSRTAELKKALKEKENRLLLQQSIGETNVERKAK
	1	1	KKRSKSVTSSSSSSSSSSSSSSSSSSSSESETSTSSSSEDSDTDESS
		l	SSSSSASSTTSSSSSDSDSDSSSSSKQ*HQHR*QL*R*TTKEE
1	J		EKEIELLHSYWTDGLKTLM
6163	1081	785	RIRSTTEGCAVRLHPTQNTGKARIMILLSVSLGRHWAFTYKFFL
1		, , , ,	TPVVFVFFFFFFHRKE*VMQKNPMKSREDEWMEKLNNLHVQRAD
		Į	MNDI TADIO UEDGO TO A DESCRIPTION DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONT
	l		MNRLIMNYLVTEGFKEAAEKFRMESGIEPSVDLETLDERIKIRE
1		i	MILKGQIQEAIALINSLHPELLDTNRYLYFHLQQQHLIELIRQR
Į.		]	ETEAALEFAQTQLAEQGEESRECLTEMERTLALLAFDSPEESPF
1	1		GDLLHTMQRQKVWSEVNQAVLDYENRESTPKLAKLLKLLLWAQN
			ELDQKKVKYPKMTDLSKGVIEEPK
6164	90	406	PCQSPGRSRMRQDKLTGSLRRGGRCLKRQGGGVGTILSNVLKKR
1			SCISRTAPRLLCTLEPGVDTKLKFTLEPSLGQNGFQQWYDALKA
i			VARLSTGIPKEWRRKVWLTLADHYLHSIAIDWDKTMRFTFNERS
ł			NPDDDSMGIQIVKDLHRTGCSSYCGQEAEQDRVVLKRVLLAYAR
		-	WNKTVGYCQGFNILAALILEVMEGNEGDALKIMIYLIDKVLPES
			YFVNNLRALSVDMAVFRDLLRMKLPELSQHLDTLQRTANKESGG
	i l		GYEPPLTNVFTMQWFLTLFATCLPNQTVLKIWDSVFFEGSEIIL
			RVSLAIWAKIGEQIECCETADEFYSTMGRLTQEMLENDLLQSHE
]			LMQTVYSMAPFPFPQLAELREKYTYNITPFPATVKPTSVSGRHS
	[		VARDEDRENDEDDEDALBRINGE CONSCIENT STORY
1			KARDSDEENDPDDEDAVVNAVGCLGPFSGFLAPELQKYQKQIKE
1	. !		PNEEQSLRSNNIAELSPGAINSCRSEYHAAFNSMMMERMTTDIN
-	1		ALKRQYSRIKKKQQQQVHQVYIRADKGPVTSILPSQVNSSPVIN
1	! !		HLLLGKKMKMTNRAAKNAVIHIPGHTGGKISPVPYEDLKTKLNS
]			PWRTHIRVHKKNMPRTKSHPGCGDTVGLIDEQNEASKTNGLGAA
) i			EAFPSGCTATAGREGSSPEGSTRRTIEGQSPEPVFGDADVDVSA
1			VQAKLGALELNQRDAAAETELRVHPPCQRHCPEPPSAPEENKAT
1	Ì		SKAPQGSNSKTPIFSPFPSVKPLRKSATARNLGLYGPTERTPTV
			HFPQMSRSFSKPGGGNSGP*KMVFSSGTMLSRQLPGYPQEYQRN
1	l		GGERFG
6165	90	405	PCQSPGRSRMRQDKLTGSLRRGGRCLKRQGGGVGTILSNVLKKR
ļ l			SCISRTAPRLLCTLEPGVDTKLKFTLEPSLGQNGFQQWYDALKA
, !			VARLSTGIPKEWRRKVWLTLADHYLHSIAIDWDKTMRFTFNERS
]			NPDDDSMGIQIVKDLHRTGCSSYCGQEAEQDRVVLKRVLLAYAR
1 1	i		WNKTVGYCQGFNILAALILEVMEGNEGDALKIMIYLIDKVLPES
<u> </u>			YFVNNLRALSVDMAVFRDLLRMKLPELSQHLDTLQRTANKESGG
[			GYEPPLINVFTMQWFLTLFATCLPNQTVLKIWDSVFFEGSEIIL
ļ ĺ			RVSLAIWAKLGEQIECCETADEFYSTMGRLTQEMLENDLLOSHE
	į		LMQTVYSMAPFPFPQLAELREKYTYNITPFPATVKPTSVSGRHS
}			KARDSDEENDPDDEDAVVNAVGCLGPFSGFLAPELQKYQKQIKE
			TOTAL STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND STATE OF THE SECOND

SEQ	Predicted	Predicted end	Amino acid coment
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ļ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
-	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +-Ston
	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
1			PNEEQSLRSNNIAELSPGAINSCRSEYHAAFNSMMMERMTTDIN
j			ALKRQYSRIKKKQQQQVHQVYIRADKGPVTSILPSQVNSSPVIN
			HLLLGKKMKMTNRAAKNAVIHIPGHTGGKISPVPYEDLKTKLNS
1			PWRTHIRVHKKNMPRTKSHPGCGDTVGLIDEQNEASKTNGLGAA
1			EAFPSGCTATAGREGSSPEGSTRRTIEGOSPEPVFGDADVDVSA VQAKLGALELNQRDAAAETELRVHPPCQRHCPEPPSAPEENKAT
1			SKAPQGSNSKTPIFSPFPSVKPLRKSATARNLGLYGPTERTPTV
		Į	HFPQMSRSFSKPGGGNSGP*KMVFSSGTMLSRQLPGYPQEYQRN
			GGERFG
6166	2	1206	HKLWRTVAMAGAEWKSLEECLEKHLPLPDLQEVKRVLYGKELRK
1	]		LDLPREAFEAASREDFELQGYAFEAAEEOLRRPRIVHUGTVONR
			IPLPANAPVAEQVSALHRRIKAIVEVAAMCGVNIICFOEAWTMP
			FAFCTREKLPWTEFAESAEDGPTTRFCOKLAKNHDMVVVSPILE
			RDSEHGDVLWNTAVVISNSGAVLGKTRKNHIPRVGDFNESTYYM
1			EGNLGHPVFQTQFGRIAVNICYGRHHPLNWLMYSINGAEIIFNP
1			SATIGALSESLWPIEARNAAIANHCFTCAINRVGTEHFPNEFTS
			GDGKKAHQDFGYFYGSSYVAAPDSSRTPGLSRSRDGLLVAKLDL
			NLCQQVNDVWNFKMTGRYEMYARELAEAVKSNYSPTIVKE*PAS VPALG
6167	1220	1844	YGIVTGPSLCAGDKQPKKQEKNPVLVSPEFVDEALCACEEYLSN
1			LAHMDIDKDLEAPLYLTPEGWSLFLQRYYQVVHEGAELRHLDTQ
			VQRCEDILQQLQAVVPQIDMEGDRNIWIVKPGAKSRGRGIMCMD
			HLEEMLKLVNGNPVVMKDGKWVVOKYIERPLLIFGTKFDLROWF
			LVTDWNPLTVWFYRDSYIRFSTOPFSLKNLDK*APLVI.TDFGWS
	,		LFLQRYYQVVHEGAELRHLDTQVORCEDILOOLOAVVPOIDMEG
1 1			DRNIWIVKPGAKSRGRGIMCMDHLEEMLKI.VNGNPVVMKDGKWV
			VQKYIERPLLIFGTKFDLRQWFLVTDWNPLTVWFYRDSYIRFST
6168	84	1392	QPFSLKNLDK
		1332	VWPVPSVSAMPPKKQAQAGGSKKAEQKKKEKIIEDKTFGLKNKK
1 1			GAKQQKFIKAVTHQVKFGQQNPRQVAQSEAEKKLKKDDKKKELQ ELNELFKPVVAAQKISKGADPKSVVCAFFKQGQCTKGDKCKFSH
1 1	1		DLTLERKCEKRSVYIDARDEELEKDTMDNWDEKKLEEVVNKKHG
l			EAEKKKPKTQIVCKHFLEAIENNKYGWFWVCPGGGDICMYRHAL
1 1			PPGFVLKKKKKKKKKEDEISL*DLIERERSALGPNVTKITLESE
1			LAWKKRKRQEKIDKLEQDMERRKADFKAGKALVISGREVERERD
			ELVNDDDEEADDTRYTQGTGGDEVDDSVSVNDIDISI.YTPRDVD
1 1	1		ETGITVASLERFSTYTSDKDENKLSEASGGRAENGERSDLEEDN
6169	112	662	EREGTENGAIDAVPVDENLFTGEDLDELEEELNTLDLEE
	***	002	APAAAMAERPEDLNLPNAVITRIIKEALPDGVNISKEARSAISR
]	j		AASVFVLYATSCANNFAMKGKRKTLNASDVLSAMEEMEFQRFVT
1			PLKEALEAYRREQKGKKEASEQKKKDKDKKTDSEEQDKSRDEDN DEDEERLEEEEQNEEEEVDN*KGRETVAPWKVPLEMRRATCFCE
			AFPCWAE
6170	62	667	STKVMLPNTGRLAGCTVFITGASRGIGKAIALKAAKDGANIVIA
1 1		l	AKTAQPHPKLLGTIYTAAEEIEAVGGKALPCIVDVRDEQQISAA
			VEKAIKKFGGIDILVNNASAISLTNTLDTPTKRLDLMMNVNTRG
]		į	TYLASKACIPYLKKSKVAHIPNISPPLNLNPVWFKOHCGRW*VV
			G*GDGLCLICFELNLCMSDVITICT
6171	382	941	HFMQSDVELDCDIEPCGHTKFPPTLPLSTTVIVCSCHPVATAST
]			MAEAFSKTTSEEDQSIQEPKEANSMTAQKQKK*GLRGSRRRHAN
1			SGGDIFGDSFAAYFPRVLKQVHQALSLSOEAVSVMDSMVRDILD
1	1		RIATEAGHLAHYSKCVTITSRDIRMAVCLLLPGKMGKLAESOGT
6172	651		NATLRYTKSK
	627	54	GLCRAGGAHRFSRTHVEAALKMLRREARLRREYLYRKAREEAQR
<b>[</b>	ļ		SAQERKERLRRALEENRLIPTELRREALALQGSLEFDDAGGEGV
			TSHVDDEYRWAGVEDPKVMITTSRDPSSRLKMFAKELKLVFPGA

COO			
SEQ ID	Predicted beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
140.	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	Sequence	\=possible nucleotide insertion)
			QRMNRGRHEVGALVRACKANGVTDLLVVHEHRGTPVGLIVSHLP
	}		FGPTAYFTLCNVVMRHDIPDLGTMSEAKPHLITHGFSSRLGKRV
-	j		SDILRYLFPVPKDDSHRVITFANQDDYISFRHHVYKKTDHRNVE
1			LTEVGPRFELKLYMIRLGTLEQEATADVEWRWHPYTNTARKRVF
			LSTE*AAPRPLGQLL
6173	3	288	SVDHREVQVLSQSMPLTPHQAVLRGERPYMCVECGKCFGRSSHL
	1	•	LQHQRIHTGEKPYVCSVCGKAFSQSSVLSKHRTIHTGEKPYECN
1			ECGKAFRVSSDLAQHHKIHTGEKPHECLECRKAFTQLSHLIQHQ
			RIHTGERPYVCPLCGKAFNHSTVLRSHQRVHTGEKPHRCNECGK
	į		TFSVKRTLLQHQRIHTGEKPYTCSECGKAFSDRSVLIQHHNVHT
j			GEKPYECSECGKTFSHRSTLMNHERIHTEEKPYACYECGKAFVQ
1	1		HSHLIQHQKVHRKL*PTCVLSVGSALAGVPTSFSISVSTLERSP
	<b>j</b>		MCAVYVGRPSARAQSLVNTGQFTQVRSPMSVMSVEKPLE
6174	1060	959	PRPPGKRWMVAGLGNPGLPGTRHSVGMAVLGQLARRLGVAESWT
İ			RDRHCAADLALAPLGDAQLVLLRPRRLMNANGRSVARAAELFGL
			TAEEVYLVHDELDKPLGRLALKLGGSARGHNGVRSCISCLNSNA
ľ			MPRLRVGIGRPAHPEAVQAHVLGCFSPAEQELLPLLLDRATDLI
			LDHIRERSQGPSLGP*H*WFSKKA
6175	2204	334	RYFRADPRSRSGQPRAEGLGAFAEGPLRAMAAPVKGNRKQSTEG
Ì			DALDPPASPKPAGKQNGIQNPISLEDSPEAGGEREEEOEREEEO
ŀ			AFLVSLYKFMKERHTPIERVPHLGFKQINLWKIYKAVEKLGAYE
ł			LVTGRRLWKNVYNELGGSPGSTSGATCTRRHY*RLVLPYVRHLK
1	! !		GEDDKPLPTSKPRKQYKMAKENRGDDGATERPKKAKEERRMDQM
			MPGKTKADAADPAPLPSQEPPRNSTEQQGLASGSSVSFVGASGC
	ł		PEAYKRLLSSFYCKGTHGIMSPLAKKKLLAQVSKVEALQCQEEG
			CRHGAEPQASPAVHLPESPQSPKGLTENSRHRLTPQEGLQAPGG
			SLREEAQAGPCPAAPIFKGCFYTHPTEVLKPVSQHPRDFFSRLK
1 1			DGVLLGPPGKEGLSVKEPQLVWGGDANRPSAFHKGGSRKGILYP
	i		KPKACWVSPMAKVPAESPTLPPTFPSSPGLGSKRSLEEEGAAHS
1			GKRLRAVSPFLKEADAKKCGAKPAGSGLVSCLLGPALGPVPPEA
1 1			YRGTMLHCPLNFTGTPGPLKGQAALPFSPLVIPAFPAHFLATAG PSPMAAGLMHFPPTSFDSALRHRLCPASSAWHAPPVTTYAAPHF
1 1	]		FHLNTKL
6176	1040	402	PLSALRAMAEVHVIGQIIGASGFSESSLFCKWGIHTGAAWKLLS
	[		GVREGQTQVDTPQIGDMAYWSHPIDLHFATKGLQGWPRLHFQVW
			SQDSFGRCQLAGYGFCHVPSSPGTHQLACPTWRPLGSWREQLAR
			AFVGGGPQLLHGDTIYSGADRYRLHTAAGGTVHLEIGLLLRNFD
	1		RYGVEC*GTLPPTSPPSTPRTPSDGGGWHSGQEHRL
6177	1400	992	VPIESLVGKVHNFPLIAFYCCEKGKRQPHKSLHDRCFGEALDPN
1	į	i	CSHCYLDQIKRSDFLGFSGYSPHFVAISTNSEHKMQPSSMQQAL
[ ]			PSQ*PYWTDPRPALVPCCSHRPDVHRSRPGPGLPGTSGCSDRPP
			VCPI
6178	1027	254	STORGGIKGVARAASLVGRRRAGTGMALLLCLVCLTAALAHGCL
			HCHSNFSKKFSFYRHHVNFKSWWVGDIPVSGALLTDWSDDTMKE
1	j		LHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELR
j	]		NIFREQVHLIQNAIIESRIDCQHRCGIFQYETISCNNCTDSHVA
			CFGYNCESSAQWKSAVQGLLNYINNWHKQDTSMRPRSSAFSWPG
ļl			THRAAPAFLVLPALRCLEPPHLANLSLEDAA+CLKQH
6179	806	276	RGETREMAGNLLSGAGRRLWDWVPLACRSFSLGVPRLIGIRLTL
1 1			PPPKVVDRWNEKRAMFGVYDNIGILGNFEKHPKELIRGPIWLRG
	Ţ		WKGNELQRCIRKRKMVGSRMFADDLHNLNKRIRYLYKHFNRHGK
L			FR*KRKLRTSEKAHLSPWRRETVLFPVRKRLCIFSVIKWGFFGI
6180	156	1833	DHHILKAASTTHVCARGNIFAIPNTRCLEC*ATATPSSLECON*
			SHLSLCPLPATTSGLTPNSMIPEKERONIAERLLRVMCADLGAL
ļ ļ		J	SVVSGKEFLKLAQTLVDSGARYGAFSVTEILGNFNTLALKHLPR
			MYNQVKVKVTCALGSNACLGIGVTCHSQSVGPDSCYILTAYQAE

SEQ	Predicted	Predicted end	Amino agid someth
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	ļ <del>-</del>	\=possible nucleotide insertion)
			GNHIKSYVLGVKGADIRDSGDLVHHWVQNVLSEFVMSEIRTVYV
I			TDCRVSTSAFSKAGMCLRCSACALNSVVQSVLSKRTLQARSMHE
}			VIELLNVCEDLAGSTGLAKETFGSLEETSPPPCWNSVTDSLLLV
			HERYEQICEFYSRAKKMNLIQSLNKHLLSNLAAILTPVKQAVIE
1			LSNESQPTLQLVLPTYVRLEKLFTAKANDAGTVSKLCHLFLEAL
1	1	Į.	KENFKVHPAHKVAMILDPQQKLRPVPPYQHEEIIGKVCELINEV
	1		KESWAEEADFEPAAKKPRSAAVENPAAQEDDRLGKNEVYDYLQE
			PLFQATPDLFQYWSCVTQKHTKLAKLAFWLLAVPAVGARSGCVN
	1		MCEQALLIKRRRLLSPEDMNKLMFLKSNML
6181	169	1032	TRTLLSPVLLPGPRWKPWRRRPMGPLALPAWLQPRYRKNAYLFI
1	1		YYLIQFCGHSWIFTNMTVRFFSFGKDSMVDTFYAIGLVMRLCQS
Į			VSLLELLHIYVGIESNHLLPRFLQLTERIIILFVVITSQEEVQE
ĺ			KYVVCVLFVFWNLLDMVRYTYSMLSVIGISYAVLTWLSQTLWMP
}	1		IYPLCVLAEAFAIYQSLPYFESFGTYSTKLPFDLSIYFPYVLKI
			YLMMLFIGMYFTYSHLYSERRDILGIFPIKKKKM*STAFQCDTR
			KDRLWIQCSK*NTGSILVEKFLVF
6182	1769	1224	AS*IDYQLNTLLKEFQLTEENTKLRYLTCSLIEDMAAAYFPDCI
			VRPFGSSVNTFGKLGCDLDMFLDLDETRNLSAHKISGNFLMEFQ
	ĺ		VKNVPSERIATQKILSVLGECLDHFGPGCVGVQKILNARCPLVR
	1		FSHQASGFQCDLTTNNRIALTSSELLYIYGALDSRVRALVFSVR
1		•	CWARAHSLTSSIPGAWITNFSLTMMVIFFLORRSPPILPTLDSL
			KTLADAEDKCVIEGNNCTFVRDLSRIKPSQNTETLELLLKEFFE
1	j		YFGNFAFDKNSINIRQGREQNKPDSSPLYIQNPFETSLNISKNV
			SQSQLQKFVDLARESAWILOOEDTDRPSISSNRPWGIMSLILDG
			APNRKSFTKKKSNKFAIETVKNLLESLKGNRTENFTKTSGKRTI
			STQT
6183	1118	452	HLDRYIKSPGSGSSTPAPPSHLLLYLLHPQSTRTMGCCGCSRGC
i l			GSGCGGCGSSCGGCGSGCGGCGSGCGGCSSSCGGCGS
1			RCYVPVCCCKPVCSWVPACSCTSCGSCGGSKGGCGSCGGSKGGC
	1		GSCGCSQSSCCKPCCCSSGCGSSCCOSSCCKPCCCOSSCCVPVC
1	1		CQSSCCKPCCCQSNCCVPVCCQCKI*GSGPRPSGFSCLVKAFLM
6100			VP
6184	. 1	2191	IVTVREEDGAPAVAPPGVVVSRANKRSGAGPGGSGGGGARGAEE
1	1		EPPPPLQAVLVADSFDRRFFPISKDOPRVI, DIANVALTDYTLE
1 1	1		FLTATGVQETFVFCCWKAAQIKEHLLKSKWCRPTSLNVVRIITS
1 [	i		ELYRSLGDVLRDVDAKALVRSDFLLVYGDVTSNTNTTPALFFHP
1 1		i	LRRKL*KNVSVMTMIFKESSPSHPTRCHEDNVVVAVDSTTNRVL
1			HFQKTQGLRRFAFPLSLFQGSSDGVEVRYDLLDCHISICSPQVA
1	ŀ		QLFTDNFDYQTRDDFVRGLLVNEEILGNQIHMHVTAKEYGARVS
{ l	1		NLHMYSAVCADVIRRWVYPLTPEANFTDSTTQSCTHSRHNIYRG
1	1		PEVSLGHGSILEENVLLGSGTVIGSNCFITNSVIGPGCHIEPGD
]			NVVLDQTYLWQGVRVAAGAQIHQSLLCDNAEVKERVTLKPRSVL
1		l	TSQVVVGPNITLPEGSVISLHPPDAEEDEDDGEFSDDSGADQEK
1	1	ĺ	DKVKMKGYNPAEVGAAGKGYLWKAAGMNMEEEEELQQNLWGLKI
1			NMEEESESESEQSMDSEEPDSRGGSPQMDDIKVFQNEVLGTLQR
	ì		GKEENISCDNLVLEINSLKYAYNISLKEVMQVLSHVVLEFPLQQ
1			MDSPLDSSRYCALLLPLLKAWSPVFRNYIKRAADHLEALAAIED
} I	j		FFLEHEALGISMAKVLMAFYQLEILAEETILSWFSQRDTTDKGQ
6185	791		QLRKNQQLQRFIQWLKEAEEESSEDD
	, , ,	44	PCTSCVLWATLHLPASTRKAPQAECGMISITEWQKIGVGITGFG
1			IFFILFGTLLYFDSVLLAFGNLLFLTGLSLIIGLRKTFWFFFQR
			HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFFSLFKGFFPVAF
1	ľ	1	GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK
			REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR
6186	569	238	GCQEAEMQTPRRLGWGWYHTLTLYLWEEK
<del></del>		230	VYGIDSSNTNTHGAEERNRKLKKHWKLCHAQSRLDVNGLALKMA

SEQ	Predicted	I manada ah ad	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
-	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
1			KERKVKNKVKNKADTEEVFNNSPTNOEKMPTSATLPDESGSVIS
İ		ł	NIRNQMETLHSQPHQEENLCFENSFSLINLLPINAVERTSSOOT
1	1	}	PNRETSEANKERRKMTSKSSESNIYSPLTSFITADSELHDITKD
ì			LEDCLMVGLHTCGDLAPNTLRIFTSNSEIKGVCSVGCCVHLLSE
1	)		EFENQHKERTQEKWGFPMCHYLKEERWCCGRNARMSACLALERV
	1		AAGQGLPTESLFYRAVLQDIIKDCYGITKCDRHVGKIYSKCSSF
1	•		LDYVRRSLKKLGLDESKLPEKIIMNYYEKYKPRMNELEAFNMLK
			VVLAPCIETLILLDRLCYLKEQEDIAWSALVKLFDPVKSPRCYA
			VIALKKQQ*FPLKQIIRCISL*DSAGCAEEVSVGDGGPALRDAP
6187	1701	771	PSGSRVGSRYD
1	1 2.02	771	DAWGPETRLARILNPDSFIEPRPGRLPELEATRPHMEPKASCPA
1			AAPLMERKFHVLVGVTGSVAALKLPLLVSKLLDIPGLEVAVVTT ERAKHFYSPQDIPVTLYSDADEWEMWKSRSDPVLHIDLRRWADL
			LLVAPLDANTLGKVASGICDNLLTCVMRAWDRSKPLLFCPAMNT
1	j		AMWEHPITAQQVDQLKAFGYVEIPCVAKKLVCGDEGLGAMAEVG
1			TIVDKVKEVLFQHSGFQQS*PGISVMGVPLYSEWVQAKSVKMDV
			GKIGGYPHLLNGGPALSLPRGQACSRLNWTEGPGLSFFQPGEAA
			A
6188	238	1534	KGFVNAGPLMAELQVSPQWKAPEMSQICLSCGHPSA*GPRWASW
1	i i		NIGVFICIRCAGIHRNLGVHISRVKSVNLDOWTOEOIOCMOFMG
}	}		NGKANRLYEAYLPETFRRPQIDPAVEGFIRDKYEKKKYMDRSLD
			INAFRKEKDDKWKRGSEPVPEKKLEPVVFRKVKMPOKKEDPOLP
Į			RKSSPKSTAPVMDLLGLDAPVACSIANSKTSNTLEKDLDIJASV
	[		PSPSSSGSRKVVGSMPTAGSAGSVPENLNLFPEPGSKSEEIGKK
1	l		QLSKDSILSLYGSQTPQMPTQAMFMAPAQMAYPTAYPSFPGVTP
			PNSIMGSMMPPPVGMVAQPGASGMVAPMAMPAGYMGGMQASMMG
1			VPNGMMTTQQAGYMAGMAAMPQTVYGVQPAQQLQWNLTQMTQQM
6189	1297	793	AGMNFYGANGMMNYGQSMSGGNEQAANQTLSPQMWK
		,,,,	LGEPLGDLCELIPGDVQQLQMGEVHPGTGAQGSAAQSVAGEVQL TQLSHARQRPSCQGSQLIALDLQHMDISRQPRWQHVQPVARQVQ
1			RAQQAQLAEGVAVHLWAGDAVVAEVELLQEVGGGKVFAANACDL
			VVQDHEGAHAARQATGHALQRVIVQVRRVQPLEAL*RVPSGLPR
1			RVRAFMILHNQITGIGREDFATTYFLEELNLSYNRITSPQVHRD
1 1	ĺ	•	AFRKLRLLRSLDLSGNRLHMLPPGLPRNVHVLKVKRNELAALAR
(	1		GALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLOLLDTAGNO
į į	l		LTEIPEGLPESLEYLYLONNKISAVPANAFDSTPNIKGIFIREN
1 1	į		KLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKDRGRLGKEKE
			EEEEDEVEEEETR
6190	66	1309	ILVGNVSFLLSFAEYVCNCSVVGSLNVNRCNQTTGQCECRPGYQ
[		ļ	GLHCETCKEGFYLNYTSGLCQPCDCSPHGALSIPCNSSGKCOCK
	ļ	İ	VGVIGSICDRCQDGYYGFSKNGCLPCQCNNRSASCDALTGACLN
1 1			CQENSKGNHCEECKEGFYQSPDATKECLRCPCSAVTSTGSCSIK
1			SSELEPECDQCKDGY1GPNCNKCENGYYNFDS1CRKCQCHGHVY
			PVKTPKICKPESGECINCLHNTTGFWCENCL*GYVHDLEGNCIK
			KVILPTPEGSTILVSNASLTTSVPTPVINSTFTPTTLQTIFSVS
			TSENSTSALADVSWTQFNIIILTVIIIVVVLLMGFVGAVYMYRE YQNRKLNAPFWTIELKEDNISFSSYHDSIPNADVSGLLEDDGNE
] ]			VAPNGQLTLTTPIHNYKA
6191	1212	1511	VNLCHGGLLHLSTHHLGIKPSMH*LFFLMLSFPHLTPQQPKCPS
! }			MIDWIKKIWYIYTMEYYATIKRNEIMFFAGTWMEMEAIILSKLM
<b>!</b>			QDYMFSLISGS QDYMFSLISGS
6192	3	950	TRGCGNKMAGKKNVLSSLAVYAEDSEPESDGEAGIEAVGSAAEE
1	1		KGGLVSDAYGEDDFSRLGGDEDGYEBEEDENSRQSEDDDSETEK
		1	PEADDPKDNTEAEKRDPQELVASFSERVRNMSPDEIKIPPEPPG
	]		RCSNHLQDKIQKLYERKIKEGMDMNYIIQRKKEFRNPSIYEKLI
<u> </u>			QFCAIDELGTNYPKDMFDPHGWSEDSYYEALAKAQKIEMDKLEK
		<del></del>	Nath Carlos

SEQ	Predicted	Predicted end	12
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
- 1	residue of	amino acid	W=Tryptophan, Y=Tvrosine, X=Unknown +-ch
	amino acid	sequence	Codon, /=possible nucleotide deletion "
· · · · · · · · · · · · · · · · · · ·	sequence		\=possible nucleotide insertion\
j			AKKERTKIEFVTGTKKGTTTNATSTTTTTASTAVADAQKRKSKW
İ			DSAIPVITIAQPTILTTTATLPAVVTVTSASGSKTTVISAVGT
6193	3	950	IVKAKQ
		950	TRGCGNKMAGKKNVLSSLAVYAEDSEPESDGEAGIEAVGSAAEE
	ł		KGGLVSDAYGEDDFSRLGGDEDGYEEEEDENSRQSEDDDSETEK
1			PEADDPKDNTEAEKRDPQELVASFSERVRNMSPDEIKIPPEPPG
			RCSNHLQDKIQKLYBRKIKEGMDMNYIIQRKKEFRNPSIYEKLI QFCAIDELGTNYPKDMFDPHGWSEDSYYEALAKAQKIEMDKLEK
			AKKERTKIEFVTGTKKGTTTNATSTTTTTASTAVADAQKRKSKW
			DSAIPVTTIAQPTILTTTATLPAVVTVTTSASGSKTTVISAVGT
			IVKKAKQ
6194	3	950	TRGCGNKMAGKKNVLSSLAVYAEDSEPESDGEAGIEAVGSAAEE
			RGGLVSDAYGEDDFSRLGGDEDGYEEEEDENSROSEDDDSETTER
j			PEADDPKDNTEAEKRDPOELVASFSERVRNMSPDETKIDDEDDC
			RCSNHLQDKIQKLYERKIKEGMDMNYIIORKKEFRNPSIVEKLI
			QFCAIDELGTNYPKDMFDPHGWSEDSYYEALAKAOKIEMDYLEV
1	J		AKKERTKIEFVTGTKKGTTTNATSTTTTTASTAVADAQKRKSKW
f			DSAIPVTTIAQPTILTTTATLPAVVTVTTSASGSKTTVISAVGT IVKKAKO
6195	736	235	VANGLQSNMPKFYCDYCDTYLTHDSPSVRKTHCSGRKHKENVKD
			YYQKWMEEQAQSLIDKTTAAFQQGKIPPTPFSAPPPAGAMIPPP
			PSLPGPPRPGMMPAPHMGGPPMMPMMGPPPPGMMPVGPAPGMRP
			PMGGHMPMMPGPPMMRPPARPMMVPTRPGMTRPDP
6196	1512	623	KTGKRRSAAYVRNILDNAEOVISNLEARNISDRITDLIOREDCU
			QKLLMGLMVSELKDHFLRHLOGVEKKKIEOMM.DYTEKTIDI.co
			HIVETNWRKHNLHSWVLHFNSRGSAAEFAVFHIMTDILEAUNGI
1 1			FLPLPPGFHTLHTILGVOCLPLHNLLHCTDSGVIJI.TETAVIDI
			MKDLDNTEKNEKLKFSIIVRLPPLIGQKICRLWDHPMSSNIISR
			NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILITDIESS NQALYPFEGHDNVDAEFVEEAALKHTAMLLGL
6197	3	819	ADPEGTEEAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG
	1		PIVDVYIPLDFYTRPRGFAYVQFEDVRDAEDALYNLNRKWVCG
			RQTEIQFAQGDRKTPGQMKSKERHPCSPSDHRRSRSPSQRRTRS
		}	RSSSWGRNRRRSDSLKESRHRRFSYSOSKSRSKSI, PROGTER PO
1	ľ		SKTPRRNFGSRGRSRSKSLOKRSKSIGKSOSSSDOKOTSSCTVS
1			RSHGRHSDSIARSPCKSPKGYTNFETKVOTAKHSHFRSHSPSPS
6198	111	1912	IRHKNSW
1		1912	SEAALSPSFISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSE
1		1	RENHAADDSEGGALDMCCSERLPGLPQPIVMEALDEAEGLQDSQ
		1	REMPPPPPPSPPSDPAQKPPPRGAGSHSLTVRSSLCLFAASQFL LACGVLWFSGYGHIWSQNATNLVSSLLTLLKQLEPTAWLDSGTW
			GVPSLLLVFLSGGLVLVTTLVWHLLRTPPEPPTPLPPEDRRQSV
] }			SRQPSFTYSEWMBEKIEDDFLDLDPVPETPVFDCVMDIKPEADP
ł I		ļ	TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREES
1 1		1	AKEYLLSASRVLQAEELHEKALDPFLLOAEFFETPMNFVDDVEV
1 1	Ī	.1	DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSVINANVIDC
1 1	}		IGGEEKVYIATQGPIVSTVADFWRMVWOEHTDIIVMTTNIDEMN
1			EKCTEYWPEEQVAYDGVEITVOKVIHTEDYRLRLISIKGGTPED
<b> </b>			GLKHYWFTSWPDQKTPDRAPPLLHLVREVEEAAOOEGPHCARTT
		i	VHCSAGIGRTGCFIATSICCQQLRQEGVVDILKTTCQLRQDRGG
6199	144	1211	MIQHCEQYQFVHHVMSLYEKQLSHQSPE
		· ·	MARENGESSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAEEKA
		1	TGKLFAVKCIPKKALKGKESSIENEIAVLRKIKHENIVALEDIY
	J	1.	ESPNHLYLVMQLVSGGELFDRIVEKGFYTEKDASTLIRQVLDAV YYLHRMGIVHRDLKPENLLYYSQDEESKIMISDFGLSKMEGKGD
		_  ,	VMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVIAYILLCGYPP
			THE TOTAL POLICY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPER

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P-Proline O-Club P-Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
ľ	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	Į.	sequence	Codon, /=possible nucleotide deletion,
<b></b>	sequence		\=possible nucleotide insertion)
	Ţ		FYDENDSKLFEQILKAEYEFDSPYWDDISDSAKDFIRNLMEKDP
1		i	NKRYTCEQAARHPWIAGDTALNKNIHESVSAOIRKNFAKSKWRO
1	Į.	į.	AFNATAVVRHMRKLHLGSSLDSSNASVSSSLSLASQKDCASGTF
	1		HAL*
6200	702	96	LPEVPHSLRPRVKPHLCCAQPAVRVMARLPKLAVFDLDYTLWPF
-			WVDTHVDPPFHKSSDGTVRDRRGQDVRLYPEVPEVLKRLQSLGV
			PGAAASRTSEIEGANQLLELFDLFRYFVHREIYPGSKITHFERL
			OOKTGIBESOMIEEDEEDEBRUIDUSKI SURGENIS SANTHEERL
	l .		QQKTGIPFSQMIFFDDERRNIVDVSKLGVTCIHIQNGMNLQTLS
6201	2809	2362	QGLETFAKAQTGPLRSSLEESPFEA
0201	2003	2383	GQTPRVRWKMRRSLRAGKRRQTAGRKSKSPPKVPIVIQDDSLPA
1			GPPPQIRILKRPTSNGVVSSPNSTSRPTLPVKSLAQREAEYAEA
	1		RKRILGSASPEEEQEKPILDRPTRISQPEDSRQPNNVIRQPLGP
			DGSQGFKQRR
6202	2	426	INADRAAVASSLLSRPTRKMAPOKDRKPKRSTWRFNLDLTHPVE
ł	1		DGIFDSGNFEOFLREKVKVNGKTGNLGNVVHIERFKNKITVVSE
	<b>:</b>		KQFSKRYLKYLTKKYLKKNNLRDWLRVVASDKETYELRYFQISQ
	[		DEDESESED
6203	419	2550	RCPRPPATAGAAASRPDRSPPSGISGSEAAAGAGAAAAASQHPA
			TGTGAVQTEAMKQILGVIDKKLRNLEKKKGKLDDYQERMNKGER
			LNQDQLDAVSKYQEVTNNLEFAKELQRSPMALSQDIQKTIKKTA
			PREOF WREED AND AMARIE OF THE PARTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PRO
1			RREQLMREEAEQKRLKTVLELQYVLDKLGDDEVRTDLKQGLNGV
1 .			PILSEEELSLLDEFYKLVDPERDMSLRLNEQYEHASIHLWDLLE
	í		GKEKPVCGTTYKVLKEIVERVFQSNYFDSTHNHQNGLCEEEEAA
i l			SAPAVEDQVPEAEPEPAEEYTEQSEVESTEYVNRQFMAETQFTS
1			GEKEQVDEWTVETVEVVNSLQQQPQAASPSVPEPHSLTPVAQAD
į į			PLVRRQRVQDLMAQMQGPYNFIQDSMLDFENQTLDPAIVSAOPM
ļ	!		NPTQNMDMPQLVCPPVHSESRLAQPNQVPVQPEATOVPLVSSTS
i l			EGYTASQPLYQPSHATEQRPQKEPIDQIQATISLNTDQTTASSS
			LPAASQPQVFQAGTSKPLHSSGINVNAAPFQSMQTVFKMNAPVP
1	}		PVNEPETLKQQNQYQASYNQSFSSQPHQVEQTELQQEQLQTVVG
1	[		TYHGSPDQSHQVTGNHQQPPQQNTGFPRSNQPYYNSRGVSRGGS
1 1			RGARGLMNGYRGPANGFRGGYDGYRPSFSNTPNSGYTQSQFSAP
	ļ		RDYSGYQRDGYQQNFKRGSGQSGPRGAPRGRGGPPRPNRGMPQM
i l	i		NTQQVN
6204	2933	787	
		,,,	CTHNLISLLGGRALIHFNRFLNLKIQEGEAHNIFCPAYDCFQLV
1	1		PGDIIKSVVSKEMDKRYLQFDIKAFVENNPAIKWCPTPGCDRAV
ļ			RLTKQGSNTSGSDTLSFPLLRAPAVDCGKGHLFCWECLGEAHEP
[	i		CDCQTWKNWLQKITEMKPEELVGVSEAYEDAANCLWLLTNSKPC
[			ANCKSPIQKNEGCNHMQCAKCKYDFCWICLEEWKKHSFVHWEVI
İ			YRCTRYEVIQHVEEQSKEMTVEAEKKHKRFQELDRFMHYYTRFK
			NHEHSYQLEQRLLKTAKEKMEQLSRALKETEGGCPDTTFIEDAV
	i		HVLLKTRRILKCSYPYGFFLEPKSTKKEIFELMQTDLEMVTEDL
[	1		AQKVNRPYLRTPRHKIIKAACLVQQKRQEFLASVARGVAPADSP
į į		į.	EAPRRSFAGGTWDWEYLGFASPEEYAEFQYRRHRQRRRGDVHS
			LLSNPPDPDEPSESTLDIPEGGSSSRRPGTSVVSSASMSVLHSS
l	<b>f</b>		SLRDYTPASRSENQDSLQALSSLDEDDPNILLAIQLSLQESGLA
	1		I.DEETDDELCHENGLONTORGE DON'T DON'T DON'T DESCRIPTION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE P
	l		LDEETROFLSNEASLGAIGTSLPSRLDSVPRNTDSPRAALSSSE
ŀ	1		LLELGDSLMRLGAENDPFSTDTLSSHPLSEARSDFCPSSSDPDS
	1		AGQDPNINDNLLGNIMAWFHDMNPQSIALIPPATTEISADSQLP
			CIKDGSEGVKDVELVLPEDSMFEDASVSEGRGTQIEENPLEENI
			PGGGKQHPQAW
6205	1	1200	RAHRGKMALEVGDMEDGQLSDSDSDMTVAPSDRPLQLPKVLGGD
1	I		SAMRAFQNTATACAPVSHYRAVESVDSSEESFSDSDDDSCLWKR
}	İ	ł	KRQKCFNPPPKPBPFQFGQSSQKPPVAGGKKINNIWGAVLQEQN
ļ		i	QDAVATELGILGMEGTIDRSRQSETYNYLLAKKLRKESQEHTKD
1	Į.	ľ	LDKELDEYMHGGKKMGSKEEENGQGHLKRKRPVKDRLGNRPEMN
	<u></u>		TITLE ON THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF THE TAXABLE OF TAXABLE OF THE TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXABLE OF TAXAB

SEQ	Predicted	Predicted end	I Amino noid
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleofide deletion
	Bequence		\=pcssible nucleotide insertion)
1		1	YKGRYEITAEDSQEKVADEISFRLQEPKKDLIARVVRIIGNKKA
	1		1 ELLMETAEVEQNGGLFIMNGSRRRTPGGVFI.NI.I.KNTDGIGER
	ł		QIKDIFYIENQKEYENKKAARKRRTOVIGKKMKOATKELNEGED
			DDTSRETFASDTNEALASLDESQEGHAEAKLEAEEATEVDHSHD
6206	·		PDIE
8206	10	1442	IISERRERSCLHLVCIRCSCDVVEMGSVLGLCSMASWIPCLCGS
1			APCLLCRCCPSGNNSTVTRLIYALFILVGVCVACVMLTDCMFFO
	ļ		LNKIPGFCENEKGVVPCNILVGYKAVYRICEGLAMEVILLELIM
i			IKVKSSSDPRAAVHNGFWFFKFAAAIAIIIGAFFIDEGTETTMI
	1		FYVGMAGAFCFILIQLVLLIDFAHSWNESWVEKMERGNGDGWVX
1			ALLSATALNYLLSLVAIVLFFVYYTHPASCSENKAETSUNMIIG
1	1		VGASVMSILPKIQESQPRSGLLQSSVITVYTMYLTWSAMTNEPE
1	1		TNCNPSLLSIIGYNTTSTVPKEGQSVQWWHAQGIIGLILFLLCV
	1 1		FYSSIRTSNNSQVNKLTLTSDESTLIEDGGARSDGSLEDGDDVH
			RAVDNERDGVTYSYSFFHFMLFLASLYIMMTLTNWYRYEPSREM
			KSQWTAVWVKISSSWIGIVLYVWTLVAPLVLTNRDFD
6207	2924	1471	TVMAEAATPGTTATTSGAGAAAATAAAASPTPIPTVTAPSLGAG
			GGGGGSDGSGGGWTKQVTCRYFMHGVCKEGDNCRYSHDLSDSPY
1			SVVCKYFQRGYCIYGDRCRYEHSKPLKQEEATATELTTKSSLAA
			SSSLSSIVGPLVEMNTGEAESRNSNFATVGAGSEDWVNAIEFVP
	İ		GQPYCGRTAPSCTEAPLQGSVTKEESEKEQTAVETKKQLCPYAA
			VGECRYGENCVYLHGDSCDMCGLQVLHPMDAAQRSQHIKSCIEA
1 1			HEKDMELSFAVQRSKDMVCGICMEVVYEKANPSERRFGILSNCN
1 1			HTYCLKCIRKWRSAKQFESKIIKSCPECRITSNFVIPSEYWVEE
1	,		KEEKQKLILKYKEAMSNKACRYFDEGRGSCPFGGNCFYKHAYPD
1 1	i		GRREEPQRQKVGTSSRYRAQRRNHFWELIEERENSNPFDNDEEE
			VVTFELGEMLLMLLAAGGDDELTDSEDEWDLFHDELEDFYDLDL
6208	2924	1471	TVMAEAATPGTTATTSGAGAAAATAAAASPTPIPTVTAPSLGAG
] [		J	GGGGGSDGSGGGWTKOVTCRYFMHGVCKEGDNCDVSHDIGDGDV
1		l	SVVCXYFQRGYCIYGDRCRYEHSKPLKOREATATFLTTVCCT AN
		•	SSSLSSIVGPLVEMNTGEAESRNSNFATVGAGSFDMINIA TERMS
1	j		GQPYCGRTAPSCTEAPLOGSVTKEESEKROTAVETKYOLODVAA
1 1	Í		VGECRYGENCVYLHGDSCDMCGLQVLHPMDAAQRSQHIKSCIEA
1 1	ľ		HEKDMELSFAVQRSKDMVCGICMEVVYEKANPSERRFGILSNCN
1 1	1		HTYCLKCIRKWRSAKQFESKIIKSCPECRITSNFVIPSEYWVEE
1	į.	1	KEEKQKLILKYKEAMSNKACRYFDEGRGSCPFGGNCFYKHAYPD
1	[		GREEPQRQKVGTSSRYRAORRNHFWELTERERENSNDEDWOERE
<del> </del>			VVTFELGEMLLMLLAAGGDDELTDSEDEWDI.FHDFI.FDFVDI.DI
6209	1758	029	ERLCFPCMQSKIYSYMSPNKCSGMRFPLOERNSVTHURVYCOOV
	-		PLAGIYRKREEKRNAGNAVRSAMKSEEOKIKDADKGDLUDEDNO
1		ĺ	KSBAAEPPKTPPSSCDSTNAAIAKQALKKPIKGKQAPRKKAQGK
			TQQNRKLTDFYPVRRSSRKSKAELQSEERKRIDELIESGKEEGM
l l		ļ	KIDLIDGKGRGVIATKQFSRGDFVVEYHGDLIEITDAKKREALY
			AQDPSTGCYMYYFQYLSKTYCVDATRETNRLGRLINHSKCGNCQ
į	1		TKLHDIDGVPHLILIASRDIAAGEELLYDYGDRSKASIEAHPWL
			KH KH
6210	3761	387	IFGMSKLRMVLLEDSGSADFRRHFVNLSPFTITVVLLLSACFVT
			SSLGGTDKELRLVDGENKCSGRVEVKVQEEWGTVCNNGWSMEAV
	* #		SVICNQLGCPTAIKAPGWANSSAGSGRIWMDHVSCRGNESALWD
	1	· 1	CKHDGWGKHSNCTHQQDAGVTCSDGSNLEMRLTRGGNMCSGRIE
1			IKFQGRWGTVCDDNFNIDHASVICRQLECGSAVSFSGSSNFGEG
1			SGPIWFDDLICNGNESALWNCKHCGWGKHNCDHAEDAGVICSKG
- 1		1	ADISTRIAD CATEGORIE BAR ECCENTER TO THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE PO
ı			ADLSLRLVDGVTECSGRLEVRFQGEWGTICDDGWDSYDAAVACK
		1.	QLGCPTAVTAIGRVNASKGFGHIWLDSVSCQGHEPAVWQCKHHE
	İ	1	WGKHYCNHNEDAGVTCSDGSDLELRLRGGGSRCAGTVEVEIQRL
		L	LGKVCDRGWGLKEADVVCRQLGCGSALKTSYQVYSKIQATNTWL

SEO	Predicted	Predicted end	L Design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design an
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ì	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
}	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	3	\=possible nucleotide insertion)
	<del> </del>		FLSSCNGNETSLWDCKNWQWGGLTCDHYEEAKITCSAHREPRLV
			GGDIPCSGRVEVKHGDTWGSICDSDFSLEAASVLCRELQCGTVV
ı			SILGGAHFGEGNGQIWAEEFQCEGHESHLSLCPVAPRPEGTCSH
1			SRDVGVVCSRYTEIRLVNGKTPCEGRVELKTLGAWGSLCNSHWD
Ī			IEDAHVLCQQLKCGVALSTPGGARFGKGNGQIWRHMFHCTGTEQ
			HMGDCPVTALGASLCPSEQVASVICSGNQSQTLSSCNSSSLGPT
			RPTIPEESAVACIESGQLRLVNGGGRCAGRVEIYHEGSWGTICD
1	Į į		DSWDLSDAHVVCRQLGCGEAINATGSAHFGEGTGPIWLDEMKCN
1		:	GKESRIWQCHSHGWGQQNCRHKEDAGVICSEFMSLRLTSEASRE
Ì			ACAGRLEVFYNGAWGTVGKSSMSETTVGVVCRQLGCADKGKINP
		•	ASLDKAMSIPMWVDNVQCPKGPDTLWQCPSSPWEKRLASPSEET
			WITCDNKIRLQEGPTSCSGRVEIWHGGSWGTVCDDSWDLDDAQV
1			VCQQLGCGPALKAFKEAEFGQGTGPIWLNEVKCKGNESSLWDCP
	-		ARRWGHSECGHKEDAAVNCTDISVQKTPQKATTGRSSROSSFIA
[	[		VGILGVVLLAIFVALFFLTKKRRQRQRLAVSSRGENLVHQIQYR
	·		EMNSCLNADDLDLMNSSGGHSEPH
6211	3761	387	1FGMSKLRMVLLEDSGSADFRRHFVNLSPFT1TVVLLLSACFVT
			SSLGGTDKELRLVDGENKCSGRVEVKVQEEWGTVCNNGWSMEAV
1			SVICNQLGCPTAIKAPGWANSSAGSGRIWMDHVSCRGNESALWD
	į į		CKHDGWGKHSNCTHQQDAGVTCSDGSNLEMRLTRGGNMCSGRIE
			IKFQGRWGTVCDDNFNIDHASVICRQLECGSAVSFSGSSNFGEG
l i			SGPIWFDDLICNGNESALWNCKHQGWGKHNCDHAEDAGVICSKG
			ADLSLRLVDGVTECSGRLEVRFQGEWGTICDDGWDSYDAAVACK
			QLGCPTAVTAIGRVNASKGFGHIWLDSVSCQGHEPAVWQCKHHE
1			WGKHYCNHNEDAGVTCSDGSDLELRLRGGGSRCAGTVEVEIQRL
			LGKVCDRGWGLKEADVVCRQLGCGSALKTSYQVYSKIQATNTWL
			FLSSCNGNETSLWDCKNWQWGGLTCDHYEEAKITCSAHREPRLV
			GGDIPCSGRVEVKHGDTWGSICDSDFSLEAASVLCRELQCGTVV
!			SILGGAHFGEGNGQIWAEEFQCEGHESHLSLCPVAPRPEGTCSH
) j			SRDVGVVCSRYTEIRLVNGKTPCEGRVELKTLGAWGSLCNSHWD
			IEDAHVLCQQLKCGVALSTPGGARFGKGNGQIWRHMFHCTGTEQ HMGDCPVTALGASLCPSEQVASVICSGNQSQTLSSCNSSSLGPT
			RPTIPEESAVACIESGQLRLVNGGGRCAGRVEIYHEGSWGTICD
	I		DSWDLSDAHVVCRQLGCGEAINATGSAHFGEGTGPIWLDEMKCN
	1		GKESRIWQCHSHGWGQQNCRHKEDAGVICSEFMSLRLTSEASRE
			ACAGRLEVFYNGAWGTVGKSSMSETTVGVVCRQLGCADKGKINP
.[	ĺ		ASLDKAMSIPMWVDNVQCPKGPDTLWQCPSSPWEKRLASPSEET
	ì		WITCDNKIRLQEGPTSCSGRVEIWHGGSWGTVCDDSWDLDDAQV
	i	j	VCQQLGCGPALKAFKEAEFGQGTGPIWLNEVKCKGNESSLWDCP
J	j		ARRWGHSECGHKEDAAVNCTDISVOKTPOKATTGRSSROSSFIA
	ļ		VGILGVVLLAIFVALFFLTKKRRQRQRLAVSSRGENLVHQIQYR
			EMNSCLNADDLDLMNSSGGHSEPH
6212	1	1134	LKWELRPGGAVWGTGRGAGTGAPRSCCCQTNPGPPSSLRRAFRR
ļ Į			RELPFPACHEIGLGAEAGSGPPPAPAARESRSRAMEEEASSPGL
	į		GCSKPHLEKLTLGITRILESSPGVTEVTIIEKPPAERHMISSWE
ŀ	Í		QKNNCVMPEDVKNFYLMINGFHMTWSVKLDEHIIPLGSMAINSI
			SKLTQLTQSSMYSLPNAPTLADLEDDTHEASDDQPEKPHFDSRS
			VIFELDSCNGSGKVCLVYKSGKPALAEDTEIWFLDRALYWHFLT
ļ		İ	DTFTAYYRLLITHLGLPQWQYAFTSYGISPQAKQRVSMYKPITY
ļ	İ		NTNLLTEETDSFVNKLDPSKVFKSKNKIVIPKKKGPVQPAGGQK
			GPSGPSGPSTSSTSKSSSGSGNPTRK
6213	1	1134	LKWELRPGGAVWGTGRGAGTGAPRSCCCQTNPGPPSSLRRAFRR
			RELPFPACHEIGLGAEAGSGPPPAPAARESRSRAMEEEASSPGL
			GCSKPHLEKLTLGITRILESSPGVTEVTIIEKPPAERHMISSWE
- 1			QKNNCVMPEDVKNFYLMTNGFHMTWSVKLDEHIIPLGSMAINSI
			SKLTQLTQSSMYSLPNAPTLADLEDDTHEASDDQPEKPHFDSRS

SEQ	Predicted	Predicted end	Amino poid comenh
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ı	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
-	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	Daquence	\=possible nucleotide insertion)
·			VIFELDSCNGSGKVCLVYKSGKPALAEDTEIWFLDRALYWHFLT
			DTFTAYYRLLITHLGLPQWQYAFTSYGISPQAKQRVSMYKPITY
			NTNLLTEETDSFVNKLDPSKVFKSKNKIVIPKKKGPVQPAGGQK
	}		GPSGPSGPSTSSTSKSSSGSGNPTRK
6214	2	460	UPLA DEATED AND OF CHARLES
	Į	400	HELAPSAIRRAARLGLGPARWQSRAAAFYFVRGFRTGWSFVGWV
			VLGTSAKRTRLFFFLSKMAASSRAQVLALYRAMLRESKRFSAYN
İ	į		YRTYAVRRIRDAFRENKNVKDPVEIQTLVNKAKRDLGVIRRQVH
6215	2	1849	IGQLYSTDKLIIENRDMPRT
"""	-	1043	FVAGGPRGSGSAAETMPEIRVTPLGAGQDVGRSCILVSIAGKNV
l			MLDCGMHMGFNDDRRFPDFSY1TQNGRLTDFLDCVIISHFHLDH
i			CGALPYFSEMVGYDGPIYMTHPTQAICPILLEDYRKIAVDKKGE
			ANFFTSQMIKDCMKKVVAVHLHQTVQVDDELEIKAYYAGHVLGA
-			AMFQIKVGSESVVYTGDYNMTPDRHLGAAWIDKCRPNLLITEST
			YATTIRDSKRCRERDFLKKVHETVERGGKVLIPVFALGRAQELC
			ILLETFWERMNLKVPIYFSTGLTEKANHYYKLFIPWTNQKIRKT
1			FVQRNMFEFKHIKAFDRAFADNPGPMVVFATPGMLHAGQSLQIF
1			RKWAGNEKNMVIMPGYCVQGTVGHKILSGQRKLEMEGRQVLEVK
1			MOVEYMSFSAHADAKGIMQLVGQAEPESVLLVHGEAKKMEFLKQ
			KIEQELRVNCYMPANGETVTLPTSPSIPVGISLGLLKREMAQGL
			LPEAKKPRLLHGTLIMKDSNFRLVSSEQALKELGLAEHQLRFTC
			RVHLHDTRKEQETALRVYSHLKSVLKDHCVQHLPDGSVTVESVL
6216	11	393	LQAAAPSEDPGTKVLLVSWTYQDEELGSFLTSLLKKGLPQAPS
	1	333	QTTRPEPRNSALRQSRSKMAVVGVSSVSRLLGRSRPQLGRPMSS
			GAHGEEGSARMWKTLTFFVALPGVAVSMLNVYLKSHHGEHERPE FIAYPHLRIRTKPFPWGDGNHTLFHNPHVNPLPTGYEDE
6217	9	1178	TRVGRGESGLKMEVKPPPGRPQPDSGRRRRRGEEGHDPKEPEQ
1			LRKLFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDPQTKRSRG
			FGFVTYSCVEEVDAAMCARPHKVDGRVVEPKRAVSREDSVKPGA
			HLTVKKIFVGGIKEDTEEYNLRDYFEKYGKIETIEVMEDROSGK
1 1			KRGFAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALSKQEMQS
1	•		AGSQRGRGGGSGNFMGRGGNFGGGGGNFGRGGNFGGGGGGGGGG
i i			GGSRGSYGGGDGGYNGFGGDGGNYGGGPGYSSRGGYGGGGPGYG
1	į		NQGGGYGGGGGYDGYNEGGNFGGGNYGGGGNYNDFGNYSGQQQS
,			NYGPMKGGSFGGRSSGSPYGGGYGSGGGGGGGGGGGRRF
6218	1305	906	SCERRGFIMADDLKRFLYKKLPSVEGLHAIVVSDRDGVPVIKVA
		<del>-</del>	NDNAPEHALRPGFLSTFALATDQGSKLGLSKNKSIICYYNTYOV
}	l		VQFNRLPLVVSFIASSSANTGLIVSLEKELAPLFEELRQVVEVS
6219	2	890	AGPGEGAGAGTRCAGAEAEMASAGGEDCESPAPEADRPHQRPFL
	ľ	<b>-</b>	IGVSGGTASGKSTVCEKIMELLGQNEVEQRQRKVVILSQDRFYK
1 1			VLTAEQKAKALKGQYNFDHPDAFDNDLMHRTLKNIVEGKTVEVP
			TYDFVTHSRLPETTVVYPADVVLFEGILVFYSQEIRDMFHLRLF
]	1		VDTDSDVRLSRRVLRDVRRGRDLEQILTQYTTFVKPAFEEPCLP
{	į		TKKYADVIIPRGVDNMVAINLIVQHIQDILNGDICKWHRGGSNG
] [	j		RSYKRTFSEPGDHPGMLTSGKRSHLESSSRPH
6220	227	764	
]		701	EQNISLEMSCTIEKALADAKALVERLRDHDDAAESLIEQTTALN
]			KRVEAMKQYQEEIQELNEVARHRPRSTLVMGIQQENRQIRELQQ
] [	J		ENKELRTSLEEHQSALELIMSKYREQMFRLLMASKKDDPGIIMK
ţ [	1		LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEANQ NVH
6221	98	916	l l
	-3	310	RWIWDLNPVSDGLELRPKYNGILHCLTTIWKLDGLRGLYQGVTP
] [			NIWGAGLSWGLYFVFYNAIKSYKTEGRAERLEATEYLVSAAEAG
			AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKGMFDTLVKIYK
		ļ	YEGVRGLYKGFVPGLFGTSHGALQFMAYELLKLKYNQHINRLPE
<b>!</b>			AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHMFYSGVI
		l	DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHFL
			LDLREKRK

SEQ	Predicted	l Bundina	
ID	beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
ł	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
ļ	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
ſ	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion,
6222	2	2116	\=possible nucleotidc insertion)
1 0222	1 -	2116	MARELRALLLWGRRLRPLLRAPALAAVPGGKPILCPRRTTAQLG
	j		PRRNPAWSLQAGRLFSTQTAEDKEEPLHSIISSTESVQGSTSKH
1	1		EFQAETKKLLDIVARSLYSEKEVFIRELISNASDALEKLRHKLV
	]		SDGQALPEMEIHLQTNAEKGTITIQDTGIGMTQEELVSNLGTIA
	1		RSGSKAFLDALQNQAEASSKIIGQFGVGFYSAFMVADRVEVYSR
			SAAPGSLGYQWLSDGSGVFEIAEASGVRTGTKIIIHLKSDCKEF
}	1		SSEARVRDVVTKYSNFVSFPLYLNGRRMNTLQAIWMMDPKDVRE
			WOHEEFYRYVAQAHDKPRYTLHYKTDAPLNIRSIFYVPDMKPSM
			FDVSRELGSSVALYSRKVLIQTKATDILPKWLRFIRGVVDSEDI
	į i		PLNLSRELLQESALIRKLRDVLQQRLIKFFIDQSKKDAEKYAKF
1			FEDYGLFMREGIVTATEQEVKEDIAKLLRYESSALPSGQLTSLS
ŀ	l i		EYASRMRAGTRNIYYLCAPNRHLAEHSPYYEAMKKKDTEVLFCF
-	]		EQFDELTLLHLREFDKKKLISVETDIVVDHYKEEKFEDRSPAAE
1	ĺ		CLSEKETEELMAWMRNVLGSRVTNVKVTLRLDTHPAMVTVLEMG
1	ŀ		AARHFLRMQQLAKTQEERAQLLQPTLEINPRHALIKKLNQLRAS
6223	3	715	EPGLAQLLVDQIYENAMIAAGLVDDPRAMVGRLNELLVKALERH
0020		715	DAWARTMAGMVDFQDEEQVKSFLENMEVECNYHCYHEKDPDGCY
į			RLVDYLEGIRKNFDEAAKVLKFNCEENQHSDSCYKLGAYYVTGK
			GGLTQDLKAAARCFLMACEKPGKKSIAACHNVGLLAHDGQVNED
1	I		GQPDLGKARDYYTRACDGGYTSSCFNLSANFLQGAPGFPKDMDL
1			ACKYSMKACDLGHIWACANASRMYKLGDGVDKVEAKAEVLKNRA
6224	1	133	QQVHKEQQKGVQPLTFG
6225	3259	938	LRTISSMAWGPLLLTLLAHCTGSWAQSVLTQPPSVSGARIPHEK
]		230	LLSCHRLAICKLPFSVESRKTVMGPQGARRQAFLAFGDVTVDFT
1			QKEWRLLSPAQRALYREVTLENYSHLVSLGILHSKPELIRRLEQ
	ļ		GEVPWGEERRRRPGPCAGIYAEHVLRPKNLGLAHQRQQQLQFSD
	I		QSFQSDTAEGQEKEKSTKPMAFSSPPLRHAVSSRRRNSVVEIES
1	i		SQGQRENPTEIDKVLKGIENSRWGAFKCAERGQDFSRKMMVIIH
1 1	I		KKAHSRQKLFTCRECHQGFRDESALLLHQNTHTGEKSYVCSVCG
			RGFSLKANLLRHORTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECOECGRRFNDKSSYNKHLKAHSGEKPFVCKECGRGYT
1 1	1		NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK
1 1	[		PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST
	· [:	•	LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSEEK?FVC
	i		KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRRFRDKSSYNKH
1			LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE
1	•		KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH
1	ł		SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN
	ļ		WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHWRIHSKE
] }		i	KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS
			YYSKHLKRHLREKRFCTGSVGEASS
6226	29	266	TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS
			IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA
6227	2581	890	MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP
1			NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS
]			YGQLSNGEPHFLPDAMFGQPGALGSTPFLGQHGFNFFPSGIDFS
1 1			AWGNNSSQGQSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL
I · I	1		NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI
1 . [	İ	ļ	VASNSLPPATIAPPKPASWADIASKPAKQQPKLKTKNGIAGSSL
1 1	1		PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG
1	j	1	QQANNSPPVAQASVGQQTQPLPPPPPPQPAQLSVQQQAAQPTRWV
]		İ	APRNRGSGFGHNGVDGNGVGQSQAGGSTPSEPHPVLEKLRSIN
] }			NYNPKDFDWNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNK
	ļ	ļ	RLDAAYRSMNGKGPVYLLFSVNGSGHFCGVAEMKSAVDYNTCAG
[ [	ŀ	i	VWSQDKWKGRFDVRWIFVKDVPNSQLRHIRLENNENKPVTNSRD
ı î		i	ozowiegki dakati akda bus olekit krennenk PALNSKD
		1	TQEVPLEKAKQVLKIIASYKHTTSIFDDFSHYEKRQ

SEQ	Predicted	Predicted end	Amino anid
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
l	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
į	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ĺ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6228	47	1978	GRRCRRGAVMELAQEARELGCWAVEEMGVPVAARAPESTLRRL
- 1	1		CLGQGADIWAYILQHVHSQRTVKKIRGNLLWYGHQDSPQVRRKL
l			ELEAAVTRLRAEIQELDQSLELMERDTEAQDTAMEQARQHTQDT
			QRRALLLRAQAGAMRRQQHTLRDPMQRLQNQLRRLQDMERKAKV
	1		DVTFGSLTSAALGLEPVVLRDVRTACTLRAQFLQNLLLPQAKRG
			SLPTPHDDHFGTSYQQWLSSVETLLTNHPPGHVLAALEHLAAER
			EAEIRSLCSGDGLGDTEISRPQAPDQSDSSQTLPSMVHLIQEGW
1	1		RTVGVLVSQRSTLLKERQVLTQRLQGLVEEVERRVLGSSERQVL
1	1		ILGLRRCCLWTELKALHDQSQELQDAAGHRQLLLRELQAKQQRI
1			LHWRQLVEETQEQVRLLIKGNSASKTRLCRSPGEVLALVQRKVV
1	i .		PTFEAVAPQSRELLRCLEEEVRHLPHTI.I.GTI.I.DUP DGDI VDI D
İ	1		TVLPSIHQLHPASPRGSSFIALSHKI,GI,PPGKASELILDAAACI
			RQUILLLQDQRSLWCWDLLHMKTSLPPGI.PTOFILOTORSOPVO
f	1		QKENLGQALKRLEKLLKOALERIPELOGIVGDWWFODGOALER
6229			ELCQGLSLPQWRLRWVQAQGALOKLCS
0223	1571	560	GPSLLGTRGTPNPARTLOIFFLIIGRRLTGRMAAUDDLOFFFFC
			NAATSLTANPDATTVNIEDPGETPKHOPGSPPGSGPPPDDELIG
1			NDDSDKTELLAGOKKSSPFWTFEYYOTFFDUDTYOUPDDTYGGT
	]		LPIPGKNFVRLYIRSNPDLYGPFWICATIVFATATSGNIGNELT
1	1		HLGERTYHYVPEFRKVSIAATIIYAYAWI,VPI.AI,WGPI,MWDNGV
1	!		VMNIVSYSFLEIVCVYGYSLFIYIPTAILWIIPHKAUPWILLWI
į	ĺ		ALGISGSLLAMTFWPAVREDNRRVALATIVTIVLLHMLLSVGCL
6230	1723	600	AYFFDAPEMDHLPTTTATPNQTVAAAKSS
1		000	SKMSGRSGKKKMSKLSRSARAGVIFPVGRLMRYLKKGTFKYRIS
	i i		VGAPVYMAAVIEYLAAEILELAGNAARDNKKARIAPRHILLAVA
	1		NDEELNQLLKGVTIASGGVLPRIHPELLAKKRGTKGKSETILSP
1	l i		PPEKRGRKATSGKKGGKKSKAAKPRTSKKSKPKDSDKEGTSNST
1			SEDGPGDGFTILSSKSLVLGQKLSLTQSDISHIGSMRVEGIVHP TTAEIDLKEDIGKALEKAGGKEFLETVKELRKSQGPLEVAEAAV
1		İ	SQSSGLAAKFVIHCHIPQWGSDKCEEQLEETIKNCLSAAEDKKL
	ı		KSVAFPPFPSGRNCFPKQTAAQVTLKAISAHFDDSSASSLKNVY
			FLLFDSESIGIYVQEMAKLDAK
6231	149	870	LIFSSSTMDRSLRNVLVVSFGFLLLFTAYGGLQSLQSSLYSEEG
1	1		LGVTALSTLYGGMLLSSMFLPPLLIERLGCKGTIILSMCGYVAF
1 1	1		SVGNFFASWYTLIPTSILLGLGAAPI,WSAOCTVI.TITCNTUATV
			AGKRGKDMVNOYFGIFFLIFOSSGVWGNI.ISSI.WEGOTDCOTTT
1 1	' !		PEEQLISCGASDCLMATTTNSTORPSOOLVYTLICIVECCUT
6232	2690		AVENTAAFLOPIRDVORESE
0232	3679	1476	FVAGTTMAGFWVGTAPLVAAGRRGRWPPQQLMLSAALRTLKHVL
] [			IISRQCLMVSRNLGSVGYDPNEKTFDKII.VANRGETACRVIDTC
1 1		Ì	KRMG1KTVA1HSDVDASSVHVKMADEAVCVCPAPTCKCVI NIMDA
			IMEALKKTRAQAVHPGYGFLSENKEFARCI.AAFDIMETCHDTUA
l i	1		IQAMGDKIESKLLAKKAEVNTIPGFDGVVKDAEFAVDTABETCV
, ,		[	PVMIKASAGGGGKGMRIAWDDEETRDGFRISSOFAAGGRODDI
		{	LIERTION PRHIEIQVLGDKHGNALWINERECS TOPPNOVAGER
1 1	1		APSIT LUAETRRAMGEOAVALARAVKYSSAGTVFFT VIDEVINEV
] [	1	i	FLEMNTRLQVEHPVTECITGLDLVOEMIRVAKGVDLDUVOADID
J.	1		INGWAVECRVYAEDPYKSFGLPSIGRLSOYOEPI.HI.PGVPVDCC
[	ļ	1	TOPGSDISTYYDPMISKLITYGSDRTEALKRMADALDWYGTDGG
<b>!</b> [	ļ	1	THNIALLREVIINSRFVKGDISTKFLSDVVPDGFKGHMTTVCFV
			NQLLAIASSLFVAFQLRAQHFQENSRMPVIKPDIANWELSVKLH
1 1	ľ		DKVHTVVASNNGSVFSVEVDGSKLNVTSTWNLASPLLSVSVDGT
	· [		QRTVQCLSREAGGNMSIQFLGTVYKVNILTRLAAELNKFMLEKV
			TEDTSSVLRSPMPGVVVAVSVKPGDAVAEGQEICVIEAMKMQNS
6233	1	2654	MTAGKTGTVKSVHCQAGDTVGEGDLLVELE
	•		HSTRENLNAGNFNFPSEGHLVRSTGPGGSFAKHMVAQCVSPKGP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ļ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
į	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u></u>	sequence		\=possible nucleotide insertion)
ł	1	1	LACSRTYFFGATHVPYLGGDSKLPKKTEQIRLLSQIYAAVIEAV
	1	}	LAGIACYAKTSSLTKAKEVAEQTLGSGLDSFELIPFKAALRSKM
ļ	1	1	TFHIHAVNNQGRIVPLDSEDSLSFVKTACMAVYDIPDLLGGNGC
İ		į.	LGSVVFSESFLTSQILVKEKDGTVTTETSSVVLTAAVPRFCSWL
	)	1	VEDNEVKLSEKTHQAVRGDESFLGTYLTGGEGAYLYSSNLQSWP
ĺ	1	-	EEGNVHFFSSGLLFSHCRHGSIIISKDHMNSISFYDGDSTSTVA
l			ALLIDFKSSLLPHLPVHFHGSSNFLMIALFPKSKIYQAFYSEVF
			SLWKQQDNSGISLKVIQEDGLSVEQKRLHSSAQKLFSALSQPAG
1	i		EKRSSLKLLSAKLPELDWFLQHFAISSISQEPVMRTHLPVLLQQ
		1	AEINTTHRIESDKVIISIVTGLPGCHASELCAFLVTLHKECGRW
			MVYRQINDSSECFHAAHFQRYLSSALEAQQNRSARQSAYIRKKT
ļ.			RLLVVLQGYTDVIDVVQALQTHPDSNVKASFTIGAITACVEPMS
	l .		CYMEHRFLFPKCLDQCSQGLVSNVVFTSHTTEQRHPLLVQLQSL
1	<b>}</b>	1	IRAANPAAAFILAENGIVTRNEDIELILSENSFSSPEMLRSRYL
i	1	1	MYPGWYEGKLNAGSVYPLMVQICVWFGRPLEKTRFVAKCKAIQS
1			SIKPSPFSGNIYHILGKVKFSDSERTMEVCYNTLANSLSIMPVL
1			EGPTPPPDSKSVSQDSSGQQECYLVFIGCSLKEDSIKDWLRQSA
			KQKPQRKALKTRGMLTQQEIRSIHVKRHLEPLPAGYFYNGTQFV
			NFFGDKTDFHPLMDQFMNDYVEEANREIEKYNQELEQQEYHDLF ELKP
6234	1731	404	1 1 1 1
0234	1/31	404	PRVREDMDHKSPGNKGSLVYAGIKSIVKSSLGMVESSRHNWSGL DKQSDIQNLNEERILALQLCGWIKKGTDVDVGPFLNSLVQEGBW
	i		ERAAAVALFNLDIRRAIQILNEGASSEKGDLNLNVVAMALSGYT
1	}	1	DEKNSLWREMCSTLRLQLNNPYLCVMFAFLTSETGSYDGVLYEN
Į.			KVAVRDRVAFACKFLSDTQLNRYIEKLTNEMKEAGNLEGILLTG
			LTKDGVDLMESYVDRTGDVQTASYCMIQGSPLDVLKDERVQYWI
i	<b>:</b>		ENYRNLLDAWRFWHKRAEFDIHRSKLDPSSKPLAQVFVSCNFCG
			KSISYSCSAVPHQGRGFSQYGVSGSPTKSKVTSCPGCRKPLPRC
			ALCLINMGTPVSSCPGGTKSDEKVDLSKDKKLAQFNNWFTWCHN
			CRHGGHAGHMLSWFRDHAECPVSACTCKCMQLDTTGNLVPAETV
			OP
6235	1	571	EKRDHRLPSWPRAALKVPGRGGRVGTTPELAAGGIMATRNPPPO
}	-		DYESDDDSYEVLDLTEYARRHQWWNRVFGHSSGPMVEKYSVATO
			IVMGGVTGWCAGFLFQKVGKLAATAVGGGFLLLQIASHSGYVCI
I		1	DWKRVEKDVNKAKRQIKKRANKAAPEINNLIEEATEFIKONIVI
			SSGFVGGFLLGLAS
6236	i i	703	WDQNKGAAAGSGLTLPSLPSARFSAGPPTQRSRPTMSNMEKHLF
1			NLKFAAKELSRSAKKCDKEEKAEKAKIKKAIQKGNMEVARIHAE
1		1	NAIRQKNQAVNFLRMSARVDAVAARVQTAVTMGKVTKSMAGVVK
l		1	SMDATLKTMNLEKISALMDKFEHQFETLDVQTQQMEDTMSSTTT
l ·		1	LTTPQNQVDMLLQEMADEAGLDLNMELPQGQTGSVGTSVASAEQ
j		1	DELSQRLARLRDQV
6237	312	720	PTAMAEEGIAAGGVMDVNTALQEVLKTALIHDGLARGIREAAKA
l		1	LDKRQAHLCVLASNCDEPMYVKLVEALCABHQINLIKVDDNKKL
ł	1		GEWVGLCKIDREGKPRKVVGCSCVVVKDYGKESQAKDVIEEYFK
ł			CKK
6238	2	4666	ERVPTQESVKWEINVIIKNPEIVFVADMTKNDAPALVITTOCEI
1	[		CYKGNLENSTMTAAIKDLQVRACPFLPVKRKGKITTVLOPCDLF
l ·		1	YQTTQKGTDPQVIDMSVKSLTLKVSPVIINTMITITSALYTTKE
		1	TIPEETASSTAHLWEKKDTKTLKMWFLEESNETEKIAPTTELVP
	1	1	KGEMIKMNIDSIFIVLEAGIGHRTVPMLLAKSRFSGEGKNWSSL
		1	INLHCQLELEVHYYNEMFGVWEPLLEPLEIDQTEDFRPWNLGIK
			MKKKAKMAIVESDPEEENYKVPEYKTVISFHSKDOLNITLSKCG
1		1	LVMLNNLVKAFTZAATGSSADFVKDLAPFMILNSLGLTISVSPS
1			DSFSVLNIPMAKSYVLKNGESLSMDYIRTKDNDHFNAMTSLSSK
1		1	LFFILLTPVNHSTADKIPLTKVGRRLYTVRHRESGVERSIVCQI
	<u> </u>		

SEQ	Predicted	Predicted end	Amino agid access
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ŀ	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
Ì	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Trophham W-Troptonham W-Troptonham W-Troptonham W-Troptonham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-Trophham W-T
ļ	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence		Codon, /=possible nucleotide deletion,
		<del></del>	\=possible nucleotide insertion)
1	1		DTVEGSKKVTIRSPVQIRNHFSVPLSVYEGDTLLGTASPENEFN
	1		IPLGSYRSFIFLKPEDENYQMCEGIDFEEIIKNDGALLKKKCRS
	1		KNPSKESFLINIVPEKDNLTSLSVYSEDGWDLPYIMHLWPPILL
	Ī		RNLLPYKIAYYIEGIENSVFTLSEGHSAQICTAQLGKARLHLKL
1	ł	1	LDYLNHDWKSEYHIKPNQQDISFVSFTCVTEMEKTDLDIAVHMT
			YNTGQTVVAFHSPYWMVNKTGRMLQYKADGIHRKHPPNYKKPVL
			FSFQPNHFFNNNKVQLMVTDSELSNQFSIDTVGSHGAVKCKGLK
			MDYQVGVTIDLSSFNITRIVTFTPFYMIKNKSKYHISVAEEGND
			KWLSLDLEQCIPFWPEYASSKLLIQVERSEDPPKRIYFNKQENC
ļ			ILLRLDNELGGIIAEVNLAEHSTVITFLDYHDGAATFLLINHTK
			NELVQYNQSSLSEIEDSLPPGKAVFYTWADPVGSRRLKWRCRKS HGEVTQKDDMMMPIDLGEKTIYLVSFFEGLQRIILFTEDPRVFK
ſ	(		VTYESEKAELAEQEIAVALQDVGISLVNNYTKQEVAYIGITSSD
1	ļ .		VVWETKPKKKARWKPMSVKHTEKLEREFKEYTESSPSEDKVIQL
1			DTNVPVRLTPTGHNMKILQPHVIALRRNYLPALKVEYNTSAHQS
	1		SFRIQIYRIQIQNQIHGAVFPFVFYPVKPPKSVTMDSAPKPFTD
	!!!		VSIVMRSAGHSQISRIKYFKVLIQEMDLRLDLGFIYALTDLMTE
İ	i i		AEVTENTEVELFHKDIEAFKEEYKTASLVDQSQVSLYEYFHISP
1	<u> </u>		IKLHLSVSLSSGREEAKDSKQNGGLIPVHSLNLLKSIGATLTD
i	[		VQDVVFKLAFFELNYQFHTTSDLQSEVIRHYSKQAIKQMYVLIL
1	1 1	i	GLDVLGNPFGLIREFSEGVEAFFYEPYQGAIQGPEEFVEGMALG
			LKALVGGAVGCLACAASKITGAMAKGVAAMTMDEDYQQKRREAM
	]		NKQPAGFREGITRGGKGLVSGFVSGTTGTVFKPTKGAOKCGAAC
	1		FFKGVGKGLVGAVARPTGGIIDMASSTFOGIKPATETCEUTCIT
1			PPRFFNEDGVIRPYRLRDGTGNOMLOKIOFYREWIMTHSSSSDD
6239	l		UDUDUDUESDLNH
0239	2108	634	KPGMAGKGSSGRRPLLLGLLVAVATVHLVICPYTKVEESFNLQA
	[		THULLYHWQDLEQYDHLEFPGVVPRTFLGPVVTAVFGGDAVVAT
Ī	1	İ	SLLEMSKFYSQLIVRGVLGLGVIFGLWTLCKEVPPHEGAMIATMA
1			FCWVTAMQFHLMFYCTRTLPNVLALPVVI.I.AI.AAWI.DUFWADET
1			WLSAFAIIVFRVELCLFLGLLLIJAIGNRKVSVVPALBUANDAG
1 1		1	ILCLGLTVAVDSYFWRQLTWPEGKVLWYNTVLNKSSNWGTSPLL
1 1			WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVLALGFMALYSLL
ļ		1	PHKELRFIIYAF?MLNITAARGCSYLLNNYKKSWLYKAGSLLVI
1 1	. 1		GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI
[ ]	ì		DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA
			PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL ERLPRPS
6240	2202		HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF
[ ]	1	· <del>-</del>	DPLSSGSRSSSLKSAQGTGFELGQLQSIRSEGTTSTSYKSLANQ
		1	TRNGSLSYDSLLTPSDSPDFESVQAGPEPDPPLGYTSPFLSARL
, i			AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLQEREKL
1 1	. [		LRQSPPLPGREEEPGLGDSGIQSTPGSGHAPRTSSSSDDSKRSP
[	ĺ	į.	LGKTPLGRPAVPRFGKPDGLRGRGVGSPEPGPTAPYLGRSMSYS
		1	SQKAQPGVSETEEVALQPLLTPKDEVQLKTTYSKSNGQPKSLGS
<u></u>		1.	ASPGPGQPPLSSPTRGGVKKVSGVGGTTYEISV
6241	3	1341	RNAEEKKRLSLQREKI LARVSI DNRTRALVQALRRTTDPKLCIT
	İ	] 1	RVEELTFHLLEFPEGKGVAVKERIIPYLLRLRQIKDETLQAAVR
[			EILALIGYVDPVKGRGIRILSIDGGGTRGVVALQTLRKLVELTO
			KPVHQLFDYICGVSTGAILAFMLGLFHMPLDECEELYRKLGSDV
		1	FSQNVIVGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP
	İ	-	TCPKVAAVSTIVNRGITPKAFVFRNYGHFPGINSHYLGGCQYKM
1	ļ	1	WQAIRASSAAPGYFAEYALGNDLHQDGGLLLNNPSALAMHECKC
	1	1	LWPDVPLECIVSLGTGRYESDVRNTVTYTSLKTKLSNVINSATD
1		1 :	TEEVHIMLDGLLPPDTYFRFNPVMCENIPLDESRNEKLDQLQLE
		lä	GLKYIERNEQKMKKVAKILSQEKTTLQKINDWIKLKTDMYEGLP
			THE SECTION AT VEKTOWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA KERLDWA

Predicted

beginning

location

to first

amino acid

residue of

amino acid

sequence

nucleotide

corresponding

Predicted end

corresponding

nucleotide

location

to first

amino acid

residue of

amino acid

sequence

SEQ

ID

NO:

Amino acid segment containing signal peptide

(A=Alanine, C=Cysteine, D=Aspartic Acid, E=

W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop

GRRPLLIGGFGLMGLFFGTLTITLTLQDHAPWVPYLSIVGILAI IASFCSGPGGIPFILTGEFFQQSQRPAAFIIAGTVNWLSNFAVG LLFPPIQKSLDTYCFLVFATICITGAIYLYFVLPETKNRTYAEI

VPPPRMMAAVPPGLE PWNRVRI PKAGNRSAVTVQNPGAALDLCT AAVI KECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRHK PHL ALKQVEQCLKRLKKNMNLEGS I QDLFELFSSNENQPLTTKVCVVP SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHLIGLQEFI I LNLVMVGLVSRLWVLYKGVLKRLILLYEPLFGLLQEVAR I QPMP YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLINKLF LINEQSPRASEETLLGISKKAKQMKINVQNNVDLGQPVKNKRVF

SQAFSKRNKAYPPEEKIDSAVTDGKINGRP

Glutamic Acid, F=Phenylalanine, G=Glycine,

H=Histidine, I=Isoleucine, K=Lysine,

P=Proline, Q=Glutamine, R=Arginine,

S=Serine, T=Threonine, V=Valine,

\=possible nucleotide insertion)

L=Leucine, M=Methionine, N=Asparagine,

Codon, /=possible nucleotide deletion,

1773

56

6248

ű.

SEQ	Predicted	Predicted end	Draine and de
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +_Chan
	amino acid sequence	sequence	Codon, /=possible nucleotide deletion
-	sequence		\=possible nucleotide insertion)
			KEESSEFDVRAFCNQLKHKATQETSFDFKCSQSRLKTTKYSSQK
		}	VIGTPHAKSFVQRFREAESFTOLSEEIOMAVVWCRSKKI KAOAT
}			FLGNKLLKSNRLKHLEAQGTSLPKKLECIKTSICNHLLRGSGIK
-			TSKHHLRQRRSQNKFLRRQRKPQRKLQSTLLREIQQFSQGTRKS
			ATDTSAKWRLSHCTVHRTDLYPNSKQLLNSGVSMPVIQTKEKMI
6249	56	1773	HENLRGIHENETDSWTVMQINKNSTSGTIKETDDIDDIFALMGV VPPPRMMAAVPPGLEPWNRVRIPKAGNRSAVTVQNPGAALDLCI
1			AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRHKPHL
			ALKOVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP
			SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHLGLQEFII
1			LNLVMVGLVSRLWVLYKGVLKRLILLYBPLFGLLQEVARIQPMP
			YFKDFTFPSDITEFLGOPYFEAFKKKMPIAFAAKGINKII NIVI E
			LINEQSPRASEETLLGISKKAKOMKINVONNVDIGODVKNVDVE
			KEESSEFDVRAFCNQLKHKATOETSFDFKCSOSRIKTTKVSSOV
			VIGTPHAKSFVQRFREAESFTOLSEEIOMAVVWCRSKKLKAOAT
			FLGNKLLKSNRLKHLEAQGTSLPKKLECIKTSICNHLLRGSGTV
			TSKHHLRQRRSQNKFLRRQRKPQRKLQSTLLREIQQFSQGTRKS
1			ATDTSAKWRLSHCTVHRTDLYPNSKQLLNSGVSMPVIQTKEKMI
6250	232	1306	HENLRGIHENETDSWTVMQINKNSTSGTIKETDDIDDIFALMGV
		2000	LAALHIMALPFRKDLEKYKDLDEDELLGNLSETELKQLETVLDD
			LDPENALLPAGFRQKNQTSKSTTGPFDREHLLSYLEKEALEHKD REDYVPYTGEKKGKIFIPKQKPVQTFTEEKVSLDPELBEALTSA
1 1			SDTELCDLAAILGMHNLITNTKFCNIMGSSNGVDQEHFSNVVKG
			EKILPVFDEPPNPTNVEESLKRTKENDAHLVEVNLNNIKNIPIP
	,		TLKDFAKALETNTHVKCFSLAATRSNDPVATAFAFMI KUNIVELV
1			SLNVESNFITGVGILALIDALRDNETLAELKIDNOROOLGTAUE
1 [			LEMAKMLEENTNILKFGYQFTQQGPRTRAANAITKNNDLVRKRR
6251	62	972	VEGDHQ
	02	912	TPGSGPMSAWAAASLSRAAARCLLARGPGVRAAPPRDPRPSHPE
1 1	,		PRGCGAAPGRTLHFTAAVPAGHNKWSKVRHIKGPKDVERSRIFS
1 1			KLCLNIRLAVKEGGPNPEHNSNLANILEVCRSKHMPKSTIETAL
1 1	I		KMEKSKDTYLLYEGRGPGGSSLLIEALSNSSHKCQADIRHILNK NGGVMAVGARHSFDKKGVIVVEVEDREKKAVNLERALEMAIEAG
1 1			AEDVKETEDEEERNVFKFICDASSLHQVRKKLDSLGLCSVSCAL
			EFIPNSKVQLAEPDLEQAAHLIQALSNHEDVIHVYDNIE
6252	27	1897	EEFCTWIAVRVGEMETAPKPGKDVPPKKDKLQTKRKKPRRYWEE
1 1			ETVPTTAGASPGPPRNKKNRELRPQRPKNAYILKKSRISKKPQV
	i		PKKPREWKNPESQRGLSGAQDPFPGPAPVPVEVVOKECDIDVCD
1	1		KLPHSKAKTRSRLEVAEAEEEETSIKAARSELLLAEEDGELEGE
1 1			DGEDTAKICQADIVEAVDIASAAKHFDLNLROFGPVRINVSPTG
1 1			RHLAFGGRRGHVAALDWVTKKLMCBINVMEAVRDIRFLHSEALL
1 1		į	AVAQNRWLHIYDNQGIELHCIRRCDRVTRLEFLPFHFLLATASE
1 1	i		TGFLTYLDVSVGKIVAALNARAGRLDVMSQNPYNAVIHLGHSNG
1 . 1	Ì		TVSLWSPAMKEPLAKILCHRGGVRAVAVDSTGTYMATSGLDHQL
]		<u> </u>	KIFDLRGTYQPLSTRTLPHGAGHLAFSQRGLLVAGMGDVVNIWA GQGKASPPSLEQPYLTHRLSGPVHGLQFCPFEDVLGVGHTGGIT
1 1		ĺ	SMLVPGAGEPNFDGLESNPYRSRKQRQEWEVKALLEKVPAELIC
ļ <b>l</b>	<u> </u>	į	LDPRALAEVDVISLEQGKKEQIERLGYDPQAKAPFQPKPKQKGR
1			SSTASLVKRKRKVMDEEHRDKVRQSLQQQHHKEAKAKPTGARPS
6252			ALDREVR
6253	27	1897	EEFCTWIAVRVGEMETAPKPGKDVPPKKDKLQTKRKKPRRYWEE
1 1		1	ETVPTTAGASPGPPRNKKNRELRPQRPKNAYILKKSRISKKPOV
]		i	PKKPREWKNPESQRGLSGAQDPFPGPAPVPVEVVOKFCRIDKSP
[ ]	1	1	KLPHSKAKTRSRLEVAEABEEETSIKAARSELLLAEEPGFLEGE
]	}		DGEDTAKICQADIVEAVDIASAAKHFDLNLROFGPYRLNYSRTG
<u> </u>		· L	RHLAFGGRRGHVAALDWVTKKLMCEINVMEAVRDIRFLHSEALL

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ŀ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
- [	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Ston
}	amino acid	sequence	Codon, /=possible nucleotide deletion.
<u> </u>	sequence		\=possible nucleotide insertion)
			AVAQNRWLHIYDNQGIELHCIRRCDRVTRLEFLPFHFLLATASE
			TGFLTYLDVSVGKIVAALNARAGRLDVMSONPYNAVIHLGHSNG
			TVSLWSPAMKEPLAKILCHRGGVRAVAVDSTGTYMATSGLDHQL
1	1		KIFDLRGTYQPLSTRTLPHGAGHLAFSQRGLLVAGMGDVVNIWA
1	ł		GQGKASPPSLEQPYLTHRLSGPVHGLQFCPFEDVLGVGHTGGIT
1			SMLVPGAGEPNFDGLESNPYRSRKQRQEWEVKALLEKVPAELIC
i			LDPRALAEVDVISLEQGKKEQIERLGYDPQAKAPFQPKPKQKGR
		•	SSTASLVKRKRKVMDEEHRDKVRQSLQQQHHKEAKAKPTGARPS ALDRFVR
6254	155	1139	
	-3-	, 223	HALGRRGGSQELSAAACGCFALRLRAPGSGRPALAPGAAAFAGL
			GGAPRFPPRGSAAGRTMLLKEYRICMPLTVDEYKIGQLYMISKH SHEQSDRGEGVEVVQNEPFEDPHHGNGQFTEKRVYLNSKLPSWA
1			RAVVPKIFYVTEKAWNYYPYTITEYTCSFLPKFSIHIETKYEDN
}			KGSNDTIFDNEAKDVEREVCFIDIACDEIPERYYKESEDPKHFK
Í			SEKTGRGQLREGWRDSHQPIMCSYKLVTVKFEVWGLQTRVEQFV
			HKVVRDILLIGHRQAFAWVDEWYDMTMDDVREYEKNMHEQTNIK
			VCNQHSSPVDDIESHAQTST
6255	1	1444	PTRPQQELLVSLATVIFVASQKALSVESKAVIKQQLESVSNGWT.
1			VYRIARQASRMGNHDMAKELYQSLLTQVASKHFYFWLNSLKEFS
			HAEQCLTGLQEENYSSALSCIAESLKFYHKGIASLTAASTPLNP
			LSFQCEFVKLRIDLLQAFSQLICTCNSLKTSPPPAIATTIAMTI
			GNDLQRCGRISNOMKQSMEEFRSLASRYGDLYQASFDADSATLR
			NVELQQQSCLLISHAIEALILDPESASFQEYGSTGTAHADSEYE
			RRMMSVYNHVLEEVESLNGKYTPVSYMHTACLCNAIIALLKVPL
			SFORYFFOKLOSTSIKLALSPSPRNPAEPIAVQNNQQLALKVEG
1 1			VVQHGSKPGLFRKIQSVCLNVSSTLQSKSGQDYKIPIDNMTNEM EQRVEPHNDYFSTQFLLNFAILGTHNITVESSVKDANGIVWKTG
1 1			PRTTIFVKSLEDPYSQQIRLQQQQAQQPLQQQQRNAYTRF
6256	1	1542	CRGAGAEPAANPRSPRSLVPSLESTSTSVPPAPGTMATDSWALA
ľ	ì		VDEQEAAAESLSNLHLKEEKIKPDTNGAVVKTNANAEKTDEEEK
1			EDRAAQSLLNKLIRSNLVDNTNQVEVLQRDPNSPLYSVKSFEEL
) )	j		RLKPQLLQGVYAMGFNRPSKIQENALPLMLAEPPONLIAOSOSG
	j		TGKTAAFVLAMLSQVEPANKYPQCLCLSPTYELALOTGKVIEOM
( )			GKFYPELKLAYAVRGNKLERGQKISEQIVIGTPGTVLDWCSKLK
1	ļ		FIDPKKIKVFVLDEADVMIATQGHQDQSIRIORMLPRNCOMLLF
1 1	]		SATFEDSVWKFAQKVVPDPNVIKLKREEETLDTIKOYYVLCSSR
[	}		DEKFQALCNLYGAITIAQAMIFCHTRKTASWLAAELSKEGHQVA
] ]	ľ		LLSGEMMVEQRAAVIERFREGKEKVLVTTNVCARGIDVEQVSVV
<b>j</b>			INFDLPVDKDGNPDNETYLHRIGRTGRFGKRGLAVNMVDSKHSM NILNRIQEHFNKKIERLDTDDLDEIEKIAN
6257	210	615	
[			AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI
j i			TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG
			KA KA
6258	210	615	AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE
	Ī		NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI
1			TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG
<u> </u>			KA
6259	2	1540	ILEKGFPSQCHPERKWKVDDVLESSQENEDDHFWELLFHNNKTV
1	ļ		SVENGDRGSKTFNLGTDPVSLRNYPYKICDSCEMNLKNISGLII
i i	.	1	SKKNCSRKKPDEFNVCEKLLLDIRHEKIPIGEKSYKYDOKRNAI
		1	NYHQDLSQPSFGQSFEYSKNGQGFHDEAAFFTNKRSOIGETVCK
ł	ĺ	1	YNECGRTFIESLKLNISQRPHLEMEPYGCSICGKSFCMNLRFGH
		İ	QRALTKDNPYEYNEYGEIFCDNSAFIIHQGAYTRKILREYKVSD
			KTWEKSALLKHQIVHMGGKSYDYNENGSNFSKKSHLTOLRRAHT
			GEKTFECGECGKTFWEKSNLTQHQRTHTGEKPYECTECGKAFCQ
		· · · · · · · · · · · · · · · · · · ·	

SEQ	Predicted	Predicted end	Amino acid coment
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
į	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	acquence	Codon, /=possible nucleotide deletion,
	Joquence	<del></del>	\=possible nucleotide insertion)
	İ		KPHLTNHQRTHTGEKPYECKQCGKTFCVKSNLTEHQRTHTGEKP
ľ		1	YECNACGKSFCHRSALTVHORTHTGEKPFICNECGKSECUVENI
l	1	i	I VHORTHIGERPYKCNECGKTFCEKSALTKHORTHIGERPYECK
6260	2081		ACGKTFSQRSVLTKHQRIHTRVKALSTS
0200	2081	1436	GTGPEIHACAHASARAPGSRAMALRELKVCLLGDTGVGKSSIVW
			REVEDSEDENTINETIGASEMTKTVOYONELHKELTWDTACOERE
		ŀ	KALAPMYYRGSAAAIIVYDITKEETFSTIKNWVKELDOUGDDMI
ĺ		ł	VVAIAGNKCDLIDVREVMERDAKDYADSIHAIFVETCAVNATNI
			NELFIEISRRIPSTDANLPSGGKGFKLRRQPSEPKRSCC
6261	3	1188	FWYRLGPGTRSRWPRRGSWAASLVPRGPSPAALVTSPCPPDPLR
]	1		SPACEPCRPDFAPRPALLLRSGPRSAPAVTGKPALKGOPGPWDG
İ	1		MAEVSIDQSKLPGVKEVCRDFAVLEDHTLAHSLQEQEIEHHLAS
		i	NVQRNRLVQHDLQVAKQLQEEDLKAQAQLQKRYKDLEQQDCEIA
1			QEIQEKLAIEAERRRIQEKKDEDIARLLQEKELQEEKKRKKHFP
1	!		EFPATRAYADSYYYEDGGMKPRVMKEAVSTPSRMAHRDQEWYDA
			EIARKLQEEELLATQVDMRAAQVAQDEEIARLLMAEEKKAYKKA
			KEKEKSSLDKRKODPEWKPKTAKAANSKSKESDEDLUGVARDDA
			RPPPPIMTDGEDADYTHFTNQQSSTRHFSKSESSHKGFHYKH
6262	2	1759	PECHSOGLCSVHRPGKVPQARMSGLVLGQRDEPAGHRLSQEEIL
			GSTRLVSQGLEALRSEHQAVLQSISQTIECLQQGGHEEGLVHEK
1 1			ARQLRRSMENIELGLSEAQVMLALASHLSTVESEKQKLRAQVRR
1 1			LCQENQWLRDELAGTQQRLQRSEQAVAQLEEEKKHLEFLGQLRQ
1 1			YDEDGHTSEEKEGDATKDSLDDLFPNEEEEDPSNGLSRGQGATA
1 1			AQQGGYEIPARLRTLHNLVIQYAAQGRYEVAVPLCKQALEDLER
	i		TSGRGHPDVATMLNILALVYRDQNKYKEAAHLLNDALSIRESTL
1			GPDHPAVAATLNNLAVLYGKRGKYKEAEDI.COPAT.ETDEVIII Cm
	<b>!</b>		NHPDVAKQLNNLALLCQNQGKYEAVERYYQRALAIYEGQLGPDN
1 1	i		PNVARTKNNLASCYLKOGKYAEAETIJYKETIJTRAHMOEEGGUDD
1 1		ļ	DHKPIWMHAEEREEMSKSRHHEGGTPYAEYGGWYKACKUSEDTU
1 1	ſ		NTTLKNLGALYRRQGKLEAAETLEECALRSRROGTDDTSOTVIN
	ŀ	ſ	ELLGESDGRRTSQEGPGDSVKFEGGEDASVAVEWSGDGSGTLOP
6263		<u></u> }	SGSLGKIRDVLRR
0203	1	2408	RELDSLADLPERIKPPYANGLSTSHLRSSSVEDVKLIISEGRPT
l i	i		1EVRKCSMPSVICEHTKQFQTISEESNOGSLITVPGDTCBCBVB
1 . 1	ļ	- 1	EVESNVPERDLSNVSNIHSSFATSPTGASNSKVVSADDNI TVXT
] [		i	APVNTVMDSPVHLEPSSOVGVIONKSWEMPVDPLETI CTPDETC
1		1	PNSN1PDQESSLQSFCNSENKVLKENADFI,SI,DOTFI,DCNCCAO
	İ	1	DPASFMPPQQPCSFPSQSLSDAESISKHMSLSVVANOEDGILOO
1 1	İ		KNAVQI ISSALDTDNESTKDTENTFVI.GDVOKTDAFVDVVCDem
1	j	ŀ	1QEASPNFEKAYTLPVLPSEKDFNGSDASTOLNTHYA PSKLTVV
t l	1		SSSGREVENSTTDTOVISHEKENKI, ESTAM, THI SPORDED OF ANY
	i	i	AGMPKGNLNEQDPKHCPESEKCLLSIEDEESOOSTISSIENWOO
1	j		QSTQPEMHKYGQLVKVELEENAEDDKTENOT PORMTPMY NATURA
1			NOSKQILASCTLLSEKDSESSSPRGRIRLTEDDDPOTHHDDVDV
1		ſ	VSRVPQPVQVSPSLLQAKEKTQQSLAAIVDSLKLDEIQPYSSER
1 1		1	ANPYFEYLHIRKKIEEKRKLLCSVIPQAPQYYDEYVTFNGSYLL
		ŀ	DGNPLSKICIPTITPPPSLSDPLKELFRQQEVVRMKLRLQHSIE
		[	REKLIVSNEQEVLRVHYRAARTLANQTLPFSACTVLLDAEVYNV
1		!	PLDSQSDDSKTSVRDRFNARQFMSWLQDVDDKFDKLKTCLLMRQ
		1	QHEAAALNAVQRLEWQLKLQELDPATYKSISIYEIQEFYVPLVD
		į ·	VNDDFELTPI
6264	143		KHRQENNALDMAPEIHMTG PMCLIENTNGELVANPEALKILSAT
1	į		TQPVVVVAIVGLYRTGKSYLMNKLAGKNKGFSLGSTVKSHTKGI
	1	ĺ,	WMWCVPHPKKPEHTLVLLDTEGLGDVKKGDNQNDSWIFTLAVLL
1			SSTLVYNSMCTINOOMDOL VYIMEL TO TO TO THE TILAVIL
		1 :	SSTLVYNSMGTINQQAMDQLYYVTELTHRIRSKSSPDENENEDS
			ADFVSFFPDFVWTLRDFSLDLEADGQPLTPDEYLEYSLKLTQGT

SEQ	Predicted	I musakatan	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	b=beucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence	_	\=possible nucleotide insertion)
			SQKDKNFNLPRLCIRKFFPKKKCFVFDLPIHRRKLAQLEKLQDE
			ELDPEFVQQVADFCSYIFSNSKTKTLSGGIKVNGPRLESLVLTY
			INAISRGDLPCMENAVLALAQIENSAAVQKAIAHYDQQMGQKVQ
			LPAETLQELLDLHRVSEREATEVYMKNSFKDVDHLFQKKLAAQL
İ			DKKRDDFCKQNQEASSDRCSALLQVIFSPLEEEVKAGIYSKPGG
			YCLFIQKLQDLEKKYYEEPRKGIQAEEILQTYLKSKESVTDAIL
	]		QTDQILTEKEKEIEVECVKAESAQASAKMVEEMQIKYQQMMEEK EKSYQEHVKQLTEKMERERAQLLEEQEKTLTSKLQEQARVLKER
[			CQGESTQLQNEIQKLQKTLKKKTKRYMSHKLKI
6265	143	1960	KHRQENNALDMAPEIHMTGPMCLIENTNGELVANPEALKILSAI
		2500	TQPVVVVAIVGLYRTGKSYLMNKLAGKNKGFSLGSTVKSHTKGI
			WMWCVPHPKKPEHTLVLLDTEGLGDVKKGDNQNDSWIFTLAVLL
			SSTLVYNSMGTINQQAMDQLYYVTELTHRIRSKSSPDENENEDS
			ADFVSFFPDFVWTLRDFSLDLEADGQPLTPDEYLEYSLKLTQGT
			SQKDKNFNLPRLCIRKFFPKKKCFVFDLPIHRRKLAQLEKLQDE
			ELDPEFVQQVADFCSYIFSNSKTKTLSGGIKVNGPRLESLVLTY
			INAISRGDLPCMENAVLALAQIENSAAVQKAIAHYDOOMGOKVO
			LPAETLQELLDLHRVSEREATEVYMKNSFKDVDHLFQKKLAAQL
			DKKRDDFCKQNQEASSDRCSALLQVIFSPLEEEVKAGIYSKPGG
			YCLFIQKLQDLEKKYYEEPRKGIQAEEILQTYLKSKESVTDAIL
Į.			QTDQILTEKEKEIEVECVKAESAQASAKMVEEMQIKYQQMMEEK
			EKSYQEHVKQLTEKMERERAQLLEEQEKTLTSKLQEQARVLKER CQGESTQLQNEIQKLQKTLKKKTKRYMSHKLKI
6266	276	1421	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE
		4.4.4	GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD
1			ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF
Ī			PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR
			GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN
1			SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLOSROLVF
i			LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH
			RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD
6267			PVYKVATWEKQIYTCCRDGLVRRYQLSDL
6267	3	622	LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK
1			NRYVVLKGDQLYISEKEVKDEKNIQEVFDLSDYEKCEELRKSKS
			RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA
] 1	ļ J	•	ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC
6268	160	1368	HRELCQNLPAGLSSALIDNPLTLLLSIDTYVMLQEPVTFQDVAV
			DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA
			PNSDIPEEEPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV
			LKQMESAQEKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPE
			SQANSGALDTNQVLLHKIPPRKRLRKRDSQVKSMKHNSRVKIHQ
! !			KSCERQKAKEGNGCRKTFSRSTKQITFIRIHKGSQVCRCSECGK
			IFRNPRYFSVHKKIHTGERPYVCQDCGKGFVQSSSLTQHORVHS
			GERPFECQECGRTFNDRSAISQHLRTHTGAKPYKCQDCGKAFRO
[			SSHLIRHQRTHTGERPYACNKCGKAFTQSSHLIGHQRTHNRTKR
			KKKQPTS
6269	2886	1449	HASAPTRRNMAAASPLRDCHAWKDARLPLSTTSNEACKLFDATL
			TQYVKWTNDKSLGGIEGCLSKLKAADPTFVMGHAMATGLVLIGT
			GSSVKLDKELDLAVKTMVEISRTQPLTRREQLHVSAVETFANGN
i	1		FPKACELWEQILQDHPTDMLALKFSHDAYFYLGYQEQMRDSVAR
( 1	ľ		IYPFWTPDIPLSSYVKGIYSFGLMETNFYDQAEKLAKEALSINP
	i		TDAWSVHTVAHIHEMKAEIKDGLEFMQHSETLWKDSDMLACHNY
[	j		WHWALYLIEKGEYEAALTIYDTHILPSLQANDAMLDVVDSCSML
i l	j		YRLQMEGVSVGQRWQDVLPVARKHSRDHILLFNDAHFLMASLGA HDPQTTQELLTTLRDASESPGENCQHLLARDVGLPLCOALVEAE

SEQ	Predicted	Predicted end	Amino agid communi
ID	beginning	nucleotide	
NO:	nucleotide	location	
ł	location	corresponding	I CAGCUMIC ACIO, PEPARNOISIANIE A ES .
	corresponding	to first	** = ** # * * * * * * * * * * * * * * *
•	to first	amino acid	D-Deucine, Mamerhionine M. A
	amino acid	residue of	I + + Q= 111C, V=G111CAMINA D_ \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself \underself
	residue of		S=Serine, T=Threonine V_Valia-
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine y=Inknox
	sequence	sequence	
	sequence		/ \-bossible nucleofide incorpical
	'		DGNPDRVLELLLPIRYRIVQLGGSNAQRDVFNQLLIHAALNC
		ľ	SVHKNVARSLIMERDALKENG
6270	23	2086	SVHKNVARSLLMERDALKPNSPLTERLIRKAATVHLMQ
	[	1	SVTVTLGSEGDGRPPTYHLEEMEQEPQNGEPAEIKIIREAYK
	1	1	THOUSEN LDEDGUKERAKNYYKOGTOTILI DOTOTOTOTOTO
	i		TALL TO FERDING ENLIPE POSESSADOUR EURICATOR CONTRACTOR
	i		T
	1		EFYRNHSQPPPLETLGLDADELILIPNGVQIFFVNPAGEVSA
	ł .		YPGYLRIVRFLDNSLDTVLNRPPGFLQVCDWLYPLVPDRSPV
			CTAGAYMEDTMI OAACCHICINH COT
			CTAGAYMFPDTMLQAAGCFVGVVLSSELPEDDRELFEDLLRQI
ł			DLRLQANWNRAEEENEFQIPGRTRPSSDQLKEASGTDVKQLDQ
			T TO THE TENED TO SEEVING OUT TO DEPUT TO THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF THE TENED OF TH
ſ	i i		I DOMESTICATION AS MOST A KENTAGEN TO A SAME DOMESTICATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF
			THE VOUSTAVINGUI AKOANGGANGGANGGAT TROTTAMES
ľ			THE TAKE TO SEE THE STREET HERE THE TAKE TO SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SE
}			I TO SO THE CONTROL OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PRO
- 1			*** O * INITIALIZATION CHARLES TO THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE TANK THE T
6271			EGAANVNVRGEKDEQTKEVKEAKKKDK
02/1	32	1058	GCGVKTAGMVGREKELSIHFVPGSCRLVEEEVNIPNRRVLVTG
ì	1		TGLLGRAVHKEFOONMULAUGGGERRANDEN
1	i		TGLLGRAVHKEFQQNNWHAVGCGFRRARPKFEQVNLLDSNAVH
ı	ł		IIHDFQPHVIVHCAAERRPDVVENQPDAASQLNVDASGNLAKE
l			1 OTT DA A A LOODI VE DGINDDDY REEDT DADT ME VOYENCE
- 1	j		1 MODING COMPANY DRIEF LYGEVER LEPS NUTUMEDIATOR CONTROL
	i		1 . WALLETUANDALAL KOMPENDEL KOMPENDE COMPENDE COMPENDE COMPENDE COMPENDE COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA COMPENDA C
I			TAKE A COLORENDESSHIPD TO TO CANDADAN COLOREN
6272	1136		1 == A CONTENT TO TYPS UMD BUILD UM LELL
	1136	528	GAVMEDAAAPGRTEGVLEROGAPPAAGOGGATATO
- 1	- 1		VSPYHTHRAGDPLDLVALAEQVQKADEFIRANATNKLTVIAEQ
			QHLQEQARKVLEDAHRDANLHHVACNIVKKPGNIYYLYKRESGO
1	ł		OYFSIISPKEWGTSCDHDEI CANNE CHITAKAPGNIYYLYKRESGO
			QYFSIISPKEWGTSCPHDFLGAYKLQHDLSWTPYEDIEKQDAK SMMDTLLSQSVALPPCTEPNFQGLTH
6273	256	843	I STATE TEROODS AND PECTED WELKENING
	1	015	SCPRVSPECRSLGCQVMFSLPLNCSPDHIRRGSCWGRPQDLKIF
1	i		TARREST TO THE CARCAMINATION OF THE PROPERTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY
- 1	1		I TO THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF THE POST OF T
i	i	i	VICTOR VANERDIKEDIKEDIKETIR. CUDEDATURDI
6274			
32/3	56	1142	AAAAMAAAAGGGAGAARSLSRFRGCLAGALLGDCVGSFYEAHDT
	1		VDLTSVLRHVQSLEPDPGTPGSERTEALYYTDDTAMARALVQSL
i	ľ		LAKEAFDFIJMAUBEAGEUUUDDDD TAMARALVQSL
ľ		1	LAKEAFDEVDMAHRFAQEYKKDPDRGYGAGVVTVFKKLLNPKCR
	1	1	TEAR OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PR
- 1	i	1	
- 1	J	1	DECEMBER VILLARE DEVICE REVISER FOR THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPER
	i i		PROPERTY OF A LIVING THE BUILDING AND AND AND AND AND AND AND AND AND AND
- 1		1	SLGGDTDTIATMAGAIAGAYYGMDQVPESWQQSCEGYEETDILA
275			QSLHRVFQKS
-,-	20	565	SRRGRARCLARGSRRPVPRPAKTMAFMVKTMVGGQLKNLTGSLG
i	j	1	GGEDKGDGDKSAAFAOCMGDERWARMVKTMVGGQLKNLTGSLG
	Į.	1	GGEDKGDGDKSAAEAQGMSREEYEEYQKQLVEEKMERDAQFTQR
-	1		TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERT
1	i	i	DEDITED BELLAS VIGQUAS LPGLNLGSI KDKAOATI GDI VOGA
276	797		
-	.51	97	TLLPLPPLPDTEGMILLNTGLEGTVAENPVPIVHTPSGNILTLE
	1	i '	CLESCHAILLEGHWGTHFOLVEDDVI'VE L'YDL COL CA A
	f		VWVGAKISHGSFSVPCHTACDEL TOTAL THE THE TOTAL SSLGLLHWP
}	ļ	1 ,	VWVGAKISHGSFSVPGHVAGRELLTAVAEVFPHVTVAPGWPEEV
1	ļ	1 .	DOOG I REQUISIDATE FOR MODALE LOCKORS OF THE
J		1 '	LASSPRATVTVEHNPAGGDYASVRTALLAARAVDRTRVYYRLPQ

SEQ	Predicted	Drode and	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
I	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
6277	4600	2744	MAFRIEMGLYYSYFKTIVEAPSFLNGVWMIMNDKLTEYPLVINT
ĺ			LKRFNLYPEVILASWYRIYTKIMDLIGIOTKICWTVTIGEGLSP
			TESCEGLGDPACFYVAVIFILNGLMMALFFIYGTYLSGSRLGGL
	Ĭ		VTVLCFFFNHGECTRVMWTPPLRESFSYPFLVLQMLLVTHILRA
		}	TKLYRGSLIALCISNVFFMLPWQFAQFVLLTQIASLFAVYVVGY
			IDICKLRKIIYIHMISLALCFVLMFGNSMLLTSYYASSLVIIWG
			ILAMKPHFLKINVSELSLWVIQGCFWLFGTVILKYLTSKIFGIA
			NDAHIGNLITSKFFSYKDFDTLLYTCAAEFDFMEKETFLRYTKT
	}		LLLPVVLVGFVAIVRKIISDMWGVLAKQQTHVRKHQFDHGELVY
}	j		HALQLLAYTALGILIMRLKLFLTPHMCVMASLICSRQLFGWLFC KVHPGAIVFAILAAMSIQGSANLQTQWNIVGEFSNLPQEELIEW
			IKYSTKPDAVFAGAMPTMASVKLSALRPIVNHPHYEDAGLRART
			KIVYSMYSRKAAEEVKRELIKLKVNYYILEESWCVRRSKPGCSM
[			PEIWDVEDPANAGKTPLCNLLVKDSKPHFTTVFQNSVYKVLEVV
L			KE KE
6278	3	823	ILFRLVLLSLVYLLNSVATEERKPAEVLIVEGQQYAVVGTVLLL
			IRIILEYCQGVDNIPSVTTDMLTRLSDLLKYFNSRSCOLVLGAG
			ALQVVGLKTITTKNLALSSRCLQLIVHYIPVIRAHFEARLPPKO
			YSMLRHFDHITKDYHDHIAEISAKLVAIMDSLFDKLLSKYEVKA
İ			PVPSACFRNICKQMTKMHEAIFDLLPEEQTQMLFLRINASYKLH
1			LKKQLSHLNVINDGGPQNGLVTADVAFYTGNLQALKGLKDLDLN
6279	127	1687	MAEIWEQXR
i		1007	GGAMASDGARKQFWKRSNSKLPGSIQHVYGAQHPPFDPLLHGTL
1			LRSTAKMPTTPVKAKRVSTFQEFESNTSDAWDAGEDDDELLAMA AESLNSEVVMETANRVLRNHSQRQGRPTLQEGPGLQQKPRPEAE
			PPSPPSGDLRLVKSVSESHTSCPAESASDAAPLQRSQSLPHSAT
			VTLGGTSDPSTLSSSALSEREASRLDKFKQLLAGPNTDLEELRR
}			LSWSGIPKPVRPMTWKLLSGYLPANVDRRPATLQRKQKEYFAFI
			EHYYDSRNDEVHQDTYRQIHIDIPRMSPEALILQPKVTEIFER:
	1		LFIWAIRHPASGYVQGINDLVTPFFVVFICEYIEAEEVDTVDVs
1			GVPAEVLCNIEADTYWCMSKLLDGIODNYTFAOPGIOMKVKMLF
			ELVSRIDEQVHRHLDQHEVRYLQFAFRWMNNLLMREVPLRCTIR
	1		LWDTYQSEPDGFSHFHLYVCAAFLVRWRKEILEEKDFOELLLFI.
6280	857	253.5	QNLPTAHWDDEDISLLLAEAYRLKFAFADAPNHYKK
5255	03,	2515	ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEEEEEDE
ļ i	}		DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSEEENDRA
1			WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA
ł ł			QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA
	Ţ		RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD
1 }			LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ
			IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK
	ľ		PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR
İ	ì		EGMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH
}	_		GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYDLLSGHTVKK
	· [		LTNHKACVRDVSWHPFEEKIVSSSWDGNLRLWOYROAEYFODDM
- 636			PESEECASAPAPVPQSSTPFSSPQ
6281	857	2515	ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEREEDE
		ļ	DVDLAQVLAYLLRRGQVRLVQGGGAANLOFIOALLDSEEENDRA
	ł	l	WDGRLGDRYNPPVDATPDTRELEFNEIKTOVELATGOLGLRRAA
	į		QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS
- 1	j	J	YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA
ĺ	i		RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD
Į.	ļ		LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ
1			IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK
			PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR

SEQ	Predicted	Predicted end	I mine
dI.	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
Ì	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Troptophan V=man=:
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
			EGMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH
			GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK
- 1			LTNHKACVRDVSWHPFEEKIVSSSWDGNLRLWQYRQAEYFQDDM
			PESEECASAPAPVPQSSTPFSSPQ
6282	125	906	RMAACRALKAVLVDLSGTLHTEDAAVPGAOFALKELDGAGUTTE
İ	1		FVINITRESKQDLLERLRKLEFDISEDETETSI.TAARGII ERKO
			VRPMLLVDDRALPDFKGIOTSDPNAVVMGLADEUEUVOTI NOAE
			RULLUGAPLIAIHKARYYKRKDGLALGPGPFVTALFVATDTVAT
		1	VVGKPEKTFFLEALRGTGCEPEEAVMTGDDCPDDVGGAODVGWT
6283	340		GILVKIGKYRASDEEKINPPPYLTCESFPHAVDHILOUIT
0203	140	1043	LSLFGIHVMNPFWSMSTSSVRKRSEGEEKTLTGDVVTGDDDTXD
1 1			KKQLPSIPKNALPITKPTSPAPAAOSTNGTHASVCDPVIEVCI -
· I			ABETTLYVKQKLPGVYVOPSYRSALMWFGVTFTPUGTVODGVEVE
1			I VII PUNI PUGDCPREVFDIPVFHPLVDPTSGELDVKPA PAVUD !
1 1			RNHNHIWQVLMYARRVFYKIDTASPI,NPEAAVI,VEKDIOI EVEN
			VVDSVKVCTARLFDQPKIEDPYAISFSPWNPSVHDEAREKMLTQ
6284	1	2879	KKKPEEQHNKSVHVAGLSWVKPGSVQPFSKEEKTVAT
1 1	**	20,5	RSVIPGSTISSRWPGLSRPRFMAAHEWDWFQREELIGQISDIRV
1 . 1			QNLQVERENVQKRTFTRWINLHLEKCNPPLEVKDLFVDIQDGKI
1 1			LMALLEVLSGRNLHEYKSSSHRIFRLNNIAKALKFLEDSNVKL
1 1			VSIDAAEIADGNPSLVLGLIWNIILFFQIKELTGNLSRNSPSSS LAPGSGGTDSDSSFPPTPTAERSVAISVKDQRKAIKALLAWVQR
i l			KTRKYGVAVQDFAGSWRSGLAFLAVIKAIDPSLVDMKQALENST
1			RENLEKAFSIAQDALHIPRLLEPEDIMVDTPDEQSIMTYVAQFL
l i			ERFPELEAEDIFDSDKEVPIESTFVRIKETPSEQESKVFVLTEN
1 1			GERTYTVNHETSHPPPSKVFVCDKPESMKEEPI.DCVCCUALCDC
[	ļ		STEPMHQLLDQVLOGGPGKTSDTSEPSPESSTLSEPVENCESNO
	İ		LEIKKIVHFEADTYKDPFCSKNLSLCFFGSDDVAKEST DODGING
1 1			LAVEVALEKEQKQESSKIPESSSDKVAGDIFLVEGTANINGGGGG
1	į		CNGALESTARHDEESHSLSPPGENTVMADSFOTVIMI MINURAL D
1 1			EGDIFEALPLKASKENSDLIDFASTSOAFNKUDGDURTUDDED
1 1			EAFENHAEKLGKRSIKSAHKKKDSPEPOVKMDKUEDHODGGERA
1			LEGCESAPEETPVDKKPEVHEKAKRKSTPDHVERECEDDDI OGUG
1			LEDSSSPPSSCVSLETLGSHSEEGI.DFKDcppt.cvvcvrpvptp [
1	ŀ		YFPHYEVPLAAVLEAYVEDPEDLKNEEMDLEEPEGYMPDLDSRE
		i	EEADGSQSSSSSVPGESLPSASDQVLYLSRGGVGTTPASEPAP
	1		LAPHEDHOQRETKENDPMDSHQSQESPNLENIANPLEENVTKES
			ISSKKKEKRKHVDHVESSLFVAPGSVQSSDDLEEDSSDYSIPSR TSHSDSSIYLRRHTHRSSESDHFSLCSVEERSRSG
6285	2157	1331	SCKTENLLEMWWFQQGLSFLPSALVIWTSAAFIFSYITAVTLHH
			IDPALPYISDTGTVAPEKCLFGAMLNIAAVLCIATIYVRYKQVH
1	!		ALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVS
1 1			GAVLTFGMGSLYMFVQTILSYQMQPKIHGKQVFWIRLLLVIWCG
		Ì	VSALSMLTCSSVLHSGNFGTDLEQKLHWNPEDKGYVLHMITTAA
			EWSMSFSFFGFFLTYIRDFQKISLRVEANLHGLTLYDTAPCPIN
F 6386	L		MERIRGESRUI
6286	1619	276	KAGASCCGSANPYVSVGKSCVLLAMAQLQTRFYTDNKKYAVDDV
]		Ī	PFSIPAASEIADLSNIINKLLKDKNEFHKHVEFDELIVGOELDW
1			PEDAGMENISSEEVVEIEYVEKYTAPOPROCMEHDDWISSIK
[ ]	1		GALLATI I GS I DKTSKI WSLEGKSIMTI V CHTDIAIKDUA MUUVU
[	1	1	SUSCILLISASMOQTILLWEWNVERNKVKALHCCRCHAGGUDGIA
			VDGSGIRFCSGSWDKMLKIWSTVPTDEEDEMEESTNDDDVVOVT
l l		í	EQUICETRIPIVILSGHMEAVSSVLWSDAEEICSASWDUTTPUMD
		i i	VESGSLKSTLTGNKVFNCISYSPLCKRLASGSTDRHTDLWDDDT
			RDGSLVSLSLTSHTGWVTSVKWSPTHEOOLISGSLDNIVELWDT
············			RSCKAPLYDLAAHEDKVLSVDWTDTGLLLSGGADNKLYSYRYSP

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ŀ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
			TTSHVGA
6287	278	1482	MOFFFNFQIGLRSTSGKEKYSGDAGFLGDALQLFLQCLALDEDF
		l	APAKLQVQKILCDLLLPENLKEGLKESSWSSLPCTKNRPFDFHS
	j		VMEESQSLNEPSPKQSEEIPEVTSEPVKGSLNRAQSAQSINSTE
i			MPAREDCLKRVSSEPVLSVQEKGVLLKRKLSLLBQDVIVNEDGR
1			NKLKKQGETPNEVCMFSLAYGDIPEELIDVSDFECSLCMRLFFE
			PVTTPCGHSFCKNCLERCLDHAPYCPLCKESLKEYLADRRYCVT
			QLLEELIVKYLPDELSERKKIYDEETAELSHLTKNVPIFVCTMA
İ			YPTVPCPLHVFEPRYRLMIRRSIQTGTKQFGMCVSDTQNSFADY
1	1		GCMLQIRNVHFLPDGRSVVDTVGGKRFRVLKRGMKDGYCTADIE
			( APEDA
6288	1	743	VTLYPCRGLVGNLLLGASGMASGCKIGPSILNSDLANLGAECLR
1			MLDSGADYLHLDVMDGHFVPNITFGHPVVESIRKOLGODDERDM
1	1		HMMVSKPEQWVKPMAVAGANOYTFHLEATENPGALTKDIDENGM
i	į l		KVGLAIKPGTSVEYLAPWANOIDMALVMTVEPGFGGOKEMEDMM
			PKVHWLRTQFPSLDIEVDGGVGPDTVHKCAEAGANMTVGGGATM
6289			RSEDPRSVINLLRNVCSEAAOKRSLDR
0203	1	743	VTLYPCRGLVGNLLLGASGMASGCKIGPSILNSDLANLGAECLR
1 .	1		MLDSGADYLHLDVMDGHFVPNITFGHPVVESI.RKOLGODBEEDM
<b>j</b>			HMMVSKPEQWVKPMAVAGANOYTFHLEATENDGALTKDIDENGM
			KVGLAIKPGTSVEYLAPWANOIDMALVMTVEPGFGGOVEMEDMM
			PKVHWLRTQFPSLDIEVDGGVGPDTVHKCAEAGANMIVSGSAIM
6290	3	1856	RSEDPRSVINLLRNVCSEAAQKRSLDR
		1030	TLGRWLLGVYETVAPTLACLPRPRLRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
1 1			VPQSLELKGITKHALNHHPPPEKLEEISPTSDSHEKDTSSQSKS
, ,			DITRESSFTSADTGNSLSAFPSYTGAGISTEGSSDFSWGYGELD
ļ .			QNATEKVQTMFTAIDELLYEQKLSVHTKSLQEECQQWTASFPHL RILGRQIITPSEGYRLYPRSPSAVSASYETTLSQERDSTIFGIR
·			GKKLHFSSSYAHKASSIAKSSSFCSMERDEEDSIIVSEGIIEEY
i l	1		LAPDHIDIEEGFHGKKSEAATEKQKLGYPPIAPFYCMKEDVLAY
	Į.		VFDSVWCKVVSCMEQLTRSHWEGFASDDESNVAVTRPDSESSCV
}	í		LSELHPLVLPRVPQSKVLYITSNPMSLCQASRHQPNVNDLLVHG
	i		MPLQPRNLSLMDKLLDLDDKLLMRPGSSTILSTRNWPNRAVEFS
	ļ		TSSLSYTVQSTRRRNPPPRTLHPISTSHSCAETPRSVEEILRGA
i			RVPVAPDSLSSPSPTPLSRNNLLPPIGTAEVEHVSTVGDODOMY
			PHGDSSRAQSAVVDEPNYOOPOERIJI, POFFDD DWTTOERI I DW
J	į		QYRRSCAVEYPHQARPGRGSAGPQLHGSTKSOSGGRPVSRTROG
6291	1772		P
0291	1732	602	LVAKMASSASARTPAGKRVINQEELRRLMKEKQRLSTSRKRIES
- 1			PFAKYNRLGQLSCALCNTPVKSELLWOTHVLGKOHPEKVAELVC
ŀ	j		AKEASQGSSASSAPQSVKRKAPDADDODVKRAKATI.VPOVODST
j		ļ	SAWITNFDKIGKEFIRATPSKPSGLSLLPDYEDEEEEEEEEGD
Ì	i	Ì	GERKRGDASKPLSDAQGKEHSVSSSREVTSSVLPNDFFSTNPPK
l		ļ	APIIPHSGSIEKAEIHEKVVERRENTAEALPEGFFDDPEVDARV
1			RKVDAPKDQMDKEWDEFQKAMRQVNTISEAIVAEEDEEGRLDRQ
ſ	1		IGEIDEQIECYRRVEKLRNRQDEIKNKLKEILTIKELQKKEEEN
6292	1835	1142	ADSDDEGELQDLLSQDWRVKGALL
j	· <del>-</del>	4476	TCPGAMKMVAPWTRFYSNSCCLCCHVRTGTILLGVWYLIINAVV
ĺ		ļ	LICAMATYCAYYORANAYARAGOREFMDDANMCIAIAISLLMI
		ĺ	LICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAITVLIYPN
1		1	SIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISIILTFKGY
1		]	LISCVWNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA AKEPPPPYVSA
6293	2382	1035	FWCTLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL
0233			- · · · · · · · · · · · · · · · · · · ·
6293		ł	VGSRTLPVDFHIKMVPCMVVDEBOCMBI BIRDVOOVA
6293			VGSRTLPVDFHIKMVESMKYPFRQGMRLEVVDKSQVSRTRMAVV DTVIGGRLRLLYEDGDSDDDFWCHMWSPLIHPVGWSRRVGHGIK

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	I MATALANTINE, CECVSTAINA DENOMARKIE NELA E
1	location	corresponding	Grucamic Acid, F=Phenylalaning C_climin.
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
J	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine Y=Unknown + G
J	amino acid	sequence	Codon, /=possible nucleotide deletine
ļ <u>-</u>	sequence		\=possible nucleotide insertion\
1			MSERRSDMAHHPTFRKIYCDAVPYLEKKVBAVVTECCHERROWK
			DEMINE TO PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO THE PURE TO
Ţ.			TASSIBLE PATECOKNOTEL TOOKGVE A OTENHONIVE DEFINE COLOR
- 1		!	AFSKUFNMDCPNHGFKVGMKLEAVDLMEDDI.TCVAMICEDIATION
}			1 DSTAFDGWDSEYDQWVDCESPDTVPUGWCFT.TCVQTQDDV23 2 DD
1	1	İ	AT PLANEAT KKKKKOFGKKRKRT PPTKTPPT POCCEPURT A PPN
			PQGARKISSEPVPGEIIAVRVKEEHLDVASPDKASSPELPVSVE NIKQETDD
6294	354	1814	
i			AQLTTRGRTVAGGVRWIPSPFPDLELYSCCLGTDRGFPELSHHC
Į.			KNVIATASDYDMAEITNIRPSFDVSPVVAGLIGASVLVVCVSVT VFVWSCCHQQAEKKHKNPPYKFIHMLKGISIYPETLSNKKKIIK
1			VRRDKDGPGREGGRRNLLVDAAEAGLLSRDKDPRGPSSGSCIDO
	į,		LPIKMDYGEELRSPITSLTPGESKTTSPSSPEEDVMLGSLTFSV
			DIMPPREADVOTIOEAHGLDVMDDOTOGGDDVTVMTTI DDVDVD
1			T VALAVIAALIDEVEDETETEYGIPYSOLODIJI HELVI CEDDDO
J	]		T ADDVIGE VMVPLAGVDPSTGKVOLTPDTIVPNTOVOT CDODE
			1 SESTOP VACKMITOVOLKARHIOKMDITACI, COMPONICARIORICA
1	1		RIAKKTHVKKCTLNPIFNESFTVDTDTDLLDDYCTERIUSDD
1	i		RTTKNEVVGRLILGAHSVTASGAEHWREVCESPRKPVAKWHSLS
6295	2795	617	/ E1
1		01,	VSSALLTGATSGSDAAKSEGASASPLSCTNAVAMDRPDEGPPAK
}			TRRLSSSESPORDPPPPPPPPPPLIRLPLPPPPQQRPRLQEETEAA
			QVLADMRGVGLGPALPPPPPYVILEEGGIRAYFTLGAECPGWDS TIESGYGEAPPPTESLEALPTPEASGGSLEIDFQVVQSSSFGGE
1			GALETCSAVGWAPQRLVDPKSKEEAIIIVEDEDEDERESMRSSR
			RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
			AGAAF DRUKKKFIOMRRPFI.ERRDI.TIOUTDCEWRAY DE NOON
1	,		LEST THRRUEDIFRYLTNIOVODIRHISMGVVMVI VEOTINDIRE
			MIN' T V NOT QRINKSGRLVSHSTPIRWHRGOFFON PRUCNOPAGUE
1 1			PESWESNASLPEADRIAETIKNDI, WVN DI, DVVI, DEDCED TVDVVI
1			QUINARATRURCEVVIMEDAPDYVAVEDTEGET COTORRITADITAL [
1 1			13DFMETTDYFETTDNEITDINENTCDSENDDUNENDARD
1 1			NESADDHETTDNNESADDNNENPEDNNKNTDDNEENPNNHENTY
1 1			GNNFFKGGFWGSHGNNQDSSDSDNEADEASDDEDNDGNEGDNEG SDDDGNEGDNEGSDDDDDDDDDDDDDDDDDDDDDDDDDDD
1 1			SDDDGNEGDNEGSDDDDRDIEYYEKVIEDFDKDQADYEDVIEII SDESVEEEGIEEGIQQDEDIYEEGNYEEEGSEDVWEEGEDSDDS
			DLEDVLQVPNGWANPGKRGKTG
6296	727	1199	RHCGCDAQGACDSLPPTGTSSPVTAPNAIDEADCCUMITECT
	į	Í	EAVREARERLAKKELROKRMOOFSRDSAVSSNYDSDST I DEDDE
!		j	HGISHQF PSPFSGTISFGSFSDSGTFDLGGOCCICEOOFGTCGT
6297		0.00	KWALIAKKVRLSVFGARWGRIYFGK
,	1	922	QRAAAASPSSCGPRGAEYGALMAMEGYWRELDY LCCALLYCTT
ļ 1			VIFALVWVLHYREGLGWDGSALEFNWHPVLMVTGEVELGCLX X -
		i	VIRLEWIWKCSKLLMKSIHAGLNAVAATI.ATTGVVAVEEAUBURY
			NIAMMISCHSWVGLIAVICYLLOLLSGFSVFI.I.DWADI.CIDADI
! !		1	MFINVISGIVIFGTVIATALMGLTEKT, TFGLDDDAVCTEDDEGIL
		1	F VNILGBLILVFGALIFWIVTRPOWKRPKEPNSTTIUPNGCORPO
6298	3	985	GARGSMPAYSGNNMDKSDSELNNEVAARKRNLALDEAGQRSTM
J			SVPLRRLSLSGTLQGAGTTTKMAVARLAAVAAWVPCRSWGWAAV PFGPHRGLSVLLARI DORADBY DAGGER
1		.	PFGPHRGLSVLLARI PQRAPRWLPACRQKTSLSFLNRPDLPNLA
		}.	YKKLKGKSPGIIFIPGYLSYMNGTKALAIEEFCKSLGHACIRFD YSGVGSSDGNSEESTLGKWRKDVLSIIDDLADGPQILVGSSLGG
i		1	WLMLHAAIARPEKVVALIGVATAADTLVTKFNQLPVELKKEVEM
ı		ļi	KGVWSMPSKYSEBGVYNVQYSFIKEAEHHCLLHSPIPVNCPIRL
j			UNGMADDI VPWHTSMOVADRVI,STDVDVII, PKUGDVDNDANDA
			QLLVYTIDDLIDKLSTIVN
	-		

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID NO:	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, F-
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine
}	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1 1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1 1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1 [	amino acid	sequence	Codon, /=possible nucleotide deletion,
F-6300	sequence		\=possible nucleotide insertion)
6299	512	814	ECDLEGIMPNVTISLSLPTNGSPLQDILVHPCVTSLDSAILTSS
			SIDAMDDSAFSGPYKFPFTPPLESFNLCFYTSQVPVPPILGFYQ
			MKEEEVQLRNNH
6300	121	692	AAPSCWSQRGVPAAGTPSSPRLLVSRAAAPSAGPWGAWRQGARA
1 1			AQSPFSIPNSSSVPYGSQDSVHSSPEDGGGGRDRPVGGSPGGPR
1			LVIGSLPAHLSPHMFGGFKCPVCSKFVSSDEMDLHLVMCLTKPR
1			ITYNEDVLSKDAGECAICLEELQQGDTIARLPCLCIYHKGCIDE
		·	WFEVNRSCPEHPSD
6301	616	284	GKFVPVNWEPPQPLFFPKYLRCYRCLLETKELGCLLGSDICLTP
) j			AGSSCITLHKKNSSGSDVMVSDCRSKEQMSDCSNTRTSPVSGFW
6300			IFSQYCFLDFCNDPQNRGLYTP
6302	490	745	IFGFLHLFHMEHSFLLVCALFAHVFFSSSCGSSVALHSDPCLLS
L			PVLLNCLPGDLRPLDELYAQKLKYKAISEELDHALNDMTSL
6303	2	1961	YWNEYGGGLLWOSWOEKHPGQALSSEPWNFPDTKEEWEOHYSOL.
1 1			YWYYLEQFQYWEAQGWTFDASQSCDTDTYTSKTEADDKNDEKCM
			KVDLVSFLSSPIMGDNDSSGTSDKDHSEILDGISNIKLNSEEVT
1			QSQLDSCTSHDGHQQLSEVSSKRECPASGQSEPRNGGTNEESNS
ľ			SGNTNTDPPAEDSQKSSGANTSKDRPHASGTDGDESEEDPPEHK
1			PSKLKRSHELDIDENPASDFDDSGSLLGFKYGSGQKYGGIPNFS
1 1			HRQVRYLEKNVKLKSKYLDMRRQIKMKNKHIFFTKESEKPFFKK
1			SKILSKVEKFLTWVNKPMDEEASQESSSHDNGHDASTSCDSEEQ
.			DMSVKKGDDLLETNNPEPEKCQSVSSAGELETENYERDSLLATV
1 1			PDEODCVTQEVPDSRQAETEAEVKKKKKKKKKKKKKVNGLPPEIAA
			VPELAKYWAQRYRLFSRFDDGIKLDREGWFSVTPEKIAEHIAGR
1 1			VSQSFKCDVVVDAFCGVGGNTIQFALTGMRVIAIDIDPVKIALA
			RNNAEVYGIADKIEFICGDFLLLASFLKADVVFLSPPWGGPDYA
1			TAETFOIRTMMSPDGFEIFRLSKKITNNIVYFLPRNADIDQVAS
6304	1	1438	LAGPGGQVEIEQNFLNNKLKTITAYFGDLIRRPASET
""		1430	HRARVDRSRESPGGDLRHPGRVRRDITLSGHPRLSTQHVVLLRE
}	ļ		DEVGDPGTKDLGHPQHGSPIQETQSEVVTLVSPLPGSDMAALPA
			WRATSGLTLWPHTAEGRDLLGAENRALTGGQQAEDPTLASGAYQ
	1		WPGSVEKLQGSVWCDAETLLSSSRTGGQAPPWLTDHDVQMLRLL
ļ.			AQGEVVDKARVPAHGQVLQVGFSTEAALQDLSSPRLSQLCSQGL
			CGLIKRPGDLPEVLSFHVDRVLGLRRSLPAVARRFHSPLLPYRY
	1		TDGGARPVIWWAPDVQHLSDPDEDQNSLALGWLQYQALLAHSCN
1	Ĭ		WPGQAPCPGIHHTEWARLALFDFLLQVHDRLDRYCCGFEPEPSD
			PCVEERLREKCRNPAELRLVHILVRSSDPSHLVYIDNAGNLQHP
			EDKLNFRLLEGIDGF?ESAVKVLASGCLQNMLLKSLQMDPVFWE
6305	99	420	SQGGAQGLKQVLQTLEQRGQVLLGHIQKHNLTLFRDEDP
- I			NMIWRGRSTYRPRPRRSVPPPELIGPMLEPGDEEPQGEEPPTES
		. [	RDPAPGQEREEDQGAAETQVPDLEADLQELSQSKTGDECGDGPD VQGKILTKSEQFKMPEGR
6306	1	1874	
	-	10/1	PTRPSKVKVPHTFLIHSYTRPTVCQACKKLLKGLFRQGLQCKDC
i			KFNCHKRCATRVPNDCLGEALINGDVPMEEATDFSEADKSALMD
1	1	}	ESEDSGVIPGSHSENALHASEEEEGEGGKAQSSLGYIPLMRVVQ
1			SVRHTTRKSSTTLREGWVVHYSNKDTLRKRHYWRLDCKCITLFQ
1	i		NNTTNRYYKEIPLSEILTVESAQNFSLVPPGTNPHCFEIVTANA
1			TYFVGEMPGGTPGGPSGQGAEAARGWETAIRQALMPVILQDAPS
j			APGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDEVLGSGQF
1		J	GVVYGGKHRKTGRDVAVKVIDKLRFPTKQESQLRNEVAILQSLR
[		1	HPGIVNLECMFETPEKVFVVMEKLHGDMLEMILSSEKGRLPERL
		ļ	TKFLITQILVALRHLHFKNIVHCDLKPENVLLASADPFPQVKLC DFGFARIIGEKSFRRSVVGTPAYLAPEVLLNQGYNRSLDMWSVG
l			THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY O
		ŀ	WINDLESS COMPONIES OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROP
			VIMYVSLSGTFPFNEDEDINDQIQNAAFMYPASPWSHISAGAID
			VIMYVDLSGTFPFNEDEDINDQIQNAAFMYPASPWSHISAGAID LINNLLQVKMRKRYSVDKSLSHPWLQEYQTWLDLRELEGKMGER YITHESDDARWEQFAAEHPLPGSGLPTDRDLGGACPPQDHDMQG

Degining beginning incledided and incledide location corresponding to first and control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control contro	· 	SEQ	Predicted	Predicted end	
Docation   Coction   Cortisponding to first   Since   Since   Cortisponding to first   Since   Cortisponding to first   Since   Cortisponding to first   Since   Cortisponding to first   Since   Cortisponding to first   Since   Cortisponding to first   Since   Cortisponding to first   Since   Cortisponding to first   Since   Cortisponding to first   Since   Cortisponding to first   Since   Cortisponding to first   Since   Cortisponding to first   Since   Cortisponding to first   Since   Cortisponding to first   Since   Cortisponding to first   Since   Cortisponding to first   Since   Cortisponding to first   Since   Cortisponding to first   Since   Cortisponding to first   Since   Cortisponding to first   Since   Cortisponding to first   Since   Cortisponding to first   Since   Cortisponding to first   Since   Cortisponding to first   Since   Cortisponding to first   Since   Cortisponding to first   Since   Cortisponding to first   Since   Cortisponding to first   Since   Cortisponding to first   Since   Cortisponding to first   Since   Cortisponding to first   Since   Cortisponding to first   Since   Cortisponding to first   Since   Cortisponding to first   Since   Cortisponding to first   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since   Since					
corresponding to first anino acid equence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence		NO:	nucleotide		I M-Atanine, CeCysteine Debenachie acci -
corresponding to first shing acid amino acid amino acid amino acid amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequen	l		location		Gracemic Acid, F=Phenvialaning C-cl
to first amino acid residue of sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence s	ļ	!	corresponding		n=nistidine, l=1solencine V-traine
amino acid residue of amino acid amino acid sequence LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRISUL LARRIS			to first		B-Droline, M=Methionine, N=Asparagine,
residue of amino acid sequence de sequence de l'expessible nucleotide deletion, legente sequence de l'expessible nucleotide deletion, l'expessible nucleotide desertion l'expessible nucleotide desertion l'expessible nucleotide desertion l'expessible nucleotide desertion l'expessible nucleotide desertion l'expessible nucleotide desertion l'expessible nucleotide desertion l'expessible nucleotide desertion l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide l'expessible nucleotide nucleotide l'expessible nucleotide l'expessible nucleotide nucleotide nucleotide l'expessible nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleo	- 1		amino acid		S-Sering Tombus ReArginine,
amino acid sequence   Codon, /-possible nucleotide dinstion	- 1		residue of		W-Trymtonha- W. W.
Sequence					Codon (
CELEBRICA PEPERAGAAR CAPGAP CHISTORY OF CELEBRICA PEPERAGA CAPTA STATEMENT OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS OF CHILD PROCESS	- 1		sequence	1	\=possible nucleotide deletion,
6310 6310 6310 6310 6310 6310 6310 6310	- (				LAPPICUT
UPLISKIGER DKASPTVOGGTOFPULDUKSGOGAFI VPLISKIGER DKASPTVOGGTOFPULDUKSGOGAFI VPLISKIGER DKASPTVOGGTOFPULDUKSGOGAFI SAGCONVIL WINDTABELYRIDGI.HEPI VARWINDENISGES ACKOKSVAI I DPRRGTLVAEREKAHEGARPMAN IFLADGKYPTT GFSRMSERGLALWDPENLEEPPRAJGELIDGI.PDPDTSV VVCGKODSSIRYTEITERPFYIHITTESKEPOKSMASUPKR GLEVSKCEILARFYKLHERKCEPI VMTVPRESDFOOLDI.PDPDTSV VVCGKODSSIRYTEITERPFYIHITTESKEPOKSMASUPKR GLEVSKCEILARFYKLHERKCEPI VMTVPRESDFOOLDI.PDPDTSV VVCGKODSSIRYTEITERPFYIHITTESKEPOKSMASUPKR GLEVSKCEILARFYKLHERKCEPI VMTVPRESDFOOLDI.PDPDTSV VVCGKODSSIRYTEITERPFYIHITTESKEPOKSMASUPKR GLEVSKCEILARFYKLHERKCEPI VMTVPRESDFOOLDI.PDPDTSV VVCGKODSSIRYTEITERPFYIHITTESKEPOKSMASUPKR GLEVSKCEILARFYKLHERKCEPI VMTVPRESDFOOLDI.PDPDTSV PRABALRALVKEQGDRI CRLEEGIGRMGIDA GERPRAPKGALDDRILVCVQSMVLFFFENTYGVOLLLVGDI. BRANKAPITARINARGYTUM IVADILLAIRGRWENDELLAGVER LLSAFLERAFYQALDDRILVCVQSMVLFFFENTYGVOLLLVGDI. LLSAFLERAFYQALDDRILVCVQSMVLFFFENTYGVOLLLVGDI. VIFPEGGRINNFEGOTIVALSASOAPAAGRGIACHVENTURITERIT VAFPCMKNYLDAIYDTVVVSGKDDGGQRESS PTWTFELKECH KIHHLDRIDKKDVPEGGEHRRMLHERFELKOKMI.ISTETESP PERRKAPPGKSVINSKI.SIKKTLPSMI.ILSGLTAGMLTMLTGLQT KANDAVSTRITUGGENGASAGOPAGGEORICHVENTICHTURITUGGEN VANDAVISTIGTILGGLWATITA VAFPCMKNYLDAITURGGENGASAGOPAGGEORICHVENTORTHOLTGLQL KLGPALKTYEHVKYTGGFECASAGOPAGGEORICHVENTORTHOLTGLQL KLGPALKTYEHVKYTGGFECASAGOPAGGEORICHTURITUGGEN VARDAVSTRITUGGENGASAGOPAGGEORICHTURITUGGEN VARDAVSTRITUGGENGASAGOPAGGEORICHTURITUGGEN VARDAVSTRITUGGENGASAGOPAGGEORICHTURITUGGEN VARDAVSTRITUGGENGASAGOPAGGEORICHTURITUGGEN VARDAVSTRITUGGENGASAGOPAGGEORICHTURITUGGEN VARDAVSTRITUGGENGASAGOPAGGEORICHTURITUGGEN VARDAVSTRITUGGENGASAGOPAGGEORICHTURITUGGEN VARDAVSTRITUGGENGASAGOPAGGEORICHTURITUGGEN VARDAVSTRITUGGENGASAGOPAGGEORICHTURITUGGEN VARDAVSTRITUGGENGASAGOPAGGEORICHTURITUGGEN VARDAVSTRITUGGENGASAGOPAGGEORICHTURITUGGEN VARDAVSTRITUGGENGASAGOPAGGEORICHTURITUGGEN VARDAVSTRITUGGENGASAGOPAGGEORICHTURITUGGEN VARDAVSTRITUGGENGASAGOPAGGEORICHTURITUGGEN VARDAVSTRITUGGENGASAGOPAGGEORICHTURITUGGEN VARDAVSTRITUGGENGASAGOPAGGEORICHTURITUGGUN VARDAVSTRITUGGENGASAGOPAGGEORICHT		6307	2136	589	CFLIDPGPDPEDDEAGAAAAGAAAA
TUNNOUT DENGTISELTEPUVULEGHTKNGI IAMIPTARNYLL SAGCDNVUL WANGTABELYRLDSHPDLI YNVSWHINGSLECS ACKDKSVRI I DPRRGTLYDLAPREKAHEGAPMAN FLADGKVFTT GFSRMSERGLALMOPENLEEPMALQELDSSNGALLPYPDPTSV VYVGCKOBSS INYFETTEBPYTHFLITSEPDGMSMSMPKR GLEVSKCELARFYKHERKCEPI WITVPRKSDLEDOLDLY PDPTAS VYVGCKOBSS INYFETTEBPYTHFLITSEPDGMSMSMPKR GLEVSKCELARFYKHERKCEPI WITVPRKSDLEDOLDLY PDPTAS PRANEAGESHLGAPASTTTAADATPSGSLARAGGACKLEEVM DSRPAMAPGSSHLGAPASTTTAADATPSGSLARAGGACKLEEVM DSRPAMAPGSSHLGAPASTTTAADATPSGSLARAGGACKLEEVM DSRPAMAPGSSHLGAPASTTTAADATPSGSLARAGGACKLEEVM DSRPAMAPGSSHLGAPASTTTAADATPSGSLARAGGACKLEEVM LLSAFLERAFYCALDDRILGEVGLAWAGUALFFYSHVLLAG GENTREKERFYCALDDRILGEVGLAWAGUALFFYSHVLLAGGUALKWULKSGLK MULLYGWYSHAGGGILVKEVALGESAPASTTAADATPSGSLARAGGACKLEEVM VIFPEGTRYNPROTVALGASAAPAGGACHALKWULTRI KAGIK MULLYGWYSHAGGAGUALWAWATTAAGATWA VAPCUMNYNTAAGAGGILVKWULSGLAWAGUALKWULTRI KAGIK MULLYGWYSHAGGAGUALKWULTAAGATWA VAPCUMNYNTAAGAGGILVKWULSGAAWAGUALKWULTRI KAGIK MULLYGWYSHAGAGGILVKWULSGAAWAGUALKWULTRI KAGIK MULLYGWYSHAGAGGILVKWULSGAAWAGUALKWULTRI KAGIK MULLYGWYSHAGAGGILVKWULSGAAWAGUALKWULTRI KAGIK MULLYGWYSHAGAGGILWAWAGAAWAGUALKWULTRI KAGIK MULLYGWYSHAGAGGILWAWAGAAWAGUALKWULTRI KAGIK MULLYGWYSHAGAGGAAWAGUALKWULTRI KAGIK MULLYGWYSHAGAGGAAWAGUALKWULTRI KAGIK MULLYGWYSHAGAGGAAWAGAGAAWAGUALKWULTRI KAGIK MULLYGWYSHAGAGAAWAGAAWAGAAWAGAAWAGAAWAGAAWAGAAWA	- 1				OPVKNDOCYEDIDAG BANGARAPCAPGAPDMSFRKVVRQSKFRHVFG
SACCINVUL MNOTABELYRLDSLIPPLI TARNUL I SACCINVUL MNOTABELYRLDSLIPPLI SACKOKSVAI I DPRRGTLVAERIKAHEGARPMAN IFLADGKYPTT GERMENGELGLAMPPENLEEPPALGELIDAGLIPPT PUTS GERMENGELGLAMPEN GERMENGEL SACKOKSVAI I DPRRGTLVAERIKAHEGARPMAN IFLADGKYPTT GERMENGELGLAMPEN PROBABLEPTYDPDTSV VVCGKODSSIRYFE I TEBPPYI HENTFISKEPOKSMASHPKR GLEVSKCE LARFYKLHERKCEPI VMTVPAGLEPOKLDFOLD YPDTAG FEAALBAEWVSGOADP ILISLBEAVVSKORDLKISERRVLS DERPAMAPGESHLOPAD FLISLBEAVVSKORDLKISERRVLS OSLBALBALVKEQGDRI CRLEEGLERMENGE ON THE SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEARCH SEAR	- 1				VI.PLSKTGPIDKAVPTROGUTTOPER
ACKDKSVILIDERGETUVEREKALERPRIAIFADGKVFTT GESRMSERGLALMDERHLESPRMAIFATEAGKVFTT GESRMSERGLALMDERHLESPRMAIFATEAGKVFTT GESRMSERGLALMDERHLESPRMAIFATEAGRAVFTT GESRMSERGLALMDERHLESPRMAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERPRIAIFATEAGRAVERP					TVMVWOIDENCITED TERMINE POWER TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TERMINE TO THE TE
GSRMSERQLALMDERHLESPHALQESSRGALLISPTOPDTSV VVVGKGDSSIRVFEITEEPPYHFINTFTSKEPGRGMSHPKR GLEVSKCELARFYKLHERKCEPIVMFKBLFVGDHYDPTSV PVVGKGDSSIRVFEITEEPPYHFINTFTSKEPGRGMSHPKR GLEVSKCELARFYKLHERKCEPIVMFKBLFVGDHYDPTSG PFAALEAEEWSGRIADPILISLREAVYPSKOEDLKISERRIVLS DSRPAMAPGSSHLGAPASTITAADATSGSLAPAGEACKLEEVM OELBALBALVKROGDRICRLEEDLGRMENGDA  GEPTTEREKMLSSLVHTYSMRYLLESSGLAPAGEACKLEEVM OELBALBALVKROGDRICRLEEDLGRMENGDA  GEPTTEREKMLSSLVHTYSMRYLLESSGLAPAGEACKLEEVM OELBALBALVKROGDRICYVKRSAKFREKERKULGSVDAGTTMIL LLSAFLEPRRYQALDBLIYCVYGSWULFFFENYTGVOILLYGGLK MLPLYGWYFAOUGGIYVKRSAKFREKERKKLGSVVDAGTTMIL VIPFEGTRYNPEVTKVLSASOFFARGKGLAVKKHULTERIKATH VAPPCMKNINLDAITDVIVVGEKOLGGSKERWIKLGSVVDAGTTMIL VIPFEGTRYNPEVTKVLSASOFFARGKGLAVKKHULTERIKATH VAPPCMKNINLDAITDVIVVGEKOLGGSKERSTMITHIAATH VAPPCMKNINLDAITDVIVVGEKOLGGSVOKSMENGRPPDFADDA MDDVAYYFRTVGFEQASAFOGGIDKKSLLIMTENDVLTGLQ KIHLHIDRIDKKDVPEEQBMRRWHERFFSIKOKHLEFFESPD PERRKRPFOKSVNSKLS IKKTLPSML LISGLTAGMLMTDAITGCL KLGFALKTYEHVKPLYTTHIAKNINS  AGROSLASLANDAAGKMADCOOPLYFOCGICLICTWINLIGHV DLHLEENSFQQGMBRVCCGGDLOAIGLQOGEDRERRSEESROE IEFFOKLROWSULDSGOKVOOLGRMEGLICTWINLIGHV DLHLEENSFQQGMBRVCCGGDLOAIGLQOGEDRERRSEESROE IEFFOKLROWSULDSGOKVOOLGRMEGLICTWINLIGHV DLHLEENSFQQGMBRVCCGGDLOAIGLOQUEEDRERRSEESROE IEFFOKLROWSULDSGOKVOOLGRMEGLICTWINLIGHV DLHLEENSFQQGMBRVCCGGDLOAIGLQOGEDRERRSEESROE IEFFOKLROWSULDSGOKVOOLGRMEGLICTWINLIGHV ASKLKRDDGIKGSGYTAPOMLLSSLLOMDAINULKGMLIP CIPKTIGSMIEDAMKEGFDPGOAGOLITRIQGTKWADVILSE VUDHYBSSLDGKWGGGTVANFOMLLSSLLOMDAINULKGMLIP CIPKTIGSMIEDAMKEGFDPDGASGLITRIQGTKWADVILSE PVWWSCUSSLSPPSTAAAARTGHGVGRRARLACLGEFRVKAAVFLTL ASKLKRDDGIKGSGTAATAGSSTRRVSVDDLLLWEVASLEANL PVWWSCUSSLSPPSTAAAARTGHGVGRRARLACLGEFRVKAAVFLTL ASKLKRDDGIKGSGTAATAGSSTRRVSVDDLLLWEVASLEANL PVWSCUSSLSFPSTLEDOLLTHLTGREAFTYTGKNOG GKTEEPAKQLAEEMNIAFYTSRTDDLLHDOVDLVCISIPPDLW GKTSSSDSTAFTAASSTRRWSVDDLLLWEVASLEANL GKTEEPAKQLAEEMNIAFYTSRTDDLLHDOVDLVCISIPPDLA GKTEEPAKQLAEEMNIAFYTSRTDDLLHDOVDLVCISIPPDLW GKTSSSDDLATHATTYTULTHTAKNINGGGFEREKVHOLLTTVORMA IRGIHVTSDDFCFFOMLMGGGVCTVTLAFRNWFTSRVYOMA IRGIHVTSDDFCFFOMLMGGGVCTVTLAFRNWFTSW	- 1				SACCONVALTABLECTA EEL VOLDES TERRANGIIAWHPTARNVLL
GSAGSAGNAMADENIAEDEMALGELDSSNOGLIFYDDPITSU VVCGKGDSSIRYFITEDEPPYTHITTSKEPDGNGKSIPKR GLEVSKCEIARTYKLHERKCEPIVMTVPRKSDLFQDDLYPDTAG PFAALEAEMVSGRADDFILISLREPYSQRQDLLISRRAVLG DSRPAMAPGSSILGAPASTTTADATTPSGLARACEACKLEEVM OELRALEALVKROGRAICTRIEGQLGRMENGDA  2 1118 GRYTREBKMLSJVLHTYSRRYJLESVVLLGTAPTTVLAMGVRR LLSAFLEARTYQALDBLYLCVYGSWLFEHSTNYGVLLJVGDL PRINKENITIVLAHGSTUDWIVADILAIRQNALCHVRYVIKEGLK WLPIYGRYFAONGGIVKRSAKFINEFENTSGVILLIVGDL PRINKENITIVLAHGSTUDWIVADILAIRQNALCHVRYVIKEGLK WLPIYGRYFAONGGIVKRSAKFINERKLOSVUDAGTPMYL VIFPEGTRYNPROTVVLSASQAPRAQGCLAVLKHVLTPRITIATH VAFDCMKNYLDAIYDVAVSCKDDGAVALKHVLTPRITIATH VAFDCMKNYLDAIYDVAVSCKDDGAVALKHVLTPRITIATH VAFDCMKNYLDAIYDVAVYSCKDDGAVALKHVLTPRITIATH VAFDCMKNYLDAIYDVAVYSCKDDGAVALKHVLTPRITIATH VAFDCMKNYLDAIYDVAVSCKDDGAVALKHVLTPRITIATH VAFDCKMYNLDAIYDVAVSCKDDGAVALKHVLTPRITIATH VAFDCKMYLDAIYDVAVSCKDDGAVALKHVLTPRITIATH VAFDCKMYLDAIYDVAVSCKDDGAVALKHVLTPRITIATH VAFDCKMYLDAIYDVAVSCKDDGAVALKHVLTPRITIATH VAFDCKMYLDAIYDVAVSCKDDGAVALKHVLTPRITIATH VARVVEYSTEPSOLDAINAAAGLAADCDQFLYDCPMCGLICTNYHLLQBHV VARVVEYSTEPSOLDAINAAAGLAADCDQFLYDCPMCGLICTNYHLLQBHV VARVVEYSTEPSOLDAINAAAGLAADCDQFLYDCPMCGLICTNYHLLQBHV VARVEYSTEPSOLDAINAAAGLAADCDQFLYDCPMCGLICTNYHLLQBHV VARVEYSTEPSOLDAINAAAGLAADCDQFLYDCPMCGLICTNYHLLQBHV VARVHYSSTEPSOLGANGAVACHTTL KAMMESIALAFDDGSKTKTSGIIEAHTVANAATUDCLKKMLIP CTCKLYBFOQOMBVCGGGGLCAINGTGANTELVANGATUDCLKKMLIP CTCKLYBFOPDNIKLHCFQCTGSDCAAUCHCANULLKKMLIP CTCKLYBFOPDNIKLHCFQLTTYPDGAYGGKCFOFSTEVPDANM MVFPKVKCLTKIHNNITETGEICLLEREISIDGTGNAPTRIL KAYAR  6312 213 1400 GBELVKRRAGMKMDEVGVGTGSSARVLVPLILARGFTVEALW GKTEEBARGLABENMIAPYTSRTDDILLHQDVOLVCISIPPPLT ROJSVALGIGGNVVCGCARATVODAFRNVTASKYYOLMSLVGN VLRPLPARVPMKGLISEHYVGAVMICLKGARSFTVEALW GKTEEBARGLAGENMIAPYTSRTDDILLHQDVOLVCISIPPPLT ROJSVALGIGGNVVCGCARATVODAFRNVTASKYYOLMSLOGG UNGSVADAIKASGRGCGGGGRAFTNFORGFFVENWY GSAGRLVARGADIVGANGATUSELDLENGAGGECGTGCTGFTVVVMRIGGECG PLOMEAIKAGRGCCGTGTGTRWFTOVSMAASFEDGII NGCSVADAIKAGGGGCGGGGRAFTNFORGFFVENWY GSAGRLVARGADIVGANGATUSELDLENGAGGECGGGGGARTHORGECTTON THE SUBARSFEDGII NGCSVADAIKAGGGGGGGGGGGGGGGGGGGGGGGGGG	- 1				ACKDESURITORDECT IN FERNANCIA
GLEYSKEELARFYKLIERKKEEPIWTSEDLIFOODLYJPDTAG FERALEAEEWSGRIADPILISIREAYVPSKOELAFOODLKISERRIVLS OSRPAMAPGSSHLGAPASTITAADATPSGSARACGACKLEEVM OSLBALRALVKROGDRICRIEEGLORMENGDA GRYPTREBEMILSSULVHYSNRYLLESSARACGACKLEEVM OELBALRALVKROGDRICRIEEGLORMENGDA GRYPTREBEMILSSULVHYSNRYLLESSARACGACKLEEVM OELBALRALVKROGDRICRIEEGLORMENGDA GRYPTREBEMILSSULVHYSNRYLLESSARACKACKLEEVM LLSAFLEPARFYQALDDRLYCVYGSWALFFPENYTGVGILLYGGL PRINKENITVIAHHGGILYVKRSAKFREKEMRIKLGSVVDAGTFMIL ULSAFLEPARFYQALDDRLYCVYGSWALFFPENYTGVGILLYGGL MILPHYGMYFAONGGILYVKRSAKFREKEMRIKLGSVVDAGTFMIL VAPPCMENTVADAGTVUTVAYGAKDGAGAACKAHVLTPRIKATH VAPPCMENTVADAGTVUTVAYGAKDGAGARACKAHVLTPRIKATH VAPPCMENTVADAGTVUTVAYGAKDGAGACKAHVLTPRIKATH VAPPCMENTVADAGTVUTVAYGAKDGAGACKAHVLTPRIKATH VAPPCMENTVADAGTVUTVAYGAKDGAGACKAHVLTPRIKATH VAPPCMENTVADAGTVUTVAYGAKDGAGACKAHVLTPRIKATH VAPPCMENTVADAGTVUTVAYGAKDGAGACKAHVLTPRIKATH VAPPCMENTVADAGTVUTVAYGAKDGAGACKAHVLTPRIKATH VAPPTYTATAGACKAHVLTAGAGACKAHVLTAGAGACKAHVLTAGAGACKAHVLTAGAGACKAHVLTAGAGACKAHVLTAGAGACKAHVLTAGAGACKAHVLTAGAGACKAHVLTAGAGACKAHVLTAGAGACKAHVLTAGAGACKAHVLTAGAGACKAHVLTAGAGACKAHVLTAGAGACKAHVLTAGAGACKAHVLTAGAGACKAHVLTAGAGACKAHVLTAGAGACKAHVLTAGAGACKAHVLTAGAGACKAHVLTAGAGACKAHVLAGAGACKAHVLTAGAGACKAHVLTAGAGACKAHVLTAGAGACKAHVLAGAGACKAHVLAGAGACKAHVLAGAGACKAHVLAGAGACKAHVLAGAGACKAHVLAGAGACKAHVLAGAGACKAHVLAGAGACKAHVLAGAGACKAHVLAGAGACKAHVLAGAGACKAHVLAGAGACKAHVLAGAGACKAHVLAGAGACKAHVLAGAGACKAHVLAGAGACKAHVLAGAGACKAHVLAGAGACKAHVLAGAGACKAHVLAGAGACKAHVLAGAGACKAHVLAGAGACKAHVLAGAGACKAHVLAGAGACKAHVLAGAGACKAHVLAGAGACKAHVLAGAGACKAHVLAGAGACKAHVLAGAGACKAHVLAGAGACKAHVLAGAGACKAHVLAGAGACKAHVLAGAGACKAHVLAGAGACKAHVLAGAGACKAHVLAGAGACKAHVLAGAGACKAHVLAGAGACKAHVLAGAGACKAHVLAGAGACKAHVAACAACKAHVLAGAGACKAAGAACKAACKAAACKAAACKAACKAACKAACK		ı			GESRMSEROLALWDDENI EEDMALOEV BOOMEN FLADGKVFTT
GLEVANCE JUNITY PERSOL FORDULT PDTAG PERALEAEEWYSCROD PIL ISLAEV PURSOR DELICAL FERNULS DERPAMAPGESHLGAPASTITAADATPSCSLARAGEAGK LEEVM OELRALRALVEGGORI CRLEEGURMENDA  GETTEPERMILSIVLHTYSMRYLLPSVULGTAPTYULAWGVWR LLSAFLPARFYOLDDRILY CVYGAMCHAVITY PERMYTUGUILLYGIL PRINKENII YLLANDGETUDRI LYADILAI RONALGHIRYVLKEGIK WLPLYGAYFAOHGGIYVKRSAKRNEKEMINKUGSVUDAGTPMIL VIFPEGTRYPEKOTIVLAS CQPARGGALVKHULTPRIKATH VAPPCHKNII HADILAI YDVTVVYEGKUDGGQRERSFTMTEFLCKECP KIHHILDRIDKKUVPERCEHIRMENLERFETKOKMILEFYESPD PERKERPEKSVNSKLSIKKTLPSMLILSGILTAGMLMTDAGRKL VANTWIGTLLGCLWAVIKA MDVUYFRIVOFECOASAPOEGE LIGKSLLLMTRNDVLTOLLCL KLGPALKIYEYHVKPLOTIKHIKNISS  GPROKKFLILSSWOFETKIRKANPOSSGOERYWTPRTHSSASE AQRGSLABILNVAAAGLWADCOOPLOCHOCCLICTTWHILOEHV DLHLEERSPCOMDRIVOCSGOLDLOLAIQUOGEBERKRESESROE LEEFGKLQRQVGLIDNSGGYKQOGLMISELNDAYNDLIKGMLIP CIPKIOSMIEDAMKEGFDPOGASDLII ILGGTKAWIGACEVYIL LTSLKY VUMPHISSLGDKKGGGOXYRNFOMLSSLLONDAYNDLIKGMLIP CIPKIOSMIEDAMKEGFDPOGASQLII RLGGTKAWIGACEVYIL LTSLKY MYPPKKKCLTKIHWPHITTGIG ILCSLLRENSIDGTGWAPTRTIL KDVWGLMSLFTDLLNFODPINIHCROLISLICHGEPRVKAAVVLITIL ASKLKRIDDELKGSTRATABDETRAVVSRKLLIKKSVALELANL PCTCKWHPPDPINKHCFOLIVYPDEGYYOGGKPOFTEVPDAYM MYPPKKKCLTKHWPHITTGIG ILCSLLRENSIDGTGWAPTRTIL KDVWGLMSLFTDLLNFDDPINIHCROLISLAURASPRIVANDLILL KYARA GDELVKREAGMKMLPGVGVFGTGSSARVLVPLLRAEGFTVEALM OKTEERARQLAEEMINIAFYTERTDD ILLHGDVDLVCISIPPPIT RQISVKALGIGKNVVCEKAATSVDFRAVYBSKLYDKAVDLVI LIGHTAVVSDFCFFOMLMGGVCSTVTINFFMPGAFYHEVMVV GAGRGILANGANGANSATOELLINGLAURASPEDGL WOSVUNDAIRSSREGGREAVEVILLIERDLAVGGLPERGEDO VULFILAKGNVAMVQALROSFGGGCDRRTWDTTVSMAASFEDGL NOSVUNDAIRSSREGGREAVEVILLEEPITNANLGEBERANDRIVK FRIERRAHGCTISCSSFVEOPTAMEAEETHECLGFFFEHHMILLD RLNNGGREODFFTDIII LYDGHHFKAKHALAGKSEFFYKFFODFF TOEPILVEIRGUSKMAFRRILIEFTTTAKIMIGGEBERANDWKAAAE FLOMLESIKALERINKENSAPLEENTINGERKKRKKTARTSNVI TESLPSAESEPVEIFVEIRGSDDSALALADTINKRORGANKKERTERSNVI TESLPSAESEPVEIFVEIRGSBODSALAURALGSEFFYKFFODER	- 1				VYVCGKGDSSTPVEFTTEEDDYTUDE
6308 2 1118 GRPTMPERMILISTURTSSURARGERAKLEEVM OELRALBALVKEGORI CRIEEQLGRMENGDA 6308 2 1118 GRPTMPERMILISTURTSMRYLDADTISGSLARGERAKLEEVM OELRALBALVKEGORI CRIEEQLGRMENGDA 66308 2 1118 GRPTMPERMILISTURTSMRYLDAVULGTA PTYVLAMGVUR LLSAFLPARFYOALDDRIYCVQGMVLFFENYTGVOILLYGDL PRINKENI IYLAMUGOTVORI VADILAI RONALGHKYVLKEGIK MLPLYGMYFAOHGGIYVKRSAKYREMIKKLGSVDAGTPMIL VIFPEGTRIPKOTTKUSASGAFAAGRGAUKHVLTPRIKATH VAFPCMKNYLDAI YVDVTVVESGOREMIKKUGSVUNDAGTPMIL VIFPEGTRIPKOTTKUSASGAFAAGRGAUKHVLTPRIKATH VAFPCMKNYLDAI YVDVTVVESGOREMIKKUGSVUNDAGTPMIL VAFPCMKNYLDAI YVDVTVVESGOREMIKKUGSVUNDAGTMRIL VAVNTWITGTILGCLMVTIKA LVGEVKEPCSEPMLSSUNDMENKENGSVOKNSMENGRPPDPADMA VMDVVNYFRIVOFESOASAPOEGEI DGKSLLLMTRNDVLTGLQL KLGPALKVYEYHVKPLOTKHLKNNSS AQRGSLASINVAAAGLMADCOQPLYDCIMCGLICTHVHILGEHV DLHLEERNSFQCGMROVQCSGDDLGAIDLQCGEDRKRSEESRGE IBEFGKLGRQVGLNNSGGYKQQQLRMMIEVHRGNPPSEPHER KADMMSSLAGEPBUSKVTGGI IEALHEYYONAATOTREVMLSS VUDHFHISSLGDKGGCGYRTFOMILSSLLOMDAYNDCLKGMLIP CIPKIGNMIEDAMKEGFDPOGASQLIIRLQGTKAMIGACEVYIL LTSLRV FORMSCEGPELAAARTGHGVGRRARLACLGEPRVKAAVELIL ASKLKRDDGLKGSKTAATASDSTRRVSVRKLLVKKVAELEANL PCTCKVHSPDPINKHCFQLTVYPDEGYYQGGKROFETEVPDAYN MYPEKVKCLTKHIMPHITTGGI CLIBERISDGGRAPTRTL KDVVWGLASGLSTDLLHFDDPLNIEABEHLRDKEDFRNKVDDYI KRYAR GDELVKRRAMKMLPGVGFTGSSARVLVPLLRAEGFTVEALW GREENGAGLAEENIA TYTSKTDDILLDRAGGTFVEALW VLRPLPAFVMRKGLISEHYVGAVHCDARITSGSSLSPSVGWIC DELMGGGGLHTMGTI YVDLITHLIGRAFRKVYGSKYFKONAA IRGIHHVTSDDFCFFCMLMGGGVCSTVTLINFIMPGAFVHEMWV VLRPLPAFVMRKGLISEHYVGAVNATGRAREKVRGLLKFYKONAA IRGIHHVTSDDFCFFCMLMGGGVCSTVTLINFIMPGAFVHEMWV SGAGRLVARGADLYGGVASATOEBLINSLAVGAGLDEGOOPD VPLLYLKKMVYMVQALRGSFGGGGDRRTWDRTPSMAASFEDGI VMGSVUDAI KRSSRGGREAUVUTLENLAAGCKFFYFVVOMPBLGVIL FIRRRAHGCTLSCSSFYQGFTAMEABETHECLOGFFEHHKMILLD RLNGGRGORFTDITLIVDGHHFKAKLVALAGCKFFYFYFOGF TOEPLVEIRGVERKMAFRRILIEFTTTAKLMIGGBERANDWKAAE FLOGULEAIKALEVINKENSAPLEENTRARKKKRIAHTSNVI TESLPSAESEPVEIRVEIRAGGITELEEVASAKOSWK YSTGSSDDSALALALDTISKVORGAURERCHERDERDENEW		1			GLEVSKCETARFYKLHERKCERTUMTURRUNDUKAN
6308 2 1118 GERALRALVERGORI CILEGGIAMENGIA  GELARALVERGORI CILEGGIAMENGIA  GEPTREEMILSIVLHTYSIMPILLESVULIGTAPTYULAMGUWR LLSAFLPARFYQALDERILYCVQGIAPTYULAMGUWR LLSAFLPARFYQALDERILYCVQGIAPTYULAGUWR LLSAFLPARFYQALDERILYCVQGIAPTYULAMGUWR LLSAFLPARFYQALDERILYCVGIAPTYULAMGUWR LLSAFLPARFYQALDERILYCVGIAPTYULAGUWR WHITH STAFL SOAPAAQRGLAVLKHULTPRIKATH VIFPEGTRYNPEOTXULSASQAPAAQRGLAVLKHULTPRIKATH VAFORMENIDAILYDVTVVYSGKDDGGQRESPTWTEFLCKECP KIHIHIDRIKKDVPEEQEMMREKHERERIKDUKLIEFYESPD PERRKRPPGKYNSKLSIKKTLESMILISGITAGMLWTDAGRKL VYNTWIYGTLLGCLWVTIKA  6310 36 979 EPROKKEPGKSVSKLSIKKTLESMILISGITAGMLWTDAGRKL KLGPALKTYEYHVKPLOTKHIKNINSS GPRKKFLILSSVICHTIRIGKAWPGSSGGEVWTPFTHSSASSAQAGAGLACLOQPLYDCOMCLICTNYHILOSHV LHIBERSPCQMOBYCCSGDLOLAHQLQGEBDKRRSEESRQE IEFFGKLOPGVGLONSGGYKQOQLIMBIEVNRGKMPFSEFHRR KADMESIALGPDGKTKTIGII ERALHSYLOMAATUVREVMLSS VVDHPHSSLGDKKGGCYRNFOMLSSLONDAYNDLKKGMLIP CIPKIQSMIEDAWKEGFDEQGASQLITILQGTKAWIGACEVYIL LTSLKW MYPRKVGLTKHINHUNITTGIGICLBERNIKGMEPTVANN MYPRKVGLTKHINHUNITTGIGICLBERNIKGHEPTVANN MYPRKVCLTKHINHUNITTGIGICLBERNIKGHEPTVANN MYPRKVCLTKHINHUNITTGIGICLBERNITATUKKUDLY KNYMGLNSLETDLLNFODDPLNIEAABHHIRDKEDFRKVDDYI KNYMGLNSLETDLLNFODDPLNIEAABHHIRDKEDFRKVDDYI KNYMGLASLAEHNITAFYTERTDLILHGDUDLVCISIPPPIT RGISVKALGIGKNVVCLKANSTVORTARGREKVRICHLIKTVONNA IRGIHVTSDDFCFFCMIMGGGVCSTVTUNFMMPGAFYHEMWV URFLEPAFVMKQLISEHYVOLAVHAGASKFFVEYMWV URFLEPAFVMKQLISEHYVOLAVHAGASKFFVEYMWV GAGRILMAGADLYGCKNASTOBELHUSLAVGAGLEPGGPQD VPILLYLKKNVYMQALRGSFGGCGDRRTHDPTPNVNAASSFEDGL MGSVGLIAMGAGDLYGCKNASTOBELHUSLAVGAGLEPGGPQD VPILLYLKKNVYMQALRGSFGGCGCDRRTHDPTPNVNAASSFEDGL MGSVGLIAMGAGDLYGCKNASTOBELHUSLAVGAGLEPGGPQD VPILLYLKKNVYMQALRGSFGGEBAWVIGLLKTYRPDUV GAGRGLAVARGADLYGGKNSATOBELHUSLAVGAGLEPGGPQD VPILLYLKKNVYMQALRGSFFGGEBAWVIGLLKTYRPDUV GAGRGLAVARGADLYGGKNSATOBELHUSLAVGAGLEPGFTDENEN GAGRGLAVARGADLYGGKNSATOBELTHICLAUGAGLEPGFTDENEN HERMAGCTICTUTOPHERARKANILARGKKPTKYRPOFFT TOEPIVEIRGVSKMAFRHILIEFTTAKMINGBERANDKTRANASST FINGREGREAWUNGARAFETHECLGFFERNEN TESISPAGESEPVEIFVEIRGEGTTERGERSPRONGWKN		J			PEAALEAEEWYSGEDADDILIGIDEAWADGEGDDLYPDTAG
6308 2 1118 GRPTRPEMMLISUHTYSMRYLDESVYLLGTAPTYVLANGVVR LLSAFLPARFYQALDRLYCVYQSWMLPFRYYLANGVVR LLSAFLPARFYQALDRLYCVYQSWMLPFRYYTGVOILLYGDL PRINKENIIYLANIOSTVDMIVADILA IRONALGHVRYVLKEGIK WLPLYGWYFAQHGGIYVKSAKFREKEMRIKLQSYVDAGTPMYL VIFPGGTRYMEDGYKVLSASQAPAQRGLAVLKHVLTPRIKATH VAPDCMKNYLDAIYDVTVVYSEKDDGGGRRESPTMTEFLCKECP KIHHIDIRKKNVPEGGEHMRRHHERFEIKDKMLIEFYESPD PERRKRPPGKVSVSKILSIKKTDKALLISGITAGM.MTDAGRKL YNNTWIYGTLGCLWYTIKA  LVARVKPECSLPHUSJUMENKENGSVGVKNSMENGRPPPPADMA WMDVVNYFRIVGFESDASAFCBOEIDGKSLLLMTRNDVLTGLQL KLGPALKIYEYHVKPLOTTHKLKNNSS GPRCWKFLILSSVNCETLRIGKAWPOSSGQERYWTPRTHSSASS AQRGSLABILNVAAAGLWADCDQPIYDCPMGGLICTNYHHLGEHV DLHLEENSPQCGMDRVQCSGDLJAIQLQGEDRKRRSEEERQE IEBFOKLGRQYGLDNSGGYKQOQLRNMEIEVNGRMPPSEPHRR KADMMSLALGFDDGKKTTSGI IEBLHRYYONAATUVRRVWLSS VVDHFHSSLGDKGWGCGYRNFOMLSSLLONDAYNDCLKGMLIP CIEKIGSMIEDJAWKSGFDPDGASQLIIRLQGEDRKRRSEEERQE IEBFOKLGRQYGLDNSGGYKQOQLRNMEITANGRWPPSEPHRR KADMWSLALGFDDGKKTTKSGI IEBLHRYYONAATUVRRVWLSS VVDHFHSSLGDKGWGCGYRNFOMLSSLLONDAYNDCLKGMLIP CIEKIGSMIEDJAWKSGFDPQGASQLIIRLQGEDRKAADATUVRRVWLSS VVDHFHSSLGDKGWGCGYRNFOMLSSLLONDAYNDCLKGMLIP CIEKIGSMIEDJAWRSGFDPQGASQLIIRLQGEDRYKAAVMUTL ASKLKRDDGLKGSRTAATASDSTRRVSVRDKLLVKEVABELBANL PCTCKVHFPDPNKLHCPQLTVTDDEGYYGGGFQFETEVPDAYM MV PFKVKCLTKIWHNTHTETGE ICCSLLBEHSIDTGWAPTRTL KDVWGGLNSLETDLLNPDDINIEAABHHLRDKEDFRNKVDDYI KRYAR GDELWKRAGGHKMLFPGUFVFGTGSSARVLVPLLRAEGFTVEALM GTELERAKQLAEBNIAFTYSTDLLHUTURGREKWHGLKFVKONAA IRGIRHVTSDDFCFFOMLMGGGVCSTVTLINFMPGAFVHEWMV GAGGGLWRRGANTAFTYSTDLLHUTURGREKWHGLKFVKONAA IRGIRHVTSDDFCFFOMLMGGGVCSTVTLINFMPGAFVHEWMV GAGGRLVARGADLYGCKNSATGEEDDTMONLCEALQRNNL GAGGARLAFLPSFFSFACVHRSPLSFHGCWFFYVVVFRPLGVL FHRRAHGCTLSCSFVQDTMARAEETMRCLGFFEHHKMILD RINEGREORPFTDITLITURGHFKAHKAVLAACSKFYKFFGFF TQEPLVEIBCWSGMARFRHLIEFTTTAKMINGGEBANDWKAAE FLOMELGREDDRFNOWKAAE FLOMELGREDDRFNOWKAAE FLOMELGREDDRFNOWKAAE FLOMELGREDDRFNOWKAAE FLOMELGREDDRFNOWKAAE FLOMELGREDDRFNOWKAAE		- 1	İ		DSRPAMAPGSSHLGAPASTTTAADATDCCCLABAGES
GRPTRPERMLISUVLHTYSMRYLLETAPFYVLARGVUR  LLSAFLPARFYGALDDRIVCYVQSMVLFFENYTGVQILLYGDL  PRINENIIYLANNIQSTVURIVADILAIRQNALGHVRYVUKEGLK  MLPLYGMYFAOHGGIYVKRSAKFREKEMRIKLGSYVDAGTPMIL  VIFPEGTRYNPEQTKVLSASQAFAQRGLAVLKHVLTPRIKATH  VAPPCMKNYLDAIYDVTVYVEGKDDGGGRESPTMTEFICKECP  KIHHINGIJKKVDVEGQSHMRWHERFEIKOKMLIEFYESPD  PERKRFPGKSVMSKLSIKKTLPSMLILSGLTAGM_MTDAGRKL  VYNTWIYGTLLGCLWVTIKA  6309 220 563 LVAEVKEPGSLPMENKENGSVGVKNSMENGRPPDFPADMA  MDDVWNYFRTVGFEGASAPQGGIDGKSLLLMTRNDVLTGLQL  KLGPALKIYYEYHVKPLGTKHLKNNSS  GPRCWKFLLISSVNCETLRIGKAMPGSSGGRYWTFPTHSSAS  AQROSLAELNVAAAGLWADCDPJYDCPMGGLICTMYHILQSHV  DLHLEENSFQQMDRVQCSGDLQLAIQLQQEDRKRRSESRQE  IEFFGKLQRYVGLUNGGGYKQDFIYDCPMGGLICTMYHILQSHV  DLHLEENSFQQMDRVQCSGDLQLAIQLQQEDRKRRSESRQE  IEFFGKLQRYVGLUNGGGYKQDFIYDCPMGLICTMYHILQSHV  DLHLEENSFQQMDRVQCSGDLQLAIQLQQEDRKRRSESRQE  IEFFGKLQRYVGLUNGGGYKOMMEISVNRGMHPSEFHRR  KADMMSSLALGFDDKTKTSGIIBALHRYYQNAATIVRRVWLISS  VVDHPHSSLGDKWGGGYKOMMEISVNRGARPPSEFHRR  KADMMSSLALGFDDKTKTSGIIBALHRYYQNAATIVRRVWLISS  VVDHPHSSLGDKWGGGYKOMTELSLLDNDAYNDCLKGMLIP  CIPKLQSMIEDAWKEGFDPGGASGLLIRLQGTKAMIGACEVYIL  LTSLRV  ASKLKRDDGLKGSKTAATAGSTRRVSVBKLLVKEVAELBANL  PCTCKVHPPDPNKLHCCDLTYTPDEGYYQGKRQFFEVPDAYN  MVPPKVKCLTKLWHPNITETGEICLSLLREHSIDGTGWAFTRTL  KDVWGCINSLFTDLLNFDDFLYNLERAEFHTVALW  GYTTEREARQLAEEMNILFTYSTRDDILLHQDVDLUCTSIPPPIT  RGISVKALGIGKNVVCEKAATSVDAFRWYTASRYYPQLMSLVGN  VLRFLPAFVRNKQLISEHYVGAWLDARIYSGSLLSPSYGWIC  DELMGGGGLHWGTYIVDLLTHLTGRREKWHGLLKTFVRONAA  IRGIRHVTSDDFCFFGMLMGGGVCSTVTLINNMGGAFVHETWMV  GSAGRLVARGADLYGKNASATGEELLLEDSLAVAGLFEGGPQD  VPLLYLKGMVYMVQALRQSFQQGGRRTWDTFYSMAASFEDGL  VRGSGARLARGGDLKGQKNASTGEELLLEDSLAVAGLFPGGPQD  VPLLYLKGMVYMVQALRGSFGGGGGRRTWDTFYSMAASFEDGL  MGSGARLVARGADLYGKGNASTGEELLLEDSLAVAGLFPGFFOF  TOPLVEIBGVSGMAFRHLIEFTTTAKMIGGEEANDWKAAE  FURRARGCTLSCSSPVEQPTAMELEPDTMONLCEALGRNUL  TESLPSAESEPVEIEVELAEGTIEVEDGETTLEEVASAKQSVK  YGSTGSDDSALALALLALLATTSKVIGGEEANDWKAAE  FLOMLEARIKALEGULGSDDSALALLALLATTSKVIGGEEANDWKAAE  FLOMLEARIKGNENDALDEENTTGKMEAKRIATSNVI  TESLPSAESEPVEIEVELAEGTIEVEDGETTLEEVASAKGGSVK	$\vdash$			_	QELRALRALVKEOGDRICRLEEOLGRMENGDA
EISAF LEART YQALDRILYCVYQSMULFFENTYGVQILLIYGDL PRINKENIIYIANINGSTUDMI VADILAI RRONALGHVRYULKEGIK WIPLYGWYFAOHGGIYVKRSAKFNEKERHINLQSYUDACTPWYL VIFFEGTRYMPEGTWYLSASQAPAQRGIAVVKHVUTPFILCKECP KIHHIIDRIDKEDVEBEGDGMRRENHERFEIKDKMILEFYESPD PERKRPFGKSVMSKLSIKKTJEKTLORULISGITAGM-MTDAGRKL YNTWIYGTLIGCIWTTIKA VINTWIYGTLIGCIWTTIKA CASON  563  LVABEVKEPCSENDSKLSIKITKROWLITGQL KLGPALKYYEYHVKPLOTYKHLKINMSS AQROSLABLINVAAAGLWADCDOPLYDCPMCGLICTMYHLLQBHV LLGPALKYYEYHVKPLOTYKHLKINMSS AQROSLABLINVAAAGLWADCDOPLYDCPMCGLICTMYHLLQBHV LHLBENSPÇQGMBEVQCSGDLOIGLQDQBEDRKRRSEESRQE IEBFOKLQRQYGLDMSGGYKQOQURNMEIEVNRGRMPPSEFHRR KADMMSSLAGLDMSGGYKQOQURNMEIEVNRGRMPPSEFHRR KADMMSSLAGLDMSGGYKQOQURNMEIEVNRGRMPPSEFHRR KADMMSSLAGLDMSGGYKQOQURNMEIEVNRGRMPPSEFHRR KADMMSSLAGLPDDKSKTKTSGIIBALHKYYQMATDVRXWLISS VVDHFHSSLGDKGWCGYRNFOMLSSLLQNDAYNDCLKGMLIP CIPKIQSMEDDAWKSGFPDQGASQLIIRLQGTKAMIGACEVYIL LTSLRV  6311  1 675  PVWWNSCEGPRLAAARTGGGVGRARLACLGEPRVKAAVMLTI ASKLKRDOCKGSKRAATASDSTRRVYDKLLVKEVABLEANL PCTCKVHFPDPNKLHCPQLTVTPDEGYYGGKFQFETEVPDAYN MVPFKVKLIKTMIPNITETGEICLSLLEHBIDGTGWAPPRTL KDVWGGNSLFILLNDDPLNIEAABHHLRDKEDFRNKVDDYI KRYAR  6312  213  1400  GDELVKREAGMKMLPGGGVFGTGSSARVLVPLLRAEGFTVEALW GTEEBAKQLAEENNIAFYTSRTDDILLHQDVDLVCTSIPPPLT RQISVKALGIGKNVCEKAATSVDAFRWYTASRYYPQLMSLVON VLRFLPARVMKQLISEHTVGAMTASRYYPQLMSLVON VLRFLPARVMKQLISEHTVGAMTASRYYPQLMSLVON VLRFLPARVMKQLISEHTVGAMTASRYYPQLMSLVON VLRFLPARVMKQLISEHTVGAMTARRYPTVLWAAGGLPEQGPQD VPLLYLKGMVYMVQALRQSFGQGGRRTWMTPVSMAASFEDGL MQGSVUDAIKRSGRGEMBAWVLTEEDDTNONLCEALORNNI. GSAGRLVARGADLYGGWNSATQEELLLRDSLAVGAGLPEQGPQD VPLLYLKGMVYMVQALRQSFGQGGRRTWMTPVSMAASFEDGL MQGSVUDAIKRSGRGEMBAWVLTEEDDTNONLCEALORNNI. FIRRARGCTLSCSSFVEQPTAMEETTMCKMIGGEEANDWKAAE FIRRARGCTLSCSSFVEQPTAMEETTMCKMEAKKRIATSNVI TESLPSAESSPVEIEVELBEDTTTGKMEAKKRIKATSNVI TESLPSAESSPVEIEVELBEDTTTGKMEAKKRIKATSNVI TESLPSAESSPVEIEVELBEDTTGKMEAKRKIKATSNVI TESLPSAESSPVEIEVELBEGTIEVEDGEIETLEEVASAKQSVK	ı	6308	. 5	1118	GRPTRPEKMLLSLVI.HTYSMRVI.I.PSVVI.I.CTA DEVINE
### PANAENT TYLANHOST TUDNI TYADILLAR GONALGHURY ULKEGIK ### WLPPINGWYFADHGGIYVKRSAKYNEK EMMIKUKOSYNDAGTPMYL VIFPEGTRYNPEQTIKULSAS QAPAQORGLAVLKHULTPRIKATH VAPPOCMNYLDAI YUDTUVUKSAS QAPAQORGLAVLKHULTPRIKATH VAPPOCMNYLDAI YUDTUVUKSAS QAPAQORGLAVLKHULTPRIKATH VAPPOCMNYLDAI YUDTUVUKSAS QAPAQORGLAVLKHULTPRIKATH VAPPOCMNYLDAI YUDTUKUSAS QAPAQORGLAVLKHULTPRIKATH VAPPOCMONIA  6310	Į	- 1			LLSAFLPARFYOALDDRIYCVYOSMVLEERENVTCVOTA
### ### ##############################	-				PANKENII YLANHOSTVDWIVADII A TRONALGUURVUI KROLK
VAFPCMKNYLDAIYDOTVVYEKKDGGGGRESPTMTEFICKECP KIHHHIDRIDKKDUPEEGEHMRRWLHERFEICKECP KIHHHIDRIDKKDUPEEGEHMRRWLHERFEICKECP KIHHHIDRIDKKDUPEEGEHMRRWLHERFEICKECP KIHHHIDRIDKKDUPEEGEHMRRWLHERFEICKECP ERRERPEGEKSVMSKLSIKKTLPSMLILGGLTAGKMTDAGRKL VNTWIYCTLLGCLWVTIKA  LVAEVKEPCSLPMLSUPMENERDSVGVKNSMENGRPPDPADWA MDDVINYFRTYGFEEQASHOVGVKSMENGRPPDPADWA MDDVINYFRTYGFEEQASHOVGVGVKSMENGRPPDPADWA MDDVINYFRTYGFEEQASHOVGVGVKSULLMTRNDVLTGLQL KLGPALKIYEYHVKPLQTKHLKNNSS  GPRCWKFLILSSVNCETLRIGKAWPGSGGGERYWTPRTHSSASS AQRGSLASLNVAAAGLMADCDQPLYDCPMCGLICTNYHILGEHV DLHLEENSFQQGMRVQCSGDLQIAIQLQQBEDRKRRSEESRQE IEEFGKLQRQGGLNSGGYKQQQLRNMEIEVNGGMPPSFHRR KADMMESLALGFDDGKTKTSGIIEALHRYVQNAATDURKWULSS VVDHFHSSLGDKGWGGYXROQLRINGIESLLQNDAYNDCLKGMLIP CIPKLGSMIEDAWKEGFDPGGASQLIIRLQSTKAWIGACEVYIL LTSLRV  6311  1 675 PVWWNSGEGPRLAAAARTGHGVGRRARLACLGEPRVKAAVMLTL ASKLKRDDGLKGSTAATASDSTRRVSVRKLUKEVAELEANL PCTCKVHFPDPNKLHCFQLTVTTDEEGYYQGGKPGFETEVPDAXN MYPFKYKCLTKHPRNITESICLSLLKEHSIDGTGWAPTRTI. KDVWGLNSLFTDLLNFDDPLNIEAABHHLRDKEDFRNKVDDYI KRYAR  6312  213 1400 GDELVKREAGMKMLPGVGVFGTGSSARVLVPLLRAEGFTVEALW GKTEEBAKQLAEENNIAFYTSKTDDILLHQDVDLVCISIPPPLT RQISVKALGIGKNVCEKAATSVDAFRMYTASRYYPQLMSLVGN VLRFLPAFVRMQLISEHYVGAVMICDARIYSGSULSPSYGMIC DELMGGGGLHTMGTYIVDLLTHLITGRAEKVHGLLKTFVRQNAA IRGIRHVTSDDFCFFQMLMGGGVCSTVTINFMPGGFVEWMV GSAGRLVARGADLYGQKNSATQEELLRDSLAVGAGLPEQGDQD VPLILYLKGMVVMVQALRQSFGQGGDRRTWRMAASFEDGL YMQSVVDAIKRSSRSGEWAVEVLTEPPDTNQNLCEALQRNNL GSAGRLVARGADLYGCSSFFGCGGGGRRTWRMAASFEDGL YMQSVVDAIKRSSRSGEWAVEVLTEPPDTNQNLCEALQRNNL FHRRAHGCTLSCSFFVGDFTAMEAEETMFELQGFPERHMILD FHRRAHGCTLSCSFFVGDFTAMEAEETMFELQGFFERHMILD FHRRAHGCTLSCSFFVGDFTAMEAEETMFELQGFFERHMILD FLAMCGRGDRFTDTTLVDGHFFKAKKAVLAACSKFFYKFFQEF TOEPLVEIEGGSKMAFRHLIEFTTYTAKLMIGGEBERANDVWRAAE FLQMLEAIKALEVENNENSARPLEENTTGKNRAKKRKLAETSNVI TESJPSAGSSEPVEIEVEIBGEITLEEVASAKGSVK YLGSTGSSDDSALALLADJTKKYRGGDBKGOI VEDCGCGGURDRORD		i			WLPLIGWYFAQHGGIYVKRSAKFNEKEMRNKLOGVUDACTDWG
WAPICHKNYLDATYDYTVYYSEKDDGGORRESPTMTEFICKECP KIHHIDRIKNDYEEGEHMRRWHEREPE IKDKWLIEFSED PERRKRPFGKSVNSKLSIKKTLPSMLILSGITAGMLMTDAGRKL VAVTWIYGTLIGCLWYTIKA  LVAEVKEPCSLPMLSVDMENKENGSVGVKNSMENGRPPDPADWA WMDVVNYFRTVGFEGASAFCOEGIDGKSLILMTRNDVLTGLQL KLGPALKIYETVHVKPLOTKHLKNNSS  GPRCWKFILLSSVNCETLRIGKAPPGSSGGERYWTPRTHSSASE AQRGSLAELNVAAGLWADCDQPLYDCPMCGLICTNYHILQEHV DLHLEENSFQQGMDRVQCSGDLQLANGLQDEDRKRRSESRQE IEFGKLQRQYGLDNSGGYKQQQLANMEIEVNRGMPPSEFHRR KADMMESIALGFDDGKYKTSGIIEALHRYVONAATDURRWNLSS VVDHFHISLGDDKGWGCGYRNFOMLLSSLLONDAYNDCLKGMLIP CIPKIQSMIEDAWKEGFDPOGASQIIRLQGTRVWANALTI ASKLKEDDGLKGSRTAATAGDSTRRUSVRDKLILKEVBAUELEANL PCTCKVHFPDPNKLHCFQLTVTDEGGYQGGKPQFETEVPDAYN MVPFWKGLTKIHPNITETGBICLSLIKEHSIDGTGMAPTRTL KDVWGLNSLFTDLLNFDDPLNIEAABHHRDKGPDFRNKVDDVI KRYAR GATEEBAKQLAEEMNIAFYTSRTDDILLHQDVDLVCISIPPPLT RQISVKALGIGKNVCEKAATVDAFRMVTASRYYPQLMSLVGN VLRFLPAFVRMKQLISEHYVGAVMLCDARISGSSLSPYGNIC DELMGGGLHTMGTYIVDLLTHLTGRAEKVHGLLKFVRQNAA INGIRHVTSDDFCFFQMMGGGVCSTVTLNFMPGGFFVVEAWV GSAGRLVARGADLYGQKNSATQEELLRDSLAVGAGLPEQGFQQ VLLLYLKKMVVMVQALRQSFQGQGDRTWDRTPVSMAASFEDGL MQSVVDAIKRSSRSGWEAVEVUTEEDDTINDNLCEALQRINL FHRRRAHGCTLSCSFFVEDFACHERETERCLGFFPEHKMILD FHRRRAHGCTLSCSFFVEDFACHERETERCLGFPEHHKMILD FHRRRAHGCTLSCSFFVEDFACHERETERCLGFPEHHKMILD FHRRRAHGCTLSCSFFVEDFACHERETERCLGFPEHHKMILD FLOGGGARLAFLESSFFFGCHFYFFVVFWPFLGVL FHRRRHAGGTLSCSSFFVEDFACHERETERCLGFPEHHKMILD FLOGGEGDRFTDITLIVDGHFFKAKKAVLAACKKFFKKFTEEFINTIGKNRAKKRKHEETSNVI TESLPSABSEPVEIEVLIBEDTITGKNRAKKRKHEETSNVI TESLPSABSEPVEIEVLIBEGIITLEEVASAKGGWK VJCSTGSSDDSALALLALDITERCTEVEDGGIETLEEVASAKGGWK VJCSTGSSDDSALALLALDITERCTEVEDGGIETLEEVASAKGGWK VJCSTGSSDDSALALLALDITERCTEVEDGGIETLEEVASAKGGWK VJCSTGSSDDSALALLALDITERCTEVEDGGIETLEEVASAKGGWK VJCSTGSSDDSALALLALDITERCTEVEDGGIETLEEVASAKGGWK VJCSTGSSDDSALALLALDITERCTEVEDGGIETLEEVASAKGGWK VJCSTGSSDDSALALLALDITERCTEVEDGGIETLEEVASAKGGWK VJCSTGSSDDSALALLALDITERCTEVEDGGIETLEEVASAKGGWK VJCSTGSSDDSALALLALDITERCTEVEDGGIETLEEVASAKGGWK	- (	1	1		VIPPEGIRINPEOTKVLSASOAPAAORGIAM VINI TOD TVATOR
PERRKPPGKSVNSKLSIKTIPSMI LISGITAGMMITDAGRKL YVNYMIYGTLLGCLWVTIKA LVAEVKEPCSLPMLSVDMENKENGSVGVKNSMENGRPPDPADWA WMDVNYTRTVGFEQASAFOEOEIDGKSLLIMTRNDVLTGLQL KLGPALKIYEYHVKPLOTKHLKNNSS  GPRCWKFLILSSVNCETHLGKAMPGSSGGERYWTPRTHSSASE AQRGSLAELNVAAAGLWADCDQPLYDCPMCGLICTNYHILDGHV DLHLEENSFQQGMDRVQCSGDLOLAHILQGDEDKRRSEESRQE IEEFQKLQRQYGLDNSGGYKQQOLRNNEIEVNRGRMPPSEPHRR KADMMESIALGFDDGKTKTSGIFEALHRYYONAATDVRRVWLSS VVDHFHSLGGMKWGCGSPKQOQLRNNEIEVNRGRMPPSEPHRR KADMMESIALGFDDGKTKTSGIFEALHRYYONAATDVRRVWLSS VVDHFHSLGGMKWGCGSPKQOQLRNNEIEVNRGRMPPSEPHRR KADMMESIALGFDDGKTKTSGIFEALHRYYONAATDVRRVWLSS VVDHFHSLGGMKWGCGSPKQOQLRNNEIEVNRGRMPPSEPHRR KADMMESIALGFDDGKTKTSGIFEALHRYYONAATDVRRVWLSS VVDHFHSLGGMKWGCGSPKQOQLRNNEIEVNRGRMPSEPHRR KADMMESIALGFDDGKTKTSGIFEALHRYYONAATDVRRVWLSS VVDHFHSLGGMKWGGGRKQOGTRARLACLGEPRVKAAVWLTL ASKLKRDDGLKGSRTAATASDSTRRVSVRDKLLVKEVAELEANL PCTCKWHFPDPNKLHCFQLTVTFDEGYYQGGKFQFETEVPDAAVN MVPPKVKCLTKLWHPNITETGEICLSLLERHSIGGTGWAPTRTL KDVWGCLNSLFTDLLNFDDDFLNIEAAEHHLRDKEDFRNKVDDYI KRYAR GDELVKREAGMKMLPGVGVFGTGSSARVLVPLLRAEGFTVEALW GKTEEBAKQLAEENNIAFYTSSTDDILHQDVDLVGISIPPPLT RQISVKALGIGKNVVCEKAATSVDAFRWYTASRYYPQLMSLVGN VLRFLPAFVRMKQLISEHYVGAWI CDARIYSGSLLSPSYGWIC DELLMGGGGHTWGTYIVDLLTHLTGRAEKVHGLKTFVKNAA IRGIRHVTSDDFCFFQMLMGGGVCSTVTLNFNIMPGAFVHCWAW GSAGRLVARGADLYGQKNSATQEELLLRISLAVGAGLPFQCPQDQ VPLLYLKGMVYWQAALGSGCQGDRTWBTPVSMAASFEDGL YMQSVVDAIKRSSRSGBEEAVEVLTEEPDTRONLCEALQRNNL FHRRAHGCTLSCSSFVEQFTAMEAEETMECLGFFPERHKMILD RLNRQRGQDRFTDTTLIVDGHFKAHKAVLAACSKFFYKFPQEF TOEPLVEIEGGKMAFRHLIEFTYTAKLMIGGBERANDVWKAAE FLQMLEAIKALEVRNNENSAPLEENTTGKNBAKRKKLTETSNVI TESLPSAESEPVEIEVEILBEGTIEVEDEGIETLEEVASAKGSVK YIQSTGSSDDSALALLALDIERGTLYEDGGIETLEEVASAKGSVK YIQSTGSSDDSALALLALDIERGCIFFPERMSKKKKLTETSNVI		1	ļ		VAPDCMKNYLDAIYDVTVVYEGKDDGGOPDEGDTMTDET GUDGD
6310 220 563 LVAEVKEPCSLDMLSVDMENKENGSVGVKNSMENGRPPDPADWA WINDWINTERCHUNTIKA  6310 36 979 GPRCWKFILLSSVNCETLRIGKRWPGSGQERVWTPRTHSSASE AQRGSLABLNVAAAGLWADCUQGEDRKRSEESRQE IDGKSLLMTRNDVLTGLQL KLGPALKYYEYHVKPLQTYHLKNNSS  GPRCWKFILLSSVNCETLRIGKRWPGSGQERYWTPRTHSSASE AQRGSLABLNVAAAGLWADCUQGEDRKRSEESRQE IDEFQKLQRQYGLDNSGGYKQQGLQABIDKQQEBDRKRSEESRQE IDEFQKLQRQYGLDNSGGYKQQGLQNENMETEVNGRMPPSEFHRR KAADMESLALGPDDGKTKTGGI IEBLHRYYQNAATDVRRVWLSS VVDHFHSSLGDKGWGCGYRNFOMLLSSLLQNDAYNDCLKGMLIP CIPKIQSMIEDAWKEGFPDPGGASQLIIRLQGTKAWIGACEVYIL LTSLRV  6311 1 675 PVWWNSCGGPPLAAAARTGHGYGRRARLACLGEPRVKAAVMLTL ASKLKRDDGLKGSKTAATASDSTRVSVNDKLLVKEVABLEANL PCTCKVHFPDPNKLHCFQLTVTPDEGYYGGKFQPFEVPDANN MYPKVKCLTKIHHPNITETGEICLSLLREHSIDGTGWAPTRTL KDVVWGLNSLFTDLLNFDDPLNIEAAEHHLRDKEDFRNKVDDYI KRYAR  6312 213 1400 GDELVKREAGMKMLPGVGVFGTGSSARVLVPLLRAEGFTVEALW GKTEEBAKQLAEEMNIAFTYSRTDDILLHQDVDLVCISIPPPLT RQISVKALGIGKNVVCEKAATSVDAFRNVTASRTYPQLMSLUGN VLRFLPAFVRMKQLISEHYVGAWICDARISSGSLLSPSYGMIC DELMGGGLHTMSTTYUDLHTHIGRRAEKVHGLIKTFVRONAA IRGISHVTSDDFCFFGMLMGGGVCSTVTLNFNMPGAFVHEWWV GSAGRLVARGADLYQKNSATGELLLRDSLAAVGAGDFQQQD VPLLYLKGMVYMVQALRQSFQQGDRTNDNTPVSMAASFEDGL YMQSVVDAIKRSSRSGEWEAVEVLTEPDDTNQNLCEALQRNNL GRAGALVARGADLYQKNSATGELLLRDSLAAVGAGFPQGGDR DVPLLYLKGMVYMVQALRQSFQGGGDRTNDNTPVSMAASFEDGL YMQSVVDAIKRSSRSGEWEAVEVLTEPDDTNQNLCEALQRNNL CRASALAFTSNVI FRRRRAHGCTLSCSSFVEQFTAMEAEETMRCLQEFPEHHKMILD RLNSQREQDRFTDTILIVDGHHFKAHKAVLAACSKFFYKFPQEF TQEPLVSTEGVSYMARALFETSNVI TESLPSAESEPVEIEVETAEGTIEVEDGGIETLEEVASAKQSVK YIQSTGSSDSSAALLABTYKRONSAPLEENTTGKNEAKKKTAETSNVI TESLPSAESEPVEIEVETAEGTIEVEDGGIETLEEVASAKQSVK YIQSTGSSDSSAALLABTYKONSAPLEENTTGKNEAKKKTAETSNVI TESLPSAESEPVEIEVETAEGTIEVEDGGGETENDERV		Į.			VINITATORIOKKDVPEEOEHMRRWI.HERFETKDVM: TERVECES
6310  563  LVAEVKEPSIDMENSUDMENKENGSVGVKNSMENGRPPDPADMA VMDVVNYFRTVGFEEQASAFOEQEIDGKSLLLMTRNDVLTGLQL KLGPALKTYEYHVKPLQTYHLKNNSS  GPRCWKFILLSSVNCETHLGKNWPQSSGQERYWTPRTHSSASE AQROSLAELNVAAAGLWADCDQPLYDCPMCGLICTMYHLLQEHV DLHLEENSFQCGOMDRVQCSGDLQAHIQLQQEEDRKRSEESRQE IEEFQKLQRQYGLDNSGGYKQOQLRNMETEVNRGRMPPSEFHRR KADMMESLALGFDGKTKTSGIIEALHRYYQNAATDVRRWLGS VVDHFHSSLGDKGWGCGYRNFOMLLSSLLQNDAYNDCLKGMLIP CIPKIOSMIEDAWKEGFDPQGASQLIIRLGGTKAWIGACEVYIL LTSLRV  6311  1 675  PVWMNSCEGPRLAAAARTGHGVGRRARLACLGEPRVKAAVMLTL ASKLKRDDGLKGSTRAATASDSTRRVSVRDKLLVKEVABLEANL PCTCKVHFPDPNKHCFQLTVTPDEGYYQGGKFQFETEVPDAYN MVPFKVKCLTKIHHPNITETGEICLSLLREHSIDGTGWAPTRTL KDVVWGLNSLFTDLLHFDDPLNIEABEHLRDKEDFRNKVDDYI KRYAR  6312  213  1400  GDELVKREAGMKMLPGVGVFGTGSSARVLVPLLRAEGFTVEALW GKTEEBAKQLAEEMNIAFYTSRTDDILHQDVDLVCISIPPPLT RQISVKALGIGKNVVCEKAATSVDAFRNVTASRYYPQLMSLVGN VLRFFPAFVRKQLISEHYVGAVMICDARIYSGSLLSFSYGWIC DELMGGGGLHTMGTYIVDLLTHLTGRRAEKVHGLLKTFVRONAA IRGIRHVTSDDFCFFOMLMGGGVCSTVTLHFNMFGAFVHEWAVV GSAGRLVARGADLYGGKNSATQEELLLRDSLAVGAGLPEQGPQD VPLLYLKGMVYMVQALRQSFQGGDRTWDRTFVSMAASFEDGL YMGSVVDAIKRSSRSGEWBAVBVLTEPPDTNQNLCEALQRNNL GSAGRLVARGADLYGGKNSATQEELLLRDSLAVGAGLPEQGFPQD VPLLYLKGMVYMVQALRQSFQGGDRTWDRTFVSMAASFEDGL YMGSVVDAIKRSSRSGEWBAVBVLTEPPDTNQNLCEALQRNNL FHRRAHGCTLSCSSFVEQFTAMEAEETMECLQEFFEHHKMILD RLNSQREQDRTFDITLIVDGHHFKAHKAVLAACSKFFYKFFQGF TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE FLQMLEAIKALEVRNKENSAPLEENTTGRNEAKKKIAETSNVI TESLPPSAESEPVEIEVELAEGTIEVEDEGGTETLEEVASAKQSVK YIQSTGSSDDSSALALLADTSKYROGDBEGETDEVASAKQSVK		j	ŀ		PERREPERSVNSKLSIKKTLPSMLILSGLTAGMT.MTDAGDVt
LVAEVKEPCSLEMLSVDMENKENGSVGVKNSMENGRPPDPADWA WDDVANTYFRTVGFEEQASAPOQEIDGKSLLMTRNDVLTGLQL KLGPALKIYEYHVKPLQTKHLKNNSS  979 GPRCWKFILISSVNCETLRIGKAMPQSSGQERYWTFFTHSSASE AQROSLASLNVAAAGHADCDQPLYDCDMCGLICTNYHLLQEHV DLHLEENSFQQGMDRVQCSGDLQLAIQLQQEEDRKRRSEESROE IEBFQKLQRQVGLDNSGGYKQQQLRNMEIEVNRGRMPPSEFHRR KADMMESLALGPDDGKKTKTGIIELHRYYOMAATDVRRYWLSS VUDHFHSSLGDKGWGGGYRNFOMLLSSLLQNDAYNDCLKGMLTP CIPKLQSMIEDAWKEGFDPQGASQLIIRLQGTKAWIGACEVYIL LTSLRV  6311 1 675 PVWWNSCEGPRLAAAARTGHGVGRRARLACLGEPRVKAAVMLTL ASKLKRDDGLKGSRTAATASDSTRRVSVRKLLVKEVAELEANL PCTCKVHFPDPNKLHCFQLTVTPDEGYYQGKFOFETEVPDAYN MYPFKVKCLTKIWHPNITETGBICLSLLREHSIDGTGMAPTRTL KRYAR  6312 213 1400 GDELVKREAGMKMLPGVGVFGTGSSARVLVPLLRAEGFTVEALW GKTEEBAKQLAEEMNIAFYTSRTDDILLHQDVDLVCISIPPPLT RQISVKALGIGKNVVCEKAATSVDAFRMVTASRYYPQLMSLVGN VLRFLPAFVRMKQLISEHYVGAVMICDARIYSGSLLSPSYGWIC DELMGGGGLHTMGTYJTVDLLTHLTGRAEKVHGLLKTFVRONAA IRGIRHVTSDDFCFFQMLMGGGVCSTVTLNFNMPGAFVHCWNV GSAGRLVARGADLYGKNSATQEELLLEDSLAVGAGLPEQGPQD VPLLYLKGMVYMVQALRQSFCGCGRRTMDRTVSWAASFEDGL YMQSVVDAIKRSSRSGEWEAVBVUTEEPDTNONLCEALQRNNL GRGGAGRLVARGADLYGKNSATQEELLLEDSLAVGAGLPEQGPD TOEPLVETELGSKGMAFRHLIEFTTTAKHAVLAACSKFFYKFFQEF TOEPLVETELGSKGMAFRHLIEFTTTAKHAVLAACSKFFYKFFQEF TOEPLVETELGSKGMAFRHLIEFTTTAKHMIGGEBEANDVWKAAE FLQMLEAIKALEVENKENSAPLEENTIGKNRAKKRKIAETSNVI TESLPSAESEPVEIEVEILBEGTIEVEDEGIETLEEVASKOSVK YIQSTGSSDDSALALLALDISKYROGDBKGOTKPRORD	<b> </b> -	6309	320		IVNIWIYGTLLGCLWVTIKA
6310 36 979 GPRCWKFLILSSVNCETLRIGKAWPQSGQERYWTFRTHSSASE AQRGSLASLNVAAAGLWADCDQPLYDCPMCGLICTMYHILQEHV DLHLEENSFQQGMDRVQCSGDLQLAHQLQQEEDRKRRSEESRQE IEEFQKLQRQYGLDNSGGYKQQLRNMEIEVNRGRMPPSEFHRR KADMMESLALGPDDGKTKTSGI IEALHRYYQNAATDVRRWLSS VVDHFHSSLGDKGWGGYRNFOMLLSSLLQNDAYDDCLKGMLIP CIPKIQSMIEDAWKEGFDPQGASQLIIRLGGTKAWIGACEVYIL LTSLRV  6311 1 675 PWWWSCEGPRLAAAARTGHGVGRRARLACLGEPRVKAAVMLTL ASKLKRDDGLKGSRTAAAARTGHGVGRRARLACLGEPRVKAAVMLTL ASKLKRDDGLKGSRTAATASDSTRRVSVRDKLLUKEVABLEANL PCTCKVHFPDPNKLHCFQLTVYDDEGYYQGGKFQFETEVPDAYN MVPPKVKCLTKIWHPNITETGEICLSLREHSIDGTGWAPTRTL KDVVWGLNSLFTDLLNFDDPLNIEAAEHHLRDKEDFRRKVDDYI KRYAR  6312 213 1400 GDELVKREAGMKMLPGVGVFGTGSSARVLVPLLRAEGFTVEALW GKTEERAKQLAEEMNIAFYTSRTDDILLHQDVDLVCISIPPPLT RQISVKALGIGKNVVCEKAATSVDAFRMYTASRYYPOLMSLVGN VLRFLPFFYRMKQLISEHYVGAVMI CDARIYSGSLLSPSYGWIC DELMGGGGLHTMGTYIVDLLTHLTGRRAEKVHGLLKTFVRONAA IRGIRHVTSDDFYNMKDLISEHYVGAVMI CDARIYSGSLLSPSYGWIC GSAGRLVARGADLYGQNNSATQEELLLRDSLAVGAGLPEQGPQD VPLLYLKGMVYMVQALRQSFQGQGDRRTWDRTPVSMAASFEDGL YMQSVVDAIKRSRSGGEWEAVEVLTEEDDTNONLCEALQRNNL GSAGRLVARGADLYGGNNSATQEELLLRDSLAVGAGLPEQGPQD VPLLYLKGMVYMVQALRQSFQGQGDRRTWDRTPVSMAASFEDGL YMQSVVDAIKRSRSGGEWEAVEVLTEEDDTNONLCEALQRNNL FHRRRAHGCTLSCSSFVEQPTAMEAEETMELLQEFFEHHKMILD RLNGQRQDRFTDITLIVDCHHFKAHKAVLAACSKFFYKFPGEF TOEPLUEGUSGENTERTSTVALMIQGGEEANDVWKAAE FLQMLEAUSGUSGEGRANDSVK YLQSTGSSDDSALALLADITSKYRQGDRKGDIKFGGEGRANDVWKAAE FLQMLEAUSGDSSALALDITSKYRQGDRKGDIKFGGEGRANDVWKAAE FLQMLEAUSGDSSALALDITSKYRQGDRKGDIKFGGEGRANDVWKAAE FLQMLEAUSGDSSALALDITSKYRQGDRKGDIKFGGEGRANDVWKAAE FLQMLEAUSGDSSALALDITSKYRQGDRKGDIKFGGEGERNDVWKAAE FLQMLEAUSGDSSALALDITSKYRQGDRKGDIKFGGEGERNDVWKAAE FLQMLEAUSGDSSALALLDITSKYRQGDRKGDIKFGGGEGERNDVWKAAE FLQMLEAUSGDSSALALDITSKYRQGDRKGDIKFGGEGERNDVWKAAE FLQMLEAUSGDSSALALDITSKYRQGDRKGDIKFGGEGERNDVWKAE FLQMLEAUSGDSSALALLDITSKYRQGDRKGDIKFGGEGERNDVWKAE FLQMLEAUSGDSSALALLDITSKYRQGDRKGDITTLEEVASAKQSVK			220	563	LVAEVKEPCSLPMLSVDMENKENGSVGVKNSMENGRPPDPADWA
6310 36 979 GPRCWKFILLSSYNCETTRIGKAWPOSSGQERYWTPRTHSSASE AQRGSLASINVAAAGLWADCDQPLYDCPMCGLICTNYHILQEHV DLHLEENSFQQMDRYQCSGDLQLAHQLQQEDERKRSEESRQE IEEFCKLORQYGLDNSGGYKQQQLRNMEIEVNRGRMPPSEFHER KADMMESLALGFDDGKTKTSGI IEALHRYYQNAATDVRRVWLSS VVDHFHSSLGDKGWGGYRNFOMLLSSLLQNDAYNDCLKGMLIP CIPKIGSMIEDAWKEGFDPQGASQLIIRLQGTKAWIGACEVYIL LTSLRV  6311 1 675 PVWWNSCEGPRLAAAARTGHGVGRRARLACLGEPRVKAAVMLTL ASKLKRDDGLKGKRDDGKKGSRTAATASDSTRRVSVRDKLLVKEVAELEANL PCTCKVHFPDPNKLHGFQLTVTPDEGYYGGKFQFFETEVDAYN MYPKVKCLTKIWHPNITETGEICLSLLREHSIDGTGWAPTRTL KDVVWGLNSLFTDLLNFDDPLNIEABEHHLRDKEDFRNKVDDYI KRYAR  6312 213 1400 GDELVKREAGMKMLPGVGVFGTGSSARVLVPLLRAEGFTVEALW GKTEEBAKQLAEENNIAFYTSRTDDILLHQDVDLVCISIPPPLT RQISVYALGIGKNVVCEKAATSVDAFRNVTASRYYPQLMSLVGN VLRFLPBAFVRMKQLISEHYVGAVMICDARIYSGSLLSPSYGWIC DELMGGGGHTMGTTIVDLITHLTGRRAEKVHGLLKTFVRONAA IRGIHNVTSDFCFFQMLMGGGVCSTVTLNFNMPGAFVHEVMVV GSAGRLVARGADLYGQKNSATQEELLLRDSLAVGAGLPEQGPQD VPLLYLKGMVYMVQALRGSFGGGGDRTWDRTPVSMAASFEDGL YMQSVVDAIKRSSRGEWEAVEVLTEEPDTNQNLCEALQRNNL GRAGKTELLCRALGRANDLYKGARGALFEGGFTGVFVVVVFPDLGVL FHRRAHGCTLSCSSFVEQPTAMEAEFTMECLQEFPEHKMILD RLNEQREQDRFTDITLIVDGHHFKARKANLAACSKFFYNFFQEF TQFFLVEIGGVSFTDITLIVDGHHFKARKANLAACSKFFYNFFQEF TQFFLVEIGGVSFTDITLIVDGHFFKARKANLAACSKFFYNFFQEF TQFFLVEIGGVSFTDITLIVDGHFFKARKANLAACSKFFYNFFQEF TQFFLVEIGGVSGSSDDSALALADITSKYRGOGDPKGU KRECKEDDRWK		1			VMDVVNYFRTVGFEEOASAFOEOETDGKSLJ.IMTPNDVI mor or
GPRCWKFILLSSVNCETILIGKAWPOSSGQERYWTPRTHSSASE AQROSLASILNVAAAGLWADCDQPLYDCPMCGLICTNYHLLQEHV DLHLEENSFQQMDRVQCSGDLQLAHQLQQEDDRKRSEESRQE IEEFQKLQRQYGLDNSGGYKQQQLRMMEIEVNRGRMPPSEFHRR KADMMESLALGFDDGKTKTSGIIEALHRYYQNAATDVRRVWLSS VVDHFHSSLGDKGWGGGYRNFOMLLSSLLQNDAYNDCLKGMLIP CIPKIQSMIEDAWKEGFDPQGASQLIIRLQGTKAWIGACEVYIL LTSLRV  6311 1 675 PVWWNSCEGPRLAAAARTCHGVGRRARLACLGEPRVKAAVMLITL ASKLKRDDGLKGSRTAATASDSTRRVSVRDKLLVKEVAELEANL PCTCKVVHPPDPNKLHCFQLTVTPDEGYYQGGKRQFETEVPDAYN MVPKVKCLTKIWHPNITETGEICLSLLREHSIDGTGWAPTRTL KDVVWGLNSLFTDLLNFDDPLNIEABEHHLRDKEDFRNKVDDYI KRYAR GKTEEBAKQLAEENNIAFYTSRTDDILLHQDVDLVCISIPPPLT RQISVXALGIGKNVVCEKAATSVDAFFRWTASRYYYQLMSLVGN VLRFLPAFVWMKQLISEHYVGAVMICDARIYSGSLLSPSYGWIC DELMGGGGHTMGTYIVDLLTHLTGRRAEKVHGLLKTFVRONAA IRGIRHVTSDDFCFFGMLMGGGVCSTVTLNFNMPGAFVHEVMVV GSAGRLVARGADLYGQKNSATCEELLLRDSLAAVGACLPEQOPQD VPLLYLKGMVYMVQALRQSFQGGDRRTWDRTPVSMAASFEDGL YMQSVVDAIKRSSRSGEWEAVEVLTEEPDTMQNLCCALQRNNL GRSGARLAFLPSFFSPACVHRSPLSFHGCUPFYFVVVFMPLGVL FHRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFFEHKMILD RLNEQREQDRFTDITLIVOGHFKAKKAUAACSKFYKFFQEF TOFFLVEIEGVSKMAYFHLIEFTYTAKLMIQGEEANDVWKAAE FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKKKHAETSNVI TESLLPSAESEPVEIEVEIAECTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSALALALDITSKYRGGDRKGUJKRGCEREDDRGV	$\vdash$	6310	36	050	KLGPALKIYEYHVKPLOTKHLKNNSS
DIHLEENSFQOEGDRONGUCSGDLQLANGLQQEEDRKRRSESRQE IEEFQKLQRQYGLDNSGGYKQQQLRNMBIEVNRGRMPPSEFHRR KADMMESLALGFDDGKTHTSGIIEALHRYYQNAATDVRRVWLSS VVDHFHSSLGDKGWGCGYRNFQMLLSSLLQNDAYNDCLKGMLIP CIPKLQSMIEDAWKEGFDPQGASQLIIRLQGTKAWIGACEVYIL LTSLRV  6311  1 675 PVWWNSCEGPRLAAAARTGHGVGRRARLACLGEPRVKAAVWLTL ASKLKRDDGLKGSTAATASDSTRRVSVRDKLLVKEVAELEANL PCTCKVHFPDPNKLHCFQLTVTPDEGYYQGKFQFSTEVPDAYN MV>PKVKCLTKIWHPNITETGEICLSLLREHSIDGTGWAPTRTL KDVVWGLNSLFTDLLNFDDPLNIEAABHHLRDKEDFRNKVDDYI KRYAR  6312 213 1400 GDELVKREAGMKMLPGVGVFGTGSSARVLVPLLRAEGFTVEALW GKTEERAKQLAEEMNIAFYTSRTDDILLHQDVDLVCISIFPPLT RQISVKALGIGKNVVCEKAATSVDAFRMVTASRYYPQLMSLUGN VLRFLPAFVRNKQLISEHYVGAVMICDARIYSGSLLSPSYGWIC DELMGGGGLHTMGTYIVDLLTHLTGRAEKVHGLLKTFVRQNAA IRGIRHVTSDDFCFFQMLMGGGVCSTVTLNFNMPGAFVHEVMVV GSAGRLVARGADLYGQKNSATQEELLLRDSLAVGAGLPEQGPQD VPLLYLKGMVYMVQALRGSFQGQGDRRTNDRTPVSMAASFEDGL YMQSVVDAIKRSSRSGEWEAVEVLTEEPDTNQNLCEALQRNNL GSAGRLVARGADLYGCKNSATQEELLRDSLAVGAGLPEQGPQD VPLLYLKGMVYMVQALRGSFQGGDRRTNDRTPVSMAASFEDGL YMQSVVDAIKRSSRSGEWEAVEVLTEEPDTNQNLCEALQRNNL FHRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHKMILD RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFVKFFQEF FHRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHKMILD RLNEQREQDRFTDITLIVDGHPKAHKAVLAACSKFFVKFFQEF TGEPLVEIEGVSKNAFRHLIEFTTTAKLMIGGEBEANDUWKAAE FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI TESLPSAESEPVEIEVELAEGTIEVEDEGIETLEEVASAKGSVK YIQSTGSSDDSALALLADITSKVROGDBKGOT WEDCGREDDMWV				979	GPRCWKFLILSSVNCETLRIGKAWPQSSGQERYWTPRTHSSASE
IEEFQKLORQYGLDNSGGYKQQQLRMREIEVNRGRMPFSEFHRR   IEEFQKLORQYGLDNSGGYKQQQLRMMEIEVNRGRMPFSEFHRR   KADMMESLALGFDDGKTKTSGI IEALHRYYQNAATDVRVWLSS   VVDHFHSSLGDKGGGGYRNFQMLLSSLLQNDAYNDCLKGMLIP   CIPKIQSMIEDAWKEGFDPQGASQLIIRLGGTKAWIGACEVYIL   LTSLRV	-	1	1		MURUS LASLINVAAAGLWADCDOPT.VDCDMCCT.TCMTVIITT COURS
KADMMESLALGFDDGKTKKTSG I EALHRYYQNAATDVRRWILSS VVDHFHSSLGDKGWGCGYRNFQMLISSLLQNDAYNDCLKGMLIP CIPKIQSMIEDAWKEGFDPGASQLIIRLQGTKAWIGACEVYIL LTSLRV  6311 1 675 PVWWNSCEGPRLAAAARTGHGVGRRARLACLGEPRVKAAVMLTL ASKLKRDDGLKGSRTAATASDSTRRVSVRDKLLVKEVAELEANL PCTCKVHFPDPNKHHCFQLTVTPDEGYYQGGKFQFETEVPDAYN MVPFKVKCLTKIKHPNITETGEICLSLLREHSIDGTGWAPTRTL KDVVWGLNSLFTDLLNFDDPLNIEAABHHLRDKEDFRNKVDDYI KRYAR  6312 213 1400 GDELVKREAGMKMLPGVGVFGTGSSARVLVPLLRAEGFTVEALW GKTEEBAKQLAEEMNIAFYTSRTDDILLHQDVDLVCISIPPPLT RQISVKALGIGKNVVCEKAATSVDAFRMVTASRYYPQLMSLVGN VLRFLPAFVRMKQLISEHYVGAVMICDARIYSGSLLSPSYGWIC DELMGGGGLHTMGTYIVDLLTHLTGRRAEKVHGLLKTFVRQNAA IRGIRHVTSDDFCFFQMLMGGGVCSTVTLNFNNMPGAFVHEVMVV GSAGRLVARGADLYGGKNSATQEELLLRDSLAVGAGLPEQGPQD VPLLYLKGMVYMVQALRQSFQGQGDRRTWDRTPVSMAASFEDGL YMQSVVDAIKRSSRSGEWEAVEVLTEEPDTNQNLCEALQRNNL GRIGHGTHANGTSTRAGKHGLUSSESPVEUPTAMEABETMECLQEFPEHKMILD FHRRAHGCTLSCSSFVEQPTAMEABETMECLQEFPEHKMILD RLNEGREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF TQEPLVEIEGVSKMAFRHLLEFTTYTAKLMIGGEEEANDVWKAAE FLQMLEAIKALEVRNKENSAPLEENTTGKNBAKKRKIAETSNVI TESLPSAESEPVELEVEIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSALALLADITSKYRGGDRFGGTEEDDGRV	1				DURILLE NS FOOGMORVOCSGDI OLAHOI OOFFD PROPERTIES
### ALMMINISTALTS PROGREMS TEALHRY YONA TOUR TWISS VUPHFHSSLED KERGEGYRN FOM LISS LLOND A YNDEL KEMLIP CIPKIQSMIED AWKEGFDP QGASQLIIRLQGTKAWIGACE VYIL LTSLRV    1	1	i			IEEFQKLQROYGLDNSGGYKOOOLRNMFTEUNDCDMDDGGDMDDGGGT
6311 1 675 PVWWNSCEGPRLAAAARTGHGVGRRARLACLGEPRVKAAVMLTL ASKLKRDDGLKGSRTAATASDSTRRVSVRDKLLVKEVAELEANL PCTCKVHFPDPNKLHCFQLITVTPDEGYYQGGKFQFETEVPDAYN MVPPKVKCLTKIWHPNITETGEICLSLLREHSIDGTGWAPTRTL KDVVWGLNSLFTDLLNFDDPLNIEAAEHHLRDKEDFRNKVDDYI KRYAR  6312 213 1400 GDELVKREAGMKMLFGVGVFGTGSSARVLVPLLRAEGFTVEALW GKTEEBAKQLAEEMNIAFYTSRTDDILLHQDVDLVCISIPPPLT RQISVKALGIGKNVVCEKAATSVDAFFRNVTASRYYPQLMSLVGN VLRFLPAFVRMKQLISEHYVGAVMICDARIYSGSLLSPSYGWIC DELMGGGGLHTMGTYIVDLLTHLTGRRAEKVHGLLKTFVRONAA IRGIRHVTSDDFCFFQMLMMGGGVCSTVTLNFNMPGAFVHEVMVV GSAGRLVARGADLYGQKNSATQEELLLRDSLAVGAGLPEQGPQD VPLLYLKGMVYMVQALRQSFQGQGDRRTWDRTPVSMAASFEDGL YMQSVVDAIKRSSRSGEWEAVEVLTEEPDTNQNLCEALQRNNL GSAGRLVARGADLYGGKNSATCEELLRDSLAVGAGFPEHHKNILD FHRRAHGCTLSCSSFVEQPTAMEAEETMECLGEFPEHHKNILD RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI TESLPSAESEPVEIEVEIAEGTIEVEDGGIETLEEVASAKQSVK YJQSTGSSDDSALALLADITSKYRGGDRKGGIKEDCRERDRTGK					AADMMESTALGEDDGKTKTSGIIEALHRVVONAATDVBDIMIT GG
6311 1 675 PWWMNSCEGPRLAAAARTGHGVGRRARLACLGEPRVKAAVMITL ASKLKRDDGLKGSRTAATASDSTRVSVRDKLLVKEVAELEANL PCTCKVHFPDPNKLHCFQLTVTPDEGYYQGGKFQFSTEVPDAYN MVPPKVKCLTKIWHPNITETGEICLSLLREHSIDGTGWAPTRTL KDVWWGLNSLFTDLLNFDDPLNIEAAEHHLRDKEDFRNKVDDYI KRYAR  6312 213 1400 GDELVKREAGMKMLPGVGVFGTGSSARVLVPLLRAEGFTVEALW GKTEEEAKQLAEEMNIAFYTSRTDDILLHQDVDLVCISIPPPLT RQISVKALGIGKNVVCEKAATSVDAFRMVTASRYYPQLMSLVGN VLRFLPAFVRMKQLISEHYVGAVMICDARIYSGSLLSPSYGWIC DELMGGGGLHTMGTYIVDLLTHLTGRRAEKVHGLLKTFVRQNAA IRGIRHVTSDDFCFFQMLMGGGVCSTVTLNFNMPGAFVHEVMVV GSAGRLVARGADLYGQKNSATQEELLLRDSLAVGAGLPEQGPQD VPLLVILKGMVYMVQALRQSFQGQGDRTWDRTPVSMAASFEDGL YMQSVVDAIKRSSRSGEWEAVEVLTEEPDTMQNLCEALQRNNL FHRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSALALLADITSKYROGDRKGOIKEDGCDERDROK	1	1			CIPKIOSMIEDAWYDODAYNDCLKGMLIP
6311 1 675 PVWWNSCEGPRLAAAARTGHGVGRRARLACLGEPRVKAAVMLTL ASKLKRDDGLKGSRTAATASDSTRRVSVRDKLLVKEVAELEANL PCTCKVHFPDPNKLHCFQLTVTPDEGYYQGGKFQFETEVPDAYN MVPPKVKCLTKLWHPNITETGEICLSLLREHSIDGTGWAPTRTL KDVVWGLNSLFTDLLNFDDPLNIEAAEHHLRDKEDFRNKVDDYI KRYAR  6312 213 1400 GDELVKREAGMKMLPGVGVFGTGSSARVLVPLLRAEGFTVEALW GKTEEEAKQLAEEMNIAFYTSRTDDILLHQDVDLVCISIPPPLT RQISVKALGIGKNVVCEKAATSVDAFRMVTASRYYPQLMSLVGN VLRFLPAFVRMKQLISEHYVGAVMICDARIYSGSLSPSYGWIC DELMGGGGLHTMGTYIVDLLTHLTGRRAEKVHGLLKTFVRQNAA IRGIRHVTSDDFCFFQMLMGGGVCSTVTLNFNMPGAFVHEVMVV GSAGRLVARGADLYGQKNSATQEELLLRDSLAVGAGLPEQGPQD VPLLYLKGMVYMVQALRQSFQGQGDRTMDRTPVSMAASFEDGL YMQSVVDAIKRSSRSGEWEAVEVLTEEPDTNQNLCEALQRNNL GRIGHATSDSTRACHSPFSPACVHRSPLSFHGCWFYFVVVFMPLGVL FHRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHKMILD RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSALALLADITSKYRGGDRKGOIKEDGGREDDTGVK	L			1	LTSLRY
ASALKKULGEKGSTTAATASDSTRRVSVRDKLLVKEVAELEANL PCTCKVHFPDPNKLHCFQLTVTPDEGYYQGKFQFETEVPDAYN MVPPKVKCLTKIWHPNITETGEICLSLLREHSIDGTGWAPTRTL KDVVWGLNSLFTDLLNFDDPLNIEAAEHHLRDKEDFRNKVDDYI KRYAR  6312 213 1400 GDELVKREAGMKMLPGVGVFGTGSSARVLVPLLRAEGFTVEALW GKTEEBAKQLAEEMNIAFYTSRTDDILLHQDVDLVCISIPPPLT RQISVKALGIGKNVVCEKAATSVDAFRMVTASRYYPQLMSLVGN VLRFLPAFVRMKQLISEHYVGAVMICDARIYSGSLLSPSYGMIC DELMGGGGLHTMGTYIVDLLTHLTGRRAEKVHGLLKTFVRQNAA IRGIRHVTSDDFCFFQMLMGGGVCSTVTLNFNMPGAFVHEVMVV GSAGRLVARGADLYGQKNSATQEELLLRDSLAVGAGLPEQGPQD VPLLYLKGMVYMVQALRQSFQGCGDRRTWDRTPVSMAASFEDGL YMQSVVDAIKRSSRSGEWEAVEVLTEEPDTNQNLCEALQRNNL FHRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHKMILD RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE FLQMLEAIKALEVRNKENSAPLEENTTGKNRAKKRIAETSNVI TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSALALLADITSKYROGDRKGUIKEDGCDERDTKK		6311	1	675	
6312 213 1400 GDELVKREAGMKMLPGVGVFGTGSSARVLVPLLRAEGFTVEALW  KRYAR  GDELVKREAGMKMLPGVGVFGTGSSARVLVPLLRAEGFTVEALW  GKTEEEAKQLAEEMNIAFYTSRTDDILLHQDVDLVCISIPPPLT  RQISVKALGIGKNVVCEKAATSVDAFRMVTASRYYPQLMSLVGN  VLRFLPAFVRMKQLISEHYVGAVMICDARIYSGSLLSPSYGWIC  DELMGGGGGLHTMGTYIVDLLTHLTGRRAEKVHGLLKTFVRQNAA  IRGIRHVTSDDFCFFQMLMGGGVCSTVTLMFMMPGAFVHEVMVV  GSAGRLVARGADLYGQKNSATQEELLLRDSLAVGAGLPEQGPQD  VPLLYLKGMVYMVQALRQSFQGQGDRRTWDRTPVSMAASFEDGL  YMQSVVDAIKRSSRSGEWEAVEVLTEEPDTNQNLCEALQRNNL  QRSGAARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVFMPLGVL  FHRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD  RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF  TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE  FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI  TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASKQSVK  YIQSTGSSDDSALALLADITSKYRGGDRKGOIKEDGCGERDREGK	1	- 1		- · - · · ·	ASKLKRDDGLKGCPTA TA CDGMD
6312 213 1400 GDELVKREAGMKMLPGVGVFGTGSSARVLVPLLRAEGFTVEALW  GKTEEBAKQLAEEMNIAFYTSRTDDILLHQDVDLVCISIPPPLT RQISVKALGIGKNVVCEKAATSVDAFRMVTASRYYPQLMSLVGN VLRFLPAFVRMKQLISEHYVGAVMICDARIYSGSLLSPSYGWIC DELMGGGGLHTMCTYIVDLLTHLTGRRAEKVHGLLKTFVRQNAA IRGIRHVTSDDFCFFQMLMGGGVCSTVTLNFIMMPGAFVHEVMVV GSAGRLVARGADLYQQKNSATQEELLLRDSLAVGAGLPEQGPQD VPLLYLKGMVYMVQALRQSFQGQGDRRTWDRTPVSMAASFEDGL YMQSVVDAIKRSSRSGEWEAVEVLTEEPDTNQNLCEALQRNNL QRSGAARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVFMPLGVL FHRRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSALALLADITSKYRGGDRKGOIKEDGCGERDREGK	İ			1	PCTCKVHEPDPNYLLCEOX WWW.DDCC.
ADVWEINSETTDLINFDDPLNIEAAEHHLRDKEDFRNKVDDYI KRYAR  GDELVKREAGMKMLPGVGVFGTGSSARVLVPLLRAEGFTVEALW GKTEEBAKQLAEENNIAFYTSRTDDILLHQDVDLVCISIPPPLT RQISVKALGIGKNVVCEKAATSVDAFRMVTASRYYPQLMSLVGN VLRFLPAFVRMKQLISEHYVGAVMICDARIYSGSLLSPSYGWIC DELMGGGGLHTMGTYIVDLLTHLTGRRAEKVHGLLKTFVRQNAA IRGIRHVTSDDFCFFQMLMGGGVCSTVTLNFNMPGAFVHEVMVV GSAGRLVARGADLYQQKNSATQEELLLRDSLAVGAGLPEQGPQD VPLLYLKGMVYMVQALRQSFQGGDRRTWDRTPVSMAASFEDGL YMQSVVDAIKRSSRSGEWEAVEVLTEEPDTNQNLCEALQRNNL GRSGARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVFMPLGVL FHRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHKMILD RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSALALLADITSKYRGGDRKGOIKEDGCDERDREGK	1	ł	į	j	MV2PKVKCLTKTWUDNTTETTCDICK CITADOGKFQFETEVPDAYN
6312 213 1400 GDELVKREAGMKMLPGVGVFGTGSSARVLVPLLRAEGFTVEALW GKTEEEAKQLAEEMNIAFYTSRTDDILLHQDVDLVCISIPPPLT RQISVKALGIGKNVVCEKAATSVDAFRMVTASRYYPQLMSLVGN VLRFLPAFVRMKQLISEHYVGAVMICDARIYSGSLLSPSYGWIC DELMGGGGLHTMGTYIVDLLTHLTGRRAEKVHGLLKTFVRONAA IRGIRHVTSDDFCFFQMLMGGGVCSTVTLNFNMPGAFVHEVMVV GSAGRLVARGADLYQGKNSATQEELLLRDSLAVGAGLPEQGPQD VPLLYLKGMVYMVQALRQSFQGQDRRTWDRTPVSMAASFEDGL YMQSVVDAIKRSSRSGEWEAVEVLTEEPDTNQNLCEALQRNNL FHRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHKMILD RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSALALLADITSKYROGDRKGOIKEDGCDERDREGK	1	1	}	Í	KDVVWGLNSLFTDLINEDDDI NIEADERINI DOMONIA
GDELVKREAGMKMLPGVGVFGTGSSARVLVPLLRAEGFTVEALW GKTEEBAKQLAEENNIAFYTSRTDDILLHQDVDLVCISIPPPLT RQISVKALGIGKNVVCEKAATSVDAFRMVTASRYYPQLMSLVGN VLRFLPAFVRMKQLISEHYVGAVMICDARIYSGSLLSPSYGWIC DELMGGGGLHTMCTYIVDLLTHLTGRRAEKVHGLLKFTVRQNAA IRGIRHVTSDDFCFFQMLMGGGVCSTVTLNFMMPGAFVHEVMVV GSAGRLVARGADLYGQKNSATQEELLLRDSLAVGAGLPEQGPQD VPLLYLKGMVYMVQALRQSFQGQGDRRTWDRTPVSMAASFEDGL YMQSVVDDAIKRSSRSGEWEAVEVLTEEPDTNQNLCEALQRNNL YMQSVVDAIKRSSRSGEWEAVEVLTEEPDTNQNLCEALQRNNL FHRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF TOEFLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSALALLADITSKYROGDRKGOIKEDGCDERDREGK	$\vdash$				KRYAR
GKTEEBAKQLAEENNTAFYTSRTDDILLHQDVDLVCISIPPPLT RQISVKALGIGKNVVCEKAATSVDAFRMVTASRYYPQLMSLVGN VLRFLPAFVRMKQLISEHYVGAVMICDARIYSGSILSPSYGWIC DELMGGGGLHTMGTYIVDLLTHLTGRRAEKVHGLLKTFVRQNAA IRGIRHVTSDDFCFFQMLMGGGVCSTVTLNFNMPGAFVHEVMVV GSAGRLVARGADLYGQKNSATQEELLLRDSLAVGAGLPEQGPQD VPLLYLKGMVYMVQALRQSFQGQGDRRTWDRTPVSMAASFEDGL YMQSVVDAIKRSSRSGEWEAVEVLTEEPDTNQNLCEALQRNNL GSGAARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVFMPLGVL FHRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSALALLADITSKYROGDRKGOIKEDGCDESDERGEV	1	0312	213		GDELVKREAGMKMLPGVGVEGTGSSARVLVDLL DA HONEUTO
VLRFLPAFVRMKQLISEHYVGAVMICDARIYSGSLLSPSYGWIC DELMGGGGLHTMGTYIVDLLTHLTGRRAEKVHGLLKTFVRQNAA IRGIRHVTSDDFCFFQMLMGGGVCSTVTLNFNMPGAFVHEVMVV GSAGRLVARGADLYGQKNSATQEELLLRDSLAVGAGLPEQGPQD VPLLYLKGMVYMVQALRQSFQGQGDRTWDRTPVSMAASFEDGL YMQSVVDAIKRSSRSGEWEAVEVLTEEPDTNQNLCEALQRNNL QRSGAARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVFMPLGVL FHRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSALALLADITSKYROGDRKGOIKEDGCDENDERGY					GKTEEEAKQLAEEMNIAFYTSRTDDILLUODUDLUGTGT
DELMEGGGLHTMGTYIVDLITHLTGRAEKVHGLIKTFVRONAA IRGIRHVTSDDFCFFQMLMGGGVCSTVTLNFNMPGAFVHEVMVV GSAGRLVARGADLYGQKNSATQEELLLRDSLAVGAGLPEQGPQD VPLLYLKGMVYMVQALRQSFQGQGDRRTWDRTFVSMAASFEDGL YMQSVVDAIKRSSRSGEWEAVEVLTEEPDTNQNLCEALQRNNL QRSGAARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVFMPLGVL FHRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASAKGSVK YIQSTGSSDDSALALLADITSKYROGDRKGOIKEDGCDESDERGEV	1	1			RQISVKALGIGKNVVCEKAATSVDAFPMUTACHVVDOLMGT
IRGIRHVTSDDFCFFQMLMGGGVCSTVTLNFFMPGAFVHEVMVV GSAGRLVARGADLYGQKNSATQEELLLRDSLAVGAGLPEQGPQD VPLLYLKGMVYMVQALRQSFQGQGDRRTWDRTPVSMAASFEDGL YMQSVVDAIKRSSRSGEWEAVEVLTEEPDTNQNLCEALQRNNL QRSGAARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVFMPLGVL FHRRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASAKGSVK YIQSTGSSDDSALALLADITSKYROGDRKGOIKEDGCDSDDRGGV	1	Ī	į		VLRFLPAFVRMKOLISEHYVGAVMICDARIVSGSLISDSVGW
GSAGRLVARGADLYGQKNSATQEELLRDSLAVGAGLPEQGPQD VPLLYLKGMVYMVQALRQSFQGQGRRTWDRTPVSMAASFEDGL YMQSVVDAIKRSSRSGEWEAVEVLTEEPDTNQNLCEALQRNNL QRSGAARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVFMPLGVL FHRRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKKIAETSNVI TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSALALLADITSKYROGDRKGOIKEDGCDESDRTGV	ĺ	1			DELMGGGGLHTMGTYIVDLLTHLTGRRAEKVHGLLKTEVPONLR
GSAGRLVARGADLYGQKNSATQEELLLRDSLAVGAGLPEQGPQD VPLLYLKGMVYMVQALRQSFQGQGDRRTWDRTPVSMAASFEDGL YMQSVVDAIKRSSRSGEWEAVEVLTEEPDTNQNLCEALQRNNL QRSGAARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVFMPLGVL FHRRAHGCTLSCSSFVEQPTAMEAEETIMECLQEFPEHHKMILD RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF TOEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSALALLADITSKYROGDRKGOIKEDGCDESDERGEV	ı		1	1	IRGIRHVTSDDFCFFOMLMGGGVCSTVTI.NFNMDGAFIJIFIAME
VPLLYLKGMVYMVQALRQSFQGQGDRRTWDRTPVSMAASFEDGL YMQSVVDAIKRSSRSGEWEAVEVLTEEPDTNQNLCEALQRNNL QRSGAARLAFLPSFFSPACVHRSPLSFHGCWFYFVVVFMPLGVL FHRRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD RLINEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRIAETSNVI TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSALALLADITSKYROGDRKGOIKEDGCDSDRTGK		- 1	1	i	GSAGRLVARGADLYGQKNSATOEELLLRDSIAVGAGI.DECCDOD
6313 2 2071 QRSGAARLAFLPSFFSPACVHRSPLSFHGCWFYFVVVFMPLGVL FHRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE FLOMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSALALLADITSKYROGDRKGOIKEDGCDESDREGK	1	- 1	]	1	VPLLYLKGMVYMVQALROSFOGOGDRRTWDPTDVGMAAGEEDGT
GRSGAARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVFMPLGVL FHRRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSALALLADITSKYROGDRKGOIKEDGCREDDRGGV	<u> </u>	5373			IMQSVVDAIKRSSRSGEWEAVEVLTEEPDTNONI.CEALODNAT
FHRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE FLQMLEAIKALEVRNKENSAPLBENTTGKNEAKKRKIAETSNVI TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSALALLADITSKYROGDRKGOIKEDGCRENDEGV	l Ì		<b>4</b>	20/1	QRSGAARLAFLPSPFSPACVHRSPLSFHGCWEVEVAVIEWDLOUT
RUNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE FLQMLEAIKALEVRNKENSAPLBENTTGKNEAKKRKIAETSNVI TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASKQSVK YIQSTGSSDDSALALLADITSKYROGDRKGOIKEDGCRENDEGV	Ī		ļ	<u> </u>	FHRRRAHGCTLSCSSFVEOPTAMEAEETMECT.OFFDFUUVMILD
TOEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASKQSVK YIQSTGSSDDSALALLADITSKYROGDRKGOIKEDGCRENDRGV			1	1 4	RUNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFVKPFOFF
TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSALALLADITSKYROGDRKGOIKEDGCESSDERGV	Ī	1		1 3	IQEPLVEIEGVSKMAFRHLIEFTYTAKLMIGGEEEANDUWKAAE
TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSALALLADITSKYROGDRKGOIKEDGCDSDBTGV		1	}	1 -	LQMLEAIKALEVRNKENSAPLEENTTGKNRAKKPKTAFTCMUT
11QSTGSSDDSALALLADITSKYROGDRKGOTKEDGCDSDBTGV				13	PESLPSAESEPVEIEVEIAEGTIEVEDEGIETI.FEVASAVOCUP
QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMKSHSTE		1		[ ]	IQSIGSSDDSALALLADITSKYROGDRKGOIKEDGCBCDDmgv
					OVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMKSHSTE

SEQ	Predicted	Predicted end	Amino poid
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ļ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	Juguenee	\=possible nucleotide insertion)
	<del></del>	· · · · · · · · · · · · · · · · · · ·	SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKQRTGKKIHVC
			QYCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERFARNSTLKCH
	<u> </u>		LTACQTGVGAKKGRKKLYECQVCNSVFNSWDQFKDHLVIHTGDK
1		į	PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSVETRVQ
1			TEPVTSMT11EQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS
ł	ł		QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNQ
	1		MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAEAAREDHED
	1		AEDLETKPTVDSEAEKAENEDRTALPVLE
6314	2	2071	QRSGAARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVFMPLGVL
1			FHRRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD
		•	RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF
ŀ			TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE
İ	ĺ		FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI
İ			TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASAKQSVK
			YIQSTGSSDDSALALLADITSKYRQGDRKGQIKEDGCPSDPTSK
!			QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMKSHSTE
			SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKQRTGKKIHVC
			QYCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERFARNSTLKCH
1	) ]		LTACQTGVGAKKGRKKLYECQVCNSVFNSWDQFKDHLVIHTGDK
			PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSVETRVQ
1 :			TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS
1			QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNQ
			MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAEAAREDHED
			AEDLETKPTVDSEAEKAENEDRTALPVLE
6315	1	1015	LGLAVNVVTTLVLISYCPTATEEAPYWTYLLCALGLFIYQSLDA
1 1			IDGKQARRINSCSPLGELFDHGCDSLSTVFMAVGASIAARLGTY
			PDWFFSCSFIGMFVFYCAHWQTYVSGMLRFGKVDVTEIQIALVI
1 1	1		VFVLSAFGGATMWDYTIPILEIKLKILPVLGFLGGVIFSCSNYF
1	ļ		HVILHGGVGKNGSTIAGTSVLSPGLHIGLIIILAIMIYKKSATD
	1		VFEKHPCLYILMFGCVFAKVSQKLVVAHMTKSELYLQDTVFLGP
}			GLLFLDQYFNNFIDEYVVLWMAMVISSFDMVIYFSALCLQISRH
6316	1503	500	LHLNIFKTACHQAPEQVQVLSSKSHQNNMD
0310	1503	792	VSAGAGTGIMGGTTSTRRVTFEADENENITVVKGIRLSENVIDR
1			MKESSPSGSKSQRYSGAYGASVSDEELKRRVAEBLALEQAKKES
1	Į		EDQKRLKQAKELDRERAAANEQLTRAILRERICSEEERAKAKHL
1	į		ARQLEEKDRVLKKQDAFYKEQLARLEERSSEFYRVTTEQYQKAA
	ł		EEVEAKFKRYESHPVCADLQAKILQCYRENTHQTLKCSALATQY
6317	102	839	MHCVNHAKQSMLEKGG
1 1			PEAQTSAVLAREKGHLPTMRHEAPMQMASAQDARYGQKDSSDQN
			FDYMFKLLIIGNSSVGKTSFLFRYADDSFTSAFVSTVGIDFKVK
1 1	l		TVFKNEKRIKLQIWDTAGQERYRTITTAYYRGAMGFILMYDITN
1 1		İ	EESFNAVQDWSTQIKTYSWDNAQVILVGNKCDMEDERVISTERG
] [			QHLGEQLGFEFFETSAKDNINVKQTFERLVDIICDKMSESLETD
6318	1765	733	PAITAAKQNTRLKETPPPPQPNCAC
-		, , , ,	PWHPLRTLPLHHPHPRPPRAEGREGADSMSHLPGLELRREAPPL
1 1			LGPLLSPFPLPAGSWHRQMLRSSLRFPITNSAGAPCKAAGRMNI
	1		LAPVRRDRVLAELPQCLRKEAALHGHKDFHPRVTCACQEHRTGT
i l		1	VGFKISKVIVVGDLSVGKTCLINRFCKDTFDKNYKATIGVDFEM
J l		1	ERFEVLGIPFSLQLWDTAGQERFKCIASTYYRGAQAIIIVFNLN
		į	DVASLEHTKQWLADALKENDPSSVLLFLVGSKKDLSTPAQYALM
		1	EKDALQVAQEMKAEYWAVSSLTGENVREFFFRVAALTFEANVLA
6319	88	717	ELEKSGARRIGDVVRINSDDSNLYLTASKKKPTCCP
		717	AATMRLNQNTLLLGKKVVLVPYTSEHVPSRYHEWMKSEELQRLT
			ASEPLTLEQEYAMQCSWQEDADKCTFIVLDAEKWQAQPGATEES
] [	1		CMVGDVNLFLTDLEDLTLGEIEVMIAEPSCRGKGLGTEAVLAML
<u> </u>		<u></u>	SYGVTTLGLTKFEAKIGQGNEPSIRMFQKLHFEQVATSSVFQEV

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid P Dt
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	1	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	residue of	residue of	S=Serine, T=Threonine, V=Valine,
		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			TLRLTVSESEHQWLLEQTSHVEEKPYRDGSAEPC
6320	90	1111	RPRTGREKVAMAAVDSFYLLYREIARSCNCYMEALALVGAWYTA
1	1	1	RKSITVICDFYSLIRLHFIPRLGSRADLIKQYGRWAVVSGATDG
1			IGKAYAEELASRGLNIILISRNEEKLQVVAKDIADTYKVETDII
			VADFSSGREIYLPIREALKDKDVGILVNNVGVFYPYPQYFTQLS
			EDKLWDIINVNIAAASLMVHVVLPGMVERKKGAIVTISSGSCCK
			PTPQLAAFSASKAYLDHFSRALQYEYASKGIFVQSLIPFYVATS
1		<b>!</b>	MTAPSNFLHRCSWLVPSPKVYAHHAVSTLGISKRTTGYWSHSIQ
1	}		FLFAQYMPEWLWVWGANILNRSLRKEALSCTA
6321	1418	341	HRKAALGALMAGRLLGKALAAVSLSLALASVTIRSSRCRGIQAF
1			RNSFSSSWFHLNTNVMSGSNGSKENSHNKARTSPYPGSKVERSQ
			VPNEKUCHLUEWODYK DUEVENANIA ACADUS STORES
	]		VPNEKVGWLVEWQDYKPVEYTAVSVLAGPRWADPQISESNFSPK
}	1		FNEKDGHVERKSKNGLYEIENGRPRNPAGRTGLVGRGLLGRWGP
1			NHAADPIITRWKRDSSGNKIMHPVSGKHILQFVAIKRKDCGEWA
1			IPGGMVDPGEKISATLKREFGERALNSLQKTSAEKREIEEKLHK
		٠	LFSQDHLVIYKGYVDDPRNTDNAWMETEAVNYHDETGEIMDNLM
1	Ė		LEAGDDAGKVKWVDINDKLKLYASHSQFIKLVAEKRDAHWSEDS
6322	2047	1083	EADCHAL
1 0022	2017	1083	NQEILKNVESSRTVQPHFLEFLLSLGWSVDVGRHPGWTGHVSTS
1	[		WSINCCDDGEGSQQEEVISSEDIGASIFNGQKKVLYYADALTEI
			AFVVPSPVESLTDSLESNISDQDSDSNMDLMPGILKQPSLTLEL
			FPNHTDNLNSSQRLSPSSRMRKLPQGRPVPPLGPETRVSVVWVE
			RYDDIENFPLSELMTEISTGVETTANSSTSLRSTTLEKEVPVIF
			IHPLNTGLFRIKIQGATGKFNMVIPLVDGMIVSRRALGFLVRQT
	' '		VINICRRKRLESDSYSPPHVRRKQKITDIVNKYRNKQLEPEFYT
6323			SLFQEVGLKNCSS
0323	1	656	PASTTDGAQEARVPLDGAFWIPRPPAGSPKGCFACVSKPPALQA
			PAAPAPEPSASPPMAPTLFPMESKSSKTDSVRAAGAPPACKHLA
			EKKTMTNPTTVIEVYPDTTEVNDYYLWSIFNFVYLNFCCLGFIA
			LAYSLKVRDKKLLNDLNGAVEDAKTDRLINITRSGLAASCIMLW
6324			MALSVIATHRGLRSSASILVAEPHDWNTERPQVTFRERCPAL
6324	1	2061	EGAGMRRCPCRGSLNEAEAGALPAAARMGLEAPRGGRRRQPGQQ
			RPGPGAGAPAGRPEGGGPWARTEGSSLHSEPERAGLGPAPGTES
, 1			PQAEFWTDGQTEPAAAGLGVETERPKOKTEPDRSSLRTHLEWSW
1			SELGTTCLWTETGTDGLWTDPHRSDLQFQPEEASPWTOPGVHGP
			WTELETHGSQTQPERVKSWADNLWTHONSSSLOTHPEGACPSKE
1 1	1		PSADGSWKELYTDGSRTQQDIEGPWTEPYTDGSOKKODTEAARK
	1		QPGTGGFQIQQDTDGSWTQPSTDGSQTAPGTDCLLGEPEDGPLE
	<b>!</b>		EPEPGELLTHLYSHLKCSPLCPVPRLIITPETPEPEAOPVGPPS
			RVEGGSGGFSSASSFDESEDDVVAGGGGASDPEDRSGSKPWKKT
	i		KTVLKYSPFVVSFRKHYPWVOLSGHAGNFOAGRDGRTLKRRCOC
	j		EQRSLEQLMKDPLRPFVPAYYGMVLODGOTFNOMEDI,LADFEGP
į J	J		SIMDCKMGSRTYLEEELVKARERPRPRKDMYEKMVAVDPGAPTP
	]		EEHAQGAVTKPRYMQWRETMSSTSTLGFRIEGIKKADGTCNTNF
1	1		KKTQALEQVTKVLEDFVDGDHVILQKYVACLEELREALEISPFF
			KTHEVVGSSLLFVHDHTGLAKVWMIDFGKTVALPDHQTLSHRLP
			WAEGNREDGYLWGLDNMICLLQGLAQS
6325	165	944	GLRDPFRRKRRLKPQVKMSNYVNDMWPGSPQEKDSPSTSRSGGS
; 1	Į	1	SRLSSRSRSFSRSSRSHSRVSSRFSSRSRSKSRSRSRRRHQ
1			RKYRRYSRSYSRSRSRSRSRRYRERRYGFTRRYYRSPSRYRSRS
, [		٠	RSRSRSRGRSYCGRAYAIARGQRYYGFGRTVYPEEHSRWRDRSR
			TRSRSRTPFRLSEKDRMELLEIAKTNAAKALGTTNIDLPASLRT
			VPSAKETSPGTGVSSNGAVDBVGT GT GROOTEN TO THE TOTAL OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GROOTEN GARACTER OF GARACTER OF GARACTER OF GARACTER OF GARACTER OF GARACTER OF GARACTER OF GARACTER OF GARACTER OF GARACTER OF GARACTER OF GARACTER OF GARACTER OF GARACTER OF GARACTER OF GARACTER OF GARACTER OF GARACTER OF GARACTER OF GARACTER OF GARACTER OF GARACTER OF GARACTER OF GARACTER OF GARACTER OF GARACTER OF GARACTER OF GARACTER OF GARACTER OF GARACTER OF GARACTER OF GARACTER OF GA
6326	238	680	VPSAKETSRGIGVSSNGAKPEVSILGLSEQNFQKANCQI
-		380	GEPSPATQQKPSATGAGVLHQHFSSGHIYVLMGLLPPPWTISFT
	1		VQTTLQPPGGLPAAPVSGRMAFEPVGRDLARRMVPRAGKRTQTL
			GARRVAAQGARPLPEDRRPKSGERLHVTVAPCWEFVLPSVSLTA

SEQ	Predicted	Predicted end	Amino acid coment
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
- }	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Ì	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i i	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	-	\=possible nucleotide insertion)
			GAKSMWTEHKSPDGRTYYYNTETKQSTWEKPDDLKTPAEQLLSK
1	•		CPWKEYKSDSGKPYYYNSQTKESRWAKPKELEDLEGYQNTIVAG
Ī			SLITKSNLHAMIKAEESSKQEECTTTSTAPVPTTEIPTTMSTMA
		!	AAEAAAAVVAAAAAAAAAAAAAANANASTSASNTVSGTVPVVPEP
1			EVTSIVATVVDNENTVTISTEEQAQLTSTPAIQDQSVEVSSNTG
1		}	EETSKQETVADFTPKKEEEESQPAKKTYTWNTKEEAKQAFKELL
1	ł	1	KEKRVPSNASWEQAMKMIINDPRYSALAKLSEKKQAFNAYKVQT
1	1		EKK
6334	. 17	644	GGNPSGRAAGFAAAAMPSSPLRVAVVCSSNQNRSMEAHN1LSKR
i	<b>!</b>		GFSVRSFGTGTHVKLPGPAPDKPNVYDFKTTYDQMYNDLLRKDK
ļ	!		ELYTQNGILHMLDRNKRIKPRPERFQNCKDLFDLILTCEERVYD
1			QVVEDLNSREQETCQPVHVVNVDIQDNHEEATLGAFLICELCQC
			IQHTEDMENEIDELLQEFEEKSGRTFLHTVCFY
6335	82	529	AARARPGVLCCRLLGAALGDQSRVEMSYIPGQPVTAVVQRVEIH
1			KLRQGENLILGFSIGGGIDQDPSQNPFSEDKTDKGIYVTRVSEG
			GPAEIAGLQIGDKIMQVNGWDMTMVTHDQARKRLTKRSEEVVRL
			LVTRQSLQKAVQQSMLS
6336	1003	438	HEPASKGRAEVGNMRLSVAAAISHGRVFRRMGLGPESRIHLLRN
			LLTGLVRHERIEAPWARVDEMRGYAEKLIDYGKLGDTNERAMRM
1 '			ADFWLTEKDLIPKLFQVLAPRYKDQTGGYTRMLQIPNRSLDRAK
			MAVIEYKGNCLPPLPLPRRDSHLTLLNQLLQGLRQDLRQSQEAS
L			NHSSHTAQTPGI
6337	76	524	EGIQMLSVQPDTKPKGCAGCNRKIKDRYLLKALDKYWHEDCLKC
1			ACCDCRLGEVGSTLYTKANLILCRRDYLRLFGVTGNCAACSKLI
1 1			PAFEMVMRAKDNVYHLDCFACQLCNQRFCVGDKFFLKNNMILCQ
			TDYEEGLMKEGYAPQVR
6338	66	1349	APNSESGTQGPLPTPANLFWTRRANPDPTTSMSATDRMGPKAVP
			GLRLALLLLGLGTPKSGVQGQEGLDFPEYDGVDRVINVNAKNV
			KNVFKKYEVLALLYHEPPEDDKASOROFEMEELII,ELAAOVLED
			KGVGFGLVDSEKDAAVAKKLGLTEVDSMYVFKGDEVIEYDGEFS
1 }			ADTIVEFLLDVLEDPVELIEGERELQAFENIEDEIKLIGYFKSK
1 1			DSEHYKAFEDAAEEFHPYIPFFATFDSKGAKKLTLKLNEIDFYE
1			AFMEEPVTIPDKPNSEEEIVNFVEEHRRSTLRKLKPESMYETWE
			DDMDGIHIVAFAEEADPDGFEFLETLKAVAODNTENPDLSIIWI
	j		DPDDFPLLVPYWEKTFDIDLSAPOIGVVNVTDADRIWMEMDDER
6339	246		DLPSAEELEDWLEDVLEGEINTEDDDDDDDD
""	230	1813	NRCDRGGGGQAERQAGQGCRTQGAGPGFGFGHSFFSQGAMKAFH
	J		TFCVVLLVFGSVSEAKFDDFEDEEDIVEYDDNDFAEFEDVMEDS
			VTESPQRVIITEDDEDETTVELEGQDENQEGDFEDADTQEGDTE
	1		SEPYDDEEFEGYEDKPDTSSSKNKDPITIVDVPAHLQNSWESYY
			LEILMVTGLLAYIMNYIIGKNKNSRLAQAWFNTHRELLESNFTL
]			VGDDGTNKEATSTGKLNQENEHIYNLWCSGRVCCEGMLIQLRFL
	, [		KRQDLLNVLARMMRPVSDQVQIKVTMNDEDMDTYVFAVGTRKAL
]	·		VRLQKEMQDLSEFCSDKPKSGAKYGLPDSLAILSEMGEVTDGMM
			DTKMVHFLTHYADKIESVHFSDQFSGPKIMQEEGQPLKLPDTKR
1			TLLLTFNVPGSGNTYPKDMEALLPLMNMVIYSIDKAKKFRLNRE
1			GKQKADKNRARVBENFLKLTHVQRQEAAQSRREEKKRAEKERIM
6340	2	583	NEEDPEKQRRLEEAALRREQKKLEKKQMKMKQIKVKAM
	~	202	EACAHTLSCPAFARLGRARRRPWMSHRTSSTFRAERSFHSSSS
1			SSSTSSSASRALPAQDPPMEKALSMFSDDFGSFMRPHSEPLAF
		į	PARPGGAGNIKTLGDAYEFAVDVRDFSPEDIIVTTSNNHIEVRA
]			EKLAADGTVMNNFAHKCQLPEDVDPTSVTSALREDGSLTIRARR
6341	2		HPHTEHVQQTFRTEIKI
55=+	-	645	KMAVLSAPGLRGFRILGLRSSVGPAVQARGVHQSVATDGPSSTQ
1	1	{	PALPKARAVAPKPSSRGEYVVAKLDDLVNWARRSSLWPMTFGLA
1			CCAVEMMHMAAPRYDMDRFGVVFRASPRQSDVMIVAGTLTNKMA

• •
· ~-
ر دنه
۶.
10

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +-cton
1	amino acid	sequence	Codon, /=possible nucleotide deletion
L	sequence		\=possible nucleotide insertion)
1			PALRKVYDQMPEPRYVVSMGSCANGGGYYHYSYSVVRGCDPTVD
6342	<del> </del>		VDIYIPGCPPTAEALLYGILQLQRKIKRERRLOTWYRR
0342	2	1191	DPRVRAMLATLARVAALRKTCLFSGRGGGRGLWTGRPQSDMNNI
İ	1		KPLEGVKILDLTRVLAGPFATMNLGDLGAEVIKVERPGAGDDTR
	1		TWGPPFVGTESTYYLSVNRNKKSIAVNIKDPKGVKIIKELAAVC
1			DVFVENYVPGKLSAMGLGYEDIDEIAPHIIYCSITGYGQTGPIS
1	1	ł	QRAGYDAVASAVSGLMHITGPEVACLSHIAANYLIGQKEAKRWG
1		j	TAHGSIVPYQAFKTKDGYIVVGAGNNQQFATVCKILDLPELIDN
ł			SKYKTNHLRVHNRKELIKILSERFEEELTSKWLYLFEGSGVPYG
<b>]</b> -			PINNMKNVFAEPQVLHNGLVMEMEHPTVGKISVPGPAVRYSKFK
6343	2	936	MSEARPFPLLGQHTTHILKEVLRYDDRAIGELLSAGVVDQHETH
		230	GTAMVSDEDELNLLVIVVDANPIWWGKQALKESQFTLSKCIDAV MVLGNSHLFMNRSNKLAVIASHIQESRFLYPGKNGRLGDFFGDP
	1		GNPPEFNPSGSKDGKYELLTSANEVIVEEIKDLMTKSDIKGQHT
}			ETLLAGSLAKALCYIHRMNKEVKDNQEMKSRILVIKAAEDSALQ
i			YMNFMNVIFAAQKQNILIDACVLDSDSGLLQQACDITGGLYLKV
			PQMPSLLQYLLWVFLPDQDQRSQLILPPPVHVDYRAACFCHRNL
1	1		IEIGYVCSVCLSIFCNFSPICTTCETAFKISLPPVLKAKKKKLK
			VSA
6344	2508	147	TMPTATLGNLRGYGMASPGLAAPSLTPPQLATPNLQQFFPQATR
1	[		QSLLGPPPVGVPMNPSOFNLSGRNPOKOARTSSSTTPNPKDSSS
			QTMPVEDKSDPPEGSEEAAEPRMDTPEDODLPPCPEDTAKEKPT
Į.			PAPEPEPCEASELPAKRLRSSEEPTEKEPPGOLOVKAOPOARMT
	·		VPKQTQTPDLLPEALEAQVLPRFQPRVLQVQAQVQSQTQPRIPS
1	i l		TDTQVQPKLQKQAQTQTSPEHLVLQQKQVQPQLQQEAEPQKQVQ
			POVOPOAHSQGPRQVQLQQEAEPLKQVQPQVQPQAHSQPPRQVQ
			LOLOKOVOTOTYPOVHTQAQPSVQPQEHPPAQVSVQPPEQTHEQ
			PHTQPQVSLLAPEQTPVVVHVCGLEMPPDAVEAGGGMEKTLPEP VGTQVSMEEIQNESACGLDVGECENRAREMPGVWGAGGSLKVTI
1 1	į		LQSSDSRAFSTVPLTPVPRPSDSVSSTPAATSTPSKQALQFFCY
	1		ICKASCSSQQEFQDHMSEPQHQQRLGEIQHMSQACLLSLLPVPR
1 1	1		DVLETEDEEPPPRRWCNTCQLYYMGDLIQHRRTQDHKIAKQSLR
			PFCTVCNRYFKTPRKFVEHVKSQGHKDKAKELKSLEKEIAGQDE
[ [	<u> </u>		DHFITVDAVGCFEGDEEEEEDDEDEEEIEVEERLCKOVPSPDIS
			REEWKGSETYSPNTAYGVDFLVPVMGYICRICHKFYHSNSGAOL
	i	İ	SHCKSLGHFENLQKYKAAKNPSPTTRPVSRRCAINARNALTALE
6345	2	3463	TSSGRPPSQPNTQDKTPSKVTARPSOPPLPRRSTRLKT
	-	3483	PRVRTKLILLVNDKKRYERVGGGPKRLGRDVEMEEMIEQLQEKV
1 1	1		HELEKQNDTLKNRLISAKQQLQTQGYRQTPYNNVQSRINTGRRK
]			ANENAGLQECPRKGIKFQDADVAETPHPMFTKYGNSLLEEARGE
			IRNLENVIQSQRGQIEELEHLAEILKTQLRRKENEIELSLLQLR
] ]			EQQATDQRSNIRDNVEMIKLHKQLVEKSNALSAMEGKFIQLQEK
[ [			QRTLKISHDALMANGDELNMQLKEQRLKCCSLEKQLHSMKFSER RIEELQDRINDLEKERELLKENYDKLYDSAFSAAHEEQWKLKEQ
			QLKVQIAQLETALKSDLTDKTEILDRLKTERDQNEKLVQENREL
		ľ	QLQYLEQKQQLDBLKKRIKLYNQENDINADELSEALLLIKAQKE
[ ]		1	QKNGDLSFLVKVDSEINKDLERSMRELQATHAETVQELEKTRNM
·	1	1	LIMOHKINKDYOMEVEAVTRKMENLOODYELKVEQYVHLLDIRA
		į	ARIHKLEAQLKDIAYGTKQYKFKPEIMPDDSVDEFDETIHLERG
	1	1	ENLFEIHINKVTFSSEVLQASGDKEPVTFCTYAFYDFELQTTPV
1	1		VRGLHPEYNFTSQYLVHVNDLFLOYIOKNTITLEVHOAVSTEVE
1	ł		TIAACQLKFHEILEKSGRIFCTASLIGTKGDIPNFGTVEVWEDI
		}	RVPMDQAIRLYRERAKALGYITSNFKGPEHMOSLSOOAPKTAOL
ŀ	[	i	SSTDSTDGNLNELHITIRCCNHLQSRASHLOPHPYVVYKFFDFA
		1	DHDTAIIPSSNDPQFDDHMYFPVPMNMDLDRYLKSESLSFYVFD
			DSDTQENIYIGKVNVPLISLAHDRCISGIFELTDHQKHPAGTIH

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	Managanine, Catysteine, Dalaspartic hold n
1	location	corresponding	Grucdmic Acid, F=Phenvlalanine G-Clusine
ĺ	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
}	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
L	sequence	1	Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			VILKWKFAYLPPSGSITTEDLGNFIRSEEPEVVQRLPPASSVST
ļ	i		LVLAPRPKPRQRLTPVDKKVSFVDIMPHQSDVSQEGSVDEVKEN
			TEKMQQGKDDVSLLSEGQLAEQSLASSEDETEITEDLEPEVEED
		l	MSASDSDDCIIPGPISKNIKQPSEKIRIEIIALSLNDSQVTMDD
ł		}	TIQRLFVECRFYSLPAEETPVSLPKPKSGQWYYYNYSNVIYVDK
	i		ENNKAKRDILKAILQKQEMPNRSLRFTVVSDPPEDEQDLECEDI
1	}	ĺ	GVAHVDLADMFQEGRDLIEQNIDVFDARADGEGIGKLRVTVEAL
			HALQSVYKQYRDDLEA
6346	2921	533	ODRRLLRLELQKTCOPTSTMSGSHTPACGDESALTDGTMDOETL
1			AKYTQKEESAEQPEFYYDEFGFRVYKEEGDEDGGGLLANGDI MB
1			DAPORLKWQAHLEFTHNHDVGDLTWDKIAVSI.PDCERT.BCI.VI.A
Ī			GIPHGMRPQLWMRLSGALOKKRNSELSYRETVKNSSNDETT > > V
			QLEKULLRIMPSNACFASMGSIGVPRI.RRVI.RAI.AWI.VPRICVC
			QGTGMVAACLLLFLEEEDAFWMMSAI IEDIJ PASVESTTI I GVO
			TDQRVLKHLIVQYLPRLDKLLOEHDIELSI.TTI.HWELTDEDGIOL
	]		DIKLLRIWDLFFYEGSRVLFQLTLGMLHLKEEELIQSENSASI
1	}		FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETQRRKHLAYL
	}		IADQQQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGEDDLEAL KAKNIKQTELVADLREAILRVARHFQCTDPKNCSVVSRQLPGLL
	i i		PNTALTPPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH
	1		RRRAKALLDFERHDDDELGFRKNDIITIVSQKDEHCWVGELNGL
1			RGWFPAKFVEVLDERSKEYSIAGDDSVTEGVTDLVRGTLCPALK
	1		ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDFASVYSRLVL
į			CKIPKLDEDGKVLTPEELLYRAVOSVNVTHDAVHAOMDVKI.Det
1			1 TCVGLNEQVLHLWLEVLCSSLPTVEKWYODWSFI.DSDGWYOTVG
i i	[		ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHT.FSW
6347	2921	533	DVDG
	2321	533	QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL
	l		AKYTQKEESAEQPEFYYDEFGFRVYKEEGDEPGSSLLANSPLME
1 1	1		DAPORLRWOAHLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA
1	i		GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK
1 1	i		QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC QGTGMVAACLLLFLEEEDAFWMMSAIIEDLLPASYFSTTLLGVQ
	ļ		TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITLHWFLTAFASVV
		ļ	DIKLLLRIWDLFFYEGSRVLFQLTLGMLHLKEEELIQSENSASI
]			PNILSDIPSQMEDAELLLGVAMRLAGSLTDVAVFTOPPVULAVI
1 1			TADQGQLLGAGTLTNLSOVVRRRTORRKSTITALLRGEDDLEAL
1 1	ļ		NAKNIKUTELVADLREAILRVARHFOCTDPKNCSVNSPOLDGIJ
1	. 1	1	PNIALIPPIPLVGLYSLWOELTPDYSMESHOPDHENVVACCOCIT
		1	RRRAKALLDFERHDDDELGFRKNDIITIVSOKDEHCWYGEINGY
1	1		RGWFPAKFVEVLDERSKEYSIAGDDSVTEGVFDIJDGTT CDALK
]		i	ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDEAGWEDT VI
		1	CKTFRLDEDGKVLTPEELLYRAVOSVNVTHDAVHAOMDVKT.Bet
			1CVGLNEQVLHLWLEVLCSSLPTVEKWYOPWSFLRSPGWYOTYC
			ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG
6348	3	3679	
1 1			AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE
]			KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN EHLOALLTPDERDYSOCODY OFFICE ACCOUNT OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPER
1	1		EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN DDDEDVOVEVARKVOKSSSPREMOVA BEVENDENDENDN
	•		DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN
	i	1	ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA
	Į		EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN
	į	Į	ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR
	ļ	1.	DASKSLNEHLQALLTPDEPDKSOGODLOFOLAFGCPLAOUT VOV
<u> </u>			LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE
			THE THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON O

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
i	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
ŀ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	Warrentonhan Value
ì	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	<del></del>		ECAITCSNSHGPYDSNQPHRKTKITFEEDKVDSTLIGSSSHVEW
			EDAVHIIPENESDDEEEEEKGPVSPRNLQESEEEEVPQESWDEG
			YSTLSIPPEMLASYKSYSSTFHSLEEQQVCMAVDIGRHRWDQVK
1			KEDHEATGPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS
			CQPYRSAFYVLEQQRVGLAVNMDEIEKYQEVEEDQDPSCPRLSR
1		•	ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE
1			QYLGLALDVDRIKKDQEEEEDQGPPCPRLSRELLEVVEPEVLQD
ļ	]		SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIE
ĺ	i		KKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCPRLSRELLDEKG
			PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV
	1		DMDEIEKYQEVEEDQDPSCPRLSGELLDEKEPEVLQESLDRCYS
	1		TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE
	<u> </u>		DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ
	i		PYSSAVYSLEEQYLGLALDVDRIKKDQEEEEDQGPPCPRLSREL
ł	] :		LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH
	į į		VGFSLDVGEIEKKGKGKKRRGRRSKKERRRGRKEGEEDONPPCP
			RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFOHYRSVFY
6340		······	SFEEEHISFALYVDNRFFTLTVTSLHLVFQMGVIFPO
6349	3	3679	AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELOFKEE
			KLAEQLKQAEELRQYKVLVHSQERELTOLREKLREGRDASRSI.N
1			EIILQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN
1			DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS
1			NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN
			ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA
			EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN
	i		EROFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR
1	j		DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK
1 1	Ī		LSPENDNDDDBDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE
1	i		ECAITCSNSHGPYDSNQPHRKTKITFEEDKVDSTLIGSSSHVEW EDAVHIIPENESDDEEEEEKGPVSPRNLQESEEEEVPQESWDEG
			YSTLSIPPEMLASYKSYSSTFHSLEEQQVCMAVDIGRHRWDQVK
	ł	i	KEDHEATGPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS
			CQPYRSAFYVLEQQRVGLAVNMDEIEKYQEVEEDQDPSCPRLSR
]	i		ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE
1 1	1	i	QYLGLALDVDRIKKDQEEEEDQGPPCPRLSRELLEVVEPEVLQD
	i		SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIE
}	J		KKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCPRLSRELLDEKG
1			PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEOORVGLAV
1.		İ	DMDEIEKYQEVEBDQDPSCPRLSGELLDEKEPEVLOESLDRCYS
	•	}	TPSGCLELTDSCQPYRSAFYILEOORVGLAVDMDEIEKYOEVER
] [			DQDPSCPRLSRELLDEKEPEVLODSLGRCYSTPSGYLFLPDI.GO
	}	}	PYSSAVYSLEEQYLGLALDVDRIKKDOEEEEDOGPPCPRISREI.
j i		İ	LEVVEPEVLQDSLDRCYSTPSSCLEOPDSCOPYGSSFYALEEKH
]	1		VGFSLDVGEIEKKGKGKKRRGRRSKKERRRGRKEGEEDONPPCP
1 1	1	1	RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFOHYRSVFY
6350			SFEEEHISFALYVDNRFFTLTVTSLHLVFQMGVIFPQ
5530	3	3679	AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE
j	i	.	KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSIN
j l		Į.	EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN
1	1	Ì	DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS
1 1	<u> </u>	ļ	NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN
1 1	1	1	ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA
		į	EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN
} i			ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR
	•		DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK
<u> </u>			LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	A=Aldnine, C=CVSteine
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
I	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=Possible nucleotide insertion
ĺ			ECAITCSNSHGPYDSNOPHRKTKITFEEDKYDSTLIGGSSINGH
į		i	EDAVHIIPENESDDEEEEEKGPVSPRNLOESEEEEVDOESWDEG
	1		151LS1PPEMLASYKSYSSTFHSLEEOOVCMAVDTCPUPWDOVV
			REDHEATGPRLSRELLDEKGPEVLODSLDRCVSTPSGCLELTDS
			CQPYRSAFYVLEQQRVGLAVNMDEIEKYOEVEEDODBGCBBICB
1	Į.		ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGODVSGALVELER
İ			QILGLALDVDRIKKDQEEEEDOGPPCPRI.SREIJ.FIGEPEULOD
	1		SEDRCYSTPSSCLEOPDSCOPYGSSFYALEERHUGEGLDUGGTE
			KAGKGKKRRGRRSKKERRRGRKEGEEDONPPCPPLSPFLLDEVC
ł			PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV
	1 :		DMDEIEKYQEVEEDQDPSCPRLSGELLDEKEPEVLQESLDRCYS
			TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE
			DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ
			PYSSAVYSLEEQYLGLALDVDRIKKDQEEEEDQGPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH
			VGFSLDVGEIEKKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCP
			RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY
			SFEEEHISFALYVDNRFFTLTVTSLHLVFQMGVIFPQ
6351	1291	319	REARRITERSQLGRMLVVEVANGRSLVWGAEAVOALDERLCVGG
			RIVGALPRGPRONSRLGLPLLLMPEEARLLAFICAVTLVCADDD
			DSKHHSLALTSFKROOEESFOEOSALAARARETOROFILERUTER
1			GUAARRUKLEQASGASSSOEAGSSOAAKEDETSDCOAGGEOLEA
ł			GPSSSQAGPSNGVAPLPRSALLVOLATARPPDVKAPDI DUBVOC
ļ			NUMPHAGRPAHELRYSIYRDLWERGFFI.SAAGKEGGDELUVDOD
İ	İ		PURTHANTIAOCWAPEDTIPLODIADAGRICTEURUTI I CORO
6352	235	923	PDGKVVYTSLQWASLQ
l		923	WSEWLSPCHAAKCKGLSMLRITMKTRAISLAADATEFVQGRSAP
- 1			AMARSLVHDTVFYCLSVYQVKISPTPQLGAASSAEGHVGQGAPG
ì	ļ		LMGNMNPEGGVNHENGMNRDGGMIPEGGGGNQEPRQOPQPPPEE
			PAQAAMEGPOPENMOPRTRRTKFTLLQVEELESVFRHTQYPDVP TRRELAENIGUTEDKUDWEENANDARGERINGER
			TRRELAENLGVTEDKVRVWFKNKRARCRRHQRELMLANELRADP DDCVYIVVD
6353	65	672	RFAGAGAIPEARARPPDVQAAEEEKEMDLPDSASRVFCGRILSM
- 1	1		VNTDDVNAIILAQKNMLDRFEKTNEMLLNFNNLSSARLQQMSER
!	Ī		FLHHTRTLVEMKRDLDSIFRRIRTLKGKLARQHPEAFSHIPEAS
1			FUEEEDEDPIPPSTTTTIATSEOSTGSCOTSPOTVSpcrcpcrp
6354			DESTVQPGSPAINGRSOTDDEEMTGE
0354	965	510	PSLRPMEPTRDCPLFGGAFSAILPMGAIDUSDLPDUDDMORVDG
1			APVIDUSUIVELLELOAHVRGEADARVHEEDUGGVOGADAMAN (
- 1			SVQPLSLENLALRGRCQEAWVLSGKOO JAKENOOVA KOVTT HON
6355	150		TPKT-DATOLIPTT-LENODD
0333	158	1662	RGSSAAFRGSGLRGAMIRRVLPHGMGRGLLTRRPGTRRGGFSLD
1	j	ļ	WDGKVSEIKKKIKSILPGRSCDLLODTSHI.PPEHSDWITVCCCV
		ſ	LGLSVAYWLKKLESRRGAIRVLVVERDHTYSOASTGI.SVCGICO
			QFSLPENIQLSLFSASFLRNINEYLAVVDAPPI.DI.PFNDCCVII
			LASEKDAAAMESNVKVQRQEGAKVSLMSPDOLRNKFDWINTEGV
		}	ALASYGMEDEGWFDPWCLLQGLRRKVQSLGVLFCQGEVTRFVSS
i			SQRMLTTDDKAVVLKRIHEVHVKMDRSLEYQPVECAIVINAAGA
ļ	1		WSAQIAALAGVGEGPPGTLQGTKLPVEPRKRYVYVWHCPQGPGL
[			ETPLVADTSGAYFREGLGSNYLGGRSPTEQEEPDPANLEVDHD
	İ	ľ	FFQDKVWPHLALRVPAFETLKVQSAWAGYYDYNTFDQNGVVGPH
		1	PLVVNMYFATGFSGHGLQQAPGIGRAVAEMVLKGRFQTIDLSPF LFTRFYLGEKIQENNII
	354	633	TCI TCCOL DI OLD COMPANDIO
6356	334 1	033	
6356	334	1	TGLTSSCLPLQVMMTKRTKDMGKFSSVTVSTIDEEEEEIEAREV ADSYAQNAKVIEKQLERKGMSKRRLQELAELEAKKAKMKGTLID

Designing mucleotide   location   corresponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contrasponding   contr	SEQ	Predicted	Predicted end	
No:			1	Amino acid segment containing signal peptide
cortesponding   coffee   corresponding   coffirst   maino acid   residue of   amino acid   residue of   amino acid   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   se	1			Glutamic Acid E-Dhomel-Lamin C on i
Leucine, M-Methionine, N-Aspariagine,   chirst amino acid residue of amino acid sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequen				H-Histidine T-Icologia- V. I.
amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid	İ	corresponding		Laleucine Mamethioning National
smino acid residue of amino acid sequence sequence sequence code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code, per code,				P=Proline O-Glutamine D-New
residue of amino acid sequence	1			S-Serine T-Thronnine, K=Arginine,
amino acid sequence    Codon, /=possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible nucleotide literion,    -possible			· -	W-Truntonhan V-Truncing V IV
### Sequence    Sequence				Codon /-paggible musl-shide 17
G357 2 915 CLLENNALURINGTSIGNUFUCSKLIFUSPICGOGGERALS RTSGNPGUSGOGGGGSGUFGD LDI LOURNITHTEKLISTKOSP OPVERVOAFIKIIEAMGFTGPLKYSKNIKKTALENYTSCUEK TOPFEFFIKORDPTINSBETLTLIHUMGLINGGESGKYK CRI IVIHIMMEDVQORGRWMGWPYILKKNNILMTNHFYAALIGY DEGILSDDHIGLAALMAFFFRENKCEDRHLEHVYPKOTQYL DSNNGEDLLITGEVSKRPLVEKNPGSILKHBPTYNDEGL  6358 2009 1040 ASDAHESLSAPARATMTGOTALKKENPITADEG BOOGLEFFRENKLLUOVGHASKQIAADKOYKGIUDCIVETPK COUNTYPHAANAVAPIERVKLLUOVGHASKQIAADKOYKGIUDCIVETPK EOGUSFFRENKLLUOVGHASKQIAADKOYKGIUDCIVETPK EOGUSFFRENKLLUOVGHASKQIAADKOYKGIUDCIVETPK COPHEYFAGNIKANIKYFTETOLAMPAFKOKYBOFLIGGUNAH ASRTAVAPIERVKLLUOVGHASKQIAADKOYKGIUDCIVETPK EOGUSFFRENKLLUOVGHASKQIAADKOYKGIUDCIVETPK EOGUSFFRENKLLUOVGHASKQIAADKOYKGIUDCIVETPK COPHEYFAGNIKAVAPIERVKLLUOVGHASKQIAADKOYKGIUDCIVETPK EOGUSFFRENKLANIVETRYFTOLAMPAFKOKYBOFLIGGUNAH MOSGKRGADIMTYOTUDCHKRIFTPEGGKAFFYEGAMSHVULRGMM OSGKRGADIMTYOTUDCHKRIFTPEGGKAFFYEGAMSHVULRGMM OSGKRGADIMTYOTUDCHKRIFTPEGGKAFFYEGAMSHVULRGMM OSGKRGADIMTYOTUDCHKRIFTPEGGKAFFYEGAMSHVULRGMM OSGKRGADIMTYOTUDCHKRIFTPEGGKAFFYEGAMSHVULRGMM OSGKRGADIMTYOTUDCHKRIFTPEGGKAFFYEGAMSHVULRGMM OSGKRGADIMTYOTUDCHKRIFTPEGGKAFFYEGAMSHVULRGMM OSGKRGADIMTYOTUDCHKRIFTPEGGKAFFYEGAMSHVULRGMM OSGKRGADIMTYOTUDCHKRIFTPEGGKAFFYEGAMSHVULRGMPUNL ERSTWIPPREGETLERSPENDUNTTAGGGSTOLKABSSTGOTE GAFVULVULRGEKKYTTAGGETHINGOTUTKKRIFTS REFERGLOCHTAGATATATATATATATATATATATATATATATATATAT			Doqueilo	\-nossible rugloctide income:
RTSGWPGMSGGAGGSEGIPGIDICHEKHTTIRKISTKOSE  OPVEEKVGAFTKIIEAMGFTGILKYSKEKIKIAALMINTSCUEK TDFEEFFLRCOMPDITENSHFJITLHHUMCLVRMKOGGSGKYM CRITVISHMENDVORGRUWGNPYLIKAHAALMINTSCUEK TDFEEFFLRCOMPDITENSHFJITLHHUMCLVRMKOGGSKSKYM CRITVISHMENDVORGRUWGNPYLIKAHUMINIFYAALLGY DEGILSDDHGLAAALMETFFRRKEEDPRILELUEYVRROTOM ASDALHSIJSAPVIRLISGRSAARPATMTEGATSPAKOPLAGGIAA ASDALHSIJSAPVIRLISSRSAARPATMTEGATSPAKOPLAGGIAA ASDALHSIJSAPVIRLISSRSAARPATMTEGATSPAKOPLAGGIAA ASDALHSIJSAPVIRLISSRSAARPATMTEGATSPAKOPLAGGIAA ASDALHSIJSAPVIRLISSRSAARPATMTEGATSPAKOPLAGGIAA ASDALHSIJSAPVIRLISSRSAARPATMTEGATSPAKOPLAGGIAA OPMINIPAGIASGAAGAGTSLCYVYLDEAGGIAA OPMINIPAGIASGAAGAGTSLCYVYLDAGGIAAVAGTUSIPK EGGULSFWRGHLANVIRTSPTOALMIAGTVATAVAGTIVDITIPK EGGULSFWRGHLANVIRTSPTOALMIAGTVATAVAGTIVDITIPK EGGULSFWRGHLANGTATAVATTAVATTUAGTUSTAVATAVAGTU DTAKGALLPDPENTHITUVSENIATAVAGTUSPPDTVARRAM MQSGRRGADIMYTSTUTDCHRISTPTDEGGKAFFKGAMSNULRGMG MQSGRRGADIMYTSTUTDCHRISTPTDEGGKAFFKGAMSNULRGMG MQSGRRGADIMYTSTUTDCHRISTPTDEGGKAFFKGAMSNULRGMG MQSGRRGADIMYTSTUTDCHRISTPTDEGGKAFFKGAMSNULRGMG MQSGRRGADIMYTSTUTDCHRISTPTDEGGKAFFKGAMSNULRGMG MQSGRRGADIMYTSTUTDCHRISTPTDEGGKAFFKGAMSNULRGMG MQSGRRGADIMYTSTUTDCHRISTPTDEGGKAFFTGAMSNULRGMG MQSGRRGADIMYTSTUTDCHRISTPTTAGGEGGTFTPDGEGGRAFTRENES INGHFYNIKHTSVFTTAAYSTUTDGMTTATQGFSTOPVHARRSSTDSS GPLEBAEBAGDUMTKSDSAGMSGRRFWGGLIHAFTGTMKVSFTATTNOT EGGSFGLANTUNGGERGKTRAGGERATRITISGKFRHSTLINGKFRMSTHM EGGGLUCHALPOAGARCHKLOCEPULEHIGHGCKKLARIF LMSPALLVALUSVULSPERSCRVFWILIGTTMKSCTMILIGERKTLITSTUTDGATTATAGATSTUTDGATTATAGATSTUTDGATTATAGATSTUTDGATTAGATSTUTDGATTAGATSTUTDGATTAGATSTUTDGATTAGATSTUTDGATTAGATSTUTDGATTAGATSTUTDGATTAGATSTUTDGATTAGATSTUTDGATTAGATSTUTDGATTAGATTAGATTAGATTAGATTAGATTAGATTAG	6357	2	915	GLIPHMALLYPHIDNOTELECOMMUNICARY TRANSPORT
OPVERKVGAFTKI LEAMGFTGFLYSKMKIKIAALAMYTSCUEK TDFFEFFLAKCMOPTFINSKFI LTLLHUVICHMKOGGGSKYM CRI LVIHMMEDVOORGEWMSUNPY LIKKMILLMININFYAALLGY DEGILSDDIGLAAALMFFFFNKCEDERIELLUEVYEKOTOYL DSNNGEDLLLTGEVSKRPLVEKINPOSILKHISPTYNAALLGY DSNNGEDLLLTGEVSKRPLVEKINPOSILKHISPTYNAALLGY DSNNGEDLLLTGEVSKRPLVEKINPOSILKHISPTYNAALLGY A AISKTAVAP I BRVKLLLQVOHASKO TAADKQYKG I UDGUVKHT OFNYFAGNILASGGAAGATSLCFVYPLDBARTRLAADVAKSGTE REFRIGIDGUKKITKSDG I GRILVQGFSVSVQGI I YRAAYGGVV DTAKGKLPDPENTHI VVSMILAGTVAUGVUSYPPDTVARRM MOSGRKGAD HNYTOTVOCHKRIFFDEGKAFFKGMSNVLRGMG GAFVLVLVDELKKYL  CKRGEERIKKEBCLESSHPPISDSKSI GKRSLLJELLKTYNCYHE GKSFQLRHREBEGTI. I I EGILNI TRAAYGGVV DTAKGKLPDPENTHI VVSMILAGTVAUGVUSYPPDTVARRM MOSGRKGAD HNYTOTVOCHKRIFFDEGKAFFKRAMSNVLRGMG GAFVLVLVDELKKYL  CKRGEERIKKEBCLESSHPPISDSKSI GKRSLLJELLKTYNCYHE GKSFQLRHREBEGTI. I I EGILNI TRAAYGGVV DTAKGKLPDPENTHI VVSMILAGTVAUGVUSYPPDTVARRM FSTSMMPRRESCLIKERSPEORGHTAAGGELLAKTYNCYHE BOPSSFALNI VVLESGERTKI KUCCEYPLI SRI LIKGPCRKI ARII I MKROALRITMLORLEDLVEAK GFLERAERA POLMETKSDAGCMSGRPKCRAPEGRAFTERBHEST INGHFYNIKTSVTPAYAS VITNAVANSI THALOYUTLLLILLKPRY EDOPSFALNI VVLESGERTKI KUCCEYPLI SRI LIKGPCRKI ARII I MKROALRITMLORLEDLVEAK GPLERAERA POLMETKS VITNAVANSI THALOYUTLLLIKRPRY EDOPSFALNI VVLESGERTKI KUCCEYPLI SRI LIKGPCRKI ARII I MKROALRITMLORLEDLVEAK GPLERAERA POLMETKS VITNAVANSI THALOYUTLLIKA STILLAGUT HENDENG TORMYT STANDAVAN ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARIONICAL ARION			313	PTSOWPOMSOSOACCOSEOTDCTDTOTATION WITHOUT TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO THE STREET TO
TOPFEFFLECOMPDTENSHELITLEHUNGLVERMEGGESGKYM CRITUSHEMBEDVQCRGRUNGVIPTIKKNEUMTNIFTYARLIGY DEGILSDDHGLAALHRTFFRRKCEDPRILELLUEVYRKOIQYL DEGILSDDHGLAALHRTFFRRKCEDPRILELLUEVYRKOIQYL DEGILSDDHGLAALHRTFFRRKCEDPRILELLUEVYRKOIQYL DEGILSDDHGLAALHRTFFRRKCEDPRILELLUEVYRKOIQYL DEGILSDDHGLAALHRTFFRRKCEDPRILELLUEVYRKOIQHAGGIAA ASDALHSLSAPVIRLISSRSARPATHTEGATSFAKOFTLAGGTAA ASSALAHSLSAPVIRLISSRSAARPATHTEGATSFAKOFTLAGGTAA ASSALAHSLSAPVIRLISSRSAARPATHTEGATSFAKOFTLAGGTAA ASSALAHSLSAPVIRLISSRSAARPATHTEGATSFAKOFTLAGGTAA ASSALAHSLSAPVIRLISSRSAARPATHTEGATSFAKOFTLAGGTAA COMMITTED COMPANIANCE TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO COMPANIANCH TO				OPVEEKVGAETVIJEAMGETCHI VYGVIVIVI
CRIIVSHMMEDVQORGRWMGVNPILIKRMILLMTNIFYAALLEY DEGILSDDRIGLAAALMETFFRIKCEDPRILELLUEVVRKOTQYL DENNEGDLLLTGEVSKRPLVEKSRPOSILKPHISPTYNADELG  ASSADAHSISJAPVERLSSRSAARPATMTEGASFAKOPLAGGIAA AISKTAVAPIERVKLLLQVQHASKOTAADKQYKGIUDCIVRIPK EGGULSFWRGLANDIRTPTQAINFARGASFAKOPLAGGIAA AISKTAVAPIERVKLLLQVQHASKOTAADKQYKGIUDCIVRIPK CFWYYSAGNLASGGAAGATSLCFVYPLDBARTRLAADVKSGTIE REFRIGLGDCUKKITKSDGIRGLYQGFSVSVQGIIYRAAYGGVV DTAKGKLPDPKNTHIUVSMILAQTVTAVAQVVSYPPDTVRZRM MOSGRKGADINTYTTUVCKRIFIDEKGKAFFKGAMSNVLRGMG GAFULVLYDELKKVI  CYRQEEEKKKRECLESSHPPISDSKSIGKSELJGLLKTYNCYHE GKSFQLRIREEGGILIEGLINGTSKSLLJGLLKTYNCYHE PSTSMWPRRSPCCILRESSHPPISDSKSIGKSELJGLLKTYNCYHE GKSFQLRIREEGGILIEGLINGTSCKSLLJGLLKTYNCYHE PSTSMWPRRSPCCILRESSHPPISDSKSIGKSELJGLLKTYNCYHE GKSFQLRIREEGGILIEGLINGTSCKSLLJGLLKTYNCYHE BOPSSFALNIVLRSGERTKLKDCEVPLIERILMGDCKTARIF INGHFYNIKTSVTPAYSGYNTWVWSISTHUQUTLLLLKRYRY EDGPSFALNIVLRSGERTKLKDCEVPLIERILMGDCKTARIF LLMRALGGVVPHEVAQYIKHGNERI PIDRIVGSC GPLEKAERAPQLMRTKSDASCMSGRPKCRAPGEAGRIRDHEN INGHFYNIKTSVTPAYSGYNTWVWSISTHUQUTLLLLKRYRY EDGPSFALNIVLRSGERTIKLKDCEVPLIERILMGDCKTARIFSDF RLPYKVLSVVPESTPPTAVLKRAAEFKVDAATSAIITNDGIGIN PAQTAGNOVHJKHGSELRI IPDRIVGSC GROOTSTELEVVLEYBEGCKVPHILIGATTASKYSKRITINGUTGIN PAQTAGNOVHJKHGSELRI IPDRIVGSC GROOTSTELEVVLEYBEGCKVPHILIGATTASKYSKRITINGUTGINAA PAGRWRGITSGSFCHPIGGRCTFTPDGGTLHIQAGDALMER APGRWRGITSGSFCHPIGGRCTFTPDGGTLHIQAGDALMER APGRWRGITSGSFCHPIGGRCTFTPDGGTLHIQAGDALMER APGRWRGITSGSFCHPIGGRCTFTPDGGTLHIQAGDALMER GASON DSSLIAGVOTLASTYLLVFLAGSKDPRAYFKTKTWILLGLILATF GHLWYSIALLAUCKYCH ILHGSKDOPRAYFKTKTWILLGHALLAF GLLVYSAYAPADLSLIVPLAGSKOPRAYFKTKTWILLGHALLAFF GLLVYSAYAPADLSLIVPLAGSKOPRAYFKTKTWILLGHALLAFF GLLVYSAYAPADLSLIVPLAGSKOPPAYFKTKTWILLGHALLAFF ALGCLIAFLAVVLITRINGKYPTLATAGATPAYBOTHERVTHLOWN ARGCHALAGATAAA TUTANAGARALAF GARAGATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA				TOFFEREI BOOMDOWENGHEL TO LINE WAS A TOFFEREI BOOMDOWENGHEL TO LINE WAS A TOFFEREI BOOMDOWENGHEL TO LINE WAS A TOFFEREI BOOMDOWENGHEL TO LINE WAS A TOFFEREI BOOMDOWENGHEL TO LINE WAS A TOFFEREI BOOMDOWENGHEL TO LINE WAS A TOFFEREI BOOMDOWENGHEL TO LINE WAS A TOFFEREI BOOMDOWENGHEL TO LINE WAS A TOFFEREI BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD BOOMDOWENGHELD B
DEGILSDBIGLARALMRTEFFRIKCEDPRILELLUEYVERQIOLIDGENA  BONNGEDILLINGEVSKRIPLYEKRNOGILKDSTYRKIPOSLUES  ASPALMISSAPVIRLISSRSARARPATMTEGATSPAKOPLAGGITAA  ASPALMISSAPVIRLISSRSARARPATMTEGATSPAKOPLAGGITAA  ASPALMISSAPVIRLISSRSARARPATMTEGATSPAKOPLAGGITAA  ASPALMISSIPRIKULLUGVOHARSKOTARAFKORYKGI IPLICUSTIPK  BOGULSFWRGHLANVIRYSPYDQALMFREDRYKGI IPLICUSTIPK  BOGULSFWRGHLANVIRYSPYDQALMFREDRYKGI IPLICUSTIPK  BOGULSFWRGHANVIRYSPYDQALMFREDRYKGI IPLIGUDKHT  DIAKGMLIPPDENTHIVVSKMIAGVYTVARGUSSYPPTYRRRM  MOSGRKGADINYTGTUDCHRITSPEDGKAFFKGAMSHVLRGMG  GAFVULVIDDELKKYT  GAFVULVIDDELKKYT  GAFVULVIDDELKKYT  GAFVULVIDELKKYT  GAFVULVIDELKKYT  GAFVULVIDELKKYT  GAFVULVIDELKKYT  GAFVULVIDELKKYT  GAFVULVIDELKKYT  GERFOLHTEREGOTLI IERULINIAMGIREPIRLIGHDDREUVHL  BSTSMMPRRPSCPLKEPS BOGGNI TOMODDREUVHL  BSTSMMPRRPSCPLKEPS BOGGNI TOMODDREUVHL  BSTSMMPRRPSCPLKEPS BOGGNI TOMODDREUVHL  BSTSMMPRRPSCPLKEPS BOGGNI TOMODDREUVHL  BSTSMMPRRPSCPLKEPS BOGGNI TOMODDREUVHL  BSTSMMPRRPSCPLKEPS BOGGNI TOMODDREUVHLANSSTIDSS  GPELEREERDOLAMTEX BOSVINNOWN STUTTLOVUTLLLINFERV  EDGGSFPALTY VHESGERTYKLKDCEPT JOVENGAS STUTSS  INGHFYNIKHTSVFFPALDS SVANTURVNS STUTTLOVUTLLLINFERV  EDGGSFPALTY VHESGERTYKLKDCEPT JOVENGAS STUTSS  FREIGDGLOCH STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STUTSSPECT STU	<b>\</b>	1		CETTULEMMEDICODGDUMGERINGER
6358 2009 1040 ASDALHSESPAPILARSSANARPATHEOAISPANDELGGIAA AISKTAVAPIERVKLLLQUCHASKQIAADKOYKGIVDCIVEIEK BOGULSPIKKRILARVI HYPTOLAINSKOKIKKOIPLGGUNKH CPWYRFAGRLASGGAAGATSLCTVYPLDPARTELAADUGKSGTIE REFRGLGOLVKITKSGIRGIXQGFGKKYKOIPLGVKSGTIE REFRGLGOLUKITKSGIRGIXQGFGKKYKOIPLGVKSGTIE REFRGLGOLUKITKSGIRGIXQGFGKKYKOIPLGVKSGTIE REFRGLGOLUKITKSGIRGIXQGFGKKYKOIPLGVKSGTIE REFRGLGOLUKITKSGIRGIXQGFGKKYKOIPLGAWGWUL DTAKGHLPDPKNITHIVVSIMIAOTUTAVAGVYSYPPTVRRMM MOSGKKADIMYTGTVOCHKKIFRDEGGKAFFKGAMGENULKGMG GAFVLVILDDELKKVI  VCRQEEEKMKEDCLESSHVPISDSKSIQKSELLGLLKTYNCYHE GKSFQURREEEGTILI EGLLAITAMGLKRIPIKLQMQDDREQVHL PSTSMMPRRESCFLKEPSOMONITAGGSIGOPVIKARSSTDSS GPLERAEEROPLIMETKSDASCNSGRRPKCRAPGEAQRIRGHRENFS INGHFKNIKTSVFTPAYGSVTAVRVNSTMTTLQMQHDDREQVHL PSTSMMPRRESCFLKEPSOMONITAGGSIGOPVIKARSSTDSS GPLERAEEROPLIMETKSDASCNSGRRPKCRAPGEAQRIRGHRENFS INGHFKNIKTSVFTPAYGSVTAVRVNSTMTTLJGMCPGLOPVIKAPSSTDSS INGHFKNIKTSVFTPAYGSVTAVRVNSTMTTLJGAGSIGOPVIKAPSSTDSS INGHFKNIKTSVFTPAYGSVTAVRVNSTMTTLJGAGSGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	1		DECILED DUCLA A ALEXEMBER DECILED DUCLA A ALEXEMBER DECILED DUCLA A ALEXEMBER DECILED DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCLA A ALEXEMBER DUCL
ASDALHSLSAPVIRLISSRSANRAMTROALSPROUPELING ASSALANDIRYTETOALMAPRIKOKUGUVELEN OGUSSPINGRILANDIRYTETOALMAPRIKOKUGUVELEN OGUSSPINGRILANDIRYTETOALMAPRIKOKUGUVELEN OGUSSPINGRILANDIRYTETOALMAPRIKOKUGUTUVELEN OGUSSPINGRILANDIRYTETOALMAPRIKOKUGUTUVELEN OFWRYENGALSGGRAGATSLCYVYDLDPARTELAADUVSGTE REFRGLGDCLVKLTKKSGGIRGLYQGFSUSVOGIITYRAAYFGYV DTAKGHLAPPRINTIVUVSINIAOTUTAVAGUVSYPEPTUVRRHMI MOSCRIKCADIMYTGTVDCWRKIFRDEGKSFFKGAMSNVLIGMG CAFVLVLYDELIKKVI  6359 98 1086 VCRGEBERNKRBCLDFSSHVPISDSKSIQKEELIGLLKTYNCYHE GKSFGLRHHEBEGTLIIEGLLANAMGERRIRLOMODDREQVHL BYSTSWIMPREPSCPLKEPSPQNONITAGGPSIQPVHKARSSTDDS GPLEBAERAPQLMRTKSDASCNSGRRPKCRAPGRAGRIRRHRSS INGHFYNHKTSVPFPAGYSUTAVUNTATLQVLITLLIKHPEV EDOPSSPALIYIVHBSGERTKLKDCEYPLIERILHOPCEKTARIF LMBALIGVEVHEVAGYIKFEMPVLOERILLOMPERVATASIITINDGIGIN MKPQALRLIMLORLEQLVEAK  6360 1 345 GTRGAVPSTLEEVVLIPPSGCEVPHIHSGTTMSKVSFKXTLTFSDF RLPYKVLSVPESTPTTAVLKFFAREFFKVPAATSAIITNDGIGIN PADTAGNVPLKHGSEURI I PRDRVGSC REFRGLGGLOHCALAPQAGNRRCRFHGREHALTRSTHRGKPMSIMQ FKDTLMTPLPDSSSVAVPLIGADIAVASTLSVEHNDGVETIWAC AGGRIRGITSQBFCHFI QGRCTTPIDOGETLHIQAGDAMLPA NSTGIWDJQBFVKRTVVLILL GHLVSFANAFALBLUQUPPTSSSSAVSEASFSYKENLIGALLAFF GHLVVSIALNLQVXCHIRLAGSKOPRAYFKTTWILLIFMLLGS GLUVPASVAPAPLISLIVLYYKEKNANDILLIFITISTEMPKOPDF LRRYVLSFUGGILAVGTYLLUTAPAPSHEKMTGENTTHRLUSS PELLMULVILIYALLISTTATTAGIITIFI KEMPKPOF LRRYVLSFUGGILAVGTYLLUTAPAPSHEKMTGENTTHRLUSS PELLMULVILIYALLISTTATTAGIITIFI KEMPKPOF LRRYVLSFUGGILAVGTYLLUTAPAPSHEKMTGENTTHRLUSS PELLMULVILIYALLISTTATTAGIITIFI KEMPKPOF LRRYVLSFUGGILAVGTYLLUTARAPSHEKMTOMYTHRLUSS TUPPLLARSFSYGALENDINISETYAPATLFVMGEGERGRASG VPYRULEHTKKB  1201 REFRIGSSFPERRBSSAMESYDVIANQPVUIDNGSGVIKAGFAG DOIPKYCFPNYVGRPKHVRVMAGALEDIFTGFRAEEHRGLLSI RYPMHGITVKOMNDER WQVYSKDOLGTFSEHPVLLTEAPL NPRKNERRAABEVFFETFNAPALFISMPLITTRKAYPUDD SGGGTHAVPINGSGSTLAKGFGORLLISSVILATGRTTGVVLD SGGGTHAVPINGSGAMENSTURALSPOVLIANGOVICHORS TIEIGPSRFRAPSILARDOVKRIANDRVKKEYEDGARSIHRTTP RYKNERRAAAEVFFETFNAPALFISMPULLYTAKARDOVKTRIADOV NRNKRERRAAEVFFETFNAPALFISMPULLTETKAQVYUD SGGGVTHAVDINGGSTLAKGTVARDFVUTNONGY FRAGERBIG RYPMIGGSTLAKGTVARDFV	İ			DEGITSDUNGHAMALWRIT FINKKCEDPRHLELLVEYVRKQIQYL
ASSENSABLE RUNKLLLQVQHASKQIADDKYKGIVDCIVEIPK EOGYLSFWEGHLANVIRYPFTQALMFARKOKAQIVDLKGIVDE OGFWSFWEGHLANVIRYPFTQALMFARKOKKGIVDCIVEIPK COFWSFWEGHLANVIRYPFTQALMFARKOKKGIVDCIVEIPK OFFWSFWEGHLANVIRYPFTQALMFARKOKKGIVDCIVEIPK COFWSFWEGHLANVIRYPFTQALMFARKOKKGIVDCIVEIPK DTAKGHLOPKHALSGGAAGATSLCFVYPLDFARTELAADVGKSGTE REFFGLGDCLVKITKSDGIRGLYQGFSUSVQGIITYRAAVFGVY DTAKGHLOPKHALIVOEMKKIFRDEGGKAFFKGAWSNVLRGMG GAFVULVIDELKKVI  GKSFQLRHEBEGGLIITGGLANGAGERIRGLIKTYNCYHE GKSFQLRHEBEGGLIITGGLANGAGERIRGLIKTYNCYHE GKSFQLRHEBEGGLIITGGLANGAGERIRGLIKTYNCYHE BSTSWMPRRPSCPLKEPSPQMGNITAGGFSIQDVIKARSSTDSS GPLEEAEARQUKHTKSDASCASGRREKCARDGEAQRIRKHRSS INGHFINIKTISVFTPAGSSUTNZWNSTMTLQULTLLIKNFPV EDGPSEFALIYLVHESGERTKLKDCSYPLISRILHOPCEKLARIF IMFADLGVVPHEWGYDIYFEMYVLDSFYEKKKEEEREIIKLT MKRQALRUTMLQRLEQLVEAK GTRGAVPSTLEEVVLIPPBSCRVFWIHSGTTMSKVSFKITLTSDF RLPYKULSVPESTFTTAVLKFFAEEFKVPAATSAIITNDGIGIN PAOTAGNVPLHGSEERI IPRDRVSC GTRGAVPSTLEEVVLIPPBSSRVAYHAGAFIAVASTLEVEHINDGVETGIWAC APGRWENQITSOBFCHPIQORCTFTPDDGETLHIQAGDALMLPA NSTGINDIQETVRKTYVLII  APGOTAGNVPLHASSESTI IPRDRVSC APGRWENQITSOBFCHPIQORCTFTPDDGETLHIQAGDALMLPA NSTGINDIQETVRKTYVLII  GHLVVSIALALQKYCHIRLAGSKOPRAYFKTETWHLGLFHMLIG GHLVVSIALALQKYCHIRLAGSKOPRAYFKTETWHLGLFHMLIG GHLVVSIALALQKYCHIRLAGSKOPRAYFKTETWHLGLFHMLIG GHLVVSIALALQKYCHIRLAGSKOPRAYFKTETWHLGLFHMLIG GHLVVSIALALQKYCHIRLAGSKOPRAYFKTETWHLGLFHMLIG GHLVVSIALALQKYCHIRLAGSKOPRAYFKTETWHLGLFHMLIG FRITZIGSSFFRAPILISLIVYYKGMANINUTLILIVALLISMTVV TVAAVAGHLUSITGGHLQLDYPIFYMFOWANATAVQAAPISQ ASGMTDSSILASVGYILISTTATTAGIFYLDPIGGEVUHICMF ALSCLIAPLGYFITTNRKXFIPPEPYISMDAMPGMOMMEDKGM VPYKULEHTKKE  ODIFNYCFPNYVGRPKHVEWAGALBGDIFTGGFRAEEHRGLISI RYPMBGIVKOMMOMERUWYXKOLOLGTSEEHFYLLTEAPL NREKNERAADEVFFETTWALFISMOADLISATVGRTTOVVLD SCOGYTHAVPIXEGSTLAKGTOPRALESKYLLAPROVLITARADQE RIYSTWIGGSILASLDTYKMWYSKEYEGOABSIHRUTP PRINSERFERAAEVFFETTWALFISMOADLISATVGRTTOVVLD SCOGYTHAVPIXEGSTLAKGFGFORLLISSVKLLAPROVLETISADQE RIYSTWIGGSILASLDTYKMWYSKEYEGOABSIHRUTP ROPHRSSEFFETVARIKERGFORLLISATORTOVVLD SCOGYTHAVPIXEGGANGISTIGFFRACHRIGLISI RYPMEHGIVKOMMOMERUWGYVYSKOOLOGTSEEHFVLLTEAPL	6358	2009	1040	ASDA HOLGADILL OCCUPANT OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE
EOGYLSFMEGNLANNIRYFPTQALNFAFKDKYKQIFI.GGUDKHT QFMYYFAGNLASGGAGATSI.CYUDFARRTRLAADVGKSGTE REFFGLGDCLVKITKSDGI.RGLYQGFSVSVQGI.IYTRAAYEGVY DTAKGMLPPDKRHTLVSWMIADVAJAQGVYSPTDYVRRMM MOSGRKGADIMYTGTVDCHRKIFRDEGGKAFFKGAMSNVLRGMG GAFVULYDELKAVI  6359 98 1086 VCRQEEEKMKEDCLPSSHYPISDKSIQKSELLGLLKTYNCYHE GKSFQLRHREBEGTI.IIEGLINIAMGLRRPIRLDMQDDREQUWL PSTSMWPRRPSCPLKEEPSPQNGHTIAMGLAGGSIQPYKAGASSTDSS GPLEBAEBAPQLMRTKSDASCMSQRRPKGRAPGEAQRIRRHRRS INGHFYMHRISVFTPAVGSVTNVVAUGSTOPVHKAESSTDSS GPLEBAEBAPQLMRTKSDASCMSQRRPKGRAPGEAQRIRRHRRS INGHFYMHRISVFTPAVGSVTNVVAUTSTTLQULTLLIMKFRV EDGPSFFALYIVHESGERTKLKDCEYPLISHLHGPCEKLARIF LMBADLGVEVHEWAQYIKFMBVYDLSFVELKKEEEREIIKLI MKRQALRITMLQRLEGUVEAK GTRGAVPSTLEEVVLPPRSCRVFWIHISGTTMSKVSFRITLTSDP RLPYKVLSVPBSTPFTAVLKFAAEEFKVPAATSAITTNDGIGIN PADTAGNVELKHGSELRII IPDRUSKYSFRITLTSDP RLPYKVLSVPBSTPFTAVLKFAAEEFKVPAATSAITTNDGIGIN PADTAGNVELKHGSELRII IPDRUSKYSFRITLTSDF RLPYKVLSVPBSTPFTAVLKFAAEEFKVPAATSAITTNDGIGIN PATTAGNVELKHGSELRII IPDRUSKYSFRITLTSDF RSGLGOLOHCALAPQAGNRRCRFHGRLHAITRSTHRGKPMSIMQ FKDTLMTPLPDSSPVAVPLAGAITAVSTLSVURDGWTTGIMAC APGRWRQITSQBFCHFIQGRCTFTDDGETLHQAGDALMLPA NSTGIMDJQBFVVRKTYULIL  GSGCYNTAVPLYSVGGGLAVVGTYLLVFFAPNSHEMTGENVTHHLUSW PFLLYMLUSILIFICLLYFYKERNALIGIIFIKEKMEPKDF LRRYVLSFVGGGLAVVGTYLLVFFAPNSHEMTGENVTHHLUSW PFLLYMLUSILIFICLLYFYKERNALIGIIFIKEKMEPKDF LRRYVLSFVGGGLAVVGTYLLVFFAPNSHEMTGENVTHHLUSW PFLLYMLVEILIFFCLLYFYKERNATIVULLLUVALLGSMTVV TVAVAGMLVUSILGGNLQLDYPFFYMPFCVANTAVYQAAFLSQ ASGMYDSLLASVGYLISTTIATTAGAFFYDDFTGBVALFIGG ALGCLIAFLGYFLTTRNRKYFIFPFPYISMDAMPGMQNMHDKGM TVOPBLKASFSYGGLISTIATTAGAFFYDDFTGBKAEEHFGLLSI RFYMBHGIVKOMNDMERIMQVYSKDQLOFTSEEHPVLLTEAPL NSKKRERRAAEVFFETTNYPALFIFEDTHLEFREGULSI RFYMBHGIVKOMNDMERIMQVYSKDQLOFTSEEHPVLLTRAPL NSKKRERRAAEVFFETHVNPALFFISHGFTLIFFRENGLSINGR TILGPSFFRRAEVFSFETHVNPALFFISHGOVLISTATAGTTGVVLL SGDGYTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLVRREGG TILGPSFFRRAEVFFFFTNYPALFTISMGAVLSLVATGRTTGVVLL SGDGYTHAVPIYEGFAMPHSIMRIDIAGRDVSRFRRLVLTRAPL NSRKNERRAAEVFFETHVNPALFFISMGAVLSLVATGRTTGVVLL SGDGYTHAVPIYEGFAMPHSIMRIDIAGRDVSRFRREGLLSI NPRKNERREARAEVFFFTHVNPALFFISM	0000	1 2009	1040	ASDALHSLSAPVLKLSSRSAARPATMTEQAISFAKDFLAGGIAA
GFWRYFAGNIA-SGGAGATSIC-FVYPLDFARTRALADUKSGTE REFREIGEDCLVKITSDGIRGLIGGS-SVSVQGIITYRAAYFGVV DTAKGMLPPDFKNTHTVVSWMIAGTVTAVAGVVSYPFDTVRRMM MOSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRMM GAGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRMM GAGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRMM GAFVLULYDELLKVI  1000 1000 1000 1000 1000 1000 1000 1	Ì			AISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVRIPK
REFEGLOCUNITISDE IRLIQGEPSUSUGGI IIYRAAYFGUY DTAKGMLPPDKNITHUVSMIADVANGUVSYPEDTVRRAMM MOSGRKADIMYTGZUDCHRIFFDEGGKAFFKGAMSNVLRGMG GAFVULYDELKKUY  OVERQEEEKMKEDCLPSSHVPISDSKSIQKSELLGLLKTYNCYHE GKSFQLRHEEBEGTLI IIEGLINIAWGLREPIRLOMQDDREQUVIL PSTSWMPRRESCHLEREPSPQNGRITHAWGLREPIRLOMQDDREQUVIL PSTSWMPRRESCHLEREPSPQNGRITHAWGLREPIRLOMQDDREQUVIL PSTSWMPRRESCHLEREPSPQNGRITHAWGLGREIQPSIQPHKAESSTDSS GPLEEAEEAPQLMRTKSDASCMSQRRPKCRAPGEAQRIRPHRES INGHFYNHRISVFTPAYGSVTNIVASTNTTIQULTLLIMKPEV EDGPSEPALYIVHESGERTKLKDCEVPLISRILHGPCEKTARIF LMEADLGVEVPHEUAQYI KPEMPVLDSFVEKLKEEEEREII KLT MKPQALRLIMLQRLEQUVEAX  6360  1 345 GTRGAVPSTLEEVVLPPRSCRVFWIHSGTIMSKVSFKITLTSDP RLPYKVLSVPESTEPTAVLKFAAEEKVPAATSAI TINNDIGIGIN PAQTAGNIVELKHGSELRI I PRDRVGSC  REPUTATIVELEGELRI I PRDRVGSC AFGRMREQITSOBE FLIPTAVLKFAAEEKVPAATSAI TINNDIGIGIN PAQTAGNIVELKHGSELRI I PRDRVGSC AFGRMREQITSOBE FLIPTAVLKFAAEEKVPAATSAI TINNDIGIN PAQTAGNIVELKHGSELRI I PRDRVGSC AFGRMREQITSOBE FLIPTAVLKFAAEEKVPAATSAI TINNDIGIN PAQTAGNIVELKHGSELRI I PRDRVGSC AFGRMREQITSOBE FLIPTIGARCTFHILIQAGDALMLFPA NSTGIMD IQETVRITYYLIL  6362  350  1576  TTMGSHSAALKLQOLPFTSSSAVSEASFSYKENLIGALLAIF GHLVVSIALINLQKYCHIRLAGSKOPRAYFKKTWMLGLFIMLIG ELGVPASVAFAPLSLIVPLSAVSVIASAI IGII FI KEKMEPKDF LRTYLISSVGGLAVVATYLLUTPANSHERMTGEMTVHHLUSM PFILVMLVEILIFCLLLYFYKERNANNI VVILLUVALLGSMTVV TVAVAQMAULUS I GGINQLQLPYFIYAPNSHERMTGENTVHHLUSM PFILVMLVEILIFCLLLYFYKERNANNI VVILLUVALLGSMTVV TVAVAQMAULUS IGUNQLQLPYFIYAPNSHERMTGHONHHKKGM TVOPELKASFSYGALEENDNISEITAPATLFVOQEBEGSRASG VYYRULEHTKKE  FRENGESSFPERKBISSAMESYDVIANQPUVIDNGSGVIKAGFAG DOIPKYCFPNYVGRPKHVRWMAGALEGIFTIGKAEEHGLLSI RYPMEHGIVKUMNDMERI MQVVYSKODQLOTFSEEHPVLLTEAPL NPRKNERAAEVFFETENVPALFISMQAVLSLYATGRTTGVVLD SCHOTHAVPIYEGFFAMPHSI MRI DI IAGROVSKFIRI SAPQE TILGEPSRFRAPFILLFREPDLIGESSGGI HEVLIFFARPL PRINGESFFFRENSSESFFFRINGAMESSYDVIANGFRAGA DOIPKYCFPNYVGRPKHVRWMAGALEGI FIGKAEEHRGLLSI RYSTWIGGSI LASLDTFKKMVSKKEYEEDGARSIHRTF PRINGESFFFRENTINGSFFFRENTSAMESTOVIANGAVILLAGEMVILLTEAPL PRENGESFFFRENTSAMESTOVIANGAVILLAGERGUS HAGFAG DOIPKYCFPNYVGRPHYRWMAGALEGI FIGKAEEHRG	İ			EUGVLSFWKGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHT
DTAKGMLPPDRNTHIVVSMINAGTTTAAAGVSYPEDTVRRAMM MOSGKSADIMTIGTUDCHKITFREGGKAFFKGAMSNVLRGMG GAFVULVIDELKKVI  OVERGEEKMERDELDESHVPISDSKSIQKSELLGLLKTYNCYHE GKSFQLRHREBGTLIIEGLLNIAWGLREIRLGMGDDREQVHL PSTSWMPRPSCPLKEPSPQNGNITAQGPSIQVVHKABSSTDSS GPLEEAEEAPQLWRFKSDASCNSGREPKCRAPGEAGRIRHRESS INGHFYNHKTSVFTEAYGSVTNVRVNSTMTLQVLTLLINKFRV EDGPSFALYIVHESGERTKLKDCSYPLIERILHGPCEKIARIF LMBADLGVEVPHEVAQYIKFEMPVLDSFVERLKEBEEREIIKLT MKPQALRITHLQRLEQLVEAK  6360  1 345 GTRGAVPSTLEEVVLPPRSCRVFMIHSGTTMSKVSFKITLTISDP RLPYKVLSVPESTPTATLKFAREFKVPAATSAIITNDGIGIN PAOTAGNVEIKHGSSLRIIPRDRVGSC  REPGLQQLQHCALAPQAGNRRCRFHGRLHALTRSTHRGKPMSIMQ FKDTLMTPLPDSSEVAVPLGAPIAVASTLEVENINDEVETGIMAC APGRWRRQITSGEFCHFIQGRCTFTPDDGGTLHIQAGDALMLPA NSTGIMDIQETVKTYVLLI  6362  350  1576  TIMDGSHSAALKLQQLPPTSSSSAVESAFSYKENLIGALLATF GHLVVSIANLQKVCHIRLAGSKDPRAYPFTKTWWLGLPIMLLG ELGVPASVAPAPLSLIVUSAVSVIASAIIGIIFIXEKWPXDF LRYVLSFVGGCLAVVGTYLLVTAPJSHEKMTGENVTHLVSW PPLLYMLVEILIFCLLLYFYXEKNANNIVVILLLVALLGSWTVV TVKAVAGHULSIQGNLQLDVFIFYVMFVCMATAVYQAAFISG ASGMYDSSLIAS VGVILISTITATAGIFFUDPIGGDVLHICMF ALGCLIAFIGVFLITRNKKXPIPPEPYISMAPMGMMMHDKGM TVOPBLKASFSGSALENDNDISETYAPATLFVMQEHGSRSASG VPYRVLEHIKKS  1201 RFREGSSFPERRDSSAMESYDVIANOPVVIDNGSGVIKAGFAG DIPKYCFPNYGRPKHVWAGALEGDIFIGFKAEEHRGLLSI NPRKNRERAAEVFFETFNVPALEISMQAVLSLYAAGRTGTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSFFLRIVLRREGY DPHSSSEFEIVKALKERACVLSINPQNVTEREQPYLDDGS TIEIGPSRFRAPELLFRPDLIGEESRGIHEVLUFFAQYYLDDGS TIEIGPSRFRAPELLFRPDLIGEESRGIHEVLUFFAQYYLDDGS TIEIGPSRFRAPELLFRPDLIGGERSRGIHRVLUFFAQY PRIVSTWIGGSSILASLDTFKKWWSKKEYEEDGARSTHRKTF RTRIGSSFPERRAPELLFRPDLIGGERSRGIHRVLUFFAQPT DQIPKYCFPNYVGRPKHVVMAGALEGDIFIGRKAEHRGLLSI RYPMEHGIVKOMNDMERIMQVYVSKOLQTFSEEHPVLLITRAPJ PRKRRERAAEVFFETFNVVALBEJSMQAVLSLYAAGRTGGTGVVLD SGDGVTHAVPIYEGSFPAPFELISMQAVLSLYAAGRTGGTGVVLD SGDGVTHAVPIYEGSFPAPFELISMQAVLSLYAAGRTGGTTGVVLD SGDGVTHAVPIYEGSFPAPFELISMQAVLSLYAAGRTGRTGVVLD SGDGVTHAVPIYEGSFPAPFELISMQAVLSLYAAGRTGRTGVVLD SGDGVTHAVPIYEGFFAMPHSIMRIDIAGRDVSFFLRIVLREGY DQIPKYGFFANFUSHSMAMSIMPANIMOGVVISNGCTGGTTGVVLD SGDGVTHAVPIYEGFFAMPHSIMRIDAGRDVSFFLRIVLTRAPJUSH	i	i		DEEDGL COOLUMINATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PR
MQSGRKGADIMYTGTUDCHRKIFRDEGKAFFKGAMSNVLRGMG GAFVULVIPELKKVI  6359  98  1086  VCRQEEKMREDCLESSHVPISDSKSIQKELLGLLKTYNCYHE GKSFOLHRERBGTLI I BGLLNIAWGLRRIFILQMQDDEGVUH. PSTSWMPRPSCPLKEPSPQNGNITAGGPSIQVHKAESSTDSS GPLEEAEEAPQLMRTKSDASCNSQRPKCRAPGEAGRIRHRES INGHFYNHRTSVFTPAYGSVITNVNSTMTLQVILLLILKKPEV EDGPSFFALVIVHESGERTKLKDCEYPLIERILHGPCEKIARIF LMEADLGVEVPHEVAQYIKFPHVLDSFVEKLKEEEREIIKLT MKFÇALRLTMLQRLEQLVEAK  6360  1 345  GTRGAVPSTLEEVVLDFPRSCRYWHINSGTTMSKVSFKITLTSDF RLPYKVLSVPESTPFTAVLKFAAEEFKVPAATSAIITNDGIGIN PAQTAGNVPSTLEEVVLDFPRSCRYWHINSGTTMSKVSFKITLTSDF RLPYKVLSVPESTPFTAVLKFAAEEFKVPAATSAIITNDGIGIN PAQTAGNVPSTLEEVVLDFPRSCRYFWINGSVEFKITLTSDF RFOTLMTPLPDSSPVAVPLGAPIAVASTLSVEINDGVETGINAC AFGRWRRQITSGEFCHFIQGRAFHGELHALTRSTHRGKPMSIMQ FKDTLMTPLPDSSPVAVPLGAPIAVASTLSVEINDGVETGINAC AFGRWRRQITSGEFCHFIQGRAFHGELHALTRSTHRGKPMSIMQ FKDTLMTPLPDSSPVAVPLGAPIAVASTLSVEINDGVETGINAC AFGRWRRQITSGEFCHFIQGRAFHGELHALTRSTHRGKPMSIMQ FKDTLMTPLPDSSPVAVPLGAPIAVASTLSVEINDGVETGINAC AFGRWRRQITSGEFCHFIQGRAFHGENHALTRSTHRGKPMSIMQ FKDTLMTPLPDSSPVAVPLGAPIAVASTLSVEINDGVETGINAC AFGRWRRQITSGEALAVGTYLLVTPDGGETVHLIGAGDALLAFF GHLVVSIALNLQXYCHLITPASSSVSEASFSYKENLIGALLAFF GHLVVSIALNLQXYCHLITPASSSVSIASAIIGIFTIKEKKKPKDF FELLYMLVEILIFCCLLYFYXERNANNIVVILLLVALLGSMTVV TVAVAGRHULSI GGENLOLDVIFTASSHEKMTGERVTHHLVSW PFILLYMLVEILIFCCLLYFYXERNANNIVVILLLVALLGSMTVV TVAVAGRHULSI LITRRIKKSI PTEYSISHEKMTGERVTHHLVSW PFILLYMLVEILIFCCLLYFYXERNANNIVVILLLVALLGSMTVV TVAVAGRHULSI LITRRIKKSI PEYISHSHEKMTGEFVITHICMS AGGMTSSLLASVGYILSTTATTAGAIFFLDPIGGEDVLHICMF AGGCLIAFLGVFLITRRIKKSI PEYISHSHEKMTGERVTHHLVSW TVOPELKASFSYGALENNDNISEIYAPATLFVMQEHGSRSAG DDIPKYCFPNVQRPKHVWAGALEGDIFIGFKAEEHRGLLSI NPRKRERABEVFFETTNVPALFISMQAVLSLYATGRTTGVVLD SGGGVTHAVPTYEGFAMPHSIMENIMFVITONGSVYKAGFAG DPHSSSEFEIVKAIKERACULSINPQKVITSERHVLLTRAPL NPRKNRERAAEVFFETTNVPALFISMQAVLSLYATGRTTGVVLD NPRKNRERAAEVFFETTNVPALFISMQAVLSLYATGRTTGVVLD NPRKNRERAAEVFFETTNVPALFISMQAVLSLYATGRTTGVVLD SGGGVTHAVPTYEGFAMPHSIMENIDLAGREGOTFFSEHPVLLITEAPL NPRKNRERAAEVFFETTNVPALFISMQAVLSLYATGRTTGVVLD SGGGVTHAVPTYEGFAMPHSIMENIDLAGREGOTFFSEHPVLL				REFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIYRAAYFGVY
6359 98 1086 VCRGEEKKMEDCLESHVPISDSKSIQKSELUGLIKTYNCYHE GKSFQLRHREBGGTLI IEGLIMIAWGLRRPIRLQMQDDREQVHL PSTSWMPRRPSCPLKEPSPONGNITAGGEPSIQVPHKABSSTDSS GPLEEAEEAPQLMRTKSDASCNSGRRRCRAPGEAGRIRHRES INGHFYNHKTSVFTEAYGSVTNVRVNSTMTLQVLTLLINKFRV EDGPSFPALYIHVESGERTKLKDCSYPLIERILIBGPCEKIARIF LMEADLGVBVPHEVAQYIKPEMPVUDSFVEKLKEEEEREIIKLT MKFQALRITMLQRLGQLVEAK  6360 1 345 GTRGAVPSTLEEVVLPPRSCRVFWHINSGTTMSKVSFKITLTSDP RLPYKVLSVPESTPTTAVLKFAAEEFKVPAATSAIITNDGIGIN PAQTAGNVPLKHEGSERT IPROPKSC  6361 615 158 RPGLGGLGCHCALAPQAGRRRCRFHGRLHALTRSTHRGKPMSIMQ FKDTLTMTPLPDSSPVAVPLGADIVASTLSVEINDGUFTGIWAC APGRWRRQITSGBFCHPIGGRCTFTPDDGETLHIQAGDALMLFA NSTGIMDIQETVRKTYVLIL  6362 350 1576 TTMDGSHSAALKLQQLPPTSSSSAVSEASFSYKENLIGALLAIF GHLVVSIALNLQKYCHIRLAGSKDPRAYPTKTWWLGLFIMLLG ELGVPSAYAPAPLSLUVPLSAVYIASAIIGHIFIKEKWRCPHTLVSW PFLLVMUVSIALNLQKYCHIRLAGSKDPRAYPTKTWWLGLFIMLLG ELGVPSAYAPAPLSLUVPLSAVYIASAIIGHIFIKEKWRCPHTLVSW PFLLVMLVBILIFICLLLYPYYKGAMINIVVILLUVALLGSMTVV TVKAVAGMLVLSIQGNLQLDYPIFYVMFVCMVATAVYQAAFLSQ ASGMTDSSLIASVGYILSTTIATAGAIFYLDPIGGDVLHICMF ALGCLIAFLGYULITRNRKK71PEPPISDSAMPGMOMNHOKGM TVOPELKASFSYGALENNDNISEIYAPATLPVMQEEHGSRSASG VYPRVLEHTKKE PVENULEHTKKE RPTRLGSSFPRRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCPPNVQRPKHVWAGALBGDIFIGFKAEEHRGLISI RPTMBGIVKOWNDMERIWQVVYSKOQLOTFSEEHPVLLTEAPL NPRKNRERAABVFFETTNVPALFISMQAVLSLYATGRTTGVVLD SCHMAVPTYEGFAMPHSIMRIDIAGROVSFRLEVLVLREGY DPHSSSSFEIVKAIKERACVLSINPOKDETLETEKAQYYLPDGS TIEIGPSRFRAPFLLFRPDLIGEESGRASHRKTF RRTHSNTVLSGSSTLFRGFGDRLLSSVKKLARKDVKRISAPQE RLYSTWIGGSILASLDTFKKMWVSKEYESGGARSIRKKTF RRTHSNTVLSGSFTLFRRSSAMESTYDVIANOPVVIDNGSGVIKAGFAG DQIPKYCPPNVQRPKHVMAGALBGDIFIGPKAEEHRGLLSI NPRKNRERAAEVFFETTNVPALFISMQAVLSLYATGRTTGVVLD SGGGVTHAVPTYEGFAMPHSIMRIDIAGRGDVFFLEVLLTEAPL NPRKNRERAAEVFFETTNVPALFISMQAVLSLYATGRTTGVVLD SGGGVTHAVPTYEGFAMPHSIMRIDIAGRGDUSTFLINLTREGY DDIPKYGSPFRVQRPKHVMAGALBGDTFIGPKAEEHRGLLSI NPRKNRERAAEVFFETTNVPALFTSDAQAVLSLYATGRTTGVVLD SGGGVTHAVPTYEGFAMPHSIMRIDIAGRDUSTFLULTRADPS DFHSSSSFETVIKAIKERACVLSINPOKDETLETEKAQYYLPDGS DFHSSSSFETVIKAIKERACVLSINPOKDETLETEKAQYYLPDGS DFHSSSSFETVIKAIKERA	1	•		DIAKGMDPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
6359  98  1086  VCROEEEKMREDCLESSHVEISDSKSIOKEELGLLKTYNCYHE GKSFOLRHREEGTLI IEGLLNIAWGLRRPIRLOMDDEROVHL PSTSWMPRRESCPLKEPSBONGNITAGOPSIOPVHKABSSTDSS GPLEKAEEAPQLMRTKSDASCMSQREPKCRAPGEAGRIRHRES INGHFYNHKTSVFTPAYGSUTUNVSSMTLQUTLLLLKKFEV EDGPSFFALVIVHESGERTKLKDCEYPLIERILHGPCEKLARIF LMEADLGVEVPHEVAQYIKPEMPVUDSFVEKLKEEERIIKLT MKPQALRLTMLQRLEQLVEAK MKPQALRLTMLQRLEQLVEAK GTRGAVPSTLEEVVLPPRSCRVFWIHSGTTMSKVSFKITLTSDP RDATAGNVELLEVVLSPRSCRVFWIHSGTTMSKVSFKITLTSDP RDATAGNVELKIGSELRIIPRDRVGSC  6361  6361  615  158  RPGLGCLOMCALAPGAGNERCRFHGELHALTRSTHRGKPMSIMQ FKDTLNTPLPDSSPVAVPLGAPIAVASTLSVEINDGVETGINAC APGRWERGITSGEFCHFIGGRCTFTPDDGSTLHIQAGDALMLPA NSTGIMDIGETVKTYVLLI  6362  350  1576  TTMDGSHSAALKIQOLPPTSSSSAVESESFYKENLIGALLAIF GHLVVSIALNIQKYCHIRLAGKSUPRAYFKTKTWALGLFHALG ELGVFASYAFAPLSLIVPLSAVSVIASALIGIIFIKEKWKPGFF LRRYVLSSVGCLAVVGTYLLVTFAPASHEKMTGENVTHHLVSW PFLLYMLVEILIFCLLLYFYKEMANIVVILLUALLGSMTVV TVAVAGMINUSIQGNLQIDVFIFYVMFVCMVATAVYQAAPLSQ ASGMYDSSLLASVGVILSTTLATGAIFFLOPGUVLHICMF ALGCLIAFLGVFLITRNKKPIPPPPYISMDAMPGMQMMHDKGM TVOPELKASFSYGALENNDNISEIYAPATLFVMQEHGSRSASG VPYRLJEHTKKE  6363  21  1201  RRTRIGSSFFRRRDSSAMESYDVIANOPVVIDNGSGVIKAGFAG DOIPKYCFPNYGRPKHVPWMAGALEGDIFIGFKAEEHRGLISI RYPMBHGIVKDWNDMERIWQYVYSKQLQTFSEEHPVLLTEAPL NPRKNRERAABVFFETENVPALFISMQAVLSLYATGRTTGVVLD SCHYSTHIGGSLASDTFKKMWASKLEYBEGDARSIHKVTF RTLFSNIVLSGSSTLFKGFGGRILLSEVKKLAPKDVKRISAPQE RIJSTNIGGSILASDTFKKMWASKLEYBEGDARSIHKTF RTLFSNIVLSGSSFFRRRDSSAMESYDVIANOPVVIDNGSGVIKAGFAG DOIPKYGFPNYGRPKHVPWMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWGYVYSKOOLQTFSEEHPVLLTEAPL NPRKNRERAABVFFETENVPALFISMQAVLSLYATGRTTGVVLD SCHYSTYGGSILASDDTFKKMWASKLEYBEGDARSIHKTF RTLFSNIVLSGSSFFRRRDSSAMESYDVIANOPVVIDNGSGVIKAGFAG DOIPKYGFPNYGRPKHVPWMAGALEGDIFIGPKAEEHRGLLSI NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SCHYNTYMGGSLASDFFRENDSAMESYDVIANOPVVIDNGSGVIKAGFAG DOIPKYGFPNYGRPKHVPWMAGALEGDIFIGPKAEEHRGLLSI NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGGGVTHAVPIYEGFFAMPHSIMRIDIAGRDUSPFLIRLYLRKEGY DFHSSSSFFEINKALKREACVLSINOPQADTLETERAGYYLPDGS	1			MOSGRAGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMG
GKSFQLRHREBEGTL1 IEGLINTAWGLRRP IRLQMQDDREQUHL PSTSWMPRRPSCPLKEPSPONGNITAGPSIQPVHKAESSTDSS GPLEEAEEAPQLWRITKSDASCMSQRRPKCRAPGEAGRIRHERS INGHFYNHKTSVFTPAYGSVTNVRVISTMTTLQVLTLLLINKEPLV EDGPSFPAIVIVHESGERTLKLCCEYPLISRILHGPCEKIARIF LMEADLGVEVPHEVAQYIKFEMPVLDSFVEKKKEEEERSIIKLT MKPQALRITMLQRUEQLVEAK  6360 1 345 GTRGAVPSTLEERCVWIFPRSCRVWHISGTTMSKVSFKITLTSDP RLPYKVLSVPESTPFTAVLKFAAEEFKVPAATSAIITTNDGIGIN PAOTAGNVFIKHAGSERIIVAFAAEEFKVPAATSAIITTNDGIGIN PAOTAGNVFIKHAGSERIIVAVASTLSVEHNDGVETGIWAC APGRWRQITSGEFCHFIGGRCTFFTDDGETLHIQAGDALMPA NSTGIMDIGETVRKTYVLIL  6362 350 1576 TTEDGSHSAALKIQOLPPTSSSSAVSEASFSYKENLIGALLAFF GHLVVSIALNLQKYCHIRAGSEKDPRAYFKTRTWKLGFLMLLG GHLVVSIALNLQKYCHIRAGSEKDPRAYFKTRTWKLGFLMLLG ELGVFASYAFAPLSLIVUPLSAVSVIASAIIGIFIKEKWKPKDF LRFYULSFVGCGLAVVGTYLLVTFAPNSHEKMTGENVTRHLVSN PFLLYMLVEIILFCLLLYFYKSKNANNIVVILLLVALIGSMTVV TVKAVAGMLVLSIQGNIQLDYFIFTWFYGWAVTAVVQAAFLSQ ASGMYDSSLIASVGYILSTTIATGAIFYLDFIGEDVLHTCMF ALGCLIAFIGGVLITNRTKYLPFPPYISMDAMPMONMHNKM TVOPBLKASFSYGALENDNISEIYAPATLPVMQEEHGGRSASG VPYRVLEHTKKE  6363 21 1201 RRTRLGSSFPRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMGALEGIFIGPKAEEHRGLLSI NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTGVVLD SGGGVTHAVPITEGFAMPHSIMDIIAGGDVSRFLRILLYREGY DPHSSSEFFIVKAIKERACYLSINPQKDETLETEKAQYYLDDGS TIEIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIGKSDMDLR RTLFSNIVLSGGSTLFKGFGORDLISEVKLARMOVKRISAPQE THYSWIGGSFLASLDTFKKMWVSKKEEEDGASIRKTF PRINGSSFFFRREDSAMESYDVIANQPVOTDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRWAGALEGIFIGPKAEEHRGLLSI RYPMEGISVKOMNDMERIWGVYSKDQLOGTFSEEHPVLLTEAPL NPRKNRERAAEVFFETRVPALFISMQAVLSLYATGRTTGVVLD SGGGVTHAUPTIEGGSPTLFKGFGORDLISEVKLARMOVKRISAPQE TIEIGPSRFRAPELLFRPDLIGEFSEGIHEVLVFAIGKSDMDLR RTLFSNIVLSGGSTLFKGFGORDLISEVKLARMOVKRISAPQE THEIGPSRFRAPELLFRPDSAMESTVVINOPVVTONGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRWAGALEGIFIGDRAEEHRGLLSI RYPMEHGIVKOMNDMERIWQTVYSKDQLOGTFSEEHPVLLTEAPL NPRKNRERABEVFFETRVPALFISMQAVISLYATGRTTGVVLD SGGGVTHAUPTIEGGSPHFFISMANSILVATGRTTGVVLD SGGGVTHAUPTIEGGSPHFFISMANSILVATGRTTGVVLD SGGGVTHAUPTIEGGRWHSTWRIDLAGRDVSRFLRKLIPLERPLU	6359	98	1006	
PSTSWMPRRPSCPLKEPSPONGNITAGGESIOPUHKAESSTDSS GPLEEAEEAPQLMRTKSDASCMSGRPKCKAPGEAGRIRRHRS INGHFYNHKTSVFTPAYGSVTNVVNSTMTTLQVLTLLLNKFRV EDGPSEPALYIVHESGERTKLKDCERYPLISRILHGPCEKIARIF LMEADLGVEVPHEVAGYIKPEMPVLDSFVEKLKEEEEREIIKLT MKRQALRITMLQRLEGLVEAK  6360 1 345 GTRGAVPSTLEEVVLPPSGCRVFWIHSGTTMSKVSFKITLTSDP RLPYKULSVPESTPFTAVLKFAAEEFKVPAATSAIITNDGISIN PAQTAGNVFLKHGSELRIIPRDRVGSC  6361 615 158 RPGLGGLQHCALAPQAGNIRACRPHGRLHALTRSTHRGKPMSTMQ FKDTLMTPLPDSSPVAVPLGAPIAVASTLSVERINGGVETGIMAC APGRWRRQITSDEFCHFIQGEFTHPJDGGTLHIQAGDALMLPA NSTGIMDIQETVRKTYVLIL  6362 350 1576 TTMDGSHAALKLQQLPPTSSSAVESAFSYKENLIGALLAIF GHLVVSIALNLQKYCHIRLAGSRDPRAYFKTTWMLGLFLMLLG ELGVFASYAFAPLISLIVPLSAVSVIASAIGIIFIXERMKPKDF LRRYVLSFUGCGLAVVGTVLYFAPNSHERMTGENVTHLVSW PFLLYMLVEILIFCLLLYFYKEKNANNIVVILLLVALLGSMTVV TVKAVAGMUVLSIQGNLQLDYFIFTYMPCWWATAVYQAAFLSQ ASGMYDSSLLASVGVILSTTIATAGAIFYLDFIGEDUHTCMF ALGCLIAFIGVELITRNRKFJPFFBYJSMDAMPGMOMMHDKGM TVQPBLKASFSVGALLENNDNISEIYAPATLPVMQEHGSRASG VPYRVLEHTKKE  6363 21 1201 RRTRLGSSFPRRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DOIPKYCFPNYVGPRKHURWAGALEGDIFTGFKAEEHRGLLSI RYPMBEGIVKOWNDMERIWQYVSKDQLGTPSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLVATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGROVSRFLRIVLRKEGY DPHSSSEFEIVKAILSLDTFKKMVVSKEYEEGGARSIRKTTF RTLFSNIVLSGCSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTWIGGSILASLDTFKKMVVSKEYEEGGARSIRKTTF DQIPKYCFPNYVGRPKHURVMAGALEGDIFTGFKAEEHRGLLSI RYPMBEGIVKOWNDMERIWQVYVSKDQLOTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLVRAGRAGG TIEIGPSRFRAPFLLSFRPDLIGEFSGFHEULVRALOKSDMDLR RTLFSNIVLSGCSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTWIGGSILASLDTFKKMVVSKEYEEGGARSIRKTTF DQIPKYCFPNYVGRPKHURVMAGALEGDIFTGFKAEEHRGLLSI RYPMBEGIVKOWNDMERIWQVYVSKDQLOTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLVRAGFRAG DQIPKYCFPNYVGRPKHURVMAGALEGDIFTGFKAEEHRGLLSI NPRKNRERAAEVFFETFNVPALFISMQAVLSLVRAGFRAG DQIPKYCFPNYVGRPKHURVMAGALEGDIFTGFKAEHRGLLSI NPRKNRERAAEVFFETFNVPALFISMQAVLSLVRAGRAGALSI NPRKNRERAAEVFFETFNVPALFISMQAVLSLVRAGRAGALSI PVPKSSEFEIVKAARMENTURDINGARDVSRFLKHLYLERGY DPHSSSEFEIVKAARRERCYLSINPQKOETLETEKAQYYLDGS DFHSSSEFEIVKAAR			1000	CKSEOL BUDGERSCHILL TERRETARIES OF THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE CHARACTER TO THE C
GPLEEAEAPQLMRTKSDASCMSGRPKCRAPGEAQRIRRHRES INGHYNHKTNSTPTAYOUTNURVINSTMTTLQVLTLLLIKFRV EDGPSEFALYIVHESGERTKLKDCEYPLISRILHGPCEKIARIF LMEADLGVEVPHEVAQYIKFEMPVLDSFVEKLKEEEREIIKLT MKRQALRLITHLQRLEGUVEAK GTRGAVPSTLEEVVLIPERSCRVFMIHSGTTMSKVSFKITLTSDP RLPYKVLSVYBSTPPTAVLKFAAEEFKVPAATSAITTNDGIGIN PAQTAGNVFLKHGSELRIIPRDRVGSC  6361 615 158 RFGLGGLQHCALAPQAGNRRCRFHGRLHAITRSTHRGKPMSIMQ FKDTLATPHOSSPVAVLPDSSPVAVLPDSSPVAVLSVEHNDGVETGIWAC APGRWRRQITSQBFCHFIQGRCTFTPDDGETLHIQAGDALMLPA NSTGIWDIQETVRKTVULIL GHLVVSIALNLQXPCHTRLAGSKDPRAYFKKTWWLGLFLMLLG ELGVFASYAPAPLSLIVPLSAVSVIASAIIGIIFIKEKWKPDF LRRYVLSFVGCGLAVVGTYLLVTFAPRSHEKMTGENVTRHLVSW PFLLYMLVSIILFCLLLYFYKEKNANNIVVILLUVALLGSMTVV TVAVAGMLVLSIGGRILDYFIFYVMFVAVATAVVQAPLSQ ASGMYDSSLIASVGYLLSTTIATTAGAIFYLDFIGEDVLHICMF ALGCLIAFLGVFLITRNRKKPIPFFFYISMDAMPGMONMIDKGM TVQPELKASFSVGALENNDMISEIYAPATLFVMQEEHGSRSASG VPYRVLEHTKKB  6363 21 1201 RRPRLGSSFPRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALBGDIFIGFKAEEHRCLLSI RYPMBEGIVKOMNDMBRIMGYVVSKDOLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNYPALFISMQAVLSLVATGRTTGVVLD SGGGVTHAVPIVEGGSTLASLDTFKKMWVSKKEVEEDGARSIHRKTF TIEIGPSFRAPFLLFRPDLIGEESGGHEVLVFAIQKSMDLR RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPLDVKIRISAPQE RLYSTWIGGSILASLDTFKKMWVSKKEVEEDGARSIHRKTF RYPMBEGIVKOMNDMERIMGYVYSKDOLQTFSEEHPVLLTEAPL NPRKNERAABEVFFETFNVPALFISMQAVLSLVATGRTTGVVLD SGGGVTHAVPIVEGGFAMPHSIMRIDIAGRDVSRFLRKJERGFAG DCIPKYCFPNYVGRPKHVRVMAGALEGDIFIGFKAEHRGLLSI RYPMEGIVKOMNDMERIMGVVYSKDOLQTFSEEHPVLLTEAPL NPRKNERAAEVFFFTROYSKMWVSKKEVEEDGARSIHRKTF RYPMEHGIVKOMNDMERIMGVVYSKDOLQTFSEEHPVLLTEAPL NPRKRERAAEVFFFTFNVPALFISMQAVLSLVATGRTTGVVLD SGGGVTHAVPIYEGFAMPHSIMRIBIARDVSRFLHYLRKEGY DPHSSSFFEIVKALIFERGYVYSKDOLQTFSEEHPVLLTEAPL NPRKRERAAEVFFFTFNVPALFISMQAVLSLYATGRTTGVVLD SGCGVTHAVPIYEGFAMPHSIMRIBIARDVSRFRLHYLRKEGY DPHSSSFFEIVKALIFERGYVLNDESIMPGVYSKDOLGTFSEEHPVLLTEAPL NPRKRERAAEVFFFTFNVPALFISMQAVLSLYATGRTTGVVLD SGCGVTHAVPIYEGFAMPHSIMRISMINIDADDVSRFRLHYLRKEGY DPHSSSFFEIVKALTRACTVLSTINPQKDETLETTEKAQYVLDDGS FRISHEGIVKANDMERIMGVYVSKDOLGTFSEEHPVLTTERAGYVLDDF	1			GASFQLRHREEEGTLITEGLLNIAWGLRRPIRLQMQDDREQVHL
INGHFYNHKTSVFTPAYGSVITIVUTISTILHOFCEKIARIF EDGSSPALIVINESGERTKIKRDCEYPLISRILHOFCEKIARIF LMEADLGUEVPHEVAQYIKFEMPVLDSFVEKIKEEEREEIIKLI MKPQALRITVHESGERTKIKRDCEYPLISRILHOFCEKIARIF LMEADLGUEVPHEVAQYIKFEMPVLDSFVEKIKEEEREEIIKLI MKPQALRITVHSEGERTSCEVFHIHSGTTMSKVSFKITLTSDP RLPYKVLSVSESTPFTAVLKFABEEFKVPAATSAIITNDGIGIN PAOTAGNVPKIKHGSELRI PRDRVGSC  6361 615 158 RPGLGQLQHCALAPQAGNRRCRFHGRLHALTRSTHRGKPMSIMQ FKDTLATPIPLBDSSPVAVPLGAPIAVASTLSVEHBGVETGIMAC APPGRWRRQ ITSQEFCHFI POGRTFTPDDGSTLHI QAGDALMLPA NSTGIMDIQETVRKTYVLIL 6362 350 1576 TTMDGSHSAALKLQQLPPTSSSSAVSEASFSYKENLIGALLAIF GHLVVSIALINLOKYCHIRLAGSKDPRAYFKKTWHLGLHIMLIG ELGVFASYAFAPLSLIVPLSAVSVIJASAIIGIIFIKEKWKPKOF LRRYULSFVGCGLAVVGTYLLVTFAPNSHERMTGENTYTHLUSW PFLLYMLVSILISPCLLLYFYXEKNANNIVVILLLVALLGSMTVV TVKAVAGMLVLSIQGNLQLDYPIFYWFVCWATAVYQAAFLSQ ASGMYDSSLIASVGYILSTIATTAGAIFYLDFIGEDVHICTMF ALGCLIAFIGVFLITRNRKKPIPFEPYISMDAMPGMONMHDKGM TVOPBLKASFSYGALENDISEIYAPATLFVMQEEHGSRSASG VPYRVLEHTKKB RTTELGSSFPRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DIPKYCFPNYVGRPKHVRWAGALBEDIFIGFKAEHRGLLSI RYFMBEGIVKDWNDMERIWQYVYSKDOLOTFSEEHPVLLTEAPL NPRKNRERAABVFFETFNVBALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMEIDIAGROVSRFLRIYLKREGY DPHSSSEFFILVAIKERACYLSINDPKODETLETEKAQYVLDDGS TIEIGPSRFRAPFELFFPDLIGEESIGHEVLUFAIQKSMDLR RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSHRKTF RYPMBEGIVKOMNDMERIWGYVYSKDOLOTFSEEHPVLLTEAPL NPRKNRERABEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMEIDIAGROVSRFLRELYLRKEGY DCIPKYCFPNYVGRPKHVRWMAGALEGDIFIGFKAEHRGLLSI RYPMBEGIVKOMNDMERIWGYVYSKDOLOTFSEEHPVLLTEAPL NPRKNRERABEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMEIDIAGROVSRFLRELYLRKEGY DPHSSSFFELWAIKERSPSDVIANQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMEIDIAGROVSRFLRELYLRKEGY DPHSSSFFELWAIKERGAPLSIMPSIMEIDIAGROVSRFLRELYLRKEGY DPHSSSFFELWAIKERGAPLSIMPSIMEIDIAGROVSRFLRELYLREGGY DPHSSSFFELWAIKERGAVLSINPQKDETTETEKAQYVLDDGS DFHSSSFFELWAIKERGAVLSINPQKDETTETEKAQYVLDDGS DFHSSSFFELWAIKERGAVLSINPQKDETTETEKAQYVLDDGS DFHSSSFFELWAIKERGAPLSIMEIDIAGROVSRFLRELYLREGGY DFHSSSFFELWAIKERGAPL		]		CDI FENDEN POLYTER SPONGNITA OG PSI OPVHKAESSTDSS
EDGPSFPALYIVHESGERTKLKDCEYPLIGRILHGPCEKIARIF LMEADLGUEVPHEVAQYIKPEMPVLDSFVEKLKEEEEREIIKLT MKFQALRLTMLQRLEQLVEAK  6360  1 345 GTRGAVESTLEEVVLPPRSCRYWHIGSTTMSKYSFKITLTSDP RLPYKVLSVESTPFTAVLKFAAEEFKVPAATSAIITNDGIGIN PAGTAGNVFLKHGSELRIIPRDRVGSC  6361 615 158 RPGLGQLQHCALAPQAGNRRCRFHGRLHAITRSTHRGKPMSIMQ FKDTLMTPLPDSSSVAVPLGAPIAVASTLSVEHNDGVETGIWAC APGRWRRQITSOBFCHFIQGRCTFTPDDGETLHIQAGDALMLPA NSTGIMBIQETVRRTYVLIL  6362 350 1576 TTMDGSHSAALKLQOLPPTSSSSAVSEASFSYKENLIGALLAIF GHLVVSIALINLQKYCHIRLIAGSKDPRAYFKTKTWMLGLFIMLLG ELGVFASYAFAPLSLIVLSAVSVIASAIIGIIFIKEKWRKDGF LRRYVLSFVGCGLAAVGTYLLUTFAPNSHEKMTGENVTRHLVSW PFLLYMLVEIILFCLLLYFYXEKNANNIVVILLUVALLGSMTVV TVKAVAGMLVLSIQGNLQLDYPIFTVMFCGMATAVYQAAFLSQ ASGMYDSSLLASVGYILSTTIAITAGAIFYLDPIGEDVLHICMF ALGCLLAFLGVFLITRNKKYIPFEPPYISMDAMPGMONMIDKGM TVOPBLKASFSYGALENNDNISEIYAPATLPVMQEEHGSKSASG VPYRVLEHTKKE  APTRLGSSFPRRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPXYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDMDMERIWQVYSKDQLGTFSEEHPVLLTEAPL NPRKNRERAABVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGGGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERGYTJSNQVBCTFSEEHPVLLTEAPL RYLSTWIGGSILASLDTFKKMWSKKEYEDGARSIHRKTF  6364 21 1201 RRTRLGSSFPRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPXYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVGKDMYDMERIWQVVSKDQLGTFSEEHPVLLTEAPL NPRKNRERAABVFFFTFNVPALFISMQAVLSLYATGRTTGVVLD SGGGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRKUFF PXPMEHGIVKDMYDMERIWQVVSKDQLGTFSEEHPVLLTEAPL NPRKNRERAAEVFFFTFNVPALFISMQAVLSLYATGRTTGVVLD SGGGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRKTF PXPMEHGIVKDMYDMERIWQVYSKDQLGTFSEEHPVLLTEAPL NPRKNRERAAEVFFFTFNVPALFISMQAVLSLYATGRTTGVVLD SGGGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRKTFR PXPMEHGIVKDMYDMERIWQVYSKDQLGTFSEEHPVLLTEAPL NPRKNRERAAEVFFFTFNVPALFISMQAVLSLYATGRTTGVVLD SGGGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRKTFR PXPMEHGIVKDMYDMERIWQVYSKDQLGTFSEEHPVLLTEAPL NPRKNRERAAEVFFFTFNVPALFISMQAVLSLYATGRTTGVVLD SGGGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRKTFR				THE THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPER
LMEADLGVEVHEWQYIKPEMPVLDSFVEKLKEEEEREIIKLT  MKPÇALRITMLQRLEQLVEAK  G16360  1  345  GTRGAVPSTLEEVVLPPRSCRVFWIHSGTTMSKVSFKITLTSDP RLPYKVLSVESSTPTTAVLKFAAEEFKVPAATSAIITNDGIGIN PAQTAGMYKKHGSEIR IPRDRVGSC  6361  615  158  RPGLGQLQHCALAPQAGNRRCRFHGRLHALTRSTHRGKPMSIMQ FKDTLMTPLEDSSPVAVPLGAFIAVASTLSVEINDGWETGIWAC APGRWRRGJUTSQEFCHF GQRCTFTPDDGETLHIQAGDALMLPA NSGIMDIQETWRITYVLIL  6362  350  1576  TIMDGSHSAALKLQQLPPTSSSSAVSEASFSYKENLIGALLAIF GHLVVSIALALQKYCHIRLAGSKDPRAYFKTKTWWLGLFLMLLG ELGVFASYAFAPLSLIVPLSAVSVIASAIIGIIFIKEKWKPKDF LRRYVLSFVGCGLAVVGTYLLVTFAPNSHEKMTGENTTHLVSW PFLLYMLVEILLFCLLVFYKEKNANNIVVILLUVALLGSMTVV TVKAVAGMLVLSIGGNLQLDYPIFYMFVCMVATAVYQAAPLSQ ASQMYDSSLLASVGYILSTTIATAGAIFYLDPIGEDVLHICMF ALGCLIAFLGVFLITRNKK7IPFBYISMDAMPGMONMHDKGM TVOPBLKASFSYGALENNDNISEIYAPATLFVMQEEHGSRSASG VPYRVLEHTKKE  6363  21  1201  RRTRLGSSFPRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPXYCFPNYVGRPKHVVVMAGALEGDIFIGFKAEEHRGLLSI RYPMBGIGIVKDMYDMERIMQVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSFFLKIVLKKEGY DPHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLDDGS TIEIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR RTLFSNIVLSGGSILASLDFFKKMVSKKEYEBGAARSHRKTF  6364  21  1201  RRTRLGSSILASLDFFKKMVVSKGEVESDEARSHRKTF  EXPMENGIGVGSILASLDFFKKMVVSKGEVESDEARSHRKTF  PHYMEHGIVGVGPKHVVVVGRAGLEGDIFIGPKAEEHRGLLSI RYPMEHGIVGVGPKHVVVVGRAGLEGDIFIGPKAEEHRGLLSI RYPMEHGIVGVGPKHVVVGPKHVVVGRAGLEGDIFIGPKAEEHRGLLSI RYPMEHGIVKONDMERINGVYVSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLKLYLKEGY DFHSSSEFFIVKAIKERACYLSIMPQKDETLETEKAQVYLDPGS  DFHSSSEFFIVKAIKERACYLSIMPGKDETLETEKAQVYLDPGS DFHSSSEFFIVKAIKERACYLSIMPGKDETLETEKAQVYLDPGS DFHSSSEFFIVKAIKERACYLSIMPGKDETLETEKAQVYLDPGS DFHSSSEFFIVKAIKERACYLSIMPGKDETLETEKAQVYLDPGS				EDGDGEFAL VIULEGGEDWY VDGRUDY TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE TOO THE
6360 1 345 GRGAVPSTLEEVULPPRSCRVPWIHSGTTMSKVSFKITLTSDP RLPYKVLSVPESTPFTAVLKFAREEFKVPAATSAIITNDGIGIN RLPYKVLSVPESTPFTAVLKFAREEFKVPAATSAIITNDGIGIN PAGTAGNVFLKHGSELRIIPROVGSC  6361 615 158 RFGLGGLOHCALAPQAGNRRCRFHGRLHALTRSTHRGKPMSIMQ FKDTLATPLPDSSPVAVPLGAPIAVASTLSVEHNDGVETGIWAC APGRWRRQITSQEFCHFIQGRCTFTFDDGETLHIQAGDALMLPA NSTGIMDIQETVRKTYVUIL  6362 350 1576 TTMDGSHSAALKLQQLPPTSSSSAVSEASFSYKENLIGALLAIF GHLVVSIALNLQKYCHIRLAGSKDPRAYFKTKTWMLGLFIMLLG ELGVFASYARAPISLIVPLSAVSVIASAIIGIIFIXEKWKKKDF LRRYVLSFVGCGLAVVGTYLLVYTARNSHEKMTGENTTRHLVSW PFLLYMLVEIILFCLLYFYXEKNANNIVVILLLVALLGSMTVV TVKAVAGMLVLSIQGNLQLDYPIFYVMFVCMVATAVYQAAFLSQ ASGMYDSSLTASVGYILSTTIAITAGAIFYLDPIGEDVLHICMF ALGCLLAFLGVFLITRNRKK?PFEFFYISMDAMPGMOMMENGM TVQPELKASFSYGALENNDNISEIYAPATLFVMQEEHGSRSASG VPYRVLEHTKKE  6363 21 1201 RRTRLGSSFFRRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DOIPKYCFPNYVGRPKHVRVMAGALEGDIFIGKAEEHRGLLSI RYFMBHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NFRKNERRAEVFFETTNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DPHSSSEFEIVKAIKERRAYLSINPOKDETLETEKAQYYLPDGS TIEIGPSRFRAPELLFRPDLIGEESEGHEVLVFAIQKSDMDLR RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRTSAPQE RLYSTWIGGSILASLDFKKWVSKKEVSEEDGARSIHRKTF OQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGI VKDMYDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNERRAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRRLTF PROMEHGIVKDMYDMRRIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNERRAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRRLTF PROMEHGIVKDMYDMRRIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNERRAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFFIVKAIKERAGVLSINPQKDETLETEKAQVYLDFGS				EDGPSEFALITVHESGERTKLKDCEYPLISRILHGPCEKIARIF
GTRGAVPSTLEEVLIPPRSCRVFWIHSGTTMSKVSFKITLTSDP RLPYKVLSVPBSTPFTAVLKFAREEFKVPAATSAIITNDGIGIN PAQTAGNVFLKHGSELRIIPRDRVSC  6361 615 158 RPGIGQLOHCALAPQAGNRRCRPHGRLHALTRSTHRGKPMSIMQ FKDTLNTPLPDSSPVAVLPAATLSVEHNDGVSCTGIWAC APGRWRRQITSQEFCHFIQGRCTFTPDDGETLHIQAGDALMPA NSTGIWDIQEFVRKTYVLIL  6362 350 1576 TTMDGSHSAALKLQQLPPTSSSAVSEASFSYKENLIGALLAIF GHLVVSIALNLQKYCHIRLAGSKDPRAYFKTKWWLGLFIMLLG ELGVFASYAFAPLSLIVPLSAVSVIASAIIGIIFIXEKWKPKDF LRRYVLSFVGCGLAVVGTYLLVTFAPNSHEKMTGENVTRHLVSW PFLLYMLVEIILFCLLLYFYKENKANNIVVILLLVALLGSMTVV TVKAVAGMLVLSIQGNLQLDPJFIYVMFVCWVATAVYQAAFLSQ ASGMYDSSLIASVGYLSTTIATTAGAIFYLDFIGEDVLHICMF ALGCLIAFLGVFLITRNRKKPIPPFPYISMDAMPGMQNMHDKGM TVCPBLKASFSYGALENNDNISEIYAPATLPVMQEEHGSRSASG VPYRVLEHTKKE  6363 21 1201 RRTRLGSSFPRRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVEWMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDNNDMERIMQYVVSKDQLOTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DPHSSESFEIVKAIKERACYLSINPOKDETLEETEKAGYYLIPDGS TIEIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR RTLFSNIVLSGGSTLFKGFGDLLISEVKKLAPKOVKIRISAPQE RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF FRYMEHGIVKDWNDMERIWQVYVSKODLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFIGMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYGGFAMPHSIMRIDIAGRDVSRFLRLYLFRAPL NPRKNRERABEVFFETFNVPALFIGMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYGGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DQIPKYCFPNYVGRPKHVRWMGKKEYEEDGARSIHRKTF RYPMEHGIVKDWNDMERIWQVYVSKODLQTFSEEHPVLLTEAPL NPRKNRERABEVFFETFNVPALFIGMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYGGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DPHSSEFFIVKAIKERACYLSINPQKOETLETEKAQYYLIPGGS DFHSSEFFIVKAIKERACYLSINPQKOETLETEKAQYYLPGGS		į		MKEONI OF EOTHERN OF EOTHERN
RIPYKVISVPBSTPTTAVLKFAREFFKVPAATSAIITNDGIGIN PAOTAGNVFLKHGSELRI IPPDRVGSC  6361 615 158 RFGLGQLQHCALAPQAGNRRCRFHGRLHALTRSTHRGKPMSIMQ FKDTLNTPLPDBSPVAVPLGAPIAVASTLSVEHNDGVETGIWAC APGRWRRQITSQEFCHFJQGRCTFTPDDGETHHIQAGDALMLPA NSTGIMDIQETVRKTYVLIL  6362 350 1576 TTMDGSHSAALKIQQLPPTSSSSAVSEASFSYKENLIGALLAIF GHLVVSIALNLQKYCHIRLAGSKDPRAYFKTKTWWLGLFLMLLG ELGVFASYAFAPLSLIVPLSAVSVIASAIIGIFIKEKWKPKDF LRRYVLSFVGGGLAVVGTYLLVTFAPNSHEKMTGENVTRHLVSW PFLLYMLVGILIFCLLLYFYKERNANNIVVILLLVALLGSMTVV TVKAVAGMLVLSIQGNLQLDYPIFYVMFVCWAVATAVYQAAFLSQ ASGMYDSSLIASVGYILSTTIAITAGAIFYLDFIGEDVLHICMF ALGCLIAFLGVFLITRNRKKPIPFEPYISMDAMPGMQNMHDKGM TVOPELKASFSYGALENNDNISEIYAPPATLPVMQEEHGSRSASG VPYRVLEHTKKE  6363 21 1201 RRTRLGSSFFRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQVVYSKDQLQTFSEEHPVLLTEAPL NFRKNRERAABVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS TIEIGFSRFRAPFLLFRCPLIGEESGGIHEVLVFAIQKSDMDLR RTLFSNIVLSGGSTLFKGFGGDRLLSEVKKLAPKDVKIRISAPQE RLYSTWIGGSILASLDTFKKMVVSKKEYEEDGARSIHRKTF 6364 21 1201 RRTRLGSSFFRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWDDMERIWQVYYSKOQLQTFSEEHPVLLITEAPL NPRKNRERABEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLREGY NPRKNRERABEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLREGY NPRKNRERABEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFFIVKAIKERACYLSINPQKDETLETEKAQYYLRREGY DFHSSSEFFIVKAIKERACYLSINPQKDETLETEKAQYYLRREGY DFHSSSEFFIVKAIKERACYLSINPQKDETLETEKAQYYLRREGY DFHSSSEFFIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS	6360	1	345	
6361 615 158 RPGLQQLQHCALAPQAGNRCRFHGRLHALTRSTHRGKPMSIMQ FKDTLNTPLPDSSPVAVPLGAPIAVASTLSVEHNDGVETGIWAC APGRWRRQITSQBFCHFIQGRCTFTPDDGETLHIQAGDALMLPA NSGIGWIDQGETVRKTYVLIL  6362 350 1576 TTMDGSHSAALKLQQDPPTSSSSAVSEASFSYKENLIGALLAIF GHLVVSIALNLQKYCHIRLAGSKDPRAYFKTKTWMLGLFIMLLG ELGVFASYAFAPLSLIVPLSAVSVIASAIIGIIFIKEKWKKPKDF LRRYVLSFVGGGLAVVGTYLLVTFAPNSHEKMTGENVTHHLVSW PFLLYMLVEIILFCLLLYFYXEKNANNIVVILLLVALLGSMTVV TVAVAGMLVLSIQGNLQLDYPIFYVMFVCMVATAVYQAAFLSQ ASQMYDSSLIASVGYILSTTIAITAGAIFYLDFIGEDVLHICMF ALGCLIAFLGGYFLITRNRKKFIPFBFYISMDAMPGMQMMHDKGM TVOPBLKASFSYGALENNDNISEIYAPATLPVMQEEHGSRASG VPYRVLEHTKKE  6363 21 1201 RRTRLGSSFPRRDSSAMESVDVIANQPVVIDNGSGVIKAGFAG DQIPXYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYFMEHGIVKDWNDMERIWQVYSKDQLQTFSEEHPVLLTEAPL NFRKNRERAABVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSIMPQKDSTLETEKAQYYLPDGS TIEIGPSRFRAPELLFRPDLIGEESEGIHBVLVFAIQKSDMDLR RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHKKTF 6364 21 1201 RRTRLGSSFPRRDSSAMESYDVIANOPVVIDNOSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYFMEHGIVKDWNDMERIWQVVSKDQLQTFSEEHPVLLTEAPL NPRKNRERAABVFFETFNVPALFISMQAVLSLVATGRTGVULD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLREHRGLLSI RYPMEHGIVKDWNDMERIWQVYSKDQLGTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLVATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRREGY DFHSSSEFEIVKAIKERACYLSIMPQKDETLETEKAQYYLPDGS SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRREGY DFHSSSEFEIVKAIKERACYLSIMPQKDETLETEKAQYYLPDGS	1			PLDYKYL SYPRETDETRYL YEAR PERKUDANGA THEY
6361 615 615 616 6362 6362 6362 6360 6362 6360 6360 636	1			PAOTAGNUFIKHGSELDI LDDDDUGGG
FKDTLNTELPDSSPVAVPLGAPIAVASTLSVEINDGVETGIWAC APGRWRQITSQEFCHFIQGRCTFTPDDGETLHIQAGDALMLPA NSTGIWDIQETVRKTYVLIL  6362 350 1576 TTMDGSHSAALKLQQLPPTSSSSAVSEASFSYKENLIGALLAIF GHLVVSIALINLQKYCHILLAGSKDPRAYFKTKTWWLGGFIMLLG ELSVFASYAFAPLSLIVPLSAVSVIASAIIGIIFIKEKWKPKDF LRRYVLSFVGCGLAVVGTYLLVTFAPNSHEKMTGENVTRHLVSW PFLLYMLVEIILFCLLLYFYKEKNANNIVVILLLVALLGSMTVV TVKAVAGMLVLSIQGNLQLDYPIFYVMFVCMVATAVYQAAFLSQ ASQMYDSSLIASVGYILSTTIATTAGAIFYUDFIGEDUHICMF ALGCLIAFLGVFLITRNRKKPIPFEPYISMDAMPGMQNMHDKGM TVOPBLKASFSYGALENNDNISEIYAPATLPVMQEEHGSRSASG VPYRVLEHTKKE  6363 21 1201 RRTRLGSSFPRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGFKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQVVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETTNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS TIBIGPSRFRAPELLFRPDLIGESSEGIHEVLVFAIQKSDMDLR RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTNIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF RYPMEHGIVKDWNDMERIWQVVYSKDQLQTFSEHFVLLTGAPL NPRKNRERAAEVFFETTNVPAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQVVYSKDQLQTFSEHFVLLTGAPL NPRKNRERAAEVFFETTNVPAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQVVYSKDQLQTFSEHFVLLTGAPL NPRKNRERAAEVFFETTNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLTGAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLTGEGY DFHSSSEFEIVKAIKERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLDDGS	6361	615	158	
APGRWRRQTTSQEFCHFIQGRCTFTPDDGETLHIQAGDALMLPA NSTGIWDIQETVRKTYVLIL  6362 350 1576 TTMDGSHSAALKLQQLPPTSSSSAVSEASFSYKENLIGALLATF GHLVVS1ALNLQKYCHIRLAGSKDPRAYFKTKTWWLGLFLMLLG ELGVYASYAFAPLSLIVPLSAVSVIASAIIGIFIIXEKWKPKDF LRRYVLSFVGCGLAVVGTYLLVTFAPNSHEKMTGENVTRHLVSW PFLLYMLVEIILFCLLLYFYKEKNANNIVVLLLLVALLGSMTVV TVKAVAGMLVLSIQGNLQLDYPIFYVMFVCWVATAVYQAFLSQ ASQMYDSSLIASVGYILSTTIAITAGAIFYLDFIGEDVLHICMF ALGCLIAFLGVFLITRNRKKPIPFEPYISMDAMPGMONMHDKGM TVQPELKASFSYGALENNDNISEIYAPATLPVMQEEHGSRSASG VPYRVLEHTKKE DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMBHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNERAABEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS TIEIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR RTLFSNIVLSGSSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTMIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF 6364 21 1201 RRTRLGSSFPRRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG CLYSTMIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF FRAFELSSFFRRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG RLYSTMIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF OQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGRAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS	1			FKDTINTDI.DDGCDVAVDI GADIAVACTI GVEVDVDGCTDT
6362 350 1576 TTMDGSHSAALKLQQLPPTSSSAVSEASFSYKENLIGALLAIF GHLVVSIALINLQKYCHIRLAGSKDPRAYFRTKTWWLGLFLMLLG ELGVFASYAFAPLSLIVPLSAVSVIASAIIGIIFIKEKWKPKDF LRRYVLSFVGCGLAVVGTYLLVTFAPNSHEKMTGENVTRHLVSW PFLLYMLVSIILFCLLLYFYKEKNANNIVVILLLVALLGSMTVV TVKAVAGMLVLSIQGNLQLDYPIFYVMFVCMVATAVYQAFFLSQ ASQMYDSSLIASVGYILSTTIAITAGAIFYLDFIGEDVLHICMF ALGCLIAFLGVFLITRNRKKPIPFEPYISMDAMPGMONMHDKGM TVOPELKASFSYGALENNDNISEIYAPATLPVMQEEHGSRSASG VPYRVLEHTKKE  6363 21 1201 RRTRLGSSFPRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGFKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQVYYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLDGS TIEIGPSRFRAPFLLFRPDLIGEESEGHEVLVPAIQKSDMDLR RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF 6364 21 1201 RRTRLGSSFPRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLVATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYVLDGS GGGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYVLDGS GGGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYVLDGS				APCDWPDOITEOFFCURIOCROTETEDDOGTTUTOSCOTT
6362  1576  TTMDGSHSAALKLQQLPPTSSSSAVSEASFSYKENLIGALLAIF GHLVVSIALINLQKYCHIRLAGSKDPRAYFKTKTWKLGLFIMLLG ELGVFASYAFAPLSLIVPLSAVSVIASAIIGIIFIKEKWKPKDF LRRYVLSFVGCGLAVVGTYLLVTFAPNSHEKMTGENVTRHLVSW PFLLYMLVEIILFCLLLYFYKEKNANNIVVILLLVALLGSMTVV TVKAVAGMLVLSIQGALQLDYPIFYVMFVCMVATAVYQAAFLSQ ASQMYDSSLIASVGYILSTTIAITAGAIFYLDFIGEDULHICMF ALGCLIAFLGVFLITRNRKK?IPFEPYISMDAMPGMONMHDKGM TVQPELKASFSYGALENNDNISEIYAPATLPVMQEEHGSRSASG VPYRVLEHTKKE  RRTRLGSSFPRRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS TIEIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR RTLFSNIVLSGSSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS GGDVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS	1			NSTGINDIOETUPETUVI.II.
GHLVVSIALNLQKYCHIRLAGSKDPRAYFKTKTWWLGLFLMLLG ELGVFASYAFAPLSLIVPLSAVSVIASAIIGIIFIKEKWKPKDF LRRYVLSFVGCGLAVVGTYLLVTFAPNSHEKMTGENVTRHLVSW PFLLYMLVEIILFCLLLYFYKEKNANNIVVILLLVALLGSMTVV TVKAVAGMLVLSIQGNLQLDYPIFYVMFVCMVATAVYQAAFLSQ ASQMYDSSLIASVGYILSTTIAITAGAIFYLDFIGEDVLHICMF ALGCLIAFIGVFLITRNRKKPIPFPFYISMDAMPGMQNMHDKGM TVOPELKASFSYGALENNDNISEIYAPATLPVMQEEHGSRSASG VPYRVLEHTKKE  1201 RRTRLGSSFPRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMBHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSFFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS TIEIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYGGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLDDGS	6362	350	1576	TTMDGSHSAALVLOOLDDTSSSSAVSSACSSAVSSA
ELGVFASYAFAPLSLIVPLSAVSVIASAIIGIIFIKEKWKPKDF LRRYVLSFVQCGLAVVGTYLLVTFAPNSHEKMTGENVTRHLVSW PFLLYMLVEIILFCLLLYFYKEKNANNIVVILLLVALLGSMTVV TVKAVAGMLVLSIQGNLQLDYPIFYVMFVCMVATAVYQAAPLSQ ASQMYDSSLIASVGYILSTTIAITAGAIFYLDFIGEDVLHICMF ALGCLIAFLGVFLITRNRKK?IPFEPYISMDAMPGMQMMHDKGM TVOPELKASFSYGALENNDNISEIYAPATLPVMQEEHGSRSASG VPYRVLEHTKKB  6363 21 1201 RRTRLGSSFFRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPMYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMBHGIVKDWNDMERIMGVVYSKDQLQTFSEEHPVLLITEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS TIEIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTWIGGSILASLDTFKKMVVSKKEYEEDGARSIHRKTF BQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGGGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGGGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYYLPDGS			23.0	GHIANGIAIAN OVYCUIRI ACOVODE AVENTURINA CONTRACTOR
LRRYVLSFVGCGLAVVGTYLLVTFAPNSHEKMTGENVTRHLVSW PFLLYMLVEIILFCLLLYFYKEKNANNIVVILLUVALLGSMTVV TVKAVAGMLVLSIQGNLQLDYPIFYVMFVCMVATAVYQAAFLSQ ASQMYDSSLIASVGYILSTTIAITAGAIFYLDFIGEDVLHICMF ALGCLIAFLGVFLITRNRKKPIPFEPYISMDAMPGMOMMHDKGM TVOPELKASFSYGALENNDNISEIYAPATLPVMQEEHGSRSASG VPYRVLEHTKKE  1201 RRTRLGSSFPRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS TIEIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF CG364 21 1201 RRTRLGSSFPRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYYYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS	1	1		FIGURAGYARADI GI TUDI CAUGUTAGATAGATAGATAGATAGATAGATAGATAGATAGA
PFLLYMLVEIILFCLLLYFY.KEKNANNIVVILLLVALLGSMTVV TVKAVAGMLVLSIQGNLQLDYPIFYVMFVCWWATAYYQAAFLSQ ASQMYDSSLIASVGYILSTTIAITAGAIFYLDFIGEDVLHICMF ALGCLIAFLGVFLITRNEKKPIPFEPYISMDAMPGMQNMHDKGM TVQPELKASFSYGALENNDNISEIYAPATLPVMQEEHGSRSASG VPYRVLEHTKKE  6363 21 1201 RRTRLGSSFPRRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGFKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS TIEIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTWIGGSLLASLDTFKKMWVSKKEYEEDGARSIHRKTF C364 21 1201 RRTRLGSSFPRRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS	1	i		L.D.D.V.J. S.D.J.C.C.C. M.D.C.C.C. I. L.D.D.J.C.J.C.C.C. M.D.C.C.C. M.D.C.C.C.C. M.D.C.C.C.C.C.C.C.C.C.C.C.C.C.C.C.C.C.C.
TVKAVAGMLVLSIQGNLQLDYPIFYVMFVCMVATAVYQAAFLSQ ASQMYDSSLIASVGYILSTTIAITAGAIFYLDFIGEDVLHICMF ALGCLIAFLGVFLITRNRKK?IPFEPYISMDAMPGMONMHDKGM TVOPELKASFSYGALENNDNISEIYAPATLPVMQEEHGSRSASG VPYRVLEHTKKE  6363 21 1201 RRTRLGSSFPRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS TIEIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF  6364 21 1201 RRTRLGSSFPRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS	1		•	DELLYMLUETTI POLLT VEVVENNADATTITITI TARAFA
ASQMYDSSLTASVGYILSTTIAITAGAIFYLDFIGEDVLHICMF ALGCLIAFLGVFLITRNRKKPIPFEPYISMDAMPGMONMHDKGM TVOPELKASFSYGALENNDNISEIYAPATLPVMQEEHGSRSASG VPYRVLEHTKKE  6363 21 1201 RRTRLGSSFPRRDSSAMESYDVIANOPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS TIEIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF 6364 21 1201 RRTRLGSSFPRRRDSSAMESYDVIANOPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS		ł		TWANACMINI CTOCKE OF DYDITERRATIONS OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PRO
ALGCLIAFLGVFLITRNRKKPIPFEPYISMDAMPGMQNMHDKGM TVOPELKASFSYGALENNDNISEIYAPATLPVMQEEHGSRSASG VPYRVLEHTKKE  6363 21 1201 RRTRLGSSFPRRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS TIEIGPSRFRAPFLLFRPDLIGEFSEGIHEVLVFAIQKSDMDLR RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF C364 21 1201 RRTRLGSSFPRRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS		į		ASOMYDSSI.TACUCUTI COMITATORA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTONICA TENTON
TVOPELKASFSYGALENNDNISEIYAPATLPVMQEEHGSRSASG VPYRVLEHTKKE  6363 21 1201 RRTRLGSSFPRRRDSSAMESYDVIANOPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLOTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS TIEIGPSRFRAPFLLFRPDLIGEESEGIHEVLVFAIQKSDMDLR RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF  RRTRLGSSFPRRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS	1			ALCCATAFICARI TERMERATERE PARENTE DE L'ACCATAFICARE
OPYRVLEHTKKE  6363  21  1201  RRTRLGSSFPRRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS TIEIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF  6364  21  1201  RRTRLGSSFPRRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS	1			TUODEL KA SESYCAL ENDOWS SETUP DATE TO SHORM TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE TO SETUP DATE
6363 21 1201 RRTRLGSSFPRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS TIEIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS				VDVD/U.EHTKKE
DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVUSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS TIEIGPSRFRAPFLLFRPDLIGEESEGIHEVLVFAIQKSDMDLR RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF RTRLGSSFPRRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYIPDGS	6363	21	1201	
RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS TIEIGPSRFRAPELLFRPDLIGESSEGIHEVLVFAIQKSDMDLR RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF  6364 21 1201 RRTRIGSSFPRRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS	1			
NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS TIEIGPSRFRAPFLLFRPDLIGEFSEGIHEVLVFAIQKSDMDLR RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF  6364 21 1201 RRTRLGSSFPRRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS				BYDMBUCTIVE DUDGED IN ONLY STREET OF STREET
SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS TIEIGPSRFRAPELLFRPDLIGESSEGIHEVLVFAIQKSDMDLR RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTWIGGSILASLDTFKKMVSKKEYEEDGARSIHRKTF  RTRLGSSFPRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS	1	1	i	NDDVNDEDAAEUBEEUDAUDAUEKTWQXVXSKDQLQTFSEEHPVLLTEAPL
DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS TIEIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTWIGGSILASLDTFKKMVSKKEYEEDGARSIHRKTF RTRLGSSFPRRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS	1 1	İ		SCOCUTA VIDIA CENARUS INC.
TIEIGPSRFRAPFLLFRPDLIGEFSEGIHEVLVFAIQKSDMDLR RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF RRTRLGSSFPRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPPYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS	1	Ì		DEUGGERRETURA TYRRA CYLCTONIA CHARLEGY
RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF RRTRLGSSFPRRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRWAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS				TIETCOSDEDINELL EDDDY TOWNSON THE TEKAQYYLDDGS
RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF  6364 21 1201 RRTRLGSSFPRRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKOQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS		ľ		PELECUTAL COCCER ENCECEDED CONTROL OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROP
RRTRIGSSFPRRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS	1			RI VERWICOGIL TO PERFECUENCE SEVENCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PROVINCE PR
DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS	6364	<del></del>	1201	RDISTWIGGSTLASLDTFKKMWVSKKEYEEDGARSIHRKTF
RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS	000	21	1201	KKTKLGSSFPRRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG
NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS				DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI
SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS				RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL
DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS		1		NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD
DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS TIEIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR	] ]			SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY
TIEIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR	ļ l			DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS
	L			TIEIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR

Deginning   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:   No:	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Not   Aucleotide   Corresponding to first   Samuno acid   residue of   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Security   Secu			1	(A=Alanine, C=Cvsteine D=Aspartic Acid D=
corresponding to first amino acid tresidue of sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence se				Clutamic Acid FarPhenylalanine Gaclusine
corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence schence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence seq				Halistidine Tatsoleucine Kalucine
to first amino acid residue of secrine, T-Threanine, V-Valise, amino acid amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence	1			LeLeucine MeMethionine N-Asparaging
amino acid residue of amino acid sequence surprotophan, %-Typrosine, %-Unknown, %-Stop Codon, %-possible nucleotide insertion) sequence sequence surprotophan, %-Typrosine nucleotide insertion)  ### RTUPSINIUS COSTIFICATION STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES A	İ		3	
residue of amino acid sequence    sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence	1		1	
amino acid sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence	1			
### Sequence   Lapone bile nucleotide insertion   ### RIPSINIVIS@STILESEVERLISEVERLISENSEVERT   ### STATES   RIPSINIVIS@STILESEVERLISENSEVERT   ### STATES   RIPSINIVIS@STILESEVERT   ### STATES   RIPSINIVIS@STILESEVERT   ### STATES   RIPSINIVIS@STILESEVERT   ### STATES   RIPSINIVIS@STILESEVERT   ### STATES   RIPSINIVIS@STILESEVERT   ### STATES   RIPSINIVIS@STILESEVERT   ### RIPSINIVIS@STILESEVERT   ### RIPSINIVIS@STILESEVERT   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STILESEVERT   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ### RIPSINIVIS@STATES   ###	1			Codon /-neggible puglochide folkhirm
### FILESH VLSGGSTLEKGFGDRILSEVERLANDVEKT SAROE RLYSTRIGGS LLSJLDTFEKWWYSKEVERDESTHENDES ####################################			acquence	
6 365 234 1939 KIKSRASCARAQAGYESPEREVISKRYSEGLESSISGECTE ASMITILATEDEYGRPELI KINODEKSRIMGLEALKSHIMAARAVA NIKKSRASCARAQAGYESPEREVISKRYSEGLESSISGESSISGECTE ASMITILATEDEYGRPELI KINODEKSRIMGLEALKSHIMAARAVA NIKKSRASCARAQAGYESPEREVISKRYSEGLESSISGENGE ASMITILATEDEYGRPELI KINODEKSRIMGLEALKSHIMAARAVA NIKKSRASCARAQAGYESPEREVISKRYGUEDI KINODEKSRIMGLEALKSHIMAARAVA LIMELSKSQIDDE GODTTOVVILAGALLESREQLLDRE HIP RI ADGYEQARAVA HUMELSKSQIDDE GODTTOVVILAGALLESREQLLDRE HIP RI ADGYEQARAVA LIMELSKSQIDDE SIDODEKVODAKATI LIGHMUVDHQIAK LIMELSKSQIDDE SIDODEKVODAKATI LIGHMUVDHQIAK VINSCHROMBER DAVIDEKUM KURUKSAN LICHEN KINOSULVENDAK LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN KURUKSAN LICHEN K		Doquonee		
6365 234 1989 KHKSRASCAARAGAFGSREREVISRERSGERELGESINGCETH AMSMITLAFBEVGRPELI KLODDERSILMGEALKSHIMAARAVA NTRITSLGPIGLDERMYDKDGDVYVINDGATILSMYDUTHOLAK LMVELKSGDDETGDGTTGVVVLAGALLEGELLORGHEIPER ADGYEGAARVAIGHLINKTSDSVLVDTKOTEELIGTAKTTLGSKY VNSCHROMBE TAVMAULTVAMBERDUTPERLYDEKKYGEKYGGLEF TKLIKGVIVDKDFSHPOMPKKVEDBAIALIGCGPERDEKYKHK LDVTSVEDYKALOKYKRKFFEEMTOOLIKTIVECKVYGGLEF TKLIKGVIVDKDFSHPOMPKKVEDBAIALIGCGPERDE ANHLLIGNNLEAVRWYGGETELIATGGRIVPERSELTAEKL GEGAGLVGET ISFGTYKKOKMIV EGCKNSRAVITEIRGGINGT AKSSLHDALGVIRNLIEDNKVYGGGAARTSCALAVSGEADKCE TLBGYAMMAFADALEVIPAGLSENSGMIPTEIRGGINGTEIL AKSSLHDALGVIRNLIEDNKVYGGGAARTSCALAVSGEADKCE TLBGYAMMAFADALEVIPAGLSENSGMIPTEIRGGINGTEIL AKSSLHDALGVIRNLIEDNKVYGGGAARTSCALAVSGEADKCE TLBGYAMMAFADALEVIPAGLSENSGMIPTEIRGGINGTEIL AKSSLHDALGVIRNLIEDNIGSSESSE NPALGTDCHINGTTURKKOOJSLATOWVRMILK TDDIRRYGESSE  GNIKKGAISSTFPVLLSIPLGAVAALCKEGGTVLGINAVFDTLIV TLBGYAMMAFADALSEVIPAGLSENSCHAMVITYITYSGGA MLYVFRRIMGTOPPATTEVDHOASFADSMIPTAVTVIYTYSIAA MLLCDWALCTPWSMYGTEILKSIDDHUSTEPTILTSGGAA MLYVFRRIMGTOPPATTEVDHOASFADSMIPTAVTVIYTYSIAA HLLCDWALCTPWSMYGTEILKSIDDHUSTAPTILTSGGAA MLYVFRRIMGTOPPATTEVDHOASFADSMIPTAVTVIYTYSIAA HLLCDWALCTPWSMYGTEILKSIDDHUSTAVTVIYTYSIAA HLLCDWALCTPWSMYGTEILKSIDDHUSTAVTVIYTYSIAA HLLCDWALCTPWSMYGTEILKSIDDHUSTAVTVIYTYSIAA RYYREAVPLINDRYVIYAMDHUSTIANTURGILDHUSTAVTVIYTYSIAA RYYREAVPLINDRYVIYAMDHUSTANTURGILDIKATURGATURGATAVTYTYTYSIGAA RYYREAVPLINDRYVIYAMDHUSTANTURGILDIKATURGATURGATAVTYTYTYSIGAA RYKREAVPLINDRYVIHAMATVIKAPHILDAKKAYPEISLGLDAVOYTRISTALFURA RYREAVPLINDRYVIHAMATVIKAPHILDAKKAYPEISLGLDAVGAA KENNYGLARVAYRIGHALAVIKAYBGILDAKKAYPEISLGLDAVGAA KENNYGLARVAYRIGHADAVATATTARTITAVTATATATATATATATATATATATATATATATATAT				
ASMOTLAPDEVGRPPILITRODRESIMMELBALKSHIVAAKAVA NTHRTSLEGENGLDKOWNDEXDOTYTVINDGRILISM/DUDRICAK LMVELSKSQDDBIGDGTTGVVVLAGALLEREQLLDRSIHPIRI ADGYEGARRVAIEHLDKISDSVLUDIKDTEPLIQTAKTILGSKY VNSCHRQWAE ZAWANLIYHAMBERRUPTELVEGKVQGKED TKLIKGVIVDLDFSHPQMPKKVEDAKIALLTGFEFEPKYKKKK LDVTSVEDYKALOKYNKKKFEEMIQOIKETABLAICOWGPDDE ANHLLIQNNLEAVRWGGPEIELIALATGGRIVPRESELTAEKI GFAGLUQEISTGTKKNAWLUEQCKNSRAVTIFIRGGNAMISE AKRSLHDALCVIRNLIRDNRVVYGGGABAISCALAVGEANKCP TLRGYMMRAFADALEVIPMALSENSGMURJOITMTEVRARQVKEM NPALGIDCILHKGYNDKKQQHVIETLIGKKQQISLATOWURNILK TLRGYMMRAFADALEVIPMALSENSGMURJOITMTEVRARQVKEM NPALGIDCILHKGYNDKKQQHVIETLIGKKQQISLATOWURNILK GRANVLETUKQKUHKRKSLENLGMLRNGGLFRMTLITSGGA MLYVRRIMGTOPPATTEVDNPASFADSMURJAWNYYYSINA WLLICPWHLCPUMSMCGIPLKSISDNRVALAVNYYYSINA WLLICPWHLCPUMSMCGIPLKSISDNRVALAVNYYYSINA WLLICPWHLCPUMSMCGIPLKSISDNRVALAVNYYYSINA WLLICPWHLCPUMSMCGIPLKSISDNRVALAVNYYSINA WLLICPWHLCPUMSMCGIPLKSISDNRVALAVNYYYSINA WLLICPWHLCPUMSMCGIPLKSISDNRVALAVNYYSINA WLLICPWHLCPUMSMCGIPLKSISDNRVALAVNYIGKSLALAMFCLIGLIC QALCSBOCHKRRILITGGFLVIFFIPASNLFRVYDAKRYY YLESVAYCULITRIFGGALSKHTKKKLILAAVULGILFITURCV LRSGEWRSEEQLFRSALSVCPLNAKVHYNIGKSLALAMFCYDCYMAERVI YLESVAYCULITRIFGGALSKHTKKKKLIAAVULGILFITURCV LRSGEWRSEEQLFRSALSVCPLNAKVHYNIGKSLALAMFCYDCYYMERVI YLESVAYCULLTRIFGGALSKHTKKKKLIAAVULGILFITURCV LRSGEWRSEEQLFRSALSVCPLNAKVHYNIGKSLALAMFCYDCYYMERVI GRLYADLNARTVLKPHSIAAVULGKSQKYKESSALPLKX IKANPMASFYKGIAAULYHRGHLDLAKKHYNIGKLALAMFCYDCYMAERVI GRLYADLNARTVLKPHSIAAVULGKSQKYKESSALPLKX IKANPMASFYKGIAAULYHRGHLDLAKKHYNIGKLALAMFCYCCGCGKFFCG GRSYFFINIACHHRGHLDLAKKYNIGKSQCGCAFTRSTTLPPHRE THTGVWADDECGCCNAFFFFFF ISHSCIGRWYNGCOGCAFFCG GRSYFFINIACHHRGHLDLAKCCCCCAAFFCGSTCYCCCCCCGCAFFCCGCGCAFFCGGFCCGCGCAFFCGGFCGG	6365	224	1000	
MTRRTSLGPNGLDEMMUNDGATILSMMUNDHQIAK LMWELKSGDDEIGDGTGVVVLAGALLEGGLDRGIHPIRI ADGYGQARAVAIEHLDKISDSVLUDI KUTGELIGTAKTTLGSKY VNSCHROME LAWANLIVAMMERRUDY ELIGTAKTTLGSKY AKK LDYTSVEDI KALOKYRKE FEEMIOQI KENGARISTET SPELTAKK GRAGLVOET SPOTTKOMMUN TEQUK NSRAVITIF SPELTAKK GRAGLVOET SPOTTKOMMUN TEQUK NSRAVITIF SPELTAKK GRAGLVOET SPOTTKOMMUN TEQUK NSRAVITIF SPELTAKK LDYAMRAFADALEVI PRALSENSGWYE IGTHTE WAROKEM PALGIDCHKOMMUN TEQUK SKOQISLATOWNYMILK IDDIRKPGESBE GNEGGAHSSTWULESI PLGAVAMLCKEGGITVLGLAAVFOLLV IGKENVLETVOKVLHKOKSLENLGMURNGGLEPMITLISGGAG MLYVRWELMGTOPAPP SPENDAMRANGLIVANNINYYSLAN WLLLCPWILCPDWSMCIPLLKSI SDWRVIALAALMFCLIGLIC QALCSBOCHKERILITIGSI FVJETFIJARSVARAVNINYYSLAN WLLLCPWILCPDWSMCIPLLKSI SDWRVIALAALMFCLIGLIC QALCSBOCHKERILITIGSI FVJETFIJARSVARAVNINYYSLAN WLLLCPWILCPDWSMCIPLLKSI SDWRVIALAALMFNINTYSLAN WLLLCPWILCPDWSMCIPLLKSI SDWRVIALAALMFNINTYSLAN WLLLCPWILCPDWSMCIPLLKSI SDWRVIALAALMFNINTYSLAN WLLLCPWILCPDWSMCIPLLKSI SDWRVIALAALMFNINTYSLAN WLLLCPWILCPDWSMCIPLLKSI SDWRVIALAALMFNINTYSLAN WLLLCPWILCPDWSMCIPLL WERE SELVEN TOTT STATE QALCSBOCHKERILITIS GRAPH TOTT STATE WARPERVEN SELVEN TOTT STATE RYYERAVRIANG SVANNAMINI SERVELSLANDIO GREYADLANHUNG SUMMANNAMANATULK PEHISLANDINI LLDINTGIL AQAENGRABELEI PROBLEMFALDE SANDANI SERVELCHOKKAN AQAENGRABLEI PROBLEMFALDE SANDANI SERVELCHOKKAN AQAENGRABLEI PROBLEMFALDE SANDANI SERVELCHOKKAN AQAENGRABLEI PROBLEMFALDE SANDANI SERVELCHOKKAN TOTT SERVELCHOKKAN AQAENGRABLEI PROBLEMFALDE SANDANI SERVELCHOKKAN AQAENGRABLEI PROBLEMFALDE SANDANI SERVELCHOKKAN TOTT SERVELCHOK SERVELCHOK SERVELCHOK SERVELCHOK SERVELCHOK SERVELCHOK SERVELCHOK SERVELCHOK SERVELCHOK SERVELCHOK SERVELCHOK SERVELCHOK SERVELCHOK SERVELCHOK SERVELCHOK SERVELCHOK SERVELCHOK SERVELCHOK SERVELCHOK SERVELCHOK SERVELCHOK SERVELCHOK SERVELCHOK SERVELCHOK SERVELCHOK SERVELCHOK SERVELCHOK SERVELCHOK SER	6365	234	1989	KHKSRASCAARAQAFGPSREREVHSRFRSGLRRLGESNSGCCTM
LIMVELSKSONDEIGDGTTGVVVLAGALEBABGQLLDRGTHEIRT ADDGYEGARAVIEHLINKI EJDSVLVDI KUTELJTAKTILGSKV VNSCHRÖMBEINVADIKTVADMERRDVDFELIXVEGKVGGRIEGE TKLIKGVIVÜDKDFSHPOMEKVEDANTALIQTAKTILGSKV VNSCHRÖMBEINVADKSHVENDEN KUTENDALIQTAKTILGSKV VNSCHRÖMBEINVADKSHVENDEN KUTENDALIQTAKTURGEN KUTENDE BENEVIKER KUNDEN BENEVIKURGANIA LOOMGPDDE ANNILLGUNDLEVBRWIGGDETELIA TATOUPERSEETAEKL GPAGLUQEISGTTKKKMLVIEGCKNSRAVIEPIRGGNIMI IEE AKRSLIGDLGVIRKINGAVVIVGGGABEVDEPSELATAEKL GPAGLUQEISGTTKKKMLVIEGCKNSRAVIEPIRGGNIMI IEE AKRSLIGDLGVIRKINGAVVIVGGGABEVDEPSELATAEKL GPAGLUQEISGTTKKKMLVIEGCKANAVVIGTETLAGKKOQISLATOVKREL NDELKKRIGHTEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUNDEN KUND				
ADGYEQARVAIEHIDKISDSULVDIKOTEPLIQUAKTIGSKY VNSCHRAMBLIAVNAUTVADMERRDYBLIAVEGKYGGIED TKLIKGYUVINDSHPOMPKKVEDAKIAILITCPFEPPKPKTKHK LDUTSVEDVKALQVYRKEKPEEMIQIEGAMLAIQOGPDDE ANHLLIONNIPAVRWOGPSIELIALATGGRIVPRESELTAEKI GRAGLUGEISFOTTKORUMVISGOGABEISCALAVSGEARCP TLEQYAMRAPADALEVIPHALSENSGMPTQTPTEVARGNKMIIEE AKRSIHDALCVIRNLIPDRIVVYGGGAAPISCALAVSGEARCP TLEQYAMRAPADALEVIPHALSENSGMPTQTHEVRARQVKEN NPALGITOLHKOTTADMKOQPVIETLIGKKQJISLATOWYKMILK IDDIRKPGESEE GRNEGARISSTFWULISIFLGKQGISLATOWYKMILK IDDIRKPGESEE GRNEGARISSTFWULISIFLGKQGISLATOWYKMILK IGKRIVLETVGKYUHKOKSLENIGHLENSGLIFRTLITSGGAG MLYVRWRIGTOPPAFTEVUNDASFADAMLARAVYNTYYYSIKA MLLICDWMLCPDWSMGCIPLIKSIBDWAVIALAAMFCLIGLIC QALCSEBGHKRRILLIGLGFLUFPIPALFRVGFVYAERVL YLESVGYCVLITFGFGALSKHTKKKKLIAAVVLGIFITNTLRCV LRSGEMRSEGLFRSALSVCPLINAVYHYNIGKIALDKGNOTAAI RYYREAVRINPRYYHAMNILGSILKERNELGRAEELLISLAVGIQ PDERAAMMMIGIVONSKKPERAEGSYRTHKIKKKLIAAVVLGIFITNTLRCV LRSGEMRSEGLFRSALSVCPLINAVYHYNIGKIALDKGNOTAAI RYYREAVRILIPRYYHAMNILGHLIFERSELLSLAVGIQ PDERAAMMMIGIVONSKKPERAEGSYRTHKIRKKYEDGYML GRLYADLINGHUNDALINAWRNATVLKPEHSLAWNMIILLDDTGKL AQAEAVGREAELEI PROHSIMPSILANYKSKYKYESDALFFRCGYVAL GRLYADLINGHUNDALINAWRNATVLKPEHSLAWNMIILLDDTGKL AQAEAVGREAELEI PROHSIMPSILANYKSKYKYESDALFFRCGYVAL GRLYADLINGHUNDSTFKILLTSVCKTWKVONISGKYXESSELFLKA IKANPARASYKGNILAVVIHRWGHLDLAKKHYEISLQLDPTASGT KENYGLIRGKKLELMOKKAV  91GFFWHLVLSILLYTCEMFODSVAFEDVAVSFTOEBKALLDRS KLCCSKESHHCGESFNOLADDMINRKTLPGITPCESSVCGEVOT GHSSLNTHIRANTOTHKSSKYSKYGNEPYRNKGKKAFSYLDSSTQ SHIKACTKSKYYDOKSCTSTFTISHCJKRYMHIGGOPYKCKF CGKAFIFANTATTHERSTYSKYGKYKCKOCKAFTSTTLEVHER THIGWADABCKECOANSPSPSEIRRHKSTEGEKYSEKCKGGKFCA SQLQIHERTHSGEKPIECKGCKVFKKYSSLEHERTHTGEKPH ECKQCKKAFRYFSSLHHERTHTGGKYPECKOCKAFTSTTLEVHER FRYEGROGGAFRCTSDLOHENKTTERDEFYGCKOGKGFCA SQLQIHERTHSGEKPIECKGCKVFKKYFSSLRIHERTHTGEKPH CCKQCKAFRYFSSLHHERTHTGGNEYPECKCCKYFCKYGCAFTCSSSIR YHERTHTGEKPYECKGGKAFTCSSLACTTTRTHGEKPHCCKGCKFC GKAFIFASCCEHERTHINR  6369  1 1745  AGCCROTERTPPFRORGSLCHMCKAFSTLDSKORGHLAKCTKEKPY DRECTETTPYPFRORGSLCHMCKAFSTLDSKORGHLAKCTKEKPY DRECTETTPYPFROGSLCHMCKAFSTLDSKORGHLAKCTK	i	1		
VINSCHRÖMAEIAVIANULTVADMERRÜVDFELIKYEGKVOGGILED TKLIKGVIUVDKOFSHBOMPKKVEDAKAILITCPFEPPPKPKIKH LDVTSVEDYKALQKYRKEKFEEMIQOIKETGANLAICOMGFDDE ANNILLIONNIEPAVRWAGGPEIELIALOGGIVPRESELTAEKL GRAGLVOEISFOTTKDKMLVIEQKINSRAVTIFIRGORKMIIEE AKRSLHDALCVIRRLIRDURVVYGGGAABISCALAVSGEADKCP TLBQYAMRAFADALEVIPALSENSGMPTQTYMTEVRARGOKEM NPALGIDCHKSTNDMKQGHVIETLIGGKQGISLATOMVRNILK 1DDIRKPGESEE GNKEGAHSSTFWVLLSIFLGAVAMLCKEQGITVLGLINAVPDILV IGKENVLETVQKVLHKOKSLENLGALKRGGLIFRMTLITGGAG MLYVGRRINGTOPPAFTEVDNDASFADSMURAVAYNNYYSIKNA WILLCEPWHLCPWSMGGIPLIKISIGAVUGALAVUGILFITTURCV LGKENVLETVQKVLHKOKSLENLGALKRGGLIFRMTLITGGAG MLYVGRRINGTOPPAFTEVDNDASFADSMURAVAYNNYYSIKNA WILLCEPWHLCPWSMGGIPLIKISIGAVUGALAVUGILFITTURCV LRSGGENSEGQIPKSALSVCPLUNAKVHYNIGKNILADKGNOTAAI RYYGEAVGLITPGFGADSKHYKKKLAVUGILFITTURCV LRSGGENSEGQIPKSALSVCPLUNAKVHYNIGKNILADKGNOTAAI RYYGEAVGLINFYGYBAANNILGHILKENGLEFRMTLILGLIG QALCSEDGHKRILITUGLGFLUYFLPASALFRYGFVVABEVU. LRSGGENSEGQIPKSALSVCPLUNAKVHYNIGKNILADKGNOTAAI RYYGEAVGLINFYGYBAANNILGHILKENGJABELLSLAVQIQ PDFRAAMMILGIVONSLKREBABGSYRTAIKHRKYPDCYYML GRLYADLNRHVDALINAWGNILGHIKKNICAGRETLSLAVQIQ PDFRAAMMILGIVONSLKREBABGSYRTAIKHRKYPDCYYML GRLYADLNRHVDALINAWGNILGHIKKNICAGRETELAVQIG PDFRAAMMILGIVONSLKREBABGSYRTAIKHRKYPDCYYML GRLYADLNRHVDALINAWGNILDEKKRYESGAFTETSLAG IKANPAASYRGNILAVUHYRNGHLDLAKKRYEISJQDPTAGGT GRAFYFAILHTRADTOHKSSYOPSGENDVASFTQEEWALLDFS GNALYSHUNGSTFKNILTSGKTWKON IEDEKKNFRRNLSLMBE KLCESKESHHGGESFROLADMINRKTLPGITPCESSUCGEVOT GHSSLINTHIRADTOHKSSYOPSGENFRECKKAFSYLDSFQ SHOKACTKSKPYDGKECTETFISHSCIQRIRVMHSGODPYKCK GGAFFYFINLCLIHERIHTGVKPYKCKGCKAFTESTTLPVHER THTGVADADECKECGNAFFSTSHGENFRECKAGGSPYCCGCGKAFTCSSIR YHBRTHTGERFYBCKGGGAFTSTTLPVHERTHTGERPYC EKPYECGQGGAFFRYSSLLIHERTHTGRKPYBCKCGCKAFTSSTTL EKPYECGCGGAFFTPTPFORGFREYPECKCGCKAFTESSTR YHBRTHTGERFYBCKGGGAFTSSTTLPVHERTHTGSPHD DSSTYYFYPCGGONFSITTENDLENDEDVATCPSCSLIIKVIYDK DGPVCGETVPAPSANKELUKG ESFNQIADDMLARKTLPGITPGEWALLDDSORLYRDVMQGT TKMLTSVKTYKKOKGAGFTSSTTLPVHERTHTGVNDDECK CGMAFFIFSSEIRHKRKTIGGKPYECKGCKGKFTSTSLINTHINAD TGHKSSEYQEVGGGGGGGAFTGSSLINTHIRAD TGHKSSEYQEVGCKGGKGFRGSG			}	
TKLIKGYIVIDKDSSHPOMPKKUBDAKIAILITCPEPPPKPITKIK LDVISWEDVKALQKYRKEKEEMIQAILATQWGPDDE ANHLLLONNLDAVRWOGPSIELIALATGGRIVPRSELTAEKI. GPAGLVUGET SFOTTENDKINUVIEQCKNSRAVITPIRGGNKMIIEE AKRSLHDALCVIRHLIRDRIVVYGGGABEISCALAVSGEADKCP TLEGYAMRAFADALEVIPRALEENSGMMPIQTMTEVRARQVEEM NPALGIIDCHKRITDRINGQHVETIGKGOSIALTQWRMILK IDDIRKPGESEE  6366 257 1898 GNKEGAINSTFWLLSIFLGAVAMLCKEGGITVLGLNAVFDILV IGKRNVLETVQKVLHKNKSLENLGHLRNSGLLFRWTLLTSGGAG MLYVRWRINGTPPAFTEVUNDASTABUKRAVYNYYYSLAN WLLLCPWMLCPDWSMGCIPLIKSIDDWRVIALAALMFCLIGLIC QALCSEDGHKRRILITLGAFUVPJENLFRVGPVVAREVL YLPSVGYCVLITPGGALSKHTKKKKLIAAVVLGILFINTIRCV LRSGEWRSEEQLFRRALSVCPLINKVHYNIGKHLAMFCLIGLIC QALCSEDGHKRRILITLGAFUVPJENLFRVGPVVAREVL YLPSVGYCVLLTPGGALSKHTKKKKLIAAVVLGILFINTIRCV LRSGEWRSEEQLFRRALSVCPLINKVHYNIGKHLAMFCTIGLIC QALCSEDGHKRRILITLGAFUVPJENLFRVGPVVAREVL YLPSVGYCVLLTFGGRALSKHTKKKKLIAAVVLGILFINTIRCV LRSGEWRSEEQLFRRALSVCPLINKVHYNIGKHLAMKNTILLDNIGKL AQAEAVGREALELIPRDHSLMFSLANVLGKSQKYKESEALPLKA IKANDNAASYHGNLAVLYHRWGHLDLAMMNILILDNIGKL AQAEAVGREALELIPRDHSLMFSLANVLGKSQKYKESEALPLKA IKANDNAASYHGNLAVLYHRWGHLDLAWMNILILDNIGKL AQAEAVGREALELIPRDHSLMFSLANVLGKSQKYKESEALPLKA IKANDNAASYHGNLAVLYHRWGHLDLAUMNNILLDDTGLL AQAEAVGREALELIPRDHSLMFSLANVLGKSQKYKESEALPLKA KENYGLLRRKLELMQKKAV SIGFPWLVSHRUGHTGHTSVGKYKWONIEDEYKNPRRILSLMME KLCESKESHIGGESFORLDDMINKRYHYEISISQLDPTAGST KENYGLKRKLELMQKKAV SIGFPWLVSHILGHTHTUSVGKYKKOOKAFTESTLUBERQ KLCESKESHIGGESFORLDDMINKRYHEISISCLOPHTROHEDEVEN CGGAPYFINLCLIHERIHTGVKYYKKOCKAFTESTLUPHER THIGVAPKCGCGKAFTRCTSDLQRHRWHSGOPYKCKF CGGAPYFINLCLIHERIHTGVKYYKKOCKAFTSTLUPHER THIGVAPACKGGKAFTROTSDLQRHRWHSGOPYKCKF CGGAPYFINLCHHORTERYPECKOCGKAFTRCOSHLQKHGRHTGENPH EKCCGCKAFTRYSSLHHBRTHTTGKPYPCCCGCGKAFTROTSDLQRHRWHSOOPHYKCK PHERTTTGKPPYECCGCGKAFTCGSBLAYHTGKPHYCCKCC GKAFTLASSCEBHERTHTINR  PREVERKTGREYPECKGCGKAFTROTSDLANGBLAYHTROMADSCKE CGGAPYFINGERCKAFSVERCOCKAFTROTSCHAP THRETTTGKPPYECCGCGKAFTROTSDLANGBLAYHTUTHAD TGHKSSEVGCGCGCGCAFTROTSDLANGBCHACHTGWARDLYCHOCKENPY DGKCCETTPISHSCIQRHRVHTSGDGPYKCKCKFSCSCILTHVUND TRAGECPECTPICHERNICHTGKTPYCCCCGCKAFTSTTLCPUBERTHISC COMAPSTS SIC	1		s	
LDUTSVEDVRALOKYRKEKFEEMIQOIKERGANLAICOMGFDDE ANNHLLONNI PADKWOOGPS IELIAIG TAPEKL GFAGLUQEISFOTTKORMIVI EGCKNSRAYTIFIRGGINKHIIEE AKRSLHADICVIRKLIFURNVVYGGAGGIVPRESICTAEKL GFAGLUQEISFOTTKORMIVI EGCKNSRAYTIFIRGGINKHIIEE AKRSLHADICVIRKLIFURNVVYGGAGGIVPRESICALAVSQEADKCP TLEQYAMRAFADALEVIPMALSENSGMPTOTMTEVRARGVKEM NFALGICLHKOTNOMMOGNUTETLIGKKQUISLATOMYRMILK IDDIRKPGESEE GNKKGAHSSTFWVLLSIFLGAVAMLCKEQGITVLGLINAVPDILV IGKENVLETVQKVLHKUKSLEMIGHLKNGGLIFRMTLITIGGGAG MLYVRWRIMSTOPPAFTEVDNDASFADSMLVRAVWYNYYYSIMA WILLICPWMLCPDSWRGCIPLIKISIGAVUGILFITNTLIGGGAG MLYVRWRIMSTOPPAFTEVDNDASFADSMLVRAVWYNYYYSIMA WILLICPWMLCPDSWRGCIPLIKISIGAVUGILFITNTLICV LRSGENRSEGOJKRRILITLGLGFLUYIPFLPASHLFFRVGFVVABRVL YLBSVGYCULTFGFGGALSKHYKKKLAVVIGILFITNTLICV LRSGENRSEGOJKRRILITLGLGFLUYPFLPASHLFRVGFVVABRVL YLBSVGYCULTRFGGALSKHYKKKLAVVIGILFITNTLICV LRSGENRSEGOJKRRILITLGLGFLUYPFLPASHLFRVFPVGFVVABRVL YLBSVGYCULTRFGGALSKHYKKKLAVVIGILFITNTLICV LRSGENRSEGOJKRRALIVITSKHYVINTIGNALADKONOTAAI RYYREAVRLDPKYVHANNIGNILKERLGEBELLSLAVOIO PDPRAAMMSLGIVONSLKFERABGSVYTTAIKHRKYPDCYYLL GRIYADLANHAVALINARRANTULKERJEAPELSLAVOI OPDERAAMMSLGIVONSLKFERABGSVYTTAIKHRKYPDCYYLL GRIYADLANHAVALINARRANTULKOKSQKYKESEALFILAA IKANPARASYKGNLAVLYRRWGHLDLAKKYEISLJOLDPTASGT KENYGLIKRKLEMDQKKRAV SIGFFFMILVISILLYTCENFODSVAFEDVAVSFTQEEMALLDFS GKALYTRAKLEMOWGETFKNILTSVGKTWKONI EIDEKKNEKKERSTULDFS GKHLYRAUMOGETFKNILTSVGKTWKONI EIDEKKNEKKAFYLLDSFQ SHOKACTKSKFYDGKECTSTFISHSCIQRIRVMHSGDGPYKCKF GGRAFFYINLLCLIHERITHTGVKPYKCKGCKAFTESTILDFWHE THTGVANADECKECONAFSFPSEIRRHKRSHTGEKFYECKOCGKY PLSFSSIGVHMOMTTGEKFYECKCGCKAFTESTILDFWHE THTGVANADECKECONAFSFPSEIRRHKRSHTGEKFYECKOCGKFRCA SQLOILERTHGSEKPHECKCCKYFYENECKAGAFTCSSIG KHERTHTGEKFYECKGGGAFTSTTLEPHERTHTGEKPH EKVGCGGKAFFRYSSLHHERTHTINR PECKOCGKAFFRYSSLHHERTHTTGKPH EKCCGCKAFTSTFTRODLENBENGLTEKFYTCKOCKG SSTYTYPCGGONNFSITTEDLENBENDVATCSSCSLIIKVIYDK DGFVCGETVPAPSANKELUKC GKAFIFANSCHEMPTTIKN DGSTYTPPFPGGADNFSITKHELENSLEMBENLORGENLYDMOGT FREMMFODSVAFEDVANSFTOGEWALLDDSORLYDDMOGT FRANCTSBLORGFFFFFFFFTANTTHEDENSPCCKCCKOFTFTSTLIPVHERTHTGVANDECK CGNAFFFFFFFFFFFTAN				
ANHLLIONNIPAURWGOPEIELIAIANTGRIVPRFSELTABKI. GPAGLUVEISFGTTEKKMLUIEDCRINKMIIEE AKRSLHDALCVIRNLIRDINRVYGGGABLISCALAVSQEADKCP TLEGYAMRAFADALEVIPMALSENGMIPIGTMTEVRARGVEEN NPALGIDCLHKGTNDMKQGRVIETLIGKKQGISLATOMYRMILK IDDIRKPGESEB  6366 257 1898 GNKGGARISSTFWILLSIPLGAVAMLCKEGGTTVLGLNAVFDILV IGKPNVLEIVQRVLHKDKSLENLGMLRNGGLIFEMTLLTSGGAG MLYVRWIEMTGTPPAFTEVDINPASDAKUPAUNYNYYSLMA MLLLCPWILCFDWSMGCIPLIKSISDWRVIALAALWFCLIGLIC QALCSBCHKRRILITLGLGFLVIPBOSMLVPAUNYNYYSLMA MULLCPWILCFDWSMGCIPLIKSISDWRVIALAALWFCLIGLIC QALCSBCHKRRILITLGLGFLVIPBOSMLVPAUNYNYYSLMA MULLCPWILCFDWSMGCIPLIKSISDWRVIALAALWFCLIGLIC QALCSBCHKRRILITLGLGFLVIPBOSMLVPAUNYNYYSLMA MULLCPWILCFDWSMGCIPLIKSISDWRVIALAALWFCLIGLIC QALCSBCHKRRILITLGLGFLVIPBOSMLVPAUNYNYYSLMA MULLCPWILCFDWSMGCIPLIKSISDWRVIALAALWFCLIGLIC QALCSBCHKRRILITLGLGFLVIPBOSMLVPAUNYNYYSLMA MULLCPWILCFDWSMGCIPLIKSISDWRVIALAALWFCLIGLIC QALCSBCHKRRILITLGLGFLVIPBOSMLVPAUNYNYYSLMA MULLCPWILCFDWSMCORPHVANIGHTELGLICIC QALCSBCHKRRILITLGLGFLVYPBOSMLVPAUNYNYYSLMA MULLCPWILCFDWSMCORPHVANIGHTELGLIC GRAYPKENSENGLOPSALAVENIGHTENCH THRCV RYYREAVRINPKYVHAMNNIGNILKRRNELGEAELLISLAVQIQ PDFARAWMNIGIVONSLKREAEGOSYRTAKHRRKYPDCYYNL GRAYANDASHNALNYTHNWGHLAKKHREILGDPTAGAT KENYGLIRRKLELMMCKAV  6367 287 1934 SIGGFWHULVSILLITLTCHFFODSVAFEDVANSFTQEEWALLDPS QKNLYRDWNGETFKNLTSVGKTWKVONIEDEYKPPRNLLDPS QKNLYRDWNGETFKNLTSVGKTWKVONIEDEYKPPRNLLDPS QKRLYRDWYDGKECTETFISHSCIQHRVMHSGDGPYKKCF GGASPYFINLCLIHERIHTGVKPYKKKQCGAFFRSTTLFVHER THTGSVADBCKECONAPSPSBLTRRIKKSHTWEGTPYECKQCGKV FISFSSIQYHMMTHTGEKPYECKQCGKAFRCGSHLQKGGRTHTG EKPYECRQCGKAFRCTSDLQRHEKKTTEDKPYECKQCGKY FROSSIGVHTMTTGEKPYECKQCGKAFRCGSHLQKGGRTHTG EKPYECRQCGKAFRCTSDLQRHEKKTTEDKPYECKQCGKY FROSSIGVHTREGKPYECKHCGKAFISHTHGEKPYECKQCGKY FROSSIGVHTREGKPYECKHCGKAFISHTHTGEKPYECKQCGKY FROSSIGVHTREGKPYECKHCGKAFISHTHTGEKPYECKQCGKY FROSSIGVHTREFTTGEKPYECKGRAFISHTHTGEKPYECKQCGKAFRCSSLIKTHTIRAD TGKSSESTIQHKWMSGDGPYKCKFCGKAFTYFTLIND TGKSSESTIQHKW THRTTGGKPYECKUGCKAFRCSSHLQKKETTRRD TGKSSESTIQHKW THRTTGGKPYECKUGCKAFRCSSHLQKKETHTTIRAD TGKSSESTORIADMLNRKTLGGTTPCESSVCGEVGTGHSSLUTHTIRAD TGKSSESTORIAD		ļ		
GPAGLIVĢEISFGTTENMINITEORRAVUSGAENISCALAVSGEADKCH  AKRSLIPDALCVIRMIRDNRVVJGABASEISCALAVSGEADKCH  TLEQYAMRAPADALEVI PMALSENSGMNPIQTMTEVRARQVKEM NPALGIDCHKKGTNDMKQQIVIETLIGKKQDISLATOMVRMILK  IDDIRKPGESEB  GNKEGARISETFWLLISIPLGAVAMLCKEQGITVLGLNAVFDILV IGKRNVLETVQKVLUKKUSLENLGMLRNGGLIFRMTLLTSGGAG MLYVRWRIMGTGPPAFTEVDNPASFADSMLVRAVNYMYYSLNA WLLLCPWMLCFDWSMGCPLJKKSINVANYMYYSLNA WLLLCPWMLCFDWSMGCDLJKKSINVANYMYYSLNA WLLLCPWMLCFDWSMGCDLJKKSINVANYMYYSLNA WLLLCPWMLCFDWSMGCDLJKKSINVANYMYYSLNA WLLLCPWMLCFDWSMGCDLJKKSINVANYMISKNLADKSNOTAAI RYYREAVRLNPKYVIANNNIGNILKERABLEAELLSLAVQIQ PDFARAAMNIGIVONSLKREBABGYRTAIKHRKKYPDCYYML GRLYADLNRHUPALNAWRNATVLKEPENSLAWNNIIILDDTGML AQAEAVSCREALELI PINDHSIMFSLAVCLIGAKVEPCCYMARKVL GRLYADLNRHUPALNAWRNATVLKPENSLAWNNIIILDDTGML AQAEAVGREALELI PINDHSIMFSLAVILKSKSKYKESEALFLKA IKANPNAASYHONLAVLYHRNGHLDLAKKHYEISLQLDPTASGT KENYGLIRRKLEIMOKKAV  6367  287  1934 SIGFFVMLVLSILLYTCEMFODSVAFEDVAVSFTQEEWALLDPS QKNLYRDWGCFFKNILTSVGKTWKVONIEBERYRPRKNISLINE KLCES KESHIGGESFNQIADDMLINKTLLEGITPCESSVCGEVGT GHSSLNTHIRADTGHKSSRVOEYGENFYRNRECKKAPSYLDSFQ SHKACTKSKYDYDGKECTEFTI SINGIPRKSPSVCGEVGT GHSSLNTHIRADTGHKSSRVOEYGENFYRNRECKKAPSYLDSFQ SHKACTKSKYDYDGKECTEFTI SINGIPRKSPSVCGVGKYFC CGRAFYFLMLCLIHERHHTGVKPYKCKQCGKAFTRSTTLFVHER THGVMADBCKKECOMAPSPPSEIRGORPYKCKF CGGAFTFLANSCGREFFTTING EKPYECRQCGKAFRYSSLHHBERTHTGKPYPCKQCGKOFRCA SQLQIHERTHSGEKPHECKGCKYFYFSSLRHERTHTGEKPH ECKQCGKAFRYFSSLHHBERTHTGKPYPCKVCGKAFTCSSSIR YHBRITHTGKFYPCKHGKGKAFINTIRVHERTHTGEKPYPCKNG GKAFIRASSCGEHERTHTING  AGCCRDTRFFFFRGGSLCHNFCRSAACTVTRTTHGSPREDTGT PRSREMMFQDSVAFEDVANSFTQEEWALLDNSKKSHTHIRAD TGHKSSSVGYGSBPFYNRECKKAFSYLDSFOGHDKACTKEKPY DGKCCTETTJESSCGCEVGTOHSSLNTHIRAD TGHKSSSVGYGSBPFYNRECKKAFSVLDSFOGHDKACTKEKPY DGKCCTETTJESSCGCEVGTOHSSLNTHIRAD TGHKSSSVGYGSBPFYNRECKKAFSVLDSFOGHDKACTKERFY DGKCCTETTJESSCGCAFRCTSSCCCVGTCHSSLNTHITRAD TGHKSSSVGYGSBPFYNRECKKAFTSTLLYVLERTHTGVNADACKE CGNAFSFPSEIRRKKSHTGERFYFTGCKOCKYFTSSSTQTHKM THTGEKPYECKQCCKAFRCSSLLOKKHTTITGKPPPECRCCKKA FRCTSSLOHDRIKTHTEKDKYPCKCQCGKFFRCSACQUTHTGKPPLECCKAR THIGEKPECCCCKKAF				
AKRSLHDALCVIRNLIENDRIVYGGGAAEISCALAVSOEADKCP TLEGYMRAFADALEVIPMALSENDRIPIGTMETVARQVEEM NPALGIDCHKGTNDMKQQHVIETLIGKKQQISLATOMYRMILK IDDIRKEGSESE GNEEGAHSSTFWULSIFLGAVAMLCKEGGITVLGLNAVFDILV IGKRNVLEIVQKUHKUKSLENIGMLRNGGLIFENTLLTSGGAG MLYVRWRIMGTOPPAFTEVDNPASFADSMLVAANWYNYYSINA WLLLCPWMLCFWSMSCIPLIKSISDWRVIALAALWFCLIGLIC QALCSSEGKRRILITLGGFLVIFLPSANLFRRGVEFVAERVL YLPSVGYCULLTFGGFGALSKHTKKKKLIAAVVLGILFINTLRCV LRSGEMSEGGLFRSALSVCPLNAVHJNIGNILAALWFCLIGLIC QALCSSEGKRRILITLGGFLVIFLPSANLFRRGVEFVAERVL YLPSVGYCULLTFGGFGALSKHTKKKKLIAAVVLGILFINTLRCV LRSGEMSEGGLFRSALSVCPLNAVHJNIGNILABKNOTAAI RYYREAVRLNPKYVHAMNIGNILKERNSLDERELLSLAVUTO PDFAAAMMAGITVONSLKRFBAAEOGSYRTAIKHRKYPDCYYNL GRLYADLNRHVDALNAWRHATVLKREHSLANNNNI ILLDDTICNL AQAEAVGREALBLIFNDHSLMFSLANVLGKSCKYKESEALFLKA IKANPMAASYHCHLAVLYHNRMGHDLAKKHVEISLGLDFTASGT KENYGLURRKLELMMCKAV  6367 287 1934 SIGFFWLVLSILLYTCEMFODSVAFEDVAVSFTQEENALLDFS OKNLYRDVMGETFKNLTSVGKTWKVONIEDEVKPFRNLSLMEE KLCESKESHCGESFNOLADDMINSTEGTPTCESVCGEVOT GHSSLNTHIRADTGHKSSRVGEYGENPYNNECKKAPSYLLDSFO SHDKACTCKEKPYDGECFTFT ISHCGNPRUMSGDPYKCKY CGKAPYFLNLCLIHERIHTGKYPKCKQCGKAFTRSTTLDVHER THTGVWADBCKRECONAFSFSEIRRHKKRHTGERPYECKQCGKY FISFSSI GYHKMTHTGKKPYECKYGCKAFRGGSHLGMGRTHTG EKPYECCQCGKAFRCTSDLORHEKTTEDENYGCKQCGKGFRCA SQLQIHERTHSGEKPHECKGGKAFISDLARHTTGEKPYPECKYGCKYGKGRCTHTG EKCYCCKAFRYFSSLHHERTHTGDKPYKCKVCGKAFTCSSSIR YHRRTHTGEKPYECKHGCKGKAFISHTHTGEKPYPECKYGCKYGKGRGTHTG EKCYCCKAFRYFSSLHHERTHTGDKPYKCKVCGKAFTCSSSIR YHRRTHTGEKPYECKHGCKGKAFISHJAMPELEDFOYDE DSSTYFYPCCGONFSITKEDLENGEDVATCPSCSIIIKVITDK DGPVCGETVPABSANKELVKG  6369 1 1745 AGCCRITREFTFTGERFSLAMFECKFCGKYTFSSLHREKKERSESHHCG ESFNQIADDMINRTLEGITPCESSVCGEVCTHSSLNTHIRRD TGHKSSEVYCCTGOTHSSLMRELKCESKSHHCH ESFNQIADDMINRTLEGITPCESSVCGEVCTHSSLNTHIRRD TGHKSSEVYCCTGOTHSSLMRELKCESKSHHCH ESFNQIADDMINRTLEGITPCESSVCGEVCTHSSLNTHIRRD TGHKSSEVYCCTGOTHSPINKECKHAFSYLDSFOSHDKACTKEKPY DGKCCTETTJSHSCIQRHEKTHTENYCCKQCGKFTCSSLQHHRTHSC CGNAPSFFSEIRRKKSHTGEKPYECKOCGKFTSISIQTHKM THTGEKPYECKQCCKAFRCSSHLQKKGKTCKEKPY DGKCCTETTJSHSCIQRHEKTHTENYCCYCCCKAF				
TLEGYAMRAPADALEVI PMALSENSGMAPIGTMTEVERAGVERM NPALGIDCHKGTNDMKQQHVIETLIGKKQQISLATOMVRMILK IDDIRKPGESEB GNKEGAHSSTFWULLSI FIGAVAMLCKEQGITVLGLNAVFDILV IGKPNVLETVQKVLHKDKSLENLGMLRNGGLEFEMTLLTEGGAG MLYVRWRIMTGPPAFTEVDNPASFADSBAUFANVNYYYSINA WLLLCPWULCFDWSMAGIPLIKSI SIDWRVIALAALMPCLIGLIC QALCSEDGHKRRILTI.GLGFLVIFFLPASMLFREVGFVVAERVL VLPSVGVCVLLTPGFADS.KHTKKKKLTAAVUGILFINTLRCV LRSGEWSSEBQLFRSALSVCPLNAKVHYNIGKNLADKGNOTAAI RYYREAVRLNPKYVHAMNNLGNILKERNELDEAEELLSAVQIQ PDFRAAMMNLGIVQNSLKFFEAEGSYKTAIKHRRKYPDCYYNL GRLYADLNRHVDALNAWRNATVLKFEHSLANNINIILLDNTGKL AQAEAVGREALELI PNDHSLHFRANVGKSYKESEALFIKA IKANPNASYHGNLAVLYHRWGHLDLAKKHYEISLQLDPTASGT KENYGLHRRILELMGKKAV IKANPNASYHGNLAVLYHRWGHLDLAKKHYEISLQLDPTASGT KENYGLHRRILELMGKKAV SCHULKRDVMQETFKNLTSVGKTWKVONIEDEYKNFRRNLSIMRE KLCESKESHHCGESFNQLADDMLNRKTLPGITPCESSVCGEVGT GHSSLNTHIRADTGHKSSRYGEYGENFYRNECKKAFSYLDSFQ SHOKACTKEKPYDGKGCTETFI SHSCIQRHRVWHSGDGFYKCFF CGRAFYFLNLCLIHERIHTGVKPYKCKQCGKAFTRSTTLPVHER THGGVANADECKEGGNAFSFDSI SHSCICGREVFYECKQCGKVF PISFSSIQHKWHTTGERFYECKQCGKAFTRGTHLPVHER EKPYECRQCGKAFRYFSSLHHERTHTGBKFYECKQCGKAFTRG EKPYECRQCGKAFRYFSSLHHERTHTGBKFYECKQCGKAFTRG EKPYECRQCGKAFRYFSSLHHERTHTGBKFYECKQCGKAFTCSSIR THGTWANDECKEGCTSULTSTHEDKYPCCKQCGKAFTCGSSIR VHERTHTGRKPYECKCGKAFKGTSHLQKHGRTHTG EKPYECRQCGKAFRYFSSLHHERTHTGBKFYECKQCGKAFTCGSSIR THERTHTGRKPYECKNCKAKISTSNIRYHERTHTGEKPYCKQC GKAFIRASSCREHETHTINR  327 RPVPAKLNIRTSGRFRTAGALPLEPPPLTMAVFHDEVEIEDFQVDE DSTYFFYCPCGDNFSITKEDLENGEDVATCPSCSLIKVIYDK DGFVCGETVPAPSAMKEUKG  6368 1 327 RPVPAKLNIRTSGRFRTAGALPLEPPPLTMAVFHDEVEIEDFQVDE DSSTYFFYCPCGDNFSITKEDLENGEDVATCPSCSLIKVIYDK DGFVCGETVPAPSAMKEUKG ESFNQIADDMLNRKTLPGITPCESSVCGEVGTHGSKRHCG ESFNQIADDMLNRKTLPGITPCESSVCGEVGTHGSLATHIRAD TGHKSSEYQEVGGNFPRANSLEKKELCESKESHLCG ESFNQIADDMLNRKTLPGITPCESSVCGVGTHGTHSCHYMOGET FKNLTSVGTTWKVQNIEDEVKNSLSMERLLCESKESHLCG ESFNQIADDMLNRKTLPGITPCESSVCGVGTHCASSIIVIRCL HERIHTGVKPYCKCCGCKAFTCASGLQCHETTHSG CGRAFFFSEIRRHKRSHTGEKPYECKQCKVFGKAFFCTSGIQHKACTKERPY DGKECTETFISHSCIQRKFNTEKCKAFGSLOGHFCTSSIQHHEM THIGGKPYECKQCGKAFFCSSHLQKHGFTTTGVKPCQCCKA FRCTSSILGHENTHTE	l			
NPALGIDCLHKGTNDMKQQHVIETLIGKKQQISLATQMVRMILK  1D11RFGGSEB  GNKEGAHSSTFWULLS IFLGAVAMLCKEQGITVLGLNAVFDILV IGKFNVLETVQKVLHKDKSLENLGMLRRSGLFFRMTLLTSGGAG MLYVRMSIMGTGPAFTEVUNDASFADSMLVRAVNYYYSINA WLLLCPWWLCFDWSMGCIPLIKSISDWSVALANUVNYYYSINA WLLLCPWWLCFDWSMGCIPLIKSISDWSVALAALWFCLIGLIC QALCSBOGHKRRILTLGLGGFLVIFPLPASNLFFRVGFVVAERVL YLPSVGYCULLTBGFGALSKHTKKKKLLAAVUGILFINTLRCV LRSGEWRSEEQLFRSALSVCPLNAKVHYNIGKNLADKGNQTAAI RYYREAVRINPKYVIAMNILDHILKERNELQEAFELLISLAVQIQ PDFAAANMALGIVQNSLKRFEAAEGSYRTAKHRRKYPDCYYML AQAEAVGREALELIPNDHSLMFSLANVLGKSQKYKBSEALFLKA IKANPNAASYHGHAAVLYHRWEHLAANNITILLDHTGNL AQAEAVGREALELIPNDHSLMFSLANVLGKSQKYKBSEALFLKA IKANPNAASYHGHAAVLYHRWEHLAAKHYSISLQLDPTASGT KENYGLIRRKLELMQKKAV  SIGFFVMLVLSILLYTCEMFQDSVAFEDVAVSFTQEEWALLDFS QKNLYRDVMCGFTKKLTSVGKTWKVQNIEDEYKNPRRNLSLMRE KLCESKESHHCGESFNQLADMLRNKTLPGITPCESSVCGEVGT GHSSLNTHIRADTGHKSSSYCYGEPYPKNECKKAFSVLDSFQ SHDKACTKKFPYDGKSCTETFISHSCIGRRVMHSGDGPYKCKF CGKAPFVELNCLIHRRIHTGVKFYKCKQCGKAFTRTSTLPVHER THTGVNADECKECGNAFSPSEIRRHKRSHTGKFYECKQCGKV FISFSSIQVHKMTHTGEKFYECKQCGKAFTRTTLPVHER THTGVNADECKECGNAFSPSEIRHHERTHTGEKPH ECKQCGKAFTKFSSLHHIERTHTGBKPYECKQCGKAFTCASSIR YHRETHTGEKPHECKECGKVFKYTSSLRTHERTHTGEKPH ECKQCGKAFTKFSSLHHIERTHTGBKPYECKQCGKAFTCASSIR YHRETHTGEKPPECKCGCKAFTSSLRTHERTHTGEKPH ECKQCGKAFTKFSSLHHIERTHTGBKPYECKQCGKAFTCASSIR YHRETHTGEKPPECKHCKKAFISNJRYHERTHTGEKPH CGKGAFTFFSSLHHIERTHTGBKPYECKQCGKAFTCASSIR YHRETHTGEKPPECKGCGKVFKYTSSLRTHERTHTGEKPH ECKQCGGAFTKFFTFTGGKPYECKCTCKAFTTLGEKPH DGFVCGETVPAFSSHLHIERTHTGBKPHECKCGSKFHTGEKPT THAACCGGRAFTFFTFTGGFSSLCHMFCRSAACTTVRTTHGSPREDTGT PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET FKNLTSVGKTMKVQNIBDEYKNFCKSGASCTVTRTTHGSPREDTGT PRSREMMFQDSVAFEDVAVSFTQESSVCSUTGHSSLNTHIRAD TGHKSSEYQEVGENPYNKECKKKAFSVLDSFGSHKACTKERPY DGKCCTETFISHSCIQHRWHSGGGPYKCKFGKAFFYLNCLL HER HITGWAPYKCKQCCKAFTGCSSLQCHAFTTSVCLL HER HITGWAPYKCKQCCKAFTGCSSLQCHERTHSG				
1DDIRREGESEE 10366 257 1898 GIRKERJAISSTRWILLSIPIGAVAMLCKEQGITVLGINAVFPIIJV IGKFNVLEIVQKVLHKDKSLENLGMLRNGGLIFRMTLLITSGGAG MLYVRWRIMTGPPAFTEVDAPASFADSMURAVNYNYYSINA WLLLCPWRLCFDWSMCCIPLIKSIBMRVIALAALWFCLIGLIC QALCSEDGHKRRILTIGLGFLVIFFLPASNLFPRVGFVVAERVL YLPSVGVCVLLTBFGADS.KHYRKKKLIAAVUGLIFINTLRCV LRSGEWRSEEQLFRSALSVCPLNAKVHYNIGKNLADKGNQTAAI RYYREAVRLNPKYVIAMNNLENILKERNELGEAFELLSLAVQIQ PDFAAANMNLGIVONSLKRFEASVYSTAIKHRKYPDCYYNL GRLYADLNRHVDALNAWRATVIKPEHSLAANNNIIILLDNTGNL AQAEAVGREALBIL PNDHSLHBSCYSTATAIKHRKYPDCYYNL GRLYADLNRHVDALNAWRATVIKPEHSLAANNNIIILLDNTGNL AQAEAVGREALBIL PNDHSLHBSCYSTATAIKHRKYPDCYYNL GRLYADLNRHVDALNAWRATVIKPEHSLAANNIIILLDNTGNL AQAEAVGREALBIL PNDHSLHBSCYNTAIGNAVUGKSGALPKL LENSYSHONLAVIHRWGHLDLAKKHYEISLQLDPTASGT KENYGLLRRKLELMKKAV GNELYRDVWGETFKNILTSUGKTWKVONIEDSYKNPRRNLSLMRE KLCESKESHCGESFNOLADDHANKKTLPGITPCESSVCGEWGT GHSSLNTHIRADTGHKSSBYOEYGENPYRKECKKAFSYLDSFO SHDKACTKEKPYDGKECTETFISHGIQRHRWHISGDGYKCKF GGKAFYFLMLCLIHERIHTGKPYECKQCKXAFTGSTTLPVHER THGSVADBCKECGRAFSPSSEIQRHRWHSTGEKPYECKQCKV GISSSIQYHKWHTGEKPYECKQCKAFKGGKAFKGSHLOKHGRTHTG EKPYECRQCGKAFRCTSDLQRHEKTHTEDKPYCCKQCKGGGGGFRCA SQLQIHERTHSGEKPHECKECGKVFKYFSSLRIHERTHTGEKPH EKPYECRQCGKAFRCTSDLQRHEKTHTEDKPYCCKQCKGGGGGKAFCGSHRAGSHLOKHGRTHG EKPYECRGCGKAFRCTSDLQRHEKTHTEDKPYCCKQCGKGGGGKAFRGFRCASGLQHAFFSSIR YHERTHTGEKPYECKHCKKAFISNIFYHERTHTGEKPH EKCQCKAFRYFSSLHHERTHTGKPYECKUGKAFTCSSIR YHERTHTGEKPYECKHCKKAFISNIFYHERTHTGEKPH EKCQCKAFRYFSSLHHERTHTGKPYECKUGKAFTCSSIR YHERTHTGEKPYECKHCKKAFISNIFYHERTHTGSPREDTGT PRSEEMMFODSUAFEDVANSTTOEBWALLDPSQKMLYRDVMQGT FKMLTSUGTWWAYANIEDVANSTTOEBWALLDPSCKMLYRDVMQGT FKMLTSUGTWWAYANIEDVANSTTOEBWALLDRACKEKPY DGKCCTETFISHSCIQHRWHSGOGPYKKKFGGKAFFYLNLCL HER IHTGVKPYKKCKQCKAFTGSTHLVKHTGEKPYECKQCKAF TGHKSSEYQEYGENPYRNKECKKAFSYLDSFOSHDKACTKERPY DGKECTETFISHSCIQHRWHSGOGPYKKKFGGKAFFYSLOYLKM THTGSERPYECKQCCKOKGGKGGGGGGAGASGLQIHBERTHSG				
6366  257  1898  GNKEGAHSSTFWULLSLYLGAVAMLCKEQGITVLGLNAVFDILV IGKPNVLBIUQKVLHKUKSLENLGMLRNGGLIFRMTLLTSGGAG MLYVRNEIMGTGPPAFTEVDNPASFADSMLYRAVNNYYYSLNA WLLLCPWWLCFDWSMGCIPLIKSISDWVIALAALMFCLIGLIC QALCSEDCHKRILITLGIGLIC VIPFIPASHIFRVGFVVAERVL YLPSVGVCVLLTRGFGALSKHTKKKKLIAAVULGILFINTLRCV LRSGEWSESGLPFRSALSVCHAKVWYNIGKNLADKGNQTAAI RYYREAVRLNPKYVHAMNNLGNILKERNELQEREELISLAVQTQ PDFAAAMMNLGIVQNSLKKFEAAGGSYRTAIKHRKKYPDCYYNL AQAEAVGREALELIPINDHSLMFSLANVLGKSQKYKESEALFLKA IKANPNASSYHGHLAVLYHRWGHLDLAKKHYEISLQLDPTASGT KENYGLLRRLELMQKKAV  6367  287  1934  SIGFFVMLVLSILLYTCEMFQDSVAFEDVAVSFTQEEWALLDFS QKNLYRDVMQETFKNLTSVGKTWKVONIEDEYKNPRNNSLMRE KLCESKESHICGESFRQIADDMLNRKTLPGITTCESSVCGEVGT GHSSLNTHIKADTGHKSSFVOERFWFRNKEKKAFSYLDSFQ SHDKACTKEKPYDGKSCTETFISHSCIQRRWMHSGDGPYKCKF CKRAFYENLALLHERIHTDSVFKCKQCKAFTRSTTLPVHER THTGVNADECKECGNAFSPFSEIRRKRSHTGEKPYECKQCKV FISFSSIQYHKWTHTGEKPYECKQCKAFTRSTTLPVHER THTGVNADECKECGNAFSFFSEIRHRKRSHTGEKPYECKQCKV FISFSSIQYHKWTHTGEKPYECKUGKAFTCSSIR YHERTHTGEKPYECKUGKAFTCSSIR YHERTHTGEKPYECKUGKAFTCSSIR YHERTHTGEKPYECKUGKAFTCSSIR YHERTHTGEKPYECKUGKAFTCSSIR YHERTHTGEKPYECKUGKAFTCSSIR YHERTHTGEKPYECKUGKAFTCSSIR YHERTHTGEKPYECKUGKAFTCSSIR YHERTHTGEKPYECKUGKAFTCSSIR YHERTHTGEKPYECKUGKAFTCSSIR YHERTHTGEKPYECKUGKAFTCSSIR YHERTHTGEKPYECKUGKAFTCSSIR YHERTHTGEKPYECKUGKAFTCSSIR YHERTHTGEKPYECKUGKAFTCSSIR YHERTHTGEKPYECKUGKAFTCSSIR YHERTHTGEKPYECKUGKAFTCSSIR YHERTHTGEKPYECKUGKAFTCSSIR YHERTHTGEKPYECKUGKAFTCSSIR YHERTHTGEKPYECKUGKAFTCSSIR YHERTHTGEKPYECKUGKAFTCSSIR YHERTHTGEKPYECKUGKAFTCSSIR YHERTHTGEKPYECKUGKAFTCSSIR THKKSSYQSTYGNPYNNECKKAFSYLDSFGSHIKACTKERPY DGKCCTETFISHSCIGRRWMHSGDGPYKCKCGKAFTCSSIR TGHKSSEYQSTYGENPYNNECKKAFSYLDSFGSHIKACTKERPY DGKCCTETFISHSCIGRRWMHSGDGPYKCKCGKAFTCSIRIYHKM THTGEKPYECKUCGKAFTCSSIRIQHKM THTGEKPYECKUCGKAFTCSSIRIQHKMTHTEERPYECKQCKUCKAFTCSSIR THIGKERPYECKUCGKAFTCSSIRIQHKM THTGEKPYECKUCGKAFTCSSIRIQHKMTHTEERPYECKUCKAFFTCSIRIYHKM THTGEKPYECKUCGKAFTCSSIRIQHKMTHTEERPYECKUCKAFFTCSIRIYHKM	ļ	1		
IGKPNVLETUQKVLHKDKSLENIGMIRNGSLLFRMTLLTSGGGG MLYVRWRIMTGGPPAFTEVDNPASFADSMURAVNYNYYYSINA WLLLCPWALCPDWSMGGIPIKSISDWRVIALAALMFCLIGIIC QALCSEDGHKRRILITIGLGFLVTPFIPASNLFRVGFVVAERVL YLPSVGVCVLLTFGFGALSKHYKKKLLAAVUGIIFINTLRCV LRSGEWRSEEQLFRSALSVCPLNAKVHYNIGKNLADKGNGTAAI RYYREAVRLAPKVYHANNAIGNIIKSENELQEAEELISLAVQIQ PDFAAAMMNLGIVONSLKRFEAAEGGYRTAIKHRRKYPDCYVNL GRLYADLNRHVDALNAWRNATVLKPEHSLAWNIMTILLDNTGNL AQAEAVGREALELIPADHAINAWRNATVLKPEHSLAWNIMTILLDNTGNL AQAEAVGREALELIPADHAINAWRNATVLKPEHSLAWNIMTILLDNTGNL KENYGLLRRKLELMQKRAV 1KANPNAASYHGNLAVLYHRWGHLDLAKKHYEISLQLDPTASGT KENYGLLRRKLELMQKRAV QKNLYRBVMQETFKNLTSVGKTWKVONTEDEYKNPRRNLSLMRE KLCESKESHIGGESFROLADMIRKTLPGITTCESSVGGEVGT GHSSLNTHIRADTGHKGSBYOEVGEMPYRNKECKKAFSYLDFQ SHDKACTKEKPYDGKECTETFISHSCIQHRWMHSGDGPYKCKF CGRAFYFLNLCLHREIHTGVKPYKCKQCGKAFTRSTTLPVHER THGTGVNADECKECGNAFSFPSETRRKKSHTGEKPYECKQCGKV FISFSSIQVIKWHTTGSKPYECKQCGKAFTRSTTLPVHER THGTGVNADECKECGNAFSFPSETRRKKSHTGEKPYECKQCGKV FISFSSIQVIKWHTTGSKPYECKQCGKAFTRSTTLPVHER EKPYECRQCGKAFRYFSSLHIHERTHTGEKPYGCKQCGKGFRCA SQLQIHERTHSGEKPHECKECKYKYFSSLRIHERTHTGEKPY ECKQCGKAFRYFSSLHIHERTHTGEKPYQCKQC GKAFTRASSCREHERTHTING 6368 1 327 RPUPAKLNPRSWRTAGALPLRPPPLTMAVFHDEVEIEDFQVDE DSETYFYPCCGDNFSITKEDLENGEDVATCPSCSLIKVIYDK GKAFTRASSCREHERTHTING FRRSKMFGDBYKKCKCESKESHCG BSPGMFGDSVAFDEVAUSTGDEBVAKLTKERPY DGFVCGETVPAPSANKELVKC ESPNQIADDMLNRKTLPGTTPCESSVCEVGFGFSLSINTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFGSHDKACTKERPY DGKCTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFFTSLUNLCL HERIHGVKPYKCKQCGKAFTCSTSLIKVINGCK CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQVHKM THTGEKPYECKQCGKAFRCGSLQKHGRTHTGEKPYGCCGCKA FREIDDMLNRKTTLPGTTPCESSVCEVGGFFSISHATCHKERPY DGKCTETFISHSCIQRHRVMHSGDGPYKCKCGKAFFTSLUNLCL HERIHGVKPYKCKQCGKAFFTCSSLQKHGRTHTGEKPYCCQCKCK FRCTSDLQRHEKTHTGEKPYECKQCGKVFISFSSIQVHKM THTGEKPYECKQCGKAFRCGSLQCKGRFTCSSLQVHKM THTGEKPYECKQCGKAFRCGSLQCKGRFTCSSLQVHKM THTGEKPYECKQCGKAFRCGSLGCCGKGFCCASQQCCKAF	63.55	<u> </u>		
MLYVRWIMGTGPPAFTEVDNPASFADSMUVRAVNYNYYYSLMA WLLLCPWWLCFDWSMGCIPLIKSISDWVVIALAALWFCLIGLIC QALCSBDGHKRILTIGLGFLVIPFIPASMLFFRVGFVVAERVL YLESVGVCVLLTRGFGALSKHTKKKKLIAAVVIGILFINTLRCV LRSGEWSESGLFFRSALSVCHAKVHYNIGKNLADKGROTAAI RYYREAVRLMPKYVHAMNILGNILKERNELQEAFELLSLAVQIQ PDFAAAWMNIGIVONSLKKFEAAEGSYRTAIKHRKKYPDCYYNL AQAEAVGREALELIPHDHSLMFSLANVLGKSQKYKESEALFLKA LKANPNASSYHGMLAVLYHRWGHADLAKKHYEISLQLDPTASGT KENYGLLRRKLELMQKKAV  31GFPVMLVISILLYTCEMFODSVAFEDVAVSFTQEEWALLDPS CKNLYRDVMGSTFKNLTSVGKTWKVONIEDEYKNPRNNSLMRE KLCESKESHICGESFNOLADDMLMRKTLPGITPCESSVCGEVGT GHSSLNTHIRADTGHKSSEYOGYGENPYRKECKKAFSYLDSFQ SHOKACTKEKPYDGKSCTETFISHSCIQRRWHHSGDGFYKCKF CGRAFYFLNLCLIHERIHTGVKPYKCKQCKAFTRSTTLPVHER THTGVANDECKECGGAFFSPSIRRKRSHTGEKPYECKQCKV FISFSSIQYHKMTHTGEKPYECKQCKAFTCSSIR YHERTHTGEKPYECKYCGKAFTCSSLIR SCHQLHERTHSGEKPHECKECKVFKYFSSLHHERTHTGEKPH ECKQCGAFFKYFSSLHHERTHTGEKPYECKVCGKAFTCSSIR YHERTHTGEKPYECKYCGKAFTSNTLPVHER SCHQCGKAFFKSSHPICKBCGKVFKYFSSLHHERTHTGEKPH ECKQCGKAFFKSSHPICKBCGKVFKYFSSLHRCHTGEKPYH ECKQCGKAFFKSSKPSCHERTHTINR  6368  1 327 RPVPAKLNRRSWFRTAGALPLREPPLTMAVFHGEVPYCKQC GKAFIRASSCREHERTHTINR  6369 1 1745 AGCCRDTRFPTFRGGSLCHNFCRSAACTVTRTHGSEPPEDTGT FRSREMMFQDSVAFEDVAVSFTQEBWALLDPSQKKLYRDVMGET FKNLTSVGKTWKVQNIEDEYKNPRRNLSLMREKLCESKESHICG ESPNQIADDMLANKTLPGITPCSSVCGEVGTGHSSLNTHIRAD TGHKSSEYQEYGENPYNKECKKAFSYLDSFQSHCKATKERPY DGKECTETFISHSCIQRHKVMHSGDGPYKCKFCGKAFFILNLCL HERTHTGKFYKYKCKQCGKAFTRSTTLPVHERTHTGRERPY DGKECTETFISHSCIQRHKVMHSGDGPYKCKFCGKAFFILNLCL HERTHTGKFYKYKCKQCGKAFTRSTTLPVHERTHTGVAPAGCKC CGMAFSFPSEIRRHKRSHTGEKPYECKQCGKYFISSSIQTHKM THTGEKPYECKQCGKAFTRSTTLPVHERTHTGVAPAGCKC CGMAFSFPSEIRRHKRSHTGEKPYECKQCGKYFISSICTHMSC CGMAFSFPSEIRRHKRSHTGEKPYECKQCGKYFISSICTHMSC FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASOLQLHERTHSG	6366	257	1898	
WLLLCPWMICEDWSMGCIPLIKSIBWRVIALAALMFCLIGLIC QALGSEDCHKRRILTLGLGFLVIPFLPASNLPFRVGFVVAERVI, YLPSVGYCVLLTFGFQALSKHTKKKKLIAAVVLGILFINTLRCV LRGGEWRSEEQLFRSALSVCPLMARVHYMIGKNLADKGNQTAAI RYYKEAVRLBMKYVHAMNIGNILKERMELQEAFELLSLAVQIQ PDFAAAMMNLGIVONSLKRFEABGSYRTAIKHRRKYPDCYYNL GRLYADLMRHVDALNAMRATVLKPEHSLAMNNMIILLDNTGNL AQAEAVGREALELIPNDHSLMFSLANVLGKSQKYKESEALFLKA IKANPNAASYHGNLAVLYHRWGHLDLAKKHYEISLQLDPTASGT KENYGLLRRKLELMQKKXA IKANPNAASYHGNLAVLYHRWGHLDLAKKHYEISLQLDPTASGT KENYGLLRRKLELMQKKXA GSGPVMLVLSILLYTCEMFQDSVAFEDVAVSFTQEEWALLDPS QKNLYRDVMQSTFKNLTSVGKTWKVQNIEDSYNOPRRNLSLMRE KLCESKESHHCGESFNQIADDMLMRKTLPGITPCESSVCGEVGT GHSSLNTHIRADTGHKSSEYQEYVGENPYRNKECKKAFSYLDSFQ SHDKACTKEKPYDGKCETETFISHSCIQRRWMHSGDGFYKCKF CGKAFYFINLCLIHERHTGVKPYKCKQCGKAFTRSTTLPVHER THTGVNADECKECGNAFSFPSEIRHKRSHTGEKPYECKQCGKV FISFSSIQYHKMTHTGEKPYECKQCGKAFRCGSHLQKHGRTHTG EKYPECRQCGKAFRCTSDLQRHENTHTEDKPYGCKQCKGKGFRCA SQLQIHERTHSGEKPHECKGGKVFKYFSSIRIHERTHTGEKPH ECKQCGKAFRYFSSLHHERTHTGKPYECKVQCKGKGFRCA SQLQIHERTHSGEKPHECKGGKVFKYFSSIRIHERTHTGEKPH ECKQCGKAFRYFSSLHHERTHTGKPYDECKQCKGKFTCASSIR YHERTHTGEKPYECKHCKKGKFISNYIRYHERTHTGEKPYQCKQC GKAFIRASSCREHERTHTIINR  6368 1 327 RPUPAKLNPRSWRTAGALPLRPPPLTMAVFHDEVEIEDFQVDE DSSTYFYPGFGONFSITKBDLENGEDVATCPSCSLIIKVIYDK DGFVCGETVPAPSANKELVKC 6369 1 1745 AGCCNDTRFFFFFRGGSLCHNFCTSAACTVTRTTHGSFREDTGF PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET FKNLTSVGKTWKVQNIEDEYKNPRNLSLMREKLCESKESHICG ESFNQIADDMLNRKTLPGITPCESSVCGFGHSSLNTHIRAD TGHKSEYGEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFFILLCL HERIHTGVKPYKCKQCGKFTRSTTLPVHERTHTGVMADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYYCCKQCGKAFRCGSHLQKHGRTHTGEKPYBECGCKA FRCTSDLQRHRVHTSGKPYECKQCGKAFRCSSIQVHKM THTGEKPYYCCKQCGKAFRCGSHLQKHGRTHTGEKPYBECGCKA FRCTSDLQRHRVHTSGKPYECKQCGKAFRCSSIQVHKM THTGEKPYYCCKQCGKAFRCGSHLQKKGRTHTGERPYBECGCKA FRCTSDLQRHRVHTGGKPYECKQCGKAF		:		
QALCSEDCHKRRILTLGLGFLVIPFLPASNLPFRVGFVVAERVL YLPSVGYCVLLTFGFGALSKHTKKKKLIAVVLGILFINTLRCV LRRGEWRSERGLFRSALSVCFLNAKVHTNICKNLADKCNGTAAI RYYKEAVRLWRKYVHAMNILGNILKERNELQEAEELLSLAVQIQ PDEPAAMMING.GIVONSLKRFEABEGSYRTAIKHRKKYPCYYNL GRLYADLNRHVDALNAWRNATVLKPEHSLAWNINIILLDNTGNL AQAEAVGREALEILFINDHSIMFSILAVUGKSQKYKESSEALFLKA IKANPNAASYHGINLAVLYHRWGHLDLAKKHVEISLQLDPTASGT KENYGLLRRKLELMOKKAV  3IGFPVMLVLSILLYTCEMFODSVAFEDVAVSFTQEEWALLDPS QKRLYRDVMQETFKNLISVGKTWKVQNIEDEYKYPRRNLSLMRE KLCESKESHHGESFNOIADDMLNRKTLPGITPCESSVCGEVGT GHSSLNTHIRADTGHKSSEVGYGVENPYNKECKKAFSYLDSFQ SHDKACTKERVPYDGKECTETFISHSCIQRHRWHSGDGPYKCKF CGKAFYFINLCLIHERIHTGVKPYKCKQCGKAFTRSTTLPVHER THTGVNADECKECGNAFSPSEIRRHKRSHTGEKPYECKQCKV FISFSSIQYHKMTHTGEKPYECKQCGKAFRCGSHLQKKGRTHTG EKPYECKQCGKAFRCTSHORPYGCKQCGKFRCA SQLQIHERTHSGEKPHECKECGKVFKYFSSLRIHERTHTGEKPH ECKQCGKAFRYFSSLHHERTHTGDKPYCKVCCKAFTCSSSIR YHERTHTGEKPYECKGCKAFISNYIRYHERTHTGEKPYQCKQC GKAFIRASSCREHERTHTINR 6368 1 327 RPVPAKLNFRSWPRTAGALPLRPPPLTMAVFHDEVEIEDFQYDE DSSTYFYPCFGONFSITKBDLENGEDVATCPSCSLIKVTYDK DGPVCGETVPAPSANKELVKC 6369 1 1745 AGCCRDTRFPTFRGFGSLCHNFCRSAACTVTRTTHGSPREDTGT PRRSEMMFQDSVAFEDVAVSFTQESWALLDPSQKNLYBDVMQET FKNLTSVGKTWKVQNIEDEXKRPSLLDSGKNTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRWHSGGDFYKCKFCGKAFYFILNLCL HERFIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGUNADECKE CGMAFSFPSEIRRHKRSHTGEKPYECKQCGKAFTSSIQVHKM THTGEKPYECKQCGKAFTRSTTLPVHERTHTGUNADECKE CGMAFSFPSEIRRHKRSHTGEKPYECKQCGKAFTCSSIQVHKM THTGEKPYECKQCGKAFRCSSLQLHERTHSG	1	ŧ		
YLPSVGYCVLLTPGFGALSKHTKKKKLIAAVVLGILFINTLRCV LRSGEWRSEQLFRSALSVCPLNAKVHYNIGKNLADKGNQTAAI RYYREAVRLNPKYVIAMMNLGNILKERNELQEAEELISLAVQIQ PDFAAAMMNLGIVONSLKRFEAAEGSYRTAIKHRKKYPDCYYNL GRLYADLANMATULKPHELJAWNNNIILLDNTGNL AQAEAVGREALELIPNDHSLMFSLANVLGKSQKYKESEALFLKA IKANPNAASYHGNLAVLYHRWGHLDLAKKHYEISLQLDPTASGT KENYGLLKRKLELMMGKTKKVONIEDEYKNPRRNLSLMRE KLCESKESHICGESFNOLADDMINNKTILPGITPCESSVCGEVGT GHSSLNTHIRADTGHKSSEYQEVGENPYRNKECKKAPSYLDSFQ SHDKACTKEKPYDGKECTETFISHSCIQRHWHSGDGPYKCKF CGKAPYFLNLCLIHERITGVKPYKCKQCGKAFTKSTLPVHER THTGVNADECKECGNAFSFPSEIRRHKRSHTGEKPYECKQCGKV FISPSSIQYHKMTHTGEKPYECKQCGKAFRCGSHLQKHGRTHTG EKPYECRQCGKAFRCTSDLQRHEKTHTEDRYYGCKQCGKGFRCA SQLQIHBRTHSGEKPHECKECGKVFKYFSSLRIHERTHTGEKPH ECKQCGKAFRYFSSLHERTHTJNR GKAFFFLSSIR YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPH ECKQCGKAFRYFSSLHFRTHTGALPPLERPHTGEKPH CGKAFFFLSSIR YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPH CGKGFFFCA SQLQIHBRTHSGEKPHECKECGKVFKYFSSLRIHERTHTGEKPH CKQCGKAFRYFSSLHFTTINR THYDEKPYECKUCKAFFCSSIR YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPH CKQCGKAFRYFSSLHFTTINR THYDEKPYECKUCKAFFCSSLIKVIYDK DGFVCGETVPAPSANKELVKC  6368  1 327 RPVPAKLNPRSWRFRTAGALPLRPPPLTMAVFHDEVEIEDFQXDE DSETYFYPCPCGDNFSITKEDLENGEDVATCPSCSLIKVIYDK DGFVCGETVPAPSANKELVKC  GKAFIRASSCREHERTHTINR TGKGCGCPTFFFFFFGFGSCHFCFTSAACTTTRTHGSPREDGT FRILTSGKFWKKVQNIEDEYKNPRRNLLSUMREKLCESKESHLCG ESSPNQIADDMLNRKTLPGITPCESSVCGEVGTHSSINTHTRAD TGHKSSEYQEYGBHPYNRECKKAFSYLDSFGSHDKACTKEKPY DGKCTETFISHSCIQRHRVMHSGGPYKKKFGKAFYFINLCL IHERIHTGVKPYKCKQCCKAFTRSTTLPVHERTHTGVNADECKE CGMAFSFPSEIRRKRSHTGEKPYECKQCCKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCSSHLQKHGRTHTGEKPYECRQCKA FRCTSDLQRHEKTHTEDKPYCCKQCGKGFRCASQLQIHERTHSG	-	į		
LRSGEWRSEQLFRSALSVCPLMAKVHYNICKNLADKGNQTAAI RYYREAVRLNPKYVHAMNILGNILKERNELQEAEELLSAVQIQ PDERAAMMNIGIVQNSLKRFEAAEGSYRTAIKHRRKYPDCYYNL GRLYADLMRHVDALMAWRNATVLKPEHSLAWNINI ILLDNTGNL AQAEAVGREALELI PNDHSLMFSLANVLGKSQKYKESEALFLKA IKANPNAASYHGNLAVLYHRWGHLDLAKKHYEISLQLDPTASGT KENYGLIRRKLEHMQKKAV  31GFPVMLVLSILLYTCEMFQDSVAFEDVAVSFTQEWALLDPS QKNLYRDVMQETFKNLTSVGKTWKVONIEDEYKNPRRNLSLMRE KLCESKESHHGGESFNQIADDMLMRKTLPGITPCESSVCGEVGT GHSSLNTHIRADTGHKSSVQEYGENPYRNKECKKAPSYLDSFQ SHDKACTKEKPYDGKECTETFISHSCIQRHRVWHSGDGPYKCKF CGKAFYFLNLCLIHERIHTGVKPYKCKQCGKAFTRSTTLPVHER THTGVNADECKECGNAFSPPSEIRRHKRSHTGEKPYECKQCKV FISFSSIQYHKMTHTGERPYBCKQCGKAFTRCSTLPVHER THTGVNADECKECGNAFSPPSEIRRHKRSHTGEKPYECKQCKV FISFSSIQYHKMTHTGERPYBCKQCGKAFTCSSSIR EKPYECRQCGKAFRCTSDLQRHEKTHTEDKPYGCKQGKGFRCA SQLQIHERTHSGEKPYBCKCGKGKFKYFSSLRIHERTHTGEKPH ECKQCGKAFRYFSSLHHERTHTGDKPYECKVCGKAFTCSSSIR YHERTHTGEKPYECKHCGKAFISNYLRYHERTHTGEKPY CKQC GKAFIRASSCREHERTHINR  6368  1 327 RPVPAKLNPRSWPRTAGALPLRPPPLTMAVFHDEVEIEDFQYDE DSSTYFYPCPCGDNFSITKEDLENGEDVATCPSCSLIIKVIYDK DQPVCGETVPAPSANKELVKC  6369  1 1745 AGCCRDTRFPTPRGGGSLCHNFCRSAACTVTRTTHGSPREDTGT PRSREMMFQDSVAFEDVAVSFTQEEMALLDPSQKNLYRDVMQET FKNLTSVGKTMKVQNIEDEYKNPRRNLSLMREKLCESKESHHCG ESFNQIADDMLMRKTLPGITPCESSVCGEVGTCHSSLNTHTRAD TGHKSSEYQEYGEMPYNRMECKKAFSYLDSFGSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL IHERIHTGVKPYKCKQCCKAFTRSTTLPVHERTHTGVNADECKE CGMAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFTCSSHLQKHGRTHTGEKPYECRQCKA FRCTSDLQRHEKTHTEDKPYCCKQCGKOFRCASQLQIHERTHSG	<b>!</b>	ĺ		
RYYREAVRINPHYVHAMNILGNILKERNELQEAEELLSLAVQIQ PDFAAAWMNIGIVQNSLKRFEAAEQSYRTAIKHRRKYPDCYYNL GRLYADLMRHVDALNAWRNATVILKEHSLAWMMIILLDNTCNL AQAEAVGEALELIPNDHSLMFSLANVLCKSQKYKESEALFILKA IKANPNAASYHGNLAVYHRWGHLDLAKKHYEISLQLDPTASGT KENYGLLRRKLELMQKKAV  SIGFPVMLVLSILLYTCEMFQDSVAFFDVAVSFTQEEWALLDPS QKNLYRDVMQETFKNTSVGKTWKVONIEDEYKNPRRNLSLMRE KLCESKESHHCGESFNQIADDMLMRKTLPGITPCESSVCGEVGT GHSSLNTHIRADTGHKSSRYVOEYGENPYNKECKKAFSYLDSFQ SHCKACTKEKPYDGKECTETFISHSCIQRHRWHSGDGPYKCKF CGKAPYFLNLCLIHERIHTGVKPYKCKQCGKAFTRSTTLPVHER THTGVNADECKECGNAFSFPSEIRRHKRSHTGEKPYECKQCGKV FISFSSIGYHKMTHTGEKPYECKQCGKAFTRCSHLQKHGRTHTG EKPYECRQCGKAFRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCA SQLQIHERTHSGEKPHECKECGKVFKYFSSLRIHERTHTGEKPH ECKQCGKAFRYFSSLHIHERTHTGEKPYECKQCGKGAFTCASSIR YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPHQCKQC GKAFIRASSCREHERTHTINR  6368  1 327 RPUPAKLMPRSNAFRTAGALPLRPPPLTMAVFHDEVEIEDFQYDE DSTYFYPCPCGDNFSITKEDLENGEDVATCPSCSLIIKVIYDK DQFVCGETVPAPSANKELVKC  6369 1 1745 AGCCRDTRFFTFRGFGSLCHNFCRSAACTVTRTIHGSPREDTGT PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET FKNLTSVGKTWKVQNIEDEYKNPRRNLSLMREKLCESKESHHCG ESFNQIADDMLMRKTLPGITPCESSVCCEVGTGHSSLNTHTRAD TGHKSSEYQEYGENPYRNRECKKAFSYLDSFGSHDKACTKEKPY DGKECTETFISHSCIQRHRWHSGDGPYKCKFCGKAFFLNLCL IHERIHTGVKPYKCKQCGKAFTRSTTLEVHERTHTGVNADECKE CGMAFSPSEIRRHKRSHTGEKPYECKQCGKYFIGSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA FFRCTSDLQRHEKTHTEDKPYGCKQCGKFRCASQLQIHERTHSG				
PDEFAAMWNIGIVQNSLKRFEAAEGSYRTAIKHRRKYPDCYYNL GRLYADLNRHVDALNAWRNATVLKPEHSLAWNNMIILLDNTGNL AQAEAVGZEALELI PDDHSIMFSLANVLGKSGKYKESEALFIJKA IKANPNAASYHGNLAVIJYHRGHLDLAKKHYEISLQLDPTASGT KENYGLLRRKLELMQKKAV  SIGFPVMLVLSILLYTCEMFODSVAFEDVAVSFTQEEWALLDPS QKNLYRDVMQETFKNLTSVGKTWKVONIEDEYKNPRRNLSLMRE KLCESKESHHCGESFNOLADMLNRKTLPGITPCESSVCGEVGT GHSSLNTHIRADTGHKSSRYQEYGENPYRNKECKKAFSYLDSFQ SHDKACTKEKPYDGKSCTETFISHSCIQRHRVMHSGDGPYKCKF CGKAFYFLNLCLIHERIHTGVKPYKCKQCGKAFTTSTTLPVHER THTGVNADECKECGNAFSPPSEIRHKRSHTGEKPYECKQGGKV FISFSSIQYHMMTHTGEKPYECKQGGKAFRCGSHLQKHGRTHTG EKPYECRQGKAFRCTSDLQRHEKTHTEDKPYGCKQCGKV FISFSSIQYHMTHTGEKPYECKQGKYFKYFSLEHHERTHTGEKPH ECKQCGKAFRYFSSLHHERTHTGKPYECKVCGKAFTCSSIR YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPYQCKQC GKAFIRASSCREHERTHTINR  6368  1 327 RPVPAKLNPRSWPRTAGALPLRPPPLTMAVFHDEVEIEDFQVDE DSSTYFYPCPCGDNFSITKEDLENGEDVATCPSCSLIIKVIYDK DGFVCGETVPAPSANNELVKC  6369  1 1745 AGCCRDTRFFTFRGFGSLCHNFCRSAACTVTRTIHGSPREDIGT PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET FKNLTSVGKTWKVQNLEDEVKNPRNLSLMREKLCBSKESHHCG ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFGSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFFFLNLCL HERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKYFISFSSIQYHKM THTGEKPYECKQCGKAFTGCSSHLQKHGRTHTGVNADECKE CGNAFSPSEIRRHKRSHTGEKPYECKQCGKYFISFSSIQYHKM THTGEKPYECKQCGKAFTGCSSHLQKHGRTHTGVNADECKE CGNAFSPSEIRRHKRSHTGEKPYECKQCGKYFIGSSIQHHERTHSG	1	1		
GRLVADLINENDALMARINATULKPEHSLAWNMIIILLDNTGNL AQAEAVGREALELI PINDHSLMFSLAWNIGKSQKYKESEALFLKA IKANPMAASYHGMLAVLYHRWGHLDLAKKHYEISLQLDPTASGT KENYGLLRRKLELMQKKAV  SIGFPVMLVLSILLYTCEMFQDSVAFEDVAVSFTQEWALLDPS QKNLYRDVMQETFEWALLTSVGKTWKVONIEDEYKNPRRNLSLMRE KLCESKESHHCGESFNQIADDMLNRKTLPGITPCESSVCGEVGT GHSSLNTHIRADTGHKSSEYQEYGENPYRNECKKAFSYLDSFQ SHCKACKKEKPYDGKECTETFISHSCIQRHRVMHSGDGPYKCKP CGKAFYFLNLCLIHERIHTGVKPYKCKQCGKAFTRSTTLFVHER THTGVNADBCKECGNAFSFPSEIRRHKRSHTGEKPYECKQCGKV FISFSSIQYHKMTHTGEKPYECKQCGKAFTCSSLIR EKPYECRQCGKAFRYFSSLHIHERTHTGKPYGCKQCGKGFRCA SQLQIHERTHSGEKPHECKECGKVFXXFSSLRIHERTHTGEKPH ECKQCGKAFRYFSSLHIHERTHTGKPYECKVCGKAFTCSSSIR YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPYQCKQC GKAFIRASSCREHERTHTINR  6368  1 327 RPVPAKLMPRSWFRTAGALPLRFPPLTMAVFHDEVEIEDFQYDE DSTTYFYPCPCGDNFSITKEDLENGEDVATCPSCSLIIKVIYDK DQFVCGETVPAPSANKELVKC  6369 1 1745 AGCCROTRFPTPRGPGSLCHWFCRSAACTVTRTIHGSPREDTGT FRSLMTSVGKTWKVQNIEDEYKMPRRNLSLMREKLCESKESHHCG ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHKSSEYGEYGENPYRNKECKKAFSYLDSFQSHLOKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFFILNLCL IHERIHTGVKPYKCKQCGKAPTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECQCGKA FRCTSDLQRHEKTHTEDKPYCCKQCGKGFTCASQLQIHERTHSG				
AQARAVGREALELIPNDHSLMFSLANVLGKSQKYKESEALFLKA IKANPNAASYHGNLAVLYHRWGHLDLAKKHYEISQLDPTASGT KENYGLLRKLELMQKKAV  SIGFPVMLVLSILLYTCEMFQDSVAFEDVAVSFTQEEWALLDFS QKNLYRDVMQETFKNLTSVGKTWKVQNIEDEYKNPRRNLSLMRE KLCESKESHHCGESFNOLADDMLNRKTLPGITPCESSVCGEVGT GHSSLNTHIRADTGHKSSBYQEYGENPYRNKECKKAFSYLDSFQ SHDKACTKEKPYDGKECTETFISHSCIQRHRVMHSGDGPYKCKF CGKAPFYENLLCLHREITHGVKPYKCKQCGKAFTRSTTLPPHER THTGVNADECKECGNAFSPPSEIRRHKRSHTGEKPYECKQCGKV FISFSSIQYHKWTHTGEKPYECKQCGKAFRCSHLQKHGRTHTG EKPYECRQCGKAFRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCA SQLQIHERTHSGEKPHECKECGKVFKYFSSLRIHERTHTGEKPH ECKQCGKAFRYFSSLRIHERTHTGDKPYECKVCGKAFTCSSIR YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPYQCKQC GKAFIRASSCREHERTHTINR  6368  1 327 RPVPAKLMPRSWPRTAGALPLRPPPLTMAVFHDEVEIEDFQYDE DSETYFYPCPCGDNFSITKEDLENGEDVATCPSCSLIIKVIYDK DGFVCGETVPAPSANKELVKC  6369 1 1745 AGCCRDTRFPTPRGPGSLCHNFCRSAACTVTRTIHGSPREDTGT PRSREMMFQDSVAFEDVAVSTTQEEWALLDPSQKNLYRDVMQCT FKNLISVGKTWKVQNIEDEYKNPRRNLSLMREKLCESKESHHCG ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHKSSEYQEYGENPYENKECKKAFSYLDSFQSIHDKACTKEKPY DGFKCTETFTISHSEIQRRRVMHSGDGPYKCKFCGKAFYFLNLCL IHER IHTGVKPYKCKQCGKAPTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECQCGKA FFCTSDLQRHEKTHTEDKPYCCKQCGKGFRCASQLQIHERTHSG				
IKANPNAASYHGNLAVLYHRWGHLDLAKKHYEISLQLDPTASGT KENYGLRRKLELMQKKAV  SIGFPVMLVLSILLYTCEMFODSVAFEDVAVSFTQEEWALLDPS QKNLYRDVMQETFKNLTSVGKTWKVQNIEDEYKNPRRNLSLMRE KLCESKESHHCGESFNQIADDMLARKTLPGITPCESSVCGEVGT GHSSLNTHIRADTGHKSSBYQEYGENPYRNKECKKAFSYLDSFQ SHDKACTKEKPYDGKECTETFISHGIQRRRVMHSGDGPYKCKF CGKAPYFLNLCLIHERIHTGVKPYKCKQCGKAFTRSTTLPVHER THTGVNADECKECGNAFSPFSEIRHKRSHTGEKPYECKQCGKV FISPSSIQHKMTHTGERPYECKQCGKAFRCGSHLQKHGRTHTG EKPYECRQCGKAFRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCA SQLQIHERTHSGEKPHECKECGKVFKYFSSLRIHERTHTGEKPH ECKQCGKAFRYFSSLHIHERTHTGDKPYECKVCGKAFTCSSIR YHERTHTGEKPYECKHCKGKAFISNYIRYHERTHTGEKPYCKQC GKAFIRASSCREHERTHTINR  6368  1 327 RPVPAKLNPRSWPRTAGALPLRPPPLTMAVFHDEVEIEDFQYDE DSTYFYPCPCGONFSITKEDLENGEDVATCPSCSLIIKVIYDK DQFVCGETVPAPSANKELVKC  6369 1 1745 AGCCRDTRFPTPRGGSLCHNFCRSAACTVTRTTHGSPREDTGT PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET FKNLTSVGKTWKVQNIEDEYKNPRNLSLMREKLCESKESHHCG ESFNQIADDMLNRKTLPGTTPCESSVCGEVGTHSSLNTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL IHER IHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSSTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKKHTEDKPYGCKQCGKVFISFSSIQYHKM				
KENYGLLRRKLELMÇKKAV  31934 SIGFPVMLVISILIYTCEMFQDSVAFEDVAVSFTQEEWALLDPS QKNLYRDVWQETFKNLTSVGKTWKVONIEDEYKNPRRNLSLMRE KLCESKESHHCGESFNQLADDMLMRKTLPGITPCESSVCGEVGT GHSSLNTHIRADTGHKSSBYQEYGENPYRNKECKKAFSYLDSFQ SHDKACTKEKPYDGKKCTETFISHSCIQRHRVHHSGDGPYKCKF CGKAFYFLNLCLHERIHTGVKPYKCKQCGKAFTRSTTLPVHER THTGVNADECKECGNAFSFPSEIRRHKRSHTGEKPYECKQCGKV FISFSSIQYHKMTHTGEKPYECKQCGKAFTRCGSHLQKHGRTHTG EKPYECRQCGKAFRCTSDLQRHEKTHTEDKPYGCKQCGKFRCA SQLQIHERTHSGEKPHECKECGKVFKYFSSLRHERTHTGEKPH ECKQCGKAFRYFSSLHHERTHTGDKPYECKVCGKAFTCSSIR YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPYQCKQC GKAFIRASSCREHERTHTINR  6368 1 327 RPVPAKLMPRSWPRTAGALPLRPPPLTMAVFHDEVEIEDFQYDE DSETYFYPCPCGDNFSITKEDLENGEDVATCPSCSLIIKVIYDK DQFVCGETVPAPSANKELVKC  6369 1 1745 AGCCDTRFFPTPRGFGSLCHNFCRSAACTVTRTIHGSPREDTGT PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET FKNLTSVGKTWKVQNIEDEYKNPRNLSLMREKLCESKESHHCG ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFGGKAFYFINLCL IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKFGRASQLQIHERTHSG		! .		
6367  287  1934  SIGFPVMLVLSILLYTCEMFQDSVAFEDVAVSFTQEEWALLDPS QKNLYRDVMQETFKNLTSVGKTWKVQNIEDEYKNPRRNLSIMRE KLCESKESHHCGESFNQIADDMLNRKTLPGITPCESSVCGEVGT GHSSLNTHIKADTGHKSSEYQEYGENPYRNKECKKAFSYLDSFQ SHDKACTKEKPYDGKECTETFISHSCIQRHRWHSGDGPYKCKF CGKAPYFLNLCLIHERIHTGVKPYKCKQCGKAFTRSTTLPVHER THTGVNADECKECGNAFSFPSEIRRHKSHTGEKPYECKQCGKV FISFSSIQYHKMTHTGEKPYECKQCGKAFRCGSHLQKHGRTHTG EKPYECRQCGKAFRCTSDLQRHEKTETEDKPYGCKQCGKGFRCA SQLQIHERTHSGEKPHECKECGKVFKYFSSLRIHERTHTGEKPH ECKQCGKAFRYFSSLHIHERTHTGDKPYECKVCGKAFTCSSSIR YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPH ECKQCGKAFRYFSSLHIHERTHTGDKPYECKVCGKAFTCSSSIR YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPYQCKQC GKAFIRASSCREHERTHTINR DSETYFYPCPGGDNFSITKEDLENGEDVATCPSCSLIIKVIYDK DOFVCGETVPAPSANKELVKC  6369  1 1745 AGCCRDTRFPTPRGFSLCHNFCRSAACTVTRTIHGSPREDTGT PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET FKNLTSVGKTWKVQNIEDEYKNPRRNLSLMREKLCESKESHHCG ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRWMHSGDGPYKCKFGGKAFTFLNLCL IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPVECKQCGKAFTRCSSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG				
QKNLYRDVMQETFKNLTSVGKTWKYONIEDEYKNPRRILSLMRE KLCESKESHHCGESFNQIADDMLNRKTLPGITPCESSVCGEVGT GHSSLINTHIRADTIGHKSSBYQEYGENPYRNKECKKAFSYLDSFQ SHDKACTKEKPYDGKECTETFISHSCIQRHRVMHSGDGPYKCKF CGKAPYFLNLCLIHERLHTGVKPYKCKQCGKAFTRSTTLPVHER THTGVNADECKECGNAFSPPSEIRRHKRSHTGEKPYECKQCGKV FISFSSIQYHKMTHTGKRYYECKQCGKAFRCGSHLQKHGRTHTG EKFYECQCGKAFRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCA SQLQIHERTHSGEKPHECKECGKVYKYFSSLRIHERTHTGEKPH ECKQCGKAFRYFSSLHIHERTHTGDKPYECKVCGKAFTCSSSIR YHERTHTGEKPYECKCKAFISNYIRYHERTHTGEKPYQCKQC GKAFIRASSCREHERTHTINR  6368 1 327 RPVPAKLNPRSWPRTAGALPLRPPPLTMAVFHDEVEIEDFQYDE DSSTYFYPCPCGDNFSITKEDLENGEDVATCPSCSLIIKVIYDK DQFVCGETVPAPSANKELVKC  6369 1 1745 AGCCRDTRFPTPRGPGSLCHNFCRSAACTVTRTIHGSPREDTGT PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET FKNLTSVGKTWKVQNIEDEYKNPRRNLSLMREKLCESKESHHCG ESFNQIADDMLNKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHKSSEYQEYGGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYPECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG	6363		4.00-	1
KLCESKESHHCGESFNQIADDMLNRKTLPGITPCESSVCGEVGT GHSSLNTHIRADTGHKSSBYQEYGENPYRNKECKKAFSYLDSFQ SHOKACTKEKPYDGKECTETFISHSCIQRHRVMHSGDGPYKCKF CGKAPYFLNLCLIHERIHTGVKPYKCKQCGKAFTRSTTLPVHER THTGVNADECKECGNAFSFPSEIRRHKRSHTGEKPYECKQCGKV FISFSSIQYHKMTHTGEKPYECKQCGKAFRCGSHLQKHGRTHTG EKPYECRQCGKAFRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCA SQLQIHERTHSGEKPHECKECGKVFKYFSSLRIHERTHTGEKPH ECKQCGKAFRYFSSLHIHERTHTGDKPYECKVCGKAFTCSSSIR YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPH ECKQCGKAFRYFSSLHIHERTHTGDKPYECKVCGKAFTCSSSIR YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPPQCKQC GKAFIRASSCREHERTHTINR  6368  1 327 RPVPAKLNPRSWPRTAGALPLRPPPLTMAVFHDEVEIEDFQYDE DSSTYFYPCCGONFSITKEDLENGEDVATCPSCSLIIKVIYDK DQFVCGETVPAPSANKELVKC  6369 1 1745 AGCCRDTRFPTPRGPGSLCHNFCRSAACTVTRTTHGSPREDTGT PRSREMMFQDSVAFEDVAVSFTQEBWALLDPSQKNLYRDVMQET FKNLTSVGKTMKVQNIEDEYKNPRRNLSLMREKLCESKESHHCG ESFNQIADDMLNKKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL HERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG	6367	287	1934	
GHSSLNTHIRADTGHKSSEYQEYGENPYRKECKKAFSYLDSFQ SHOKACTKEKPYDGKECTETFISHSCIQRHRVMHSGDGPYKCKF CGKAFYFLNLCLIHERIHTGVKPYKCKQCGKAFTRSTTLPVHER THTGUNADECKEGNAFSFPSEIRRHKRSHTGEKPYECKQCGKV FISFSSIQYHKMTHTGEKPYECKQCGKAFRCGSHLQKHGRTHTG EKPYECRQCGKAFRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCA SQLQIHERTHSGEKPHECKECGKVFKYFSSLRIHERTHTGEKPH ECKQCGKAFRYFSSLHIHERTHTGDKPYECKVCGKAFTCSSSIR YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPYQCKQC GKAFIRASSCREHERTHTINR  6368 1 327 RPVPAKLNPRSWPRTAGALPLRPPPLTMAVFHDEVEIEDFQYDE DSETYFYPCGDNFSITKBDLENGEDVATCPSCSLIIKVIYDK DQFVCGETVPAPSANKELVKC  6369 1 1745 AGCCRDTRFPTPRGPGSLCHNFCRSAACTVTRTIHGSPREDTGT PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET FINLTSVGKTWKVQNIEDEYKNPRNLSLMREKLCESKESHHCG ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG				
SHDKACTKEKPYDGKECTETFISHSCIQRHRVMHSGDGPYKCKF CGKAPYFLNLCLIHERIHTGVKPYKCKQCGKAFTRSTTLPVHER THTGVNADECKECGNAFSPSEIRHKRSHTGEKPYECKQCGKV FISFSSIQYHKMTHTGEKPYECKQCGKAFRCGSHLQKHGRTHTG EKPYECRQCGKAFRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCA SQLQIHERTHSGEKPHECKECGKVFKYFSSLRIHERTHTGEKPH ECKQCGKAFRYFSSLHIHERTHTGDKPYECKVCGKAFTCSSSIR YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPPYQCKQC GKAFIRASSCREHERTHTINR  6368 1 327 RPVPAKLNPRSWPRTAGALPLRPPPLTMAVFHDEVEIEDFQYDE DSETYFYPCPCGDNFSITKEDLENGEDVATCPSCSLIIKVIYDK DQFVCGETVPAPSANKELVKC  6369 1 1745 AGCCRDTRFPTPRGPGSLCHNFCRSAACTVTRTIHGSPREDTGT PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMCET FKNLTSVGKTWKVQNIEDEYKNPRNLSLMREKLCESKESHHCG ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL IHER IHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFTRCSSHLQKHGRTHTGEKPYECRQCCKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG	1			
CGKAFYFLNLCLIHERIHTGVKPYKCKQCGKAFTRSTTLPVHER THTGVNADECKECGNAFSFPSEIRRHKRSHTGEKPYECKQCGKV FISFSSIQYHKMTHTGEKPYECKQCGKAFRCGSHLQKHGRTHTG EKFYECRQCGKAFRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCA SQLQIHERTHSGEKPHECKECGKVFKYFSSLRIHERTHTGEKPH ECKQCGKAFRYFSSLHIHERTHTGDKPYECKVCGKAFTCSSSIR YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPYQCKQC GKAFIRASSCREHERTHTINR  6368 1 327 RPVPAKLNPRSWPRTAGALPLRPPPLTMAVFHDEVEIEDFQYDE DSETYFYPCPCGDNFSITKEDLENGEDVATCPSCSLIIKVIYDK DQFVCGETVPAPSANKELVKC  6369 1 1745 AGCCRDTRFPTPRGPGSLCHNFCRSAACTVTRTIHGSPREDTGT PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET FKNLTSVGKTWKVQNIEDEYKNPRRNLSLMREKLCESKESHHCG ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVMADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG	i			
THTGVNADECKECGNAFSPPSEIRRHKRSHTGEKPYECKQCGKV FISFSSIQYHKMTHTGEKPYECKQCGKAFRCGSHLQKHGRTHTG EKPYECRQCGKAFRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCA SQLQIHERTHSGEKPHECKECGKVFKYFSSLRIHERTHTGEKPH ECKQCGKAFRYFSSLHIHERTHTGDKPYECKVCGKAFTCSSSIR YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPYQCKQC GKAFIRASSCREHERTHTINR  6368 1 327 RPVPAKLNPRSWPRTAGALPLRPPPLTMAVFHDEVEIEDFQYDE DSETYFYPCPCGDNFSITKBDLENGEDVATCPSCSLIIKVIYDK DQFVCGETVPAPSANKELVKC  6369 1 1745 AGCCRDTFPTPRGPGSLCHNFCRSAACTVTRTIHGSPREDTGT PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET FKNLTSVGKTWKVQNIEDEYKNPRRNLSLMREKLCESKESHHCG ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG	ļ			
FISFSSIQYHKMTHTGEKPYECKQCGKAFRCGSHLQKHGRTHTG EKPYECRQCGKAFRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCA SQLQIHERTHSGEKPHECKECGKVFKYFSSLRIHERTHTGEKPH ECKQCGKAFRYFSSLHIHERTHTGDKPYECKVCGKAFTCSSSIR YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPYQCKQC GKAFIRASSCREHERTHTINR  6368 1 327 RPVPAKLNPRSWPRTAGALPLRPPPLTMAVFHDEVEIEDFQYDE DSETTFYPCPCGDNFSITKEDLENGEDVATCPSCSLIIKVIYDK DQFVCGETVPAPSANKELVKC  6369 1 1745 AGCCRTTFPTPRGPGSLCHNFCRSAACTVTRTIHGSPREDTGT PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET FKNLTSVGKTWKVQNIEDEYKNPRRNLSLMREKLCESKESHHCG ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG	Ī			
EKPYECRQCGKAFRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCA SQLQIHERTHSGEKPHECKECGKVFKYFSSLRIHERTHTGEKPH ECKQCGKAFRYFSSLHIHERTHTGDKPYECKVCGKAFTCSSSIR YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPYQCKQC GKAFIRASSCREHERTHTINR  6368 1 327 RPVPAKLNPRSWPRTAGALPLRPPPLTMAVFHDEVEIEDFQYDE DSETYFYPCPCGDNFSITKEDLENGEDVATCPSCSLIIKVIYDK DQFVCGETVPAPSANKELVKC  6369 1 1745 AGCCRDTRFPTPRGPGSLCHNFCRSAACTVTRTIHGSPREDTGT PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET FKNLTSVGKTWKVQNIEDEYKNPRRNLSLMREKLCESKESHHCG ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG	1			
SQLQIHERTHSGEKPHECKECGKVFKYFSSLRIHERTHTGEKPH ECKQCGKAFRYFSSLHIHERTHTGDKPYECKVCGKAFTCSSSIR YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPYQCKQC GKAFIRASSCREHERTHTINR  6368 1 327 RPVPAKLNPRSWPRTAGALPLRPPPLTMAVFHDEVEIEDFQYDE DSETYFYPCGDNFSITKEDLENGEDVATCPSCSLIIKVIYDK DQFVCGETVPAPSANKELVKC  6369 1 1745 AGCCRDTRFPTPRGPGSLCHNFCRSAACTVTRTIHGSPREDTGT PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET FKNLTSVGKTWKVQNIEDEYKNPRRNLSLMREKLCESKESHHCG ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG				
ECKQCGKAFRYFSSLHIHERTHTGDKPYECKVCGKAFTCSSSIR YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPYQCKQC GKAFIRASSCREHERTHTINR  6368  1 327 RPVPAKLNPRSWPRTAGALPLRPPPLTMAVFHDEVEIEDFQYDE DSETYFYPCPCGDNFSITKEDLENGEDVATCPSCSLIIKVIYDK DQFVCGETVPAPSANKELVKC  6369  1 1745 AGCCRDTRFPTPRGPGSLCHNFCRSAACTVTRTIHGSPREDTGT PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET FKNLTSVGKTWKVQNIEDEYKNPRRNLSLMREKLCESKESHHCG ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG		[		
YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPYQCKQC GKAFIRASSCREHERTHTINR  6368  1 327 RPVPAKLNPRSWPRTAGALPLRPPPLTMAVFHDEVEIEDFQYDE DSETYFYPCPCGDNFSITKEDLENGEDVATCPSCSLIIKVIYDK DQFVCGETVPAPSANKELVKC  6369  1 1745 AGCCRDTRFPTPRGPGSLCHNFCRSAACTVTRTIHGSPREDTGT PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET FKNLTSVGKTWKVQNIEDEYKNPRRNLSLMREKLCESKESHHCG ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG	1			
GKAFIRASSCREHERTHTINR  6368  1 327  RPVPAKLNPRSWPRTAGALPLRPPPLTMAVFHDEVEIEDFQYDE DSETYFYPCPCGDNFSITKEDLENGEDVATCPSCSLIIKVIYDK DQFVCGETVPAPSANKELVKC  6369  1 1745  AGCCRDTRFPTPRGPGSLCHNFCRSAACTVTRTIHGSPREDTGT PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET FKNLTSVGKTWKVQNIEDEYKNPRRNLSLMEEKLCESKESHHCG ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG	1			
6368 1 327 RPVPAKLNPRSWPRTAGALPLRPPPLTMAVFHDEVEIEDFQYDE DSETYFYPCPCGDNFSITKEDLENGEDVATCPSCSLIIKVIYDK DQFVCGETVPAPSANKELVKC  6369 1 1745 AGCCRDTRFTTPRGPGSLCHNFCRSAACTVIRTIHGSPREDTGT PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET FKNLTSVGKTWKVQNIEDEYKNPRRNLSLMREKLCESKESHHCG ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG	] .			l
DSETYFYPCPCGDNFSITKEDLENGEDVATCPSCSLIIKVIYDK DQFVCGETVPAPSANKELVKC  1 1745 AGCCRDTRFPTPRGPGSLCHNFCRSAACTVIRTIHGSPREDTGT PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET FKNLTSVGKTWKVQNIEDEYKNPRRNLSLMREKLCESKESHHCG ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG	6360		202	
DQFVCGETVPAPSANKELVKC  6369  1 1745  AGCCRDTRFPTPRGPGSLCHNFCRSAACTVTRTIHGSPREDTGT PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET FKNLTSVGKTWKVQNIEDEYKNPRRNLSLMREKLCESKESHHCG ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG	0368	<b>-</b>	321	
AGCCRDTRFPTPRGPGSLCHNFCRSAACTVIRTIHGSPREDTGT PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET FKNLTSVGKTWKVQNIEDEYKNPRRNLSLMREKLCESKESHHCG ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG	1			, · · · · ·
PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET FKNLTSVGKTWKVQNIEDEYKNPRRNLSLMEEKLCESKESHHCG ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG	6360			<u> </u>
FKNLTSVGKTWKVQNIEDEYKNPRRNLSLMREKLCESKESHHCG ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG	6369	<u> </u>	1745	
ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG	1			
TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG	1			
DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG				
IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG				
CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG	1			
THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG				
FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG				
EKPHECKECGKVFKYFSSLRIHERTHTGEKPHECKOCGKAFRVF				
THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE P	i			EKPHECKECGKVFKYFSSLRIHERTHTGEKPHECKQCGKAFRYF

Beginning   nucleotide   nucleotide   nucleotide   cortesponding   contesponding   to first   amino acid   amino acid   amino acid   amino acid   amino acid   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequ	SEQ	Predicted	1 20 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	
Noticetide   Cocation   Corresponding			Predicted end	Amino acid segment containing signal peptide
Cocation   Corresponding				(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence se				Glutamic Acid, F=Phenylalanine, G=Glycine,
amino acid residue of amino acid residue of amino acid amino acid amino acid amino acid amino acid sequence  Sequence  Sequence  Sequence  SEJMITERTHIROREPYTEXTUCARPTICSSISTRYHERITHTOERPY ECKNICKAR ISNYIRYHERITHTOERPY ECKNICKAR ISNYIRYHERITHTOERPY ECKNICKAR ISNYIRYHERITHTOERPY ECKNICKAR ISNYIRYHERITHTOERPY ECKNICKAR ISNYIRYHERITHTOERPY ECKNICKAR ISNYIRYHERITHTOERPY ECKNICKAR ISNYIRYHERITHTOERPY ECKNICKAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHTOERPO ELANGAR ISNYIRYHERITHTOERPO ELANGAR ISNYIRYHTOERPO ELANGAR ISNYIRYHTOERPO ELANGAR ISNYIRYHTOERPO ELANGAR ISNYIRYHTOERPO ELANGAR ISNYIRYHTOERPO ELANGAR ISNYIRYHTOERPO ELANGAR ISNYIRYHTOERPO ELANGAR ISNYIRYHTOERPO ELANGAR ISNYIRYHTOERPO ELANGAR ISNYIRYHTOERPO ELANGAR ISNYIRYHTOERPO ELANGAR ISNYIRYHTOERPO ELANGAR ISNYIRYHTOERPO ELANGAR ISNYIRYHTOERPO ELANGAR ISNYIRYHTOERPO ELANGAR ISNYIRYHTOERPO ELANGAR ISNYIRYHTOERPO ELANGAR ISNYIRYHTOERPO ELANGAR ISNYIRYHTOERPO ELANGAR IS			,	Hanscidine, Talsoleucine, Kalysine,
Samino acid   residue of amino acid   sequence   Samino acid   sequence   Samino acid   sequence   Samino acid   sequence   Samino acid   sequence   Samino acid   sequence   Samino acid   Sequence   Samino acid   Sequence   Samino acid   Sequence   Samino acid   Sequence   Samino acid   Sequence   Samino acid   Samino acid   Sequence   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid   Samino acid				D-Proline O-Clutomine N-Asparagine,
##Tryptophán, Y=Tyrosine, X=Unkom, *=Stop damino acid sequence    Sequence		amino acid	1	S=Serine T-Thronning W-Waling
Sequence    Sequence	i	residue of		W=Tryptonhan V=Tyrosine Y=Unknown # 04
SEQUENCE    SEMINIERTHORY PECKUGGAPTESSIENTERTHTGERPY	1	amino acid		Codon, /=possible nuclentide deletion
6370 1711 329 FULSEORUSTEPTWPRSFGLGRGAAAAGARTAGAGLUSILLUSGG ALVGGLRVTHTTINANANASTWELSIYELHEPTORS HOTE IAVSPRSHISSIKCPICLDALVINTTITEALISTEROSCUTVTALR SGNNECPTCRKKLVSKRSLKPPDNFDALISKIYESPSCLTVTALR SGNNECPTCRKKLVSKRSLKPPDNFDALISKIYESPSCLTVTALR SGNNECPTCRKKLVSKRSLKPPDNFDALISKIYESPSCLTVTALR SGNNECPTCRKKLVSKRSLKPPDNFDALISKIYESPSCLTVTALR SGNNECPTCRKKLVSKRSLKPPDNFDALISKIYESPSCLTVTALR SGNNECPTCRKKLVSKRSLKPPDNFDALISKIYESPSCLTVTALR SGNNECPTCRKKLVSKRSLKPPDNFDALISKIYESPSCLTVTALR SGNNECPTCRKKLVSKRSLKPPDNFDALISKIYESPSCLTGPRGPGGGGGGAG RVLLTRISLINGOQUAGNGSCEGEGGGAGGAG SSVSTGGGGTGGGGGGAGGTGGGGGGAGGAGG SSVSTGGGGTGGGGGGAGGAGGGGAGGAGGAGGAGGAG SSVSTGGGGTGGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA		sequence	-	\=possible nucleotide insertion)
6370  1711  329  FVISEGRIRTERTWERS FOLGRGAAAAGARTAGAGLIRILLIGG ALIVOGIR PUTTYPANAONASKTWELSIVELIHERTOEA MODTE I LAVSPRSIHSELMCPICLDMLKNITHTYRECHREPOSA MODTE I LAVSPRSIHSELMCPICLDMLKNITHTYRECHREPOSA THOTE I LAVSPRSIHSELMCPICLDMLKNITHTYRECHREPOSA THOTE I LAVSPRSIHSELMCPICLDMLKNITHTYRECHREPOSA THOTE ROWNELD AVAILAGE STATE AND				SSLHIHERTHTGDKPYECKVCGKAFTCSSSTRVHFRTHTGEVDV
6370 1711 329 FVLSEGRIKTERTWPRSPGLGRGAAAGGRTAGGGLIRLLIGGG ALWGGLRPVTMTTPANAQNASKTWELSIVELMRTPQGBATMGGTE IAWSPRSLHSEIMCPICLUMKNITMTIKERGSDCIVTALR SGNKECPTCRKKLUSKRSIREDRPFDALISKIVPSESPYAHOD RVLIRLSRIHMQOLLSSIEGLRMGAMERGSDCIVTALR SGNKECPTCRKKLUSKRSIREDRPFDALISKIVPSESPYAHOD RVLIRLSRIHMQOLLSSIEGLRMGAMERGSDCIPSPPBPGGGAG SSVCTGGGGTGGVGCGASSEBSGNGGGTLAPSPPFGGAGG SSVCTGGGTGGVGCGASSEBSGNGGGTLAPSPPFGAGP PPBRGGEIELVFRRHPLLVEKGEVCOTRYVTTGANTVHLSKY LALBIALERROQGEAGERGGGGAGTGOPBPPGGAPG PPBRGGEILVFRRHPLLVEKGEVCTRYVXTTGANTVHLSKY LALBIALERROQGAGAERFOGGGGGASTTUNGSLTLELWNE KWKVSRPLELCVAPTKOPK  6371 3 288 GVANMSTAMNEGTKSFOPPPDKGSFPLDHIGGCKSFKEXMKC LANNNEFALLCKYREKKEVLECTMRKIMLQEPLEKLGFGDLTSG KSRAKK SARKK SARKK SARKK SVSALASBGKARERYKKLEDLLEKSFSLVKMPSLOPVNGCVNRRL LPKVPEKKLKLVANDKELYRACAVEVRRQINGONONALFGDEVED LPKVPEKKLKLVANDKELYRACAVEVRRQINGONONALFGDEVED LPKVPEKKLKLVANDKELYRACAVEVRRQINGONONALFGDEVED CEICTVPCHKFTWCLDACITERFEVDSK KRARELOGPLDEVKKOG QVLGDLSMILCDEPAINTALSTVRHLQELVGORTHEDSEPLL LLKRLIALGGAMDHIDGOVEKEPKMEVELLTEPLEMBEPLD DYTFNVDKLDPAINTALSTVRHLQEDLFORDLEDENGLEDDEV VKVLHTKKGRNINLLELLPGLVSTVRDLAEDTIFLHIMLMSFIND DYTFNVDKLDPATRGAGAMENTALSTVRHLQELVGORTHEDSEPLL LANDEFALEDFCSSLFGGFFLASPRKENVYRHALKLIHHIPRV APSKLEALGAANDMALKGGAMPLTBAGFTFTFONTSTPLTIMLMSFIND DYTFNVDKLALEPTOGSGRAVKELVSQLGEKLECLODIRKESPA OAAETPALEIPLSVADAAPI.  6373 67 711 SSRAMASSPRALAMWSVI SERVLVI SERVLVIL GFYAYYSVANKK DIKEYVKMMWWI IFALFTDAETFTD I FILCHPPTYPLKTAFVA VHCKRGLINVAATAANMALKOGGAAERSTALAVKSKY UHCKRGLINVAATAANMALKOGGAAERSTALAVKSKY UHCKRGLINVAATAANMALKOGGAAERSTALAVKSKY UHCKRGLINVAATAANMALKOGGAAERSTALAVKSKY UHCKRGLINVAATAANMALKOGGAAERSTALAVKSKY UHCKRGLINVAATAANMALKOGGAAERSTALEDTSTRAGQVAA IRGSVIBERTIRRGEGGAAPTSTTHLESTROMS HKLFCSYTSTSEFSSTRHISCFTHTFCNYTPOTIRGDGAPASGFOPDAGGTIN DISURTYRRGEGAAHFTOTLDEGSGVULVAVMVDERRRGEMOOH SOGHI ITAVADHIFFLAKTTSWELGERFSALELDTSSTRAGOVA IRGSVIBERTIRRGEGAAHFTOTLDEGSGVULVARVKGOGEPMNIT ANEIGSBETLALLUTGLAGARSTTLEGSTRADGVARKILLISSTCH CORRENGGOVVROPTILDEGGGVULVARVKGOGEPMNIT ANEIGSBETLALLUTGLAGGASTALLEGGAAERAVET CORRENGGOVVROPTILARKGGGAAERAVET				ECKHCGKAFISNYIRYHERTHTGEKPYOCKOCGKAFIRASSCRE
ALVOGIARY VINTIT PARAGNASK WELST LEHRTPOEAI MROTE  LAVSPRSIHS SIMPLY CLUMLKNITHTIKS CHARCEGOL VTALK  SGNKECPT CRKKLVSKRSLERPONFDALISK IVESREEVEAHQD  RVLI RIJSKLHMQQALSSS IEGGLRMQAMMRAQRURP PIGSDOT  TIMSGGEGE PEGEGGGGGDGUSSSSA PADSAPPARK PRGGGAGG  SVOTTGGGTGGVGCAGSESGGRAGTIGGGTLGFB PIGSDOT  TIMSGGEGE PEGEGGGGGGGVGSSSA PADRAPRAPK PRGGGAGG  SVOTTGGGTTGVGCGAGSESGGRAGTIGGGTLGFB PIGSDOT  LARIALERRQQDEAGEPGGGGGAADTGGFDCGGGGGGAGGG  GOFEPPALPSLEGVSKKVITTI TARGGAFTILMGSLTLELVNE  KFMKVSRPLELCYAPTKOPK  6371 3 288 GVANMSTANNFGTKSFOPPPPEKGSFPLDHIGGCKSFFREXBYKC  LHNNNFENALCRKESKEYLECRMERKLMLQEPLEKLGFGDLTSG  KSEAKK  6372 2141 625 RVSALASIGKAERFYKKLEDLLEKSFSLVKNFSLQEVUNCVIKKI  LHNNNFENALCRKESKEYLECRMERKLMLQEPLEKLGFGDLTSG  KSEAKK  6372 LLKOYILEKESALFSTELSVLHNFSPPSPKTERGGEVVORLTRM  VGKNVELVDWVDLAFLKLVAADKELLYRACAVEVERGINONOALFGDEVSF  LLKOYILEKESALFSTELSVLHNFSPPSPKTERGGEVVORLTRM  VGKNVELVDWVLOFLETLFETRNWYLCTELTSVLHDONOALFGDEVSF  LLKOYILEKESALFSTELSVLHNFSPPSPKTERGGEVVORLTRM  VGKNVELVDWVLOFLETLFETRNWYLCTELTSVLHDEDSDLL  LLELLALGOGANDWLDGOVFKEPROGELITSFLEMBISCHDV  VGKNVELVDWLOFLETLFETRNWYLCTELTSVLHLTBGSDDLL  LLELLALGOGANDWLDGOVFKEPROGELITSFLEMBISCHD  VGKNVELVDWLOFLETLFETRNWYLCTELTSFLEMBISCHDLW  VGKNVELVDWLOFLETLFETRNWYLCTELTSFLEMBISCHDLW  VGKNVELVDWLOFLETLFETRNWYLCTELTSFLEMBISCHDLWGRAGG  OVIGDLSSNILLDOPAINTALSSVLHLGEVORGTHAGSLANDLUNG  EICTUPPCHKFTALSTVLHSTENDWLTGFDLITFLIMMSFLUD  DYTFNWDGALBPTGGGGAGAVKELTSGLGEKLEGLODIRKRSDL  AREKEBLOGALBPTGGGGARVELTSGLGEKLEGLODIRKRSDL  VARGREDPARLEDPLSVPAPAPLI  6373 67 711 PSERARASFARLZBAWSNILTSRLVVLIFGTLYPAYYSYKAVKK  DIESYKMMWMILTALFTTALSTVHLIFLSKKEK LIDCHTLHTHPRA  KLLSPYTKGSCALVFRYTSSTIFLSSTTPLSSTTFLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPLSSTTPL	L		j	HERTHTINR
ALVOGGRPYTHTTPANAQNASKTRELS/JELHRIPOGRAMOOTE IAVSPRSLIBSLEMCYICLDUKKITMITIKERCSDCIVTALR SGNKECPTCRKGLUSKRSIRPDNPFDALISKIYPSKEETEAHQD RVLIRISRIHMQOALSSIEGURMQAMPRIPIGSDCI TIMSGGGGPGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	6370	1711	329	FVLSEQRLRTERTWPRSPGLGRGAAAAGARTAGAGLLRLLLGCG
1 ANSPRSLHSELMOPICLDMENTIMTIKSCHRECSBOLTVTALE SGNNECTFORKKUZYSKEJKPOPNFDALITYSSKEPERAHOD RVLIRLSRIHMOGALESSIEGGLRMOAMBRAQRURPIGSBOT TTMSGGGGG PGGGGGGGUSSSSADPOSAPKAPRGGGAGG SVOTTGGGTGGVGCGAGEDSGDRGGTLGGTLGFPEPFGADD' PPBFGGEIELLVFREHPLLVEKGEVCTTRVVATTGNATUPHLSKY LABRIALERRQQDEAGEPGGGGGABTGGFDGGGAGGGGG BOFFEPALPSLEGVSKKQVTY1TAPGGGAFTLMGSLTLELWNE  6371 3 288 GYAMMSTANNFGTKSPOPPFPERGGAFTLMIGSCKEFKEKERKE LINNNFENALCRKESKEYLECRMERKLMLQEPLEKLGFGDLTGG KSEAKK 6372 2141 625 RVSALASBGKAEGRYKKLEDLLEKFSLUKHPSLOFVVMCVMKH LINNYLLDRVLGHENVELVRACAVEVRRQIMONOAALGDEVSF LLKQYILEKESALFSTELLSVIHNFFSPSFTRRGGGVVGCHTRN VGKNYKLLDRVLGHENTLFRTENVHYCTLRAELLMSHLDDLVG EICTVDPCHKRTTACLBACIRERFVDSKRARELGGFLDGVKKGG QVLGDISHILCDFFAINTLALSTVERLGELVGGCVCGRLTRN VGKNYKLLDRVLGGAMDLIBSGYKEFSPERFRGGGVVGCHTRN VGKNYKLLDRVLGGAMDLIBSGYKEFSPERFRGGGVVGCHTRN VGKNYKLLDRVLGGAMDLIBSGYKEFSPERFRGGFVGGVVGCHTRN VGKNYKLLDRVLGGAMDLIBSGYKEFFTRGGFVVGKTGG QVLGDISHILCDFFAINTLALSTVERLGELVGGGCTLPRBSPDLL LLRLLALGGGAMDLIBSGYKEFFTGGFFLTAPKRELGGLDGKKKGG QVLGDISHILCDFFAINTLALSTVERLGELVGGGTLPRBSPDLL LARPHALEDFCSSLFFGFFTLTAPFRRENVHRHALRLLHLHPRK APSKLEALGGAMDLIBSGYKEFFTGGFFTFLTAPKRELGGLDIKKFSPA QAAETTALEDFLSVARAPPI.  6373 67 711 PSSRARASPARLBAMWSH ISRLVVLIFGTLYPAYYSYKAVKSK DIRFYVKMMMYNI JPALFTTAETFTDI JFLCMFFFYYEKKLECDLDIKKFSPA QAAETTALEDFLSVARAPPI.  6374 535 2105 CHRISTORIANATAAMMASKGGGALSERLRSFSMGDLTTIRGD GAPASGGPPPPGGGRAGSKGUNGGPMSRASSASSGTA HKLFCSYTSTSTEFSSTRHISGFTHFFCNYTSSTIFLSSTDDH HSCPHTTSCHYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTDDH HSCPHTTSCHYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTDDH HSCPHTTSCHYTSSTIFLSSTRDHSCPTHTFCNYTSTIFLSSTDD HSCPHTTSCHYTSSTIFLSSTRDHSCPTHTFCNYTSTIFLSSTDD HSCPHTTSCHYTSSTIFLSSTRDHSCPTHTFCNYTSTIFLSSTDD HSCPHTTSCHYTSSTIFLSSTRDHSCPTHTFCNYTSTIFLSSTDD HSCPHTTSCHYTSSTIFLSSTRDHSCPTHTFCNYTSTIFLSSTDD HSCPHTTSCHYTSSTIFLSSTRDHSCPTHTFCNYTSTIFLSSTDD HSCPHTTSCHYTSSTIFLSSTRDHSCPTHTFCNYTSTIFLSSTDD HSCPHTTSCHYTSTIFLSTRDHSCPTHTFCNYTSTIFLSSTDD HSCPHTTSCHYTSTIFLSTRHSCPTHTFCNYTSTIFLSSTDD HSCPHTTSCHYTSTIFLSTRHSCPTHTFCNYTSTIFLSSTDD HSCRGKRYNGRAGALGOVARDARNTKLL VMIBRORDMACHTANATARAFKHULDVA	1			ALVGGLRPVTMTTPANAONASKTWELSLYELHRTPOFAIMDGTE
SGNNECPTCRKILVSKESLEPDPNDTALISKITPSREPTEAHOUN RVLIRISRIHNOQALSSISIEGLIRAMRQAVERT PIGSDOT TTMSGGEGS PEGEGDDEDVSSISAPDSAPGRAPREPREGGAGG SSVGTGGGGGGGGGGGDGUGGGTLGGGTLGFD PEP PGAPP PPBFGGEIELVFRHPLLVEKGEYCOTRYVETGRATVDHLSKY LARIALERRQOGRAFGEFGGGGGAGFDCCGGGGGGGGGGGGGGGGGGGGGGGGGGGG				IAVSPRSLHSELMCPICLDMLKNTMTTKECLHRFCSDCIVTALR
TTMSGGEG PGEGEDGEDVSDSAPDSAFREPRIGEGAGG SSVGTGGGTGGGGGEDGEDVGGTGFGFP PF PGAPS PFBFGGTGTGVGGGGGEDGGGGGGGGGGGGGGGGGGGGGGGGGG	1			SGNKECPTCRKKLVSKRSLRPDPNFDALISKIYPSREEYEAHOD
SSVOTGGGTGGVGGAGSEBGGGTLLGGFLBPBPBAGPB PPBFGGEI ELVFRPHIPLUFEKEPYOTFYVETGNATVHHLSKY LALRIALERRQQGEAGSPGGGGASTGGPDGCGGGGGAGGG GOFEEPALPSLEGVSERVTIYIAFGGAFTLNGSLTLELVNE KFMKVSRPLELCYAPTEDPK KFMKVSRPLELCYAPTEDPK KFMKVSRPLELCYAPTEDPK KFMKVSRPLELCYAPTEDPK KFMKVSRPLELCYAPTEDPK KFMKVSRPLELCYAPTEDPK KFMKVSRPLELCYAPTEDPK KFMKVSRPLELCYAPTEDPK KFMKVSRPLELCYAPTEDPK KFMKVSRPLELCYAPTEDPK KFMKVSRPLELCYAPTEDPK KFMKVSRPLELCYAPTEDPK KFMKVSRPLELCYAPTEDPK KFMKVSRPLELCYAPTEDPK KFMKVSRPLELCYAPTEDPK KFMKVSRPLELCYAPTEDPK KFMKVSRPLELCYAPTEDPK KFMKVSRPLELCYAPTEDPK KFMKVSRPLELCYAPTEDPK KFMKVSRPLELCYAPTEDPK KFMKVSRPLELCYAPTEDPK KFMKVSRPLELCYAPTEDPK KFMKVSRPLELCYAPTEDFLOHEGGEDLEKGGGDLTSG KSEAKK KSEAKK KSEAKK LHUNNIFELSELLAFTELSVLIMFFSFSFLVRGGGEDVGRUTSR VGKNVKLYDMVLQFLRTLFLRRTNNHYCTLRAELLMSLHDLDVG EICTVDPCHKFTMCLDGLTERFFUNSRELGGFLIGEVGKIGG QVLGDLSMILCDPAINTLALSTVRHLQELVGGETLPBDSDLL LLURGLLAGGABMUNDSOVFKEPKMVSELLGFLDEVKIGG QVLGDLSMILCOGPAKTHLQELVGGGTLPBDSDDLL LLURGLLAGGABMUNDSOVFKEPKMVSELLGFLDHENSFLUX VULHITKGRNINALLHLEGPLETFEDADI FLHLTGNILAL LADEFALEDFCSSLFDGFPLTAS PRKENVHRHARKLIHLHFPKV APSKLEALACKALEBTGGGAAVKELYSQLGERLEGLDHRKFSPA QAAETPALELPLPSVSPARAPL  6373 67 711 PSRARASSFRALZAMWSWIISRUVULFFTLWFSYSYKAVKSK MLLSPYTKGSSLLYRKFVHPTLSSKEKEIDDCLOWAKNSFYDAL VHGKRGLUNVATHAVMANASKGGGALSERLRSFSMODLITTIRGD GAPABGGPPPGGGGRAKGKEVLSGFOVULFDTWSSTIFLSSTTELSSTRDHS CPTHTFCNYTSSTIFLSSTRDHSCPTHTSCNYTSSTIFLSSTTELSSTEDDH SCPHLTSVNYSSTIFLSSTRDHSCPTHTSCNYTSSTIFLSSTTELSSTED SCHLITAVADHLFKLKTISSELGERSALEDDPSMAGGFBWIDHAGGFIR NUNISGUSMACCHTUSNLDLOVILLIGTEKGKNNETNILIFL SGRWLKKMERSHGTKALTALLKCGAEDHVERWELUPDHAGGIR NUNISGUSMACCHTUSNLSDLOVILLIGTEKGKNNETNILIFL SGRWLKKMERSHGTKALTALLKCGAEDHVERWELUPDHAGGEIA NEGGGAGKKGRPGCAATRVSRRMAGALLDDYSTGGARK PGGRACSMSPGLKFRYSRRMAGALLDDYSTGGARK PGGRACSMSPGLKFRYSRRMAGALLDDYSTGGARK PGGRACSMSPGLKFRYSRRMAGALLDDYSTGGARK PGGRACSMSPGLKFRYSRRMAGALLDDYSTGGARK PGGRACSMSGTERFGQAVARGFWLATALARVCLLASCLLGDER FVALILLIGTGALFSVIFTFVLUTVDPHGAGLGTFSSFA				RVLIRLSRLHNQQALSSSIEEGLRMQAMHRAQRVRRPIPGSDQT
### PP\$PGGEIELUFERPHPLLVERGEYCOTRYVKTGNATVDHLSKY LARIALBERQQGEAGEGGGGAGGGAGGGGGGGGGGGGGGGGGGGGGG				TTMSGGEGEPGEGEGDGEDVSSDSAPDSAPGPAPKRPRGGGAGG
LÄRIALERRQQEAGEFGGGGASDTGGPGGGGGGG DGFEEPALPSLESUSERQYTITJAGGAFTILDISCHTLELVNE KFWKVSRPLELCYAPTKDPK GVAMMSTAMNFGTKSFQPREPBUGSFPLDHLGECKSFREKSMKC LHNINFENALCRKESKEYLECRMERKLMLGEPLEKLGFGDLTSG KSEAKK  6372 2141 625 RVSAIASEGKAEERYKKLEDLLEKSFSLVKMPSLQPVVMCVMKH LPKVPEKKLKLVMADKELYRACAVEVRGIUMOMOALFGDEVSP LLKGYJLEKESALFSTELSVLHNFSPSFKTRGGEVOVQLTFM VGKNVKLYDMVLOFLRTI-FLRTENVMYCTLRAELLMSLHDLDVG EICTVDPCHKFTWCLDACTERPSPSFKTRGGEVOVQLTFM VGKNVKLYDMVLOFLRTI-FLRTENVMYCTLRAELLMSLHDLDVG EICTVDPCHKFTWCLDACTERPSPSFKTRGGEVOVQLTFM VGKNVKLYDMVLOFLRTI-FLRTENVMYCTLRAELLMSLHDLDVG EICTVDPCHKFTWCLDACTERPSPSFKTRGGEVAGEVGKY VULBITKGRNKNALLRIPGSFFKREVEVENTLERLLMSLHDLDVG EICTVDPCKFFWCLDACTERPSPFTLL LLLRALGOGAMMSIDSQVFKEPKMSVEVLITRLPHMMSFLVD DYFRNVDKKPAERVSYPMTLEPSFFKKLOEGORAGEVGLY YVLHITKGRNKNALLRLIPGLVETFGDLAFGDIFLHLTONLAL LADEFFALEDLPSSFDOFFITTSPSFFKLOEGORAGEVGLY YVLHITKGRNKNALLRLIPGLVETFGDLAFGDIFLHLTONLAL LADEFFALEDLPSSFDOFFITTSPSFFKLOEGORAGEVGLY APSKLEALGKALEPTGGSGEAVKELYSQLGEKLEOLDHRKPSPA APSKLEALGKALEPTGGSGEAVKELYSQLGEKLEOLDHRKPSPA APALEDLPLSSFDAFPAPAL ULSSYTKGSSLLIKKEVHPTLSSKEKSIDDCLVQARGEVGLSTHAFVA WLLSPYTKGSSLLIKRKVHPTLSSKEKSIDDCLVQARGNSTAL VHFGKKGLINVAATAAVMAASKOGGALSERLKSFMODLTTIRGD GAPAPSGSPPPPGGSGASGKHGQPKMSRSAASSSASSSTA  HKLFGYYISTSFFFSSTRHISGFFHFFCNYTSSTTFLSSTRDHS CPHTHTCNYTSSTTIFLSSTRDHSCPTHTFCNYTSSTTFLSSTRDHS CPHTHTCNYTSSTTIFLSSTRDHSCPTHTFCNYTPRPIIRLSSC CPABLOTESSNOKKEVLSGFQVVLEDTVLFPEGGGPDDRGTIN DISVLRVTRRGEQADHTTOTPLDREGGGPDDRGTIN DISVLRVTRRGEQADHTTOTPLDREGGGPDDRGTIN DISVLRVTRRGEQADHTTOTPLDREGGVVLRVDMERFFHMOMI APEIGSETTLLFILVDEKKGGLFLALAGPPASVETLGFRVAREVL GKGAGKKGRPGGKATMSRNENGADLAQNYLNDMERFHMOMI APEIGSETTLLFILVDEKKGGLFLALAGPPASVETLGFRVAREVL GKGAGKKGRFGGKATMSRNENGADLAQNYLNGNYKIL OKNNINLIRDLAVHAHSLENSPDMGGVVLINGSKKEVLESLTY SLCCITKLSODYFYLLVGBALGGLSTALLFSAFRAM PPGRACSSPSFLRFQLDFYGVYFLAALADHLOAPTLYKLYCHYPY FLEGIALTYVGGLASCTLALSCULGESTCRAK PPGRACSSPSFLRFQLDFYGVYFLAALADHLOAPTLYKLYCHYPY FLEGIALTYCTLAGAGALACHWGENYDRGAFSTCLAGGLECLLSDR RVLLLGTTQALFFSVYFTIFVTHTYTDDPHGRENGSTUFSTFTAA	1		1	SSVGTGGGGTGGVGGGAGSEDSGDRGGTLGGGTLGPPSPPGAPS
6371 3 288 GVANMSTANNFGTKSFORPPDKGSFPLDHLGECKSFAKER- KFMKVSRPLELCYAPTKOPK  GVANMSTANNFGTKSFORPPDKGSFPLDHLGECKSFAKER- LHNNNFENALCRKESKEYLECRMERKLMLQEPLEKLGFGDLTSG KSEAKK  6372 2141 625 RVSATASEGKAEERYKKLEDLLEKSFSLVKMPSLOPVVMCVMKH LPKVPEKKLKLVMADKELYRACAVEVRRQIMODNOALFGDEVSF LLKGYILEKESALFSTELSVLHNFFSPSPKTRTGGEVVORLITM VGKNVKLYDMLVQFRTHJELTSTWAYCTLRAELLMSHIDLDVG EICTVDPCHKFTWCLDACIRERFVDSKRARELOGFLDGVKKGDE OVLGDLSMILCOPPFAINTLALSTVHLOELVGOETLOGVKKGDE OVLGDLSMILCOPPFAINTLALSTVHLOELVGOETLOFDSFDLL LLURLLALGOGAMDMIDSOVFKEPKMEVELITIFLIPMLMSFLVD DYFFNVDOKLPAEREAPVSYPNTIAGSTVHCHLOELVGOETLOFDSFDLL LLURLLALGOGAMDMIDSOVFKEPKMEVELITIFLIPMLMSFLVD DYFFNVDOKLPAEREAPVSYPNTIAGSTVGAUGLAUGHTHEPRV APSKLEALGKALEPTGGSGEAVKELYSGLGEKLEGLDHRKPSPA OAAETPALELLPSVVPAPAEL LADEFALEDPCSSLFDOFFLTASPKKENVHRHARKLLIHHHPRV APSKLEALGKALEPTGGSGEAVKELYSGLGEKLEGLDHRKPSPA OAAETPALELLPSVVPAPAEL VHFCKRGLNVAATAAVMAAKGOGALSERLESFSMODLTTIRGD GAPAPSGPPPPGGGGAGGKNGGPKMSFASSASSASSAS GAPAPSGPPPPTKGSSLFUKFVPHTLSSKKEEIDDCLVQAAKGRSVDAL VHFCKRGLNVAATAAVMAAKGOGALSERLESFSMODLTTIRGD GAPAPSGPPPPTKGSSLGVKRVVHPTLSSKKEEIDDCLVQAAKGRSVDAL VHFCKRGLNVAATAAVMAAKGOGALSERLESFSMODLTTIRGD GAPAPSGPPPPTGSGAGGKKEVLSGFOVLEDTHTFCNYTTSSTIFLSSTRDH CCHTFFCNYTSSTIFLSSTRDHSCPTHTFCNYTTSSTIFLSSTRDH SCPTHTFCNYTSSTIFLSSTRDHSCPTHTFCNYTPSTIFLSSTRDH SCPTHTFCNYTSSTIFLSSTRDHSCOPTHTSCNYTTSSTIFLSSTRDH SCSTULTTAVANHLFKLKTTSBLIGFFSAULTUTELTSPLOMAA IEGSVNEKIRDRLEVNYRELSLADDFVXDVKINGNNSTKIL OKNNLNLLRDLAVHIAHSLEDLOVIKTLGFEKGKNNTINLIFL SGRNUKMMERSHGTFKALTALLKCGAEDHVEAVKNI,ONSTKIL OKNNLNLLRDLAVHIAHSLENDSPOMGGVULHHRKEGDSFFMII ANEIGSESTLLFILVODEKGGGLFLLAGPPRAVETLIFPAVAEVL SCKGRLVKMMERSHGTFKALTALLKCAGAEDLVEAVKNI,ONSTKIL OKNNLNLLRDLAVHIAHSLEGGGGFRKCMPSSRSSHSGEGGLAMMSTT CCHTRERGOQVVRGFMINTTATLAPVALLAGGLLSRCTAK PPGRACSSPSFLRFGLDFYQVYFLALAADMLOAPTLYKLYCHYYF FLEGIALLYCGLASTVLFGLUASPCLLASCLIGLERCRAK PPGRACSSPSFLRFGLDFYQVYFLALAADMLOAPTLYKLYCHYPY FLEGIALLTYCGLASTVLFGLUASPCLASCLIGLERCRAK PPGRACSSPSFLRFGLDFYQVYFLALAADMLOAPTLYKLYCHYPY FLEGIALLTYCGLASTVLFGLUASPCLASCLIGLERCRAK PPGRACSSPSFLRFGLDFYQVYFLALAADMLOAPTLYKLYCHYPY F				PPEPGGETELVFRPHPLLVEKGEYCQTRYVKTTGNATVDHLSKY
6371 3 288 GVAMMSTAMMEGTKSFÖREPPDKGSFPLDHIGECKSFKENMC LHNNNFENALCRESKEYLECRMERKLMLQEPLEKLGFGDLTSG KSEAK  6372 2141 625 RVSAIASEGKAEERYKKLEDLLEKSFSLVKMPSLQFVVMCVMKH LPKVPEKKIKLVVADKEBLYRACAVEVRGTMONDALFGEVSP LLKQYILEKSALFSTEBSVHTRSFSPKTRRGGEVVGRLTM VGKNVKLYDWLQFLRTIFLERTRNYHYCTLRAELLMSLHHDLDUG EICTVDPCHKFTVACLDACIREFTUDSKRARELGGFLDGVKKGG QVLGDLSMILCDPFAINTLALSTVEHLQELUGGETLGPRUKGGE QVLGDLSMILCDPFAINTLALSTVEHLQELUGGETLGPRUKGGE QVLGDLSMILCDPFAINTLALSTVEHLQELUGGETLGPRUKGGE QVLGDLSMILCDPFAINTLALSTVEHLQELUGGETLGPLKKGGE QVLGDLSMILCDPFAINTLALSTVEHLQELUGGETLGPRUKGGE QVLGDLSMILCDPFAINTLALSTVEHLQELUGGETLGPLKKGGE QVLGDLSMILCDPFAINTLALSTVEHLQELUGGETLGPLKKGGE QVLGDLSMILCDPFAINTLALSTVEHLQELUGGETLGPLKKGGE QVLGDLSMILCDPFAINTLALSTVEHLQEGUTLGPLHLLTONLAL LADEFFALEDFCSSLPGFFLLAFGDIFTERCLITHLHAN APSKLEALQKALEPTGQSGEAVKELYSQLGEKLEGLDHKKPSPA QAAETPALELPLPSVAPAPI. GAPEKAPALSLPLPSVAPAPI.  6373 67 711 PSRAARASPARLDAWVSWITSRLUVALIFGTLYDEXYSYKAVKSK DIKEYVKMMYWI IFAHTTAETFTDIFTLONLYSTIFLSSTROMS UNLSPYTKGGSLLYRKFVHPTLSSKEKEIDDCLVQAKORSYDAL VHFGKKGLNVAATAAVMAASKGGGALSERRSFSMQDLITIRGD GAPAPSGPPPROSGRASCKHOQFMSRSASEASSSGTA  6374 535 2105 HKLFCSYLSTSEFPSSTTHHSCPTHTFCNYTSSTIFLSSTRDHS CPPHTTCNYTSSTIFLSSTRDHSCPTHSCNYTSSTIFLSSTRDHS CPPHTTCNYTSSTIFLSSTRDHSCPTHFCNYPPPITRLSS CPAELQTEGNSJOKKRULSGFOUTHTSCNYTSSTIFLSSTRDH SCHTTTCNYTSSTIFLSSTRDHSCPTHFCNYPPPITRLSS CPAELQTEGNSJOKKRULSGFOUTHTSCNYTSSTIFLSSTRDH SCHTTTCNYTSSTIFLSSTRDHSCPTHFCNYPPPITRLSS CPAELQTEGNSJOKKRULSGFOUTHTSCNYTSSTIFLSSTRDH SCHTTTCNYTSSTIFLSSTRDHSCPTHFCNYPPPITRLSS CPAELQTEGNSJOKKRULSGFOUTHTSCNYTSSTIFLSSTRDH SCHTTTCNYTSSTIFLSSTRDHSCPTHFCNYPPPITRLSS CPAELGTEGNSTARABENDGGPDDGRGTIN DISULRVTRRGEQADHFTQTPLDPSQQVLVRUWBERFPDHMQQH SCQHITTAVADHLKYLLKTTSWELGARFKSALELDTPSMTAEQVAA INGSVENSHCROTHVREISLDDPEVEQVSGRGLDDHARGVAN SCGHITAVADHLKYLLATGBGESTALLFAGEBANSTT VNNIBSVDSNMCCGTHVSNLSDLQVIKILGFEGKKNRTNLIFL GRKGAKKRPQKATKMSRMBAQALLQDYLYRKINGHTYL GRKGAKKRPQKATKMSRMBAQALLQDYLYRKINGHLYNGHY FLEGGIALLYVGGEKGGEKCKONSFRSEISGEGGLAAMSTT CCGRRRGQQVVRGPMMLTAALLARDGLAFANSKICLELISTRCRAK PPGRACSSPSFLRRQLDFVQVYFLALAADWLQAP	Ī			DGPFFPALPSI ECVERYOVETHA PGGGA TETTA DE CO
G371  GYAMMSTAMNFGTKSFOPREPBKGSFPLDHIGECKSFKEYMKC LHINNFENALCRKESKEYLECRMERKIMLQPLIEKIGFGLTSG KSEAKK  RVSAIASEGKAEGRYKKLEDLLEKSFSLVKMPSLQPVMCVMKH LPKVPPEKKLKLVVADKELYRACAVEVRRQIMODNOALFGDEVSP LLKQYILEKSALFSTELSVLHNFFSPSPKTRRGGEVVORLTEM VGKNVKLYDMVLOFLRTIFLEFRINVHYCTLRAELLMSLHDLDVG EICTVDPCHKFTACLDACIRERFVDSKRARELGGFLLGYKKKGE QVLGDLSMILCDFFAINTLASTVHLLGELUVGGETLPRDSPDLL LLERLLALGGGADWIDSQVEKEPKMEVELITHFLPMLMSFLUL DYTFNVDQKLPAEEKAPVSYDNTLPESFTKFLOEGRNACEVGLY VULHITKQRNKWALLRLIFLGFLUTGDLAFGDIFJHLITUNLAL LADEFALEDFCSSLFDGFFLTASPRKENVHHALRLLIHHPRV APSKLERLQKALEPTGGSGEAVKLLYSQLGEKLEQLDHRKPSPA QAAETALLSLPLPSVPAPAPL  6373  67  711  PSRAARASPARLDANVSNITSRLUVLLTGGTLYPAYYSYKAVKK MLSPYTKGSSLLYKKFVHPTLSSKEKEIDDCLVOAKDRSYDAL VHEKRGLINVAATAVMASKGOALSERLRSFSMODLTIRGD GAPAPSGPPPGGSGASKHOOPMSRSASESASSGTA  HKLFCSYISTSEFPSSTRHHSCPTHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHSCPTHTFCNYPRPITRLSSC CPAELCTGSNYSKKRULSGFQVLDTVLPFPEGGGPDDRGTIN DISVLRVTRRGEQADHFTOTLDDGSQVLWVDWERRPDHMQOH SCGHLTAVADHLFKLKTTSWELDTVLPFPEGGGPDDRGTIN DISVLRVTRRGEQADHFTOTLDDGSQVLWVDWERRPDHMQOH SCGHLTAVADHLFKLKTTSWELDTVLPFPEGGPDDRGTIN DISVLRVTRRGEQADHFTOTLDDGSQVLWVDWERRPDHMQOH SCGHLTAVADHLFKLKTTSWELGTVLTVLPFPEGGPDDRGTIN DISVLRVTRRGEGADHFTOTLDDGSQVLWVDWERRPDHMQOH SCGHLTAVADHLFKLKTTSWELGTENFVSATELDTPSMTAEQVAA IEQSVMEKIRDRLPVNVRELSLDDPEVEQVSGGLPDDHAGFIR VVNIBSVDSMCCGTHYNISDLQVIKILGFEGKKNNRTNLIFL SGRRVLKWMERSHGTERALTALLGAPPASVETLGPRAVEVL EGKGAGKKGRFGCKATKWSRMSAQALLODYISTGSAKE  AMAAATRPVRIPEAGGGEFRCWNPSRSHEGGGGAARSRT CGGRRRRGQQVVRGPTMLTATALARVGLLASPLUELSPLY FLEGGIALLYCGLASTVLEGIUSTUNDLGRKNSCVLFSLTY SLCCTTKLSOPYFULLVERALGGGLSTALLFSAFEAMYTHENVER HPFPARWYPATPARAAPWNIVLAVVAQVAAEAVASWIGLIFVAP FVAAIPLLALAGLASTVLEGIUSTALLFSAFEAMYTHENVER HPFPARWYPATPARAAPWNIVLAVVLOVAQVAAEAVASWIGLIFVAP FVAAIPLLALAGTLAAFRVENVERVILDMHLLSLAVLIVFSLIFMLTFSTSP	1			KEWKVSRPLELCVARTURDE
LHNNNFENLÖRRESKEYLECRMERKLMLQEPLEKLGFGDLTSG KSEKK KSEKK KSEKK KSEKK  6372  2141  625  RVSAIASEGKAEERYKKLEDLLEKSFSLVKMPSLQPVVMCVMKH LPKVPEKKLKLVVADKEBLYRACAVEVRRQIMODNOALFGEVEP LLKQYILEKSALFSTEBSVHMINFSPSPKTRRQGEVVORLTEM VGKNVKLYDWLQFLRTLFSTENDVHNYCTLRAELLMSLHDLDVG EICTVDPCHKFTWCLDACIREFUNDKRABELGGFLGVKKGQE QVLGDLSMILCDPFAINTLALSTVRHLQELVGQETLPRDSPDLL LLLELLALGQGAWMINDSQVEKBFKMEVEURLHFLIHHDRYLVD DYTFNVDQKLPAEERAPVSYDNTLPESFTKFLGGERMACEVGLY YVLHITKQRNKAALLRLLPGLVETTGGLAFGDIFLHLLIGNLAL LADEFALEDFCSSLEFGFFLLASKENVHRHALRLLHHHDRY APSKLEALQKALEPTQGSGEAVKELYSQLGEKLEQLDHRKPSPA QAAETPALELPLSVPAPAPL  6373  67  711  PSRARARSPARLDAWSNIISRLVVLIFGTLYPAYYSYKAVKSK DIKEYVKMMYNIIFALSTTAETFDIFLOKFPFYYELKIAFVA WLLSPYTKGSGLIVKRKYMPTISKSEKEIDDCLVOAKDRSYDAL VHEGKGLNVAATAAVMAASKQQALSERLRSFSMQDLTTIRGD GAPAPSGPPPPPGSGRASGKHQQPKMSASSENASSGTA  6374  535  2105  HKLFCSYISTSFFSSTRHHSCPTHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRDH SCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYTPSTIFLSSTRD HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYTPPPITRLSSC CPABLQTESSNOKKRVLSGFQVVLEDTVLPPEGGGQPDDRGTIN DISVLRVTRRGQADHFTQTPLDPGSQVURVDWERRFPHMQQH SQQHLITAVADHLFKLKTTSWELGTRSAIELDTSMTAEQVAA IEQSVNEKIRDRLPVNVRELSLDDPEVEQVSGRGLPDDHAGPIR VNNIBSVDSNMCGTHVSNILSJURVLKILGTERSKRINTINLIFL SGNRVLKMRESHGTEKALTALLKCGAEDHVEAVKKLQNSTKIL QKNNILLRDLAVHIAHSLENSPDMGGVVLLHRKEGDSEFMNII ANEIGSETLLFTVGDEKGGGLFLLAGPPASVETLGRVAREVL ECKGAGKKGRFQGKATKMSRBAQALLQDYLVKKLQCHYY FLEGGIALLYVGGLASTVLEGUNSSLVDWLGRKNSCVLFSLITY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFRAMYIHHERVER PFGRACSNPSFLRRQLDSTVLTVASSLVDWLGRKNSCVLFSLITY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFRAMYIHHERVER HFPPBEWIPPATFARAPAWNINLVANGVAABEAVANGVLIFSEND FVAAIPLLALAGALALRNWGENYDRQRAFSTCAGGIRCLLSDR RVLLLGTIQALFSEVIFITYFUMTEVLDDRAGPLGIFISSFMAA SLLGSTVLRINGSVRYLDRMHLHLSLAVULVUFSLIFMLTFSTSP	6371	3	288	
6372 2141 625 RVSAIASEGKAEGRYKKLEDLLEKSFSLVKMPSLQPVVMCVMKH LPKVPEKKLKLVVADKELYRACAVEVRRQIWQDNQALFGDEVSP LLKQYILEKESALFSTELSVLHNFFSPSKTRRQGEVVORLTEM VGRIVKLYDDVVLQFLETLEFRTNDVHYCTT.REALLMSLLDDVG EICTVDPCHKFTVCLDACIRERFUDSKRARELQGFLDGVKKGQE QULGDLSMILLOPFAINTLALSTVRHLQELVGGETLPRDSPDLL LLURLLALGGANDM.IDSQVFKEPKMEVELITRFLPMLMSFLVD DYTFNUDKLDAEEKAPEVTNLPESFTKFLQGEQRMACEVGLY YVLHITKQRNKNALLRLPGLVETFGDLAFGDIFHLLIGNLAL LADEFALEDFCSSLFDOFFLITASPRKENVHRHALRLIHLHPRV APSKLENLOKALBFTQGSGEAVKELYSQLGEKLEGLDHRKPSPA QAAETPALEDPLSSVFAPAPL  6373 67 711 PSRRARSPRALDAMWSWIISRLVVLIFGTLYPAYYSYKAVKSK DIKEYYKWMMYWIIFALFTTAETFTDIFLCWPFFYYELKIAFVA WLLSPYTKGSSLLYKRFVHPTLSSKEKEDDCLVOAKDRSYDAL VHFGKRGLAVAATAAVMAASKGQGALSEELREFSMODLTIRGD GAPAPSGPPPPGSGRASGHGQPKMSRSASESASSGTA HKLFCSYISTSEFPSSTRHSGCPTHFTCNYTSSTIFLSSTRDHS CPHTTCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRDH HCFCSYISTSEFPSSTRHSGOPVLEDTHTFCNYTSSTIFLSSTRDHS CPHTTCNYTSSTIFLSSTRDHSCPTHTFCNYTPSTIFLSSTRD HSCPTWTSCNYTSSTIFLSSTRDHSCPTHTFCNYTPSTIFLSSTR HSCPTWTSCNYTSSTIFLSSTRDHSCPTHTFCNYTPSTIFLSSTR DISVURVTRRGEQADHFTQTPLDPESGQVLVRVDMERRFDHMQQH SQQHLITAVADHLHFKLKTTSWLGRFRSALELDTPSMTAEQVYAA IEGSWBKIRDRLPWWRELSLDDPEVQVSGRGLPDDHAGPIR VVNIBAVDSMMCCGTHVSNLSDLQVVIKILGTEKKKKNRTNLIFL GRNRVLKWMERSHGTEKALTALLKGGADHVENKILDTSMTKLIL QRNNLMLERDLAVHIAHSLRNSPDMGGVVILHRKEGDEFFNNII AMEIGSESTILLFLUTVOBEGGGLFLLAGPPBYSTELGFRVÄEVLE GKGAGKKGRFGGKATKWSRRMEAQALLQDVISTGSAKE  CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSMPSTLRFGLDFYQYTFLALAADMLQAFYLYKLVQHYY FLEGGIALLYVGLASTVILFGLASSLIVDMLGRRNSCVLPSLITY SLCCITKLSQDYFVLLVGRASTLGGSTALLFSAFRAWYHEHVER HDFPAEWTPATFARAFFANHVLAVVNGVAAEAVASWIGLGFVAP FVAAIPLLALAGALALRNWGENTYDRQRAFSKTCAGGGLRCLLSDR RVLLLGTIQALFESVIFIFFVLWTYVLUDPHAPHGIFIFSSPMAA SLLGSSIYRIATSKRYHLQPHLLSALVVLIFSTSSPHAA	1			LHNNNFENALCRKESKEYLECRMERKI.MI.OPDI.EKI.GEODI.ECO
LPRYPEKKEKUVAADKELYRACAVEVRGUWONOALFGDEVSP LLKGYILEKESALFSTELSVLHNFSPSPKTRGGEVVORLTEM VGKNKLYDMVLOPERTLETKNUWYCTLRAELLMSLHOLDVG EICTVDPCHKFTWCLDACIRERFVDSKRARELQGFLDGVKKGGE QVLGDLSMILCOPFAINTLALSTVRHLDELVGQETLPRSSPDLL LLERLALGGGAWDMLDSGVFKEPKMEVELITRFLEMLMSFLVD DYTFNVDGKLPASEKARPVSYPNTLDESFTKFLQGGRMACEVGLY YULHTKGNRKMALLKLIPGBTFTGDLAFGDIFLHLLTGNLAL LADEFALEDFCSSLFDGFFLTASPRKENVHRRALRLLIHLHPRV APSKLEALGKALEPTCGSGEAVKELYSGLGEKLEGLDHRKPSPA OAAETPALELJPLSVPAPAPA  6373 67 711 PSRAARASPARLJAMVSWIISRLVVLIFGTLYPAYYSYKAVKSK DIKEYVKWMWYMYLIFALFTTAEFTDIFLCWPFFYYELKIAFVA WLLSPYTKGSSLLYRKFVHPTLSSKEKEIDDCLVQAKDRSYDAL VHEGKRGLAVAATAAVMAASKGQGALSERLESFSMQDLTTIRGD GAPASGPPPPGSGGRASGKHGGVKNSSASSASSGTA  1535 2105 HKLFCSYISTSEFPSSTRHSCPTHFFCNYTSSTIFLSSTRDHS CPHTTFCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRDHS CPHTTSCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRDHS CPHTTSCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRDHS CPHTTGCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRDHS CPHTTSCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRDHS CPARLQTEGSNOKKBULSGFQVVLEDFTUNFDGGGQDDRGTIN DISVLEVTRERGEQADHFTOTLDEGSQVLVEVDMERREPDHAQOH SCQHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA IEQSVNEKIRDRLPUNVERLSLDDPEVRQSGGGLPDDHAGPIR VNNIBGVDSNMCCGHVSNLSDLOVIKILGFEKKKNRTNLIFL SGNRVLKWMERSHGTEKALTALLKGGABDHVEAVKKLONSTKIL OKNINLIKELLAVILAVTAHLANGLADHVISTGSAKE ANAAATRFVENDEGGGGLFLLAGPPASVETLGFRVAEVL EGKGAGKKGRFGGKATKNSRMEAQALLQVISTGSAKE CPGRRRFGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSPLRFQLDFYQVYFLALAADMUQAFYLIKKLYCHYY FLEGGIALLYVCGLASTVLHGVLAVSSLVDMLGRRNSCVLPSLTY SLCCTIKLSQDYFVLLVGRALGGISTALLFSAFFAWYHEERURE HDFPAEWTPATFARAFANHVLAVVGAVAAFANSWIGLGPVAP FVAATPLLALAGALALRNWGENYDRQRAFSRTCAGGIRCLLSDR RVLLLGTITQAFFESVIFIFFVLWTPVLUDFROEPLGIFFSSFMAA SLLGSSLYRIATSKRYHLQPHALLSLAVLIVVFSLFMLTFSTSP			Ì	KSEAKK
LPKYPEKKLUVMADKELYRACAVEVRRQIMODNOALFGDEUSP LLKQYILEKESALFSTELSVIHNFFSPSFKTRRQGEVVQRLTRM VGKNYKLYDMVLQFLRTLFLRTRNVHYCTLRAELLMSLHDLDUG EICTVDPCHKFTMCLDACITERFYDSKRARBLQGFLDGVKKGQE QVLGDLSMILCDPPAINTLASTVHRLDGELVGGTLDFBSPDLL LLURLLALGQGAMDWIDSQVFKEPKMEVELITRFLPMIMSFLVD DYFFNVDOKLDAEKKAPVSYDNTLPESFTKFLQEQRMACEVGLY YVLHITKQRNKNALLRLJGGLSFTKLGEQRMACEVGLY YVLHITKQRNKNALLRLJGGLSFTKENVHRHALRLLHHLHPRV APSKLEALQKALBFTGGGGEAVKELYSQLGEKLEQLDHRKPSPA QAAETPALEDPLSSVPAPAPL  6373 67 711 PSRAARASPARLSAMVSWIISRLVVLIFGTLYPAYYSYKAVKSK DIKEYVKWMYWIIFALFTTAEFTFDIFLCAFPFFYYELKIAFVA WLLSPYTKGSSLLYRKFVHPTLSSKEKEIDDCLVQAKDRSYDAL VHEKRGLANVAATAAVMASKGQALSERLRSFSMQDLTTIRGD GAPAPSGPPPPGSGRASGKHQPKMSRSASSASSASSGTA  6374 S35 2105 HKLFCSYISTSEFPSSTRHHSCPTHTFCNYTSSTIFLSSTRDHS CPPHTTCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRDHS CPPHTTCNYTSSTIFLSSTRDHSCPTHTFCNYPRPIIRLSSC CPAELQTEGSNGKKEVLSGFQVVLURVDWERRFDHMQGH SQCHLITAVADHLFKLKTTSWELGRFRSATELDTPSMTAEQVAA IEGSVMEKLRDRLPVNYREISLDDPEVEQVSGRGLPDDHAGFIR VVNIEGVDSNMCCGTHVSNLSDLQVIKILGTERGKKRRTINLIFL SGNRVLKWMERSHGTKALTALLKCCAEDMVEAVKHQNSTKIL QNNNLNLIKBLAVHIAHSLMNSPDWGGVVLHRKEGDSEFMNII ANEIGSESTLLFLTVGDEKGGGLFLLAGPPASVETLGPRVAEVL EGKGAGKKGRFQCKATKMSRRMEAQALLQDYISTGSAKE  6375 1 1535 ATMAAATREVRLPEAGCEGREKGMPSRSRSHSGEGGLAMSRT CPGRPRRGQQVVRGPTMLVTAYLAAFVGLLASCLGLELSRCRAK PPGRACSNPSFLFFQLDFYQVFLALAADMLQAPYLYKLYQHYY FLEGQIALLYVCGLASTULFGVASSLVOWLGRKNSCVLFESLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFFAMYIHEHVER HDFPFAEWIPATFARAAFMULAVVAVAGAAVASNIGLGPVAP FVAATPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTQALFESVIFIFVFLMTEVLDHGRAPGIFFSSFMAA SLLGSSLYRIFTSTEPFINGERYFTFTFTFTSSFMAA SLLGSSLYRIFTSTEPFINGERYFTSSFFTFTGSFFTRAMYTHENTER ASLLGSSLYRIFTSTEPFINGERYFTSFTFTTFTTSSFTMAA SLLGSSLYRIFTSTSFFTFTTFTTTTTTTTTTTTTTTTTTTTTTTTTT	6372	2141	625	RVSAIASEGKAEERYKKLEDLLEKSFSLVKMPSLOPVVMCVMKH
LLKQYILEKESALESTELSVLHNFFSPSPKTRRQGEVVQRLTRM VGKNVKLYDWVQCELTILEREILMSLHDLDVG EICTVDPCHKFTWCLDACIRERFVDSKRARELQGFLDGVKKQQE QVLGDLSMILCDPCHKFTWCLDACIRERFVDSKRARELQGFLDGVKKQQE QVLGDLSMILCDPCHFTWLLDACIRERFVDSKRARELQGFLDGVKKQQE QVLGDLSMILCDPCHIVELOGQETLPRDSPDLL LLERLALQQADMMIDSQVKEPKREVELTRFIPMMSFLVD DYFFNVDQKLPAEKAPVSYBTILDESFTKFLQEQRMACEVGLY YVLHITKQRNKNALIRLIPGLVETFGGLAFGGIFHLLITGNLAL LADEFALEDFCSSLFDGFFTTASPKENVHRHARRLIHHLHRV APSKLEALQKALBFTGQSGEAVKELYSQLGEKLEQLDHRKPSPA QAAETPALELPLSVPRPAPI.  6373 67 711 PSRAARASPARLPAMVSWITSRLVVLIFGTLYPAYYSVKAVKSK DIKEYVKWMWWIIFALFTTAEFFTDIFLCWPFFYYELKIAFVA WLLSPYTKGSSLLYRKFVHPTLSSKEKEIDDCLVQAKDRSYDAL VHEGKRGLANVAATAAVMAASKQQGALSERLRSFSMQDLTTIRGD GAPAPSGPPPPPPGGRASGKIGQPKMSRASASSASSGTA  6374 S35 2105 HKLFCSYISTSEFPSSTRHISCPTHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRDH SCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYTPSTIFLSSTRDH CPTHTFCNYTSSTIFLSSTRDHSCPTHTFCNYTPSTIFLSSTRDH SCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYTPRIFLISLSC CPABLQTEGSNGKKRULSGFQVULEDTVLFPEGGQDPDRGTIN DISULRVTRRGEQADHFTQPLDPGSQULVRVDWERRFDHMQOH SCQHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA IEQSVNEKIRDRLPPWVRELSLDDPSEVQVSGRALPDDHAGPIR VNNIBEVDSNMCCGTHVSNISDLQVIKILGTERGKKNRTNLIFL SGNRVLKWMERSHGTEALTALLKCGAEDHVEAVKKI,QNSTKIL OKNNLNLERDLAVHIAHSLENSPDWGCVVILIRKEGDSEFMNII ANEIGSESTLLFLTVGDEKGGGLFLLAGPPASVETLGPRVAEVL EEKGAGKKGRFQGKAFKMSRRMERAGALLQDYISTGSAKE  1 1535 AMMAATREVNIPEAGCEGERECWNPSTSSHSGEGGLAAMSRT CPGRRRRGQQVVRGPTMLVTAYLAAFVGLLASCLGLELSRCRAK PPGRACSNPSFLEFQLDFYQVFLALAADWLQAFLYKLVQHYY FLEGGIATLYVCGLASTULFGLASSLVDWLGRKNSCVLJESLTY SLCCLTKLSQDYFVLLVGRALGGLISTALLFSAFFAMYIHEHVER HDFPFAWIPATARAAFNHNVLAVVAQVAAAAAVASNIGLGPVAP FVAATPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSIR RVLLLGTTQALFESVIFIFVFLWTEVLDPHGAPGIIFSSFPMA SLLGSSLYRITGTQAFESVIFIFVFLWTEVLDPHGAPGIIFFSSFPMA SLLGSSLYRITGTQAFESVIFIFVFLWTEVLDPHGAPGIIFFSSFPMA				LPKVPEKKLKLVMADKELYRACAVEVRROIWODNOALFGDEVSP
VGKNVKLYDMVLOGLRTLFIRRTRNVHYCTLRABELLMSLHDLDUG EICTVDPCHKFTWCLDAGIRFFVDSKRARELQGFLDGVKKQQE QVLGDLSMILCDPFAINTLALSTVRHLQELVGQETLPRDSPDLL LLERLLALGGGAMDMIDSQVFKEPKMEVELITRFLPMLMSFLVD DYTFNVDQKLDAEKARPVSTITLPESFTKFLOGGRAMACEVGLY YVLHITKQRKNALLRLLPGLVETTFGDLAFGDIFLHLLTGNLAL LADEFALEDFCSSLFDGFFLTASPRKENVEHHARRLLTHLHERV APSKLEALQKALBFTCGSGEAVKELYSGLGEKLEOLDHRKFSPA QAAETPALELPLSSVPAPAPI.  6373 67 711 PSRARARSPARLSAMVSMIISRLUVLIFGTLYPAYYSYKAVKSK DIKEYVKWMMYWIIFALFTTAETFTDIFLCAFFFYYSELKIAFVA WILSPYTKGSSLLYRKFVHFTLSSKEKEIDDCLUQAKDRSYDAL VHERKBGLHVAATAAVMAASKGQGALSERLRSFSMQDLTTIRGD GAPAPSGPPPPGSGRASGKHGQPKMSRSASESASSGTA  6374 535 2105 HKLFCSYISTSFFPSSTRHHSCPTHTFCNYTSSTIFLSSTRDHS CPTHTTCNYTSSTIFLSSTRDHSCPTHTFCNYTPSTIFLSSTRD HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYTPSTIFLSSTR HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYTPSTIFLSSTC CPARLOTEGSNGKKEVLSGOVVLEDTVLPPEGGGQPDDRGTIN DISVLRVTRRGEQADHFTQTPLDPGSQVLVRVDWERRFDCHMQQH SQCHLITAVADHLFKLKTTSWELGRRFSATELDTPSMTAEQVAA IEGSYMEKIRDRLPVWWRERSLDDPEVEGYGRGLPDDHAGP IR VVNIB80VDSNMCCGTHVSNLSDLQVIKILGTEKGKKNRTNLIFL SGNNVLKWMERSHGTEKALTALLKCAGEDHVEAVKKI,QNSTKIL QKNNLMLERLAVHIAHSLRNSPDWGGVVLHRKEGGSEFMNII AMEIGSETILFITVGDEKGGGLFLLAGPPASVETLGPRVAEVL EKKGACKKGRFQCKATKMSRRMEAQALLQDYISTQSAKE  6375 1 1535 AIMAATRFVRLPEAGCEGRERCWNPSRSRSHSGEGGLAAWSRT CPGRRRRGQQVVRGPTMLVTAYLLAFVGLLASCLIGLELSRCRAK PCGRACKNGFFLKFLDTGVVYFLALAADMLQAPYLYKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVWMLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFFAMYIHEHVER HDFFPAEWIPATFARAAFMYLLAVVAVAGAAVASMIGLGPVAP FVAATPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPCIFFSSFMAA SLLGSSLYRIATSKRYHLQPHLSLAVLIVVVSSLFMLIFFSTSP				LLKQYILEKESALFSTELSVLHNFFSPSPKTRROGEVVORLTRM
QVIGDLSMILCDPFAINTLALSTVRHLQELVGGETLPRDSPDLL LLIRLLALGQGAMDMIDAGOPKEPKMEVELITRFLPMLMSPLVD DYTFNVDQKLPAEKAPVSYPNTLPESFTKFLGEQRMACEVGLY YVLHITKQRNKNALLRLPGLUFFGDLAFGDIFLHLLTGNLAL LAADEFALEDFCSSLFDGFFILTASPRKENVRHALRLHHLHPRV APSKLEALQKALEPTGGSGEAVKELYSQLGEKLEQLDHRKPSPA APSKLEALQKALEPTGGSGEAVKELYSQLGEKLEQLDHRKPSPA QAAETPALELPLPSVPAPAPAPL UKLSPYTKGSSLLYRKFVPPTLSSKEKEIDDCLVQAKDRSYDAL VHFGKRGLNVAATAAVMAASKGQGLSERLRSFSMQDLTTIRGD GAPAPSGPPPPGSGRASGKHGGPKMSRSASESASSGTA HKLGSYISTSEFPSSTRHSCPTHFTCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHSCPTHTFCNYTPSTIFLSSTRD HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYPRPIIRLSSC CPABLOTEGSNKKEVLSGFQVVLEDTVLPPEGGGPDDRGTIN DISVLRVTRRGEQADHFTQTPLDPGSQVLVRVDWERRFDHMQQH SCQHLITAVADHLFKLKTTSNELEDFPSMTAEQVAA IEQSVMEKIRDRJPVNYRELSLDDPEVEQVSGRGLPDDHAGPIR VVNIEGVBSMCCGTHVSNLSDLQVIKLIGFERGKKRNTTNLIFL SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKIQNSTKIL QKNNLNLLERLAVHIANSLRNSPDWGGVVILHRKEGDSEFMNII AMEIGSESTLLFITVGDEKGGGLFLLAGPPASVETLGPRVAEVL EKKGRAKKGRPQGKATMSRRMEAQALLQDYISTGQSAKE  6375 1 1535 AIMAAATRPVRLPEAGCEGRERCWNPSRSRSHSGEGGLAAWSRT CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFGLDGUSTALLFSAFEAWYIHEHVER LEGGIAILLYVCGLASTVLFGLVAASSLVDMLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGISTALLFSAFEAWYIHEHVER HUFPFAEWI PATFFARAFWINVLAVVAGVAEAVASWIGLGDPVAP FVAAT PLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFFFLHTPVLDDPHGABIGLIFSSFMAA SLLGSSLYKIATSKRYHLQPMHLLSLAVIIVFSLFMLTFSTSP				VGKNVKLYDMVLQFLRTLFLRTRNVHYCTLRAELLMSLHDLDVG
LLERLALGOGAMDMIDSQVFKEPKMEVELITRFLPMLMSFLVD DYTFNUDQKLPABEKAPVSYPNTLPES FTKFLQEQRMACEVGLY YVLHITKQRNKNALLRLLFGLVETTFGDLAFGIFLHLLTGNLAL LADEFALEDFCSSLFPGFFITASFRKENVHRHALRLLHLHEPRV APSKLEALQKALEPTGQSGEAVKELYSQLGEKLEQLDHRKPSPA QAAETPALELPLPSVPAPAPL  6373 67 711 PSRAARASPARLJAMVSWITSRLVVLIFGTLYPAYYSYKAVKSK ULSPYTKGSSLLYRKFVHPTLSSKEKEIDDCLVQAKDRSYDAL VHFGKRGLNVAATAAVMAASKGQALSERLKSFSMQDLTTTRGD GAPAPSGPPPPGSGRASGKHGQPKMSRSASSASSGTA 6374 535 2105 HKLFCSYISTSEFPSSTRHHSCPTHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHSCPTHTFCNYPRPIHRLSSC CPARLOTEGSNGKKEVLSGFQVVLEDTVLFPEGGQPDDRGTIN DLSVLRVTRRGQADHFTQTPLDPGSQVLVRVDWBERFFDHMQQH SQQHLITAVADHLFFKHKTTSWELGRFRSAIELDTPSMTAEQVAA IEQSWEKIRDRLPVNVRELSLDDPEVEQVSGRGLPDDHAGPIR VVNIEGVDSNMCCGTHVSNLSDLQVIKILGFEKGKKNRTNLIFL SGNRVLKWMERSHGTEKALTALKCGAEDHVEAVKKLQNSTKIL OKNNLMLRDLAVHIAHSLRNSPDWGGVVLLHRKEGDSEFMNII ANEIGSETLLFLTVGDEKGGGLFLLAGPPASVETLGPRVAEVL OKNNLMLRDLAVHIAHSLRNSPDWGGVVLLHRKEGDSEFMNII ANEIGSETLLFLTVGDEKGGGLFLLAGPPASVETLGPRVAEVL COKNLMLLRDLAVHIAHSLRNSPDWGGVVLLASCLGLELSRCRAK PPGRACSNSSFLRPQLDFYQVYFLALAADMLQAPYLYKLYGHYY FLEGGIAILYVCGLASTULFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYTHHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGFVAP FVAAIPLLALAGALALRNWGENYDRQRAFSTCAGGLRCLLSDR RVLLLGTIQALFESVIFITVFUTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPPHLLSLAVLTUPFSLFMITFSTSP	1			EICTVDPCHKFTWCLDACIRERFVDSKRARELQGFLDGVKKGQE
DYTFNUDCKLPAEEKAPUSYPNTLPESFIKFLQEQRMACEUGLY YVLHITKQRNKMALLRLLPGLVETFGDLAFGDI FLHLLTGNLAL LADEFALEDFCSSLFDGFFLTASPIKENVHRHALRLLHHLHPRV APSKLEALQKALEPTGGGEAVKELYSQLGEKLEQLDHRKPSPA QAAETPALELPLPSVPAPAPIL  6373 67 711 PSRAARASPARLJAMVSWIISRLVVLIFGTLYPAYYSYKAVKSK DIKEYVKWMMYWIIFALFTTAEFFTDI FILGWPFFYYELKIAFVA WLLSPYTKGSSLLYRKFVHPTLSSKEKEIDDCLVQAKDRSYDAL VHEGKRGLNVAATAAVMAASKGQGALEERLRSFSMQDLTTIRGD GAPAPSGPPPPGGGRASGKHGQPKMSRSASESASSGTA  6374 535 2105 HKLFCSYISTSEFPSSTRHHSCPTHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHSCPTHTFCNYPRPIIRLSSC CPHALQTEGSNGKKEVLSGFQVVLEDTVLPFEGGGQPDDRGTIN HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYPRPIIRLSSC CPABLQTEGSNGKKEVLSGFQVVLEDTVLPFEGGGQPDDRGTIN DISVLKVTRRGEQADHFTQTPLDPGSQVULVBWERFFDHMQQH SQCHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA IEQSVNEKIRDRLPVNVRELELDDPEVEQVSGRGLPDDHAGPIR VNNIBGVDSNNCCGTHVSNLSDLOVIKILGTEKGKKNRTKIL IFL SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKLQNSTKIL QKNNLNLLRLLAVHIAHSLRNSPDWGGVVLHRKRGDSSFMNII ANEIGSETLLFLTVGDEKGGLFFLLAGPPASVETLGPRVAEVL EGKGAGKKGRFQGKATKMSRRMEAQALLQDVISTQSAKE  6375 1 1535 AIMAAATRPVRLPBAGCEGEREKWPSRSRSHSGEGGLAAWSRT CPGRPRRPRGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADMLQAPYLYKLYQHYY FLEGGIAILYVCGLASTULFGLVSASLVDMLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHULAVVAGVAAEAVASWIGLGFVAP FVAAIFLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFITVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPPHLLSLAVLIVVFSLFMLTFSTSP	}			QVLGDLSMILCDPFAINTLALSTVRHLQELVGQETLPRDSPDLL
APERGENTUS NEUTRINGER STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL STEEL ST	İ			LLLRLLALGQGAWDMIDSQVFKEPKMEVELITRFLPMLMSFLVD
LADEFALEDFCSSLFDGFFLTASPRIENVHRHALRLLIHLHPRV APSKLEALQKALEPTGQSGEAVKELYSQLGEKLEQLDHRKPSPA QAAETPALELPLPSVPAPAPL  6373 67 711 PSRAARASPARLJAMVSWIISRLVVLIFGTLYPAYYSYKAVKSK DIKKYVKWMMYWIIFALFTTAEFFTDIFLCWFPFYYELKIAFVA WLLSPYTKGSSLIYRKFVHPTLSSKEKEIDDCLVQAKDRSYDAL VHFCKRCINVAATAAWMAASKGQGALSERLRSFSMQDLTTIRGD GAPAPSGPPPPGSGRASKIGQPKMSRSASESASSSGTA  6374 S35 2105 HKLFCSYISTSEFPSSTRHHSCPTHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHSCPTHTFCNYPPPITRLSSC CPAELOFGESNGKVLSGFQVULLDTVLPPEGGGQPDDRGTIN DISVLRVTRRGEQADHFTQTPLDPGSQVLWVUWERRFDHMQQH SQCHLITAVADHLFKLKTTSWELGRFRSATELDTPSMTAEQVAA IEGSVEKKIRDRLPVWYRELSLDDPEVEQVSGRGLPDDHAGPIR VVNIEGVDSNMCCGTHVSNLSDLOVIKILGTEKGKKNRTNLIFL SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKIQNSTKIL QKNNLNLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII ANEIGSESTLLFTUTVDEKGGGLFILLAGPPASVETLGFSVAEVL EGKGAGKKGRPGKATKMSRRMEAQALLODYISTQSAKE  6375 1 1535 AIMAAATREVRLPEAGCEGRERCWNPSRSRSHSGEGGLAAWSRT CPGRPRRPGQQVVRGPTMLVTAYLLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAFYLIYKLYQHYY FLEGGIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSITY SLCCLTKLSQDYFTLLVGRALGGLSTALLFSAFFAWYIHEHVER HDFPAEWIPATFARAAFWHVLLNVNGVAAEAVASWICLGPVAP FVAATFLLALAGALARNIGENTDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFFYLWTPVLDPHGAPLGIIFSSFNAA SLLGSSLYRTATSKRYHLQPNHLLSLAVLIVVFSLFMLIFSTSP				DITFNODQKLPAEEKAPVSYPNTLPESFTKFLQEQRMACEVGLY
APSKLEALQKALBPTGGSGEAVKELYSQLGEKLEQLDHRKPSPA QAAETPALELPLPSVPAPAPL  6373 67 711 PSRARASPARLZAMVSWIISRLVVLIFGTLYPAYYSYKAVKSK DIKEYVKWMMYWIIFALFTTAETFTDIFLCWFPFYYELKIAFVA WLLSPYTKGSSLLYRKFYHPTLSSKEKEIDDCLVQAKDRSYDAL VHFCKRGINVAATAAVMAASKGQALSERLRSFSMQDLTTIRGD GAPAPSGPPPPGSGRASGKHGQPKMSRSASESASSGTA  6374 535 2105 HKLFCSYISTSEPPSSTRHHSCPTHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHSCPTHTFCNYTPSTIFLSSTRDHS CPHTTSCNYTSSTIFLSSTRDHSCPTHTFCNYTPFIIRLSSC CPAELQTEGSNGKKEVLSGFQVVLEDTVLPPEGGGQPDDRGTIN DISVLRVTRGEQADHFTQTPLDPGSQVLVRVDWERRFDHMQQH SQQHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA IEQSVNEKIRDRLPVNVRELSLDDPEVEQVSGRGLPDDHAGPIR VVNIEGVDSNMCCGTHVSNLSDLQVIKILGTEKGKKNRTNLIFL SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKIQNSTKIL QKNNLNLLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII ANEIGSESTLLFLTVGDEKGGGLFLLAGPPASVETLGPRVAEVL EGKGAGKKGRFQGKATTKMSRRMEAQALLQDYISTQSAKE CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPYLYKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVDMLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYHEHENER HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGFVAP FVAAIPLLALAGALALRNWGENYDRGRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVVLWFPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPHHLLSLAVLIVVFSLFMLTFSTSP				LADEFALEDECCCI EDGERI WAS CRAVEN TO THE TOTAL TOTAL
GAAETPALELPESVPAPAPI  PSRAARASPARLSAMVSWIISRLVVLIFGTLYPAYYSYKAVKSK DIKEYVKMMYWIIFALFTTAETFTDIFLCWFPFYYELKIAFVA WLLSPYTKGSSLLYRKFVHPTLSSKEKEIDDCLVQAKDRSYDAL VHFGKRGLNVAATAAVMAASKGQALSERLRSFSMQDLTTIRGD GAPAPSGPPPPGGGRASGKHGQPKMSRSASSASSGTA  6374  535  2105  HKLFCSYISTSEFPSSTRHHSCPTHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHSCPTHTSCNYTSSTIFLSSTRDH HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYPRPIIRLSSC CPAELQTEGSNGKKEVLSGFQVVLEDTVLFPEGGGQPDDRGTIN DISVLRYTRRGEQADHFTQTPLDPGSQVLVRVDWERRFDHMQQH SCQHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA IEQSVNEKIRDRLPVNVREISLDDPEVEQVSGRGLPDDHAGPIR VVNIEGVDSNMCCGTHVSNLSDLQVIKILGTEKGKKNRTNLIFL SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKIQNSTKIL QKNNLNLRDLAVHIAHSLNSPDWGGVVILHRKEGDSEFMNII ANEIGSESTLLFLTVGDEKGGLFLLAGPPASVETLGPRVAEVL EGKGAGKKGRFQCKATKMSRRMEAQALLQDYISTQSAKE  6375  1  1535  AIMAATTPVRLPEAGCEGRERCWNPSRSRSHSGEGLAAWSRT CPGRPRRPGQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPYLYKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGFVAP FVAAIFLLALAGALARNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPHHLLSLAVLIVVFSLFMLTFSTSP		1		APSKLEDI OKAL EPTGOSGENUKEL MOOLGENI DOLDANI DOLDANI
6373 67 711 PSRAARASPARLJAMVSWIISRLVVLIFGTLYPAYYSYKAVKSK DIKEYVKWMYWIIFALFTTAETFTDIFLCGPFFYYELKIAFVA WLLSPYTKGSSLLYRKFVHPTLSSKEKEIDDCLVQAKDRSYDAL VHFGKRGLNVAATAAVMAASKGQGALSERLRSFSMQDLTTIRGD GAPAPSGPPPPGSGRASGKIGQPKMSRSASESASSSGTA  6374 535 2105 HKLFCSYISTSEFPSTRHHSCPTHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHSCPTHTSCNYTSSTIFLSSTRDHS HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRD HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRD HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYPRPIIRLSSC CPAELQTEGSNGKKEVLSGFQVVLEDTVLPPEGGQPDDRGTIN DISVLRVTRREGQADHFTQTPLDPGSQVLVRVDWERFDHMQQH SGQHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA IEQSVNEKIRDRLPVNVRELSLDDPEVEQVSGRGLPDDHAGPIR VVNIEGVDSNMCCGTHVSNLSDLQVIKILGTEKGKKNRTNLIFL SGNRVLKWMERSHETEKALTALLKCGAEDHVEAVKKLQNSTKIL QKNNLNLLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMMII ANEIGSESTLLFTUTGDEKGGGLFILAGPPASVETLGPRVAEVL EGKGAGKKGRFQGKATKMSRRMEAQALLQPVISTGSAKE AIMAAATRPVRLPEAGCEGGRERCNNPSRSRSHSGEGGLAAWSRT CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAFYLIYKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVCRALGGLSTALLFSAFFAWYIHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP FVAAIFLLAAGALALRWGGENTDRQRAFSRTCAGGIRCLLSDR RVLLLGTIQALFESVIFIFFYLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIAACALALRWGGENTDRQRAFSRTCAGGIRCLLSDR RVLLLGTIQALFESVIFIFFYLWTPVLDPHGAPLGIIFSSFMAA	1			OAAETPALELPI,PSVPAPAPI.
DIKEYVKWMYWIIFALFTTAEFFTDIFLCMFPFYYELKIAFVA WLLSPYKGSSLLYRKFVHPTLSKEKEIDDCLVQAKDRSYDAL VHEGKRGLNVAATAAVMASKGQGALSERLRSFSMQDLTTIRGD GAPAPSGPPPPPGSGRASGKHGQPKMSRSASESASSSGTA  6374  535  2105  HKLFCSYISTSEFPSSTRHHSCPTHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRDHS HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRD HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYPRPIIRLSSC CPABLQTEGSNGKKEVLSGFQVVLEDTVLPPEGGGQPDDRGTIN DISVLRVTRRGEQADHFTQTPLDPGSQVLVRVDWERRFDHMQQH SCQHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA IEQSVNEKIRDRLPVNVRELSLDDPEVEQVSGRGLPDDHAGPIR VVNIEGVSNMCCGTHVSNLSDLQVIKTLGTEKGKKNRTNLIFL SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKI,QNSTKIL QKNNLNLLRDLAVHIAHSLRNSPDWGGVVILHRREGDSEFMNII ANEIGSESTLLFLTVGDEKGGGLFFLLAGPPASVETLGPRVAEVL EGKGAGKKGFQGKATKMSRRMEAQALLQDYISTQSAKE  1 1535  AIMAAATRPVRLPEAGCEGRERCWNPSRSRSHSGEGGLAAWSRT CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADHQAPYLYKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVDMLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP	6373	67	711	PSRAARASPARLPAMVSWIISRLVVI.I FGTT.VDAVVCVVAUVCV
### WILSPYTKGSSLLYRKFVHPTLSSKEKEIDDCLVQAKDRSYDAL VHFGKRGLNVAATAAVMAASKGQGALSERLRSFSMQDLTTIRGD GAPAPSGPPPPGSGRASGKHGQPKMSRSASESASSGTA  6374 535 2105 HKLFCSYISTSEFPSSTRHHSCPTHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDH HSCPTHTSCNYTSSTIFLSSTRDH CCPABLQTEGSNGKKBVLSGFQVVLEDTVLFPEGGGQPDDRGTIN DISVLRVTRRGEQADHFTQTPLDPGSQVLVRVDWERRFDHMQQH SCQHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA IEQSVNEKIRDRLPVNVRELSLDDPEVEQVSGRGLPDDHAGPIR VVNIEGVOSNMCCGTHVSNLSDLQVIKILGTERGKKNRTNLIFL SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKI.QNSTKIL QKNNLNLLERDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII ANEIGSESTLLFLTVGDEKGGGLFLLAGPPASVETLGPRVAEVL EGKGAGKKGRFQGKATKMSRRMEAQALLQDYISTQSAKE  6375 1 1535 AIMAAATRPVRLPEAGCEGRERCWNPSRSRSHSGEGGLAAWSRT CPGRPRRFGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPYLYKLYQHYY FLEGQIATLYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFFAWYIHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPHHLLSLAVLIVVFSLFMITFSSSP	1			DIKEYVKWMMYWIIFALFTTAETFTDIFLCWFDFYVELKIAFWA
6374 535 2105 HKLFCSYISTSEFPSSTRHHSCPTHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRDH HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYPRPIIRLSSC CPABLQTEGSNGKKEVLSGFQVVLEDTVLFPEGGQQPDDRGTIN DISVLRVTRGEQADHFTQTPLDPGSQVLVRVDWERRFPHMQQH SCQHLITAVADHLFKLKTTSWLLGRFRSAIELDTPSMTAEQVAA IEQSVNEKIRDRLPVNVRELSLDDPEVEQVSGRGLPDDHAGPIR VVNIEGVDSNMCCGTHVSNLSDLQVIKILGTEKGKKNRTNLIFL SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKI,QNSTKIL QKNNLNLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII ANEIGSESTLLFLTVGDEKGGGLFLLAGPPASVETLGPRVAEVL EGKGAGKKGRFQGKATKMSRRMEAQALLQDYISTQSAKE AIMAAATREVRLPEAGCEGRERCWNPSRSRSHSGEGGLAAWSRT CPGRPRRPGQQVVRGPTMUVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPYLYKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPNHLLSLAVLIVVFSLFMLTFSTSP				WLLSPYTKGSSLLYRKFVHPTLSSKEKEIDDCLVOAKDRSVDAI.
6374 535 2105 HKLFCSYISTSEFPSSTRHHSCPTHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRD HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYPRPIIRLSSC CPABLQTEGSNGKKEVLSGFQVVLEDTVLFPEGGGQPDDRGTIN DISVLRVTRRGEQADHFTQTPLDPGSQVLVRVDWERRFDHMQQH SCQHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA IEQSYNBKIRDRLPVNVRELSLDDPEVEQVSGRGLPDDHAGPIR VVNIEGVDSNMCCGTHVSNLSDLQVIKILGTEKGKKNRTNLIFL SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKIQMSTKIL QKNNLNLLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII ANEIGSESTLLFLTVGDEKGGGLFLLAGPPASVETLGPRVAEVL EGKGAGKKGRFQGKATKNSRRMEAQALQDYISTQSAKE  1 1535 AIMAAATRPVRLPEAGCEGRERCWNPSRSRSHSGEGLAAWSRT CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPYLYKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLAVVGVAAEAVASWIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPNHLLSLAVLIVVFSLFMLTFSTSP				VHFGKRGLNVAATAAVMAASKGQGALSERLRSFSMODLTTIRGD
HKLFCSYISTSEFPSSTRHHSCPTHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHSCPTHTSCNYTSSTIFLSSTRD HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTSCNYTSSTIFLSSTRD HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYPRPIIRLSSC CPABLQTEGSNGKKEVLSGFQVVLLDTVLPPEGGGQPDDRGTIN DISVLRVTRRGEQADHFTQTPLDPGSQVLVRVDWERRFDHMQQH SQQHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA IEQSVNEKIRRPLPVNVRELSLDDPEVEQVSGRGLPDDHAGPIR VVNIEGVDSNMCCGTHVSNLSDLQVIKILGTEKGKKNRTNLIFL SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKLQNSTKIL QKNNLNLLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII ANEIGSESTLLFLTVGDEKGGGLFLLAGPPASVETLGPRVAEVL EGKGAGKKGRFQGKATKMSRRMEAQALLQDYISTQSAKE AIMAAATRPVLPEAGCEGRERCWNPSRSRSHSGEGGLAAWSRT CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPYLYKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTTQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP		20.00		GAPAPSGPPPPGSGRASGKHGOPKMSRSASESASSSGTA
CPTHTFCNYTSSTIFLSSTRDHSCPTHTSCNYTSSTIFLSSTRD HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYPRPIIRLSSC CPABLQTEGSNGKKEVLSGFQVVLEDTVLFPEGGQPDDRGTIN DISVLRVTRRGEQADHFTQTPLDPGSQVLVRVDWERRFDHMQQH SCQHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA IEQSVNEKIRDRLPVNVRELSLDDPEVEQVSGRGLPDDHAGPIR VVNIEGVDSNMCCGTHVSNLSDLQVIKILGTEKGKKNRTNLIFL SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKI,QNSTKIL QKNNLNLLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII ANNEIGSESTLLFLTVGDEKGGGLFLLAGPPASVETLGPRVAEVL EGKGAGKKGRFQGKATKMSRRMEAQALLQDYISTQSAKE  AIMAAATRPVRLPEAGCEGRERCWNPSRSRSHSGEGGLAAWSRT CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPYLYKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLAVVNGVAAEAVASWIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPNHLLSLAVUIVVFSLFMLTFSTSP	6374	535	2105	HKLFCSYISTSEFPSSTRHHSCPTHTFCNYTSSTIFLSSTRDHS
CPARLQTEGSNGKKEVLSGFQVVLEDTVLFPEGGGQPDDRGTIN DISVLRVTRRGEQADHFTQTPLDPGSQVLVRVDWERRFDHMQQH SCQHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA IEQSVNEKIRDRLPVNVRELSLDDPEVEQVSGRGLPDDHAGPIR VVNIEGVDSNMCCGTHVSNLSDLQVIKILGTEKGKKRRTNLIFL SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKI,QNSTKIL QKNNLNLLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII ANEIGSEETLLFLTVGDEKGGGLFLLAGPPASVETLGPRVAEVL EGKGAGKKGRFQGKATKMSRRMEAQALLQDYISTQSAKE CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPYLYKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPNHLLSLAVLIVVFSLFMLTFSTSP				CPTHTFCNYTSSTIFLSSTRDHSCPTHTSCNYTSSTIFLSSTRD
DISVLRVTRRGEQADHFTQTPLDPGSQVLVRVDWERRFDHMQQH SCQHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA IEQSVNEKIRDRLPVNVRELSLDDPEVEQVSGRGLPDDHAGPIR VVNIEGVDSNMCCGTHVSNLSDLQVIKILGTEKGKKNRTNLIFL SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKIQNSTKIL QKNNLNLLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII ANEIGSESTLLFLTVGDEKGGGLFLLAGPPASVETLGPRVAEVL EGKGAGKKGRFQGKATKMSRRMEAQALLQDYISTQSAKE AIMAAATRPVRLPEAGCEGRERCWNPSRSRSHSGEGGLAAWSRT CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPYLYKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP	1			HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYPRPIIRLSSC
SGQHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA IEQSVNEKIRDRLPVNVRELSLDDPEVEQVSGRGLPDDHAGPIR VVNIEGVDSNMCCGTHVSNLSDLQVIKILGTEKGKKNRTNLIFL SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKIQNSTKIL QKNNLNLLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII ANEIGSEETLLFLTVGDEKGGGLFLLAGPPASVETLGPRVAEVL EGKGAGKKGRFQGKATKMSRRMEAQALLQDYISTQSAKE  AIMAAATRPVRLPEAGCEGRERCWNPSRSRSHSGEGGLAAWSRT CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPYLYKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP	ĺĺ			CPARLQTEGSNGKKEVLSGFQVVLEDTVLFPEGGGQPDDRGTIN
IEQSVNEKIRDRLPVNVRELSLDDPEVEQVSGRGLPDDHAGPIR VVNIEGVDSNMCCGTHVSNLSDLQVIKILGTEKGKKNRTNLIFL SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKILQNSTKIL QKNNLNLLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII ANEIGSESTLLFLTVGDEKGGGLFLLAGPPASVETLGPRVAEVL EGKGAGKKGRFQGKATKMSRRMEAQALLQDYISTQSAKE  1 1535 AIMAAATRPVRLPEAGCEGRERCWNPSRSRSHSGEGGLAAWSRT CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPYLYKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLNVVNGVAAEAVASWIGLGPVAP FVNAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP	Į.	1		DISVLRVTRRGEQADHFTQTPLDPGSQVLVRVDWERRFDHMQQH
VVNIEGVDSNMCCGTHVSNLSDLQVIKILGTEKGKKNRTNLIFL SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKIQNSTKIL QKNNLNLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII ANEIGSESTLIFLTVGDEKGGGLFLLAGPPASVETLGPRVAEVL EGKGAGKKGRFQGKATKMSRRMEAQALLQDYISTQSAKE  1 1535 AIMAAATRPVRLPEAGCEGRERCWNPSRSRSHSGEGGLAAWSRT CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPYLYKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAEAVASWIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP		l		SEQUILITAVADRLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA
SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKI.QNSTKIL QKNNLNLLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII ANEIGSESTLLFLTVGDEKGGGLFLLAGPPASVETLGPRVAEVL EGKGAGKKGRFQGKATKMSRRMEAQALLQDYISTQSAKE  AIMAAATRPVRLPEAGCEGRERCWNPSRSRSHSGEGGLAAWSRT CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPYLYKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAFWNHVLAVVAGVAAEAVASWIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP				MANIFOUDENING COTTINGNESS DDDPEVEQVSGRGLPDDHAGPIR
QKNNLNLLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII ANEIGSEETLLFLTVGDEKGGGLFILIAGPPASVETLGPRVAEVL EGKGAGKKGRFQGKATKMSRRMEAQALLQDYISTQSAKE  AIMAAATRPVRLPPEAGCEGRERCWNPSRSRSHSGEGGLAAWSRT CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPYLYKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP	1			SGNEVI.KWMEPSHCTEKAI TALI YOGA EDINERALWA ONOMANI
ANEIGSEETLLFLTVGDEKGGGLFLLAGPPASVETLGPRVAEVL EGKGAGKKGRFQGKATKMSRRMEAQALLQDYISTQSAKE  1 1535 AIMAAATRPVRLPEAGCEGRERCWNPSRSRSHSGEGGLAAWSRT CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPYLYKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP FVAAIPLLALAGAIALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP		İ		OKNNLNLLRELAVHIAHSI,RNSPOMCGMITT HEVEGOGESTATE
EGKGAGKKGRFQGKATKMSRRMEAQALLQDYISTQSAKE  1 1535 AIMAAATRPVRLPEAGCEGRERCWNPSRSRSHSGEGGLAAWSRT CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPYLYKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP	1			ANEIGSEETLLFLTVGDEKGGGLELLAGDDAGUDELGDSSEFMNII
AIMAAATRPVRLPEAGCEGRERCWNPSRSRSHSGEGGLAAWSRT CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPYLYKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP				EGKGAGKKGRFOGKATKMSRRMEADALLODVISTOSAKE
CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPYLYKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLNVVNGVAAEAVASWIGLGPVAP FVNAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP	6375	1	1535	AIMAAATRPVRLPEAGCEGRERCWNPSRSRSHSGEGGLANGS
PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPYLYKLYQHYY FLEGQIAILYVCGLASTVIFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRAGLGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLNVVNGVAAEAVASWIGLGPVAP FVNAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP		1		CPGRPRRPGQQVVRGPTMLVTAYLAFVGLIASCLGLELSDCDAW
FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAÆAVASWIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP		[		PPGRACSNPSFLRFQLDFYQVYFLALAADWLOAPYLYKI.VOHVV
SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP			•	FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVI.FGI.TV
HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP		ļ		SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHURD
FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP				HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAD
RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP				FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR
SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP			l	RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA
GQESPVESFIAFLLIELACGLYFPSMSFLRRKVIPBTEQAGVLN		1	ļ	SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP
			<u>_</u>	GQESPVESFIAFLLIELACGLYFPSMSFLRRKVIPETEQAGVLN

SEQ	Predicted	Predicted end	·
ID	beginning	nucleotide	
NO:	nucleotide	location	In-miditing, C=CVSteine, D-Aenartic Acid n
	location	corresponding	Oldcamic Acid, F=Phenylalaning C-Clusing
1	corresponding	to first	n-nistidine, i=isolehcine V-Lyeine
İ	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
}	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
I	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
J	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
L	sequence		Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
		<del>                                     </del>	WFRVPLHSLACICILIA (DORDAY
			WFRVPLHSLACLGLLVLHDSDRKTGTRNMFSICSAVMVMALLAV VGLFTVVRHDAELRVPSPTEEPYAPEL
6376	380	1437	ISSTDIDHYRFSFLVNSKMPSKESWSGRKTNRAAVHKSKQEGRQ
1	1		QDLLIAALGMKLGSPKSSVTIWQPLKLFAYSQLTSLVRRATLKE
	1	ł	NEQIPKYEKIHNFKVHTFRGPHWCEYCANFMWGLIAQGVKCADC
-			GLNVHKQCSKMVPNDCKPDLKHVKKVYSCDLTTLVKAHTTKRPM
			VVDMCIREIESRGLNSEGLYRVSGFSDLIEDVKMAFDRDGEKAD
1	1		ISVNMYEDINIITGALKLYFRDLPIPLITYDAYPKFIESAKIMD
1			PDEQUETEREALKLEPPAHCETERYIMAHIKRUTI.UPPENTANIA
6377			ENLGIVEGPTLMRSPELDAMAAINDTRYOPIJMETT TENTENTED
1 03//	2311	1845	SKIKKKSSKKPREPPGPSRRRRRRRRPDPRTMPSEKTEVODDTPD
			QRVEDVRLIREQHPTKIPVIIERYKGEKOLPVIDVTVELUDDING
-			I MASSILLALIKKKLOLNANOAFFILLVNCHSMVSVSTDISERUNGE
6378	686	191	KDEDGFLYMVYASOETFGMKLSV
1		137	GAGPWEAFPDGIGRRSRRARLPQYKRPPGRVGGGDSGRRNMAVA
			DLAGIPDVDIDSDGVFKYVLIRVHSADDSGADAAECVETIMOVK
1	i 1		WALTHADIYDKVSGDMOKOGCDCECLGGGDTGUOGODYYTHING
6379	35	378	I ISTATOPAQUAISTEKIKAKYPDVEVTWANDOV
			ERAGSPSPSRAALRRCAPQRSQAPRWPDRAACRRSFQGSQGRAY
			LFNSVVNVGCGPAEERVLLTGLHAVADIYCENCKTTLGWKYEHA FESSQKYKEGKYIIELAHMIKDNGWD
6380	1414	462	PAVQGQRGAGPPTGRGSGNMARFALTVVRHGETRFNKEKIIQGQ
1	}		GVDEPLSETGFKQAAAAGIFLNNVKFTHAFSSDLMRTKQTMHGI
			LERSKFCKDMTVKYDSRLRERKYGVVEGKALSELRAMAKAAREE
			CPVFIPPGGETLDOVKMRGIDFFEFI.COLILVEADOVEDERGOES
1 1			FONCIDE ISLABIT PLICKNHSSKVNSDSGTDGIAACUT TOTOTTON TO
1 1			I PRODUCT EL TULKCSLPATLSRSELMSVTDNTCMCI EL TWEEDOG
			KEVRPIVQCICMNLQDHLNGLTENSLGINIPSKSNHERDIVCUD
6381	1668		MADE ISLING
	1000	218	AVVRAQGSRGFSGAGWRPRQAAAMNFSEVFKLSSLLCKFSPDGK
			I THASCVQIRDVVRDVNTLOILOLYTCI.DOIOUIPWCADGI BIT C
	j		MATERICA VOVE AND THE CONTRACT OF THE PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND A PROPERTY AND
1 1	1	'	I TETALKII VWSLCIKSVSYIKYPKACI OCTTETPDDCDVMAI ADD
1	1		TOCKDI VSIFVCSDWOLLRHFDTDTODI.TCIRWA DACCITA ALTER
1 1	i		TCLEYKILLYSLDGRLLSTYSAYEWSLGIKSVAWSPSSQFLAVG
1	j		SYDGKVRILNHVTWKMITEFGHPAAINDPKIVVYKEAEKSPQLG
			LGCLSFPPPRAGAGPLPSSESKYEIASVPVSLQTLKPVTDRANP KIGIGMLAFSPDSYFLATRNDNIPNAVWVWDIQKLRLFAVLEQL
1 1			SPVRAFQWDPQQPRLAICTGGSRLYLWSPAGCMSVQVPGEGDFA
		_	VLSLCWHLSGDSMALLSKDHFCLCFLETEAVVGTACRQLGGHT
6382	2	1062	FEEDEDRNLCLIAYPLKGDHGIVDIVDNSDCEPKSKLLRWTTNK
] [			MINUTE LEXI PROMVROHRKEEKMKSHKI.FFFFFFWI.KVCFVA.VV
1 1	j	<b>{</b>	TVERKGNISSQLKHYNPWSMKCHOOOLOPMKENAVUDAIOVVETT
]	Ì		DENDISKIEVPCVDDLKMGTROHGDDASEEKAANOTPVCOOGRO
1 1		[	AVIGVRVCGMQVYQAGSGOLMFMNKYHGRKI.SUGGEVERT PORE
i l	1		MORITRRELLGPVLKKLTELKAVI.EROESVDEVSSSI.IVIVOS
1		i	AERPE V V DOSDAEDLEDLSEESADESAGA VAVKDIGA COUDUM
] ]	ļ	1	TDFAHITCRLYGEDTVVHEGQDAGYIFGLOSLIDIVTEISERSC
6383	3159		<u> </u>
	3233	1061	SPAPGRPSPHGSQPAARAAAAPAMPSAKQRGSKGGHGAASPSEK
			GAHPSAARPLAAPTPAAPACRSPSPGGAPASEDGPADDCTACOD
[ [		1.	AARAAAAPAMPSAKORGSKGGHGAASPSEKGAUDCCGADDWAYY
1		j.	***APQQPPPPPAPHPOOHPOOHPONOAHGKGGHPGGGGGGCV
		f ·	SSSSASAAAAAAASSSASCSRRLGRALNFLFVI.AI.WAAARG
L		[ ]	GWCVHHVLEEVQQVRRSHQDFSRQREELGQGLQGVEQKVQSLQA
			TFGTFESILRSSQHKQDLTEKAVKQGESEVSRISEVLQKLQNEI

000	1 20 12 3		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID NO:	beginning nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	residue of	residue of	S=Serine, T=Threonine, V=Valine,
	1	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\-possible nucleotide insertion)
	1	1	LKDLSDGIHVVKDARERDFTSLENTVEERLTELTKSINDNIAIF
1	1		TEVQKRSQKEINDMKAKVASLEESEGNKQDLKALKEAVKEIOTS
1	1	ł	AKSREWDMEALRSTLQTMESDIYTEVRELVSLKQEQQAFKEAAD
		į.	TERLALQALTEKLLRSEESVSRLPEEIRRLEEELRQLKSDSHGP
ł		ł	KEDGGFRHSEAFEALQQKSQGLDSRLQHVEDGVLSMOVASAROT
		<u>{</u>	ESLESLLSKSQEHEQRLAALQGRLEGLGSSEADODGLASTVRSL
			GETQLVLYGDVEELKRSVGELPSTVESLQKVQEQVHTLLSODOA
ì			QAARLPPQDFLDRLSSLDNLKASVSQVEADLKMLRTAVDSLVAY
<u></u>			SVKIETNENNLESAKGLLDDLRNDLDRLFVKVEKIHEKV
6384	738	1904	IWEVPVCLTHLLHLQQANQPLPPPSSSINEEDADEANRAIGEKR
i			AAPDSGKKPKTPKTKQQKDPNEPQKPVSAYALFFRDTOAAIKGO
I			NPNATFGEVSQIVASMWDSLGEEQKQVYKRKTEAAKKEYLKALA
			AYRASLVSKAAAESAEAQTIRSVQQTLASTNLTSSLLLNTPLSO
	}		HGTVSASPQTLQQSLPRSIAPKPLTMRLPMNOIVTSVTIAANMP
ļ			SNIGAPLISSMGTTMVGSAPSTQVSPSVQTQQHQMQLQQQQQQQ
1	i		QQQMQQMQQQLQQHQMHQQIQQQMQQQHFQHHMQQHLQQQQQH
ł	1		LQQQINQQQLQQRLQLQQLQHMQHQSQPSPRQHSPVASQI
			TSPIPAIGSPQPASQQHQSQIQSQTQTQVLSQVSIF
6385	2	1584	PRVRAADVAAGAQAVVSAGMAKSNGENGPRAPAAGESLSGTRES
ļ	]		LAQGPDAATTDELSSLGSDSEANGFAERRIDKFGFIVGSOGAEG
			ALEEVPLEVLRQRESKWLDMLNNWDKWMAKKHKKIRLRCQKGIP
1	1		PSLRGRAWQYLSGGKVKLQQNPGKFDELDMSPGDPKWLDVIERD
			LHROFPFHEMFVSRGGHGQQDLFRVLKAYTLYRPEEGYCQAQAP
i			IAAVLLMHMPAEQAFWCLVQICEKYLPGYYSEKLEAIOLDGEIL
	1		FSLLQKVSPVAHKHLSRQKIDPLLYMTEWPMCAFSRTLPWSSVI.
J	į į		RVWDMFFCEGVKIIFRVGLVLLKHALGSPEKVKACQGQYETIER
			LRSLSPKIMQEAFLVQEVVELPVTERQIEREHLIOLRRWOETRG
			ELQCRSPPRLHGAKAILDAEPGPRPALOPSPSIRLPLDAPLPGS
1	j		KAKPKPPKQAQKEQRKQMKGRGQLEKPPAPNQAMVVAAAGDACP
	<u>                                       </u>		PQHVPPKDSAPKDSAPQDLAPQVSAHHRSQESLTSQESEDTYL
6386	819	195	TVCGSFYLGIMQRASRLKRELHMLATEPPPGITCWQDKDQMDDL
ì	l i		RAQILGGANTPYEKGVFKLEVIIPERYPFEPPQIRFLTPIYHPN
!	l i		IDSAGRICLDVLKLPPKGAWRPSLNIATVLTSIQLLMSEPNPDD
			PLMADISSEFKYNKPAFLKNARQWTEKHARQKQKADEEEMLDNL
	ŀ		PEAGDSRVHNSTQKRKASQLVGIEKKFHPDV
6387	1	662	PGPTHASADAWADAWAQPNMAMHNKAAPPQIPDTRRELAELVKR
			KQELAETLANLERQIYAFEGSYLEDTQMYGNIIRGWDRYLTNQK
			NSNSKNDRRNRKFKEAERLFSKSSVTSAAAVSALAGVQDQLIEK
	į		REPGSGTESDTSPDFHNQENEPSQEDPEDLDGSVQGVKPQKAAS
			STSSGSHHSSHKKRKNKNRHSPSGMFDYDFEIDLKLNKKPRADY
6388	1	662	PGPTHASADAWADAWAQPNMAMHNKAAPPQIPDTRRELAELVKR
			KQELAETLANLERQIYAFEGSYLEDTQMYGNIIRGWDRYLTNQK
			NSNSKNDRRNRKFKEAERLFSKSSVTSAAAVSALAGVQDQLIEK
			REPGSGTESDTSPDFHNQENEPSQEDPEDLDGSVQGVKPQKAAS
İ			STSSGSHHSSHKKRKNKNRHSPSGMFDYDFEIDLKLNKKPRADY
6389	1074	497	AEPGDRMAGHRLVLVLGDLHIPHRCNSLPAKFKKLLVPGKIQHI
		·	LCTGNLCTKESYDYLKTLAGDVHIVRGDFDENLNYPEQKVVTVG
			QFKIGLIHGHQVIPWGDMASLALLQRQFDVDILISGHTHKFEAF
			EHENKFYINPGSATGAYNALETNIIPSFVLMDIQASTVVTYVYQ
	i		LIGDDVKVERIEYKKP
6390	158	535	
		223	GEERKEGRAPGKAFAPERNPAKMEKEETTRELLLPNWQGSGSHG
	l		LTIAQRDDGVFVQEVTQNSPAARTGVVKEGDQIVGATIYFDNLQ
6391	5386	2007	SGEVTQLLNTMGHHTVGLKLHRKGDRFFPSLGQTWDP
	2300	2897	VRWNSKTECYLSIQTQENFPANLNELVNCIVISSLVTTQRKLKA
1			MSLLGSRNQLARAVLNPNPMDFCTKDLLTTTSERIIAYLRDFNE
			DQKKAIETAYAMVKHSPSVAKICLIHGPPGTGKSKTIVGLLYRL

SEO	Predicted		
ID	beginning	Predicted end nucleotide	
NO:	nucleotide	location	I WE THE CELVSEPING DENOMINE TO THE TENE
1	location	corresponding	
- 1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, O=Glutamine, P-Arginine
İ	amino acid	residue of	S=Serine, T=Threonine V=V=1:ne
ŀ	amino acid	amino acid	W=Tryptophan, Y=Tyrosine y-unknown to
l	sequence	sequence	Codon, /=possible micleotide dolor:
			\=Possible nucleotide incertion)
1			LTENQRKGHSDENSNAKIKQNRVLVCAPSNAAVDELMKKIILEF
1			A THE CANADA CONTROL OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION OF THE PART PROTECTION O
ŀ			MKKELPSHVQAMHKRKEFLDYQLDELSRQRALCRGGREIQRQEL
ļ	1	]	DENISKVSKERQELASKIKEVQGRPQKTQSIIILESHIICCTLS TSGGLLLESAFRGQGGVPFSCVIVDEAGQSCEIETLTPLIHRCN
Į		ļ	KLILVGDPKQLPPTVISMKAQEYGYDQSMMARFCRLLEENVEHN
		ļ	1 MADE ADOLI VOI KMMPI) I C'I. PDCNIVII VAIDATE MANNA ABRES
			ODDWET QFILVED VGDGSERRDNDSVTNVORTET TAKET THE
	İ		I WOOD AS ENTRETTHINK WORLD LOND TO THE WORLD STREET
1			L QGRQRDCVIVICVRANSIOGSTGFI A GLODI ARITEMPA 1110x -
l	·		- DUCALINATION OF TODACK DESTRUCTION ASSESSMENT OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERT
			THE VIORSUITEPPT LAPEGSR POCCI, DCCP1 VMC112 2 C-
			YHTPSDSKEITLTVTSKDPERPPVHDQLQDPRLLKRMGIEVKGG IFLWDPQPSSPQHPGATPPTGEPGFPVVHQDLSHVQQPAAVVAA
			DOSERVE VRGEPPAASPEASTCOSYCONDERED CURRER DA
6392	972		1 GEATURE THE TRANSKAUK BALLE CENTRAL F
""	972	186	GRIGVDLASSMAHRLOIRILTWDVKDTIT.DI. DUDI CRAVA CONTROL
1			I MIGHE VEPSALEUGEROAYRAOSHSEDNYCI.GUCI monorum nee
1	]		T V DO T T T DAG V UDAUAVAPI AFINI. V Y DECUDO TUO TUO TUO TO
1			ECRTRGLRLAVISNFDRRLEGILGGLGLREHFDFVLTSEAAGWP
			KPDPRIFQEALRLAHMEPVVAAHVGDNYLCDYQGPRAVGMHSFL VVGPQALDPVVRDSVPKEHILPSLAHLLPALDCLEGSTPGL
6393	2017	730	1005 KMAAVATUGSVAASTGGAWATACKCADUTECTOOPTOOPTOOPTOOPTOOPTOOPTOOPTOOPTOOPTOO
			INDSGPRENTS LAGIRPS VRNGOLLVSTGL DAL DOLL GOOT ALL
1	1		1 TOTO DOMENT LOCALIFICATION ON CONTRACTOR OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF
			I DESTEDIOUNCEREDEDVYNHKTDEGNIKMETAMDVOLLDIM.
1	1		1 101 V333RIGHI I DASKRMPOELTEA CHIMDOTTE DOUT COMT
1			EPCSLTPGYTKLLQFIQNIIYEEGFDGSNPQKKQRNILRIGIQN
			LGSPLWGDDICCAENGGNSHSLTKFLYVLRGLLRTSLSACIITM PTHLIQNKAIIARVTLSDVVVGLESFIGSERETNPLYKDYHGL
1 1			THE RESERVED TO THE PROPERTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF
6394	1418		* * OKOON IDDAESAKRIGPGCGMMAGGKKUILDE
	1410	511	GAAAGGEGARRPAAMATVMAATAAEDAVI EGERDUI
			VIRQUILIKEASLRFTLPGSGTECDAYOFMETT GOOGMOOVER
1			AD A DO DATE OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION OF A DEPOSITION O
		1	NHVSQAIYLLTSRDQSYQFKTGAEVLKLMDAVMLQLTRARNRLT TPATLTLPEIAASGLTRMFAPALPSDLLVNVYINLNKLCLTVYQ
			THE TOTAL PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROP
6395			VII WENDALVIETVSLOLCOOLKDETSVEGGVWGVDDD
55,55	13	658	PSGRPTRPLCCAARRGAARHGGSVSGWDAGDTDTETTCMTGAGGG
			ESVIPEDVAVEFIQEWALLDSARRSI.CKVPMI.DOCDEL B.CD.CT
ļ į	[	•	TOWN OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PR
		1	DEBEASSRUMQMGPGLFLRMOLVPSTEERETPI.TPPDDDDT.
6396	1		FFWSDGCTGLKAAMQIQRVVIPVPTLGHRNPWVAPDccp
1		1	ANILSSPSKRGQKGTLIGYSPEGTPLYNFMGDAFQHSSQSIPRF
1			IKESLKQILEESDSRQIFYFLCLNLLFTFVELFYGVLTNSLGLI SDGFHMLFDCSALVMGLFAALMSRWKATRIFSYGYGRIEILSGF
		1	INGLE LIVIAFFVFMESVARLIDPPELDTHMI.TPVCVCGT TIDY
ł		i	TOTCAP SHAHSHAHGASOGSCHSSDHSHSHHMHGHSDUGUGUGU
			OSAGGGMANMAGVFLHVLADTLGSTGVIVSTVI.TEOPGMETA > 1
		l l	FICSHFIAILIFESVVPLIKDACOVLLLRIPPEVEKELUTATER
		I .	TORTEGETSYRDPHFWRHSASIVAGTIHIOVTSDVI.FORTWOOM
		1	TGILKDAGVNNLTIQVEKEAYFQHMSGLSTGFHDVLAMTKQMES
6397	391		GAGGVGRFEAIRAPARMIEVVCNDRLGKKVRVKCNTDDTIGDLK
			KLIAAQTGTRWNKIVLKKWYTIFKDHVSLGDYEIHDGMNLELYY

SEQ Predicted beginning nucleotide location nucleotide location corresponding to first amino acid segment containing sign (A=Alanine, C=Cysteine, D=Aspartic Glutamic Acid, F=Phenylalanine, G=H=Histidine, I=Isoleucine, K=Lysin L=Leucine, M=Methionine, N=Asparag P=Proline, Q=Glutamine, R=Arginine S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknow Codon, /=possible nucleotide deleted insertion)  6398 353 1306 HKQMGPLINRCKKILLPTTVPPATMRIWLLGGLL RPTEGSEVAIKIDPDFAPGSFDDQYQGCSKQVME DIEAQKNYFRMWQKAHLAWLNQGKVLPQNMTTTH SNVHSDFTRAMASVARTPQQYERSFHFKYLHYYL SIMENGTLCYEVHYRTKDVHFNAYTGATIRFGQF PRGDWLQLRSTGNLSTYNCQLLKASSKKCIPDPI; VIIFSKSRV  6399 75 1245 PNLETYFGRRCEKDSMNFTPTHTPVCRKRTVVSKI RRGMADSLESTPLPSPEDRLAKLHPSKELLEYYQ; EDLLKKLELYYEACEGQHKLECDLQQREEEIAELG LFQEREHVLRLYSENDRLIRIRELEDKKKIQNLLAYFCKEPPHKVTILQKTIQAVGECEQSESSAFKAD	C Acid, E=  Glycine, ne, gine, gine, c, wn, *=Stop  cion,  DFFLLLSGLQ  EKLTQGDYFTK  IAVAILFYTLN  TSAIQLLRKD  CLSTSLLKEEA  ELFKVINMSYH  AIASLSFLTS  RGVAVSGPTK
NO: nucleotide location corresponding to first amino acid residue of amino acid sequence  6398  353  1306    Ka-Alanine, C=Cysteine, D=Aspartice Glutamic Acid, F=Phenylalanine, G=Cysteine, D=Aspartice Glutamic Acid, F=Phenylalanine, G=Cysteine, D=Aspartice Glutamic Acid, F=Phenylalanine, G=Cysteine, D=Aspartice Glutamic Acid, F=Phenylalanine, G=Cysteine, D=Aspartice Glutamic Acid, F=Phenylalanine, G=Cysteine, D=Aspartice Glutamic Acid, F=Phenylalanine, G=Cysteine, D=Aspartice Glutamic Acid, F=Phenylalanine, G=Cysteine, D=Aspartice Glutamic Acid, F=Phenylalanine, G=Cysteine, D=Aspartice Glutamic Acid, F=Phenylalanine, G=Cysteine, D=Aspartice Glutamic Acid, F=Phenylalanine, G=Cysteine, D=Aspartice Glutamic Acid, F=Phenylalanine, G=Cysteine, D=Aspartice Glutamic Acid, F=Phenylalanine, G=Cysteine, D=Aspartice Glutamic Acid, F=Phenylalanine, G=Cysteine, D=Aspartice Glutamic Acid, F=Phenylalanine, G=Cysteine, D=Aspartice Glutamic Acid, F=Phenylalanine, G=Cysteine, D=Aspartice Glutamic Acid, F=Phenylalanine, G=Cysteine, D=Aspartice Glutamic Acid, F=Phenylalanine, G=Cysteine, D=Aspartice Glutamic Acid, F=Phenylalanine, G=Cysteine, D=Aspartice Glutamic Acid H=Histidine, I=Isolectine, M=Betyline, M=Asparialanine, C=Cysteine, D=Aspartice Glutamic Acid H=Histidine, I=Isolectine, M=Betyline, M=Asparialanine, C=Cysteine, D=Aspartice Glutamic Acid H=Histidine, I=Isolectine, M=Betyline, M=Asparialanine, C=Cysteine, D=Aspartice Glutamic Acid H=Histidine, I=Isolectine, M=Betyline, M=Asparialanine, C=Cysteine, D=Aspartice Glutamic Acid H=Histidine, I=Isolectine, M=Betyline, M=Betyline, M=Betyline, M=Betyline, M=Betyline, M=Betyline, M=Betyline, M=Betyline, M=Betyline, M=Betyline, M=Betyline, M=Betyline, M=Betyline, M=Betyline, M=Betyline, M=Betyline, M=Be	C Acid, E=  Glycine, ne, gine, gine, c, wn, *=Stop  cion,  DFFLLLSGLQ  EKLTQGDYFTK  IAVAILFYTLN  TSAIQLLRKD  CLSTSLLKEEA  ELFKVINMSYH  AIASLSFLTS  RGVAVSGPTK
location corresponding to first amino acid residue of amino acid sequence  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  130	=Glycine, ne, gine, gine, e, wn, *=Stop cion, DFFLLLSGLQ EKLTQGDYFTK HAVAILFYTLN MTSAIQLLRKD ELFKVINMSYH AIASLSFLTS RGVAVSGPTK
corresponding to first amino acid residue of amino acid sequence  6398  353  1306  H=Hstidine, I=Isoleucine, K=Lysin L=Leucine, M=Methionine, N=Asparag P=Proline, Q=Glutamine, R=Arginine S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknow Codon, /=possible nucleotide delet \ =possible nucleotide insertion)  0  HKQMGPLINRCKKILLPTTVPPATMRIWLLGGLL RPTEGSEVAIKIDPDFAPGSFDDQYQGCSKQVME DIEAQKNYFRMWQKAHLAWLNQGKVLPQNMTTTH SNVHSDFTRAMASVARTPQQYERSFHFKYLHYYL SIMENGTLCYEVHYRTKDVHFNAYTGATIRFQQF PRGDWLQLRSTGNLSTYNCQLLKASSKKCIPDPIX VIIFSKSRV  6399  75  1245  PNLETYFGRRCEKDSMNFTPTHTPVCRKRTVVSKI RRGMADSLESTPLPSPEDRLAKLHPSKELLEYYQ EDLLKKLELYKEACEGQHKLECDLQQREEEIAELG LFQEREHVIRLYSENDRLRIRELEDKKKIONIJA	ne, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gine, gi
L=Leucine, M=Methionine, N=Asparage amino acid residue of amino acid sequence  6398 353 1306 HKQMGPLINRCKKILLPTTVPPATMRIWLLGGLL RPTEGSEVAIKIDPDFAPGSFDDQYQGCSKQVME DIEAQKNYFRMWQKAHLAWLNQGKVLPQNMTTTH SIMENGTLCYEVHYRTKDVHFNAYTGATIRFGQF PRGDWLQLRSTGNLSTYNCQLLKASSKKCIPDPIS PRGDWLQLRSTGNLSTYNCQLLKASSKKCIPDPIS PROMUNICATION VITESKSRV  6399 75 1245 PNLETYFGRRCEKDSMNFTPTHTPVCRKRTVVSKI RRGMADSLESTPLPSPEDRLAKLHPSKELLEYYQUEDLKKILLYKEACEGQHKLECDLQQREEEIAELLEYYQUEREHVIRLYSENDRLRIRELEDKKKIONIJA	gine,  m, *=Stop  cion,  DFFLLLLSGLQ  EKLTQGDYFTK  IAVAILFYTLN  TSAIQLLRKD  CLSTSLLKEEA  ELFKVINMSYH  AIASLSFLTS  RGVAVSGPTK
amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequen	PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLLSGLQ PFLLLSGLQ PFLLLSGLQ PFLLLSGLQ PFLLLSGLQ PFLLLSGLQ PFLLLSGLQ PFLLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PFLLSGLQ PF
residue of amino acid sequence  festidue of amino acid sequence  amino acid sequence  festidue of amino acid sequence  festidue of amino acid sequence  festidue of amino acid sequence  festidue of amino acid sequence  festidue of amino acid sequence  festidue of amino acid sequence  festidue of amino acid sequence  festidue of amino acid sequence  festidue of amino acid sequence  festidue of amino acid sequence  festidue of amino acid sequence  festidue of amino acid sequence  festidue of amino acid sequence  festidue of amino acid sequence  festidue of amino acid sequence  festidue of amino acid sequence  festidue of amino acid sequence  festidue of amino acid sequence  festidue of amino acid sequence  festidue of amino acid sequence  festidue of amino acid sequence  festidue of weTryptophan, Y=Tyrosine, X=Unknow Codon, /=possible nucleotide delet	PFLLLLSGLQ EKLTQGDYFTK IAVAILFYTLN TSAIQLLRKD LSTSLLKEEA ELFKVINMSYH AIASLSFLTS RGVAVSGPTK
amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence s	PFLLLSGLQ EKLTQGDYFTK IAVAILFYTLN TSAIQLLRKD LSTSLLKEEA ELFKVINMSYH AIASLSFLTS RGVAVSGPTK
sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence	PFLLLSGLQ EKLTQGDYFTK IAVAILFYTLN TSAIQLLRKD LSTSLLKEEA ELFKVINMSYH AIASLSFLTS RGVAVSGPTK
Tepossible nucleotide insertion	DFFLLLLSGLQ EKLTQGDYFTK IAVAILFYTLN ITSAIQLLRKD LSTSLLKEEA ELFKVINMSYH AIASLSFLTS RGVAVSGPTK
6398 353 1306 HKQMGPLINRCKKILLPTTVPPATMRIWLLGGLL RPTEGSEVAIKIDPDPAPGSFDDQYQGCSKQVME DIEAQKNYPRMWQKAHLAWLNQGKVLPQNMTTTH SNVHSDFTRAMASVARTPQQYERSFHFKYLHYYL SIMENGTLCYEVHYRTKDVHFNAYTGATIRFGQF QEFGNQTLFTIFTCLGAPVQYFSLKKEVLIPPYE PRGDWLQLRSTGNLSTYNCQLLKASSKKCIPDPI VIIFSKSRV  6399 75 1245 PNLETYFGRRCEKDSMNFTPTHTPVCRKRTVVSKI RRGMADSLESTPLPSPEDRLAKLHPSKELLEYYQI EDLLKKLELYKEACEGQHKLECDLQQREEEIAEL LFQEREHVLRLYSENDRLRIRELEDKKKIONIJA	EKLTQGDYFTK IAVAILFYTLN JTSAIQLLRKD LSTSLLKEEA LFKVINMSYH AIASLSFLTS RGVAVSGPTK
HRQMGPLINRCKKILLPTTVPPATMRIWLLGGLL RPTEGSEVAIKIDPDFAPGSFDDQYQGCSKQVME DIEAQKNYFRMWQKAHLAWLNQGKVLPQNMTTTH SNVHSDFTRAMASVARTPQQYERSPHFKYLHYYL SIMENGTLCYEVHYRTKDVHFNAYTGATIRFGQF QEFGNQTLFTIFTCLGAPVQYFSLKKEVLIPPYE PRGDWLQLRSTGNLSTYNCQLLKASSKKCIPDPIX VIIFSKSRV PNLETYFGRRCEKDSMNFTPTHTPVCRKRTVVSKI RRGMADSLESTPLPSPEDRLAKLHPSKELLEYYQI EDLLKKLELYKEACEGQHKLECDLQQREEEIAEL LFQEREHVLRLYSENDRLRIRELEDKKKIONILA	EKLTQGDYFTK IAVAILFYTLN JTSAIQLLRKD LSTSLLKEEA LFKVINMSYH AIASLSFLTS RGVAVSGPTK
RPTEGSEVAIKIDFDFAPGSFDDQYQGCSKQVME DIEAQKNYPRMWQKAHLAWLNQGKVLPQNMTTTH SNVHSDFTRAMASVARTPQQYERSFHFKYLHYYL SIMENGTLCYEVHYRTKDVHFNAYTGATIRFGQF. QEFGNQTLFTIFTCLGAPVQYFSLKKEVLIPPYE PRGDWLQLRSTGNLSTYNCQLLKASSKKCIPDPI. VIIFSKSRV PNLETYFGRRCEKDSMNFTPTHTPVCRKRTVVSKI RRGMADSLESTPLPSPEDRLAKLHPSKELLEYYQ: EDLLKKLELYKEACEGQHKLECDLQQREEEIAEL LFQEREHVLRLYSENDRLRIRELEDKKKIONIJA	EKLTQGDYFTK IAVAILFYTLN JTSAIQLLRKD LSTSLLKEEA LFKVINMSYH AIASLSFLTS RGVAVSGPTK
6399 75 1245 PNLETYFGRRCEKDSMNFTPTHTPVCRKRTVVSKI RRGMADSLESTPLPSPEDRLAKLHPSKELLEYYQ EDLLKKLELYKEACEGQHKLECDLQQREEEIAEL LFQEREHVLRLYSENDRLRIRELEDKKKIONIJA	IAVAILFYTLN TSAIQLLRKD LSTSLLKEEA LFKVINMSYH AIASLSFLTS RGVAVSGPTK
SNVHSDFTRAMASVARTPQQYERSFHFKYLHYYL SIMENGTLCYEVHYRTKDVHFNAYTGATIRFGQF QEFGNQTLFTIFTCLGAPVQYFSLKKEVLIPPYE PRGDWLQLRSTGNLSTYNCQLLKASSKKCIPDPI; VIIFSKSRV  6399 75 1245 PNLETYFGRRCEKDSMNFTPTHTPVCRKRTVVSKI RRGMADSLESTPLPSPEDRLAKLHPSKELLEYYQI EDLLKKLELYKEACEGQHKLECDLQQREEEIAEL LFQEREHVLRLYSENDRLRIRELEDKKKIONIJA	TSAIQLLRKD LSTSLLKEEA LFKVINMSYH AIASLSFLTS RGVAVSGPTK
6399 75 1245 PRICHERLEY PREDICTION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROP	LSTSLLKEEA LFKVINMSYH AIASLSFLTS RGVAVSGPTK
6399 75 1245 PRICHERT PRESENTATION OF THE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBABLE PROBAB	LFKVINMSYH AIASLSFLTS RGVAVSGPTK
FRGWLQLRSTGNLSTYNCQLLKASSKKCIPDPIX VIIFSKRV  6399 75 1245 PNLETYFGRRCEKDSMNFTPTHTPVCRKRTVVSKI RRGMADSLESTPLPSPEDRLAKLHPSKELLEYYQI EDLLKKLELYKEACEGQHKLECDLQQREEEIAELL LFQEREHVLRLYSENDRLRIRELEDKKKIONILA	AIASLSFLTS RGVAVSGPTK
6399 75 1245 PNLETYFGRRCEKDSMNFTPTHTPVCRKRTVVSKI RRGMADSLESTPLPSPEDRLAKLHPSKELLEYYQI EDLLKKLELYKEACEGQHKLECDLQQREEEIAELL LFQEREHVLRLYSENDRLRIRELEDKKKIONILA	RGVAVSGPTK
6399 75 1245 PNLETYFGRRCEKDSMNFTPTHTPVCRKRTVVSKI RRGMADSLESTPLPSPEDRLAKLHPSKELLEYYQ EDLLKKLELYKEACEGQHKLECDLQQREEEIAEL LFQEREHVLRLYSENDRLRIRELEDKKKIONIJA	KKMAECEAEN
RRGMADSLESTPLPSPEDRLAKLHPSKELLEYYQI EDLLKKLELYKEACEGQHKLECDLQQREEEIAEL( LFQEREHVLRLYSENDRLRIRELEDKKKIONILA)	KKMAECEAEN
EDLLKKLELYKEACEGQHKLECDLQQREEEIAEL LFQEREHVLRLYSENDRLRIRELEDKKKIONIJA	KKMAECEAEN
LFQEREHVLRLYSENDRLRIRELEDKKKIONIJA	01077.00
YFCKEPPHKVTILOKTIOAVGECEOGREGGDERADD	QKALSDMQVC
1 II CHEFFIRWITHORT TOAVISH BEINGGREEN	LVGTDAGEVT
ERKESSPUVODITOMI TI OVIDA I OSIDATI RADI	PKISKRRPSR
ERKESSEHYQRDIQTLILQVEALQAQLGEQTKLSI	REQIECTIED
RRIHLEEIQVQHQRNQNKIKELTKNLHHTQELLYI	ESTKDFLQLR
SENQNKEKSWMLEKDNLMSKI KQYRVQCKKKEDKI	IGKVLPVMHE
SHHAQSEYIKVMSLCRNEVVYFSGRVEGIPKNLQI 6400 2520 1053 KTMKCDEVVYFVOSA II PUNCGYAMVEGYENIN	FVM
1 THRODE VIE VOSATERING YAMKIGKEENINIA	MERKDFETWL
DNISVTFLSLTDLQKNETLDIILISLSGAVQLRHLS	SNNLETLLKR
DFLKLLPLELSFYLLKWLDPQTLLTCCLVSKQWNF	KVISACTEVW
QTACKNLGWQIDDSVQDALHWKKVYLKAILRMKQI	LEDHEAFETS
SLIGHSARVYALYYKDGLLCTGSDDLSAKLWDVST	rgqcvygiqt
HTCAAVKFDEQKLVTGSFDNTVACWEWSSGARTQH	AFRGHTGAVF
SVDYNDELDILVSGSADFTVKVWALSAGTCLNTLT	(GHTEWVTKV
VLQKCKVKSLLHSPGDYILLSADKYEIKIWPIGRE	SINCKCLKTL
SVSEDRSICLQPRLHFDGKYIVCSSALGLYQWDFA	ASYDILRVIK
TPEIANLALLGFGDIFALLFDNRYLYIMDLRTESL	JISRWPLPEY
RKSKRGSSFLAGEASWLNGLDGHNDTGLVFATSMP KEHG	DHSIHLVLW
	İ
FGAAWSRPDERGCCTGPQPALRMLVLPSPCPOPLA	FSSVETMEG
PPRRTCRSPEPGPSSSIGSPQASSPPRPNHYLLID	TQGVPYTVL
VDEESQREPGASGAPGQKKCYSCPVCSRVFEYMSY	LQRHSITHS
EVKPFECDICGKAFKRASHLARHHSIHLAGGGRPH	GCPLCPRRF
RDAGELAQHSRVHSGERPFQCPHCPRRFMEQNTLQ	KHTRWKHP
TTSQCGGTRQSSATPVASMEFAAICLRNALLLLEFE	EQQDPKQEN
GAKNSNQLGGNTESSESSETCSSKSHDGDKFIPAP	PSSPLRKQE
LENLKCS I LACSAYVALALGDNLMALNHADKI I .OO	PKI.SCST.KE
LGHLYAAEALISLDRISDAITHINDENUTDUSIGT	COMPODOGG
DKGENEAMESSGKRAPQCYPSSVNSARTVMLFNLG:	SAYCLESEV
DKARKCLHQAASMIHPKEVPPEAILLAVYLELONG	NTOLALOTY
KRNQLLPAVKTHSEVRKKPVFQPVHPIQPIOMPAFT	TTVORK
RGIHTSVLQGNLQNQMYSHNVVIMNLNNLTOVOC	ORNITTNICO
RSVDDTSQAIQRIKNDFQNLQQVFLQAKKDTDWLKF	EKVOST OTT.
AANNSALAKANNDTLEDMNSQLNSFTGOMENITTIS	SOANEONT.V
DLQDLHKDAENRTAIKFNQLEERFQLFETDIVNIIS	SNISYTAHU
LRTLTSNLNEVRTTCTDTLTKHTDDLTSLNNTLANI	IRI-DSVSt.p
MQQDLMRSRLDTEVANLSVIMEEMKLVDSKHGQLIK	KNETILOGD
PGPRGPRGDRGSQGPPGPTGNKGQKGEKGEPGPPGF	PACERCUTA
PAGPPGERGGKGSKGSQGPKGSRGSPGKPGPQGPSG	DIGDROPIG
GKEGLPGPQGPPGFQGLQGTVGEPGVPGPRGLPGLP	PEGEEGEF
KGPPGPPGPSGAVVPLALQNEPTPAPEDNSCPPHWK	CHEMPLE
FSVEKEIFEDAKLFCEDKSSHLVFINTREEQQWIKK	WEIDKCAA
WIGLTDSERENEWKWLDGTSPDYKNWKAGQPDNWGH	LOMVGRESH
AGLIYAGQWNDFQCEDVNNFICEKDRETVLSSAL	IGHGPGEDC
6404 1012 222 AAALAMADADUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUURUU TUR	
6404 1012 222 AAALAMAAPAPGLISVFSSSQELGAALAQLVAQRAA	CCLAGARA

SEQ	Predicted	Predicted end	Amino
ID	beginning	nucleotide	
No:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
İ	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
İ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ļ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	<u> </u>	\=possible nucleotide insertion)
			RFALGLSGGSLVSMLARELPAAVAPAGPASLARWTLGFCDERLV
	1		PEDMARSTYGLYRTHLLSRLPIPESOVITTNDELDVERAARDVA
ŀ	1		KKLKQAFQGDSIPVFDLLILGVGPDGHTCSI.EDDUDII OEDDUR
			VAPISUSPRPPPQRVTLTLPVLNAARTVTFVATGECVAAUT VD T
6405	<del> </del>		LEDQEBNYLPAALVQPHTGKLCWFLDRAARI, J. TVDDDDVUGDI
0403	1	1456	AALPRPTPRAPLGREGTGSDSEMAASMEYGRIAAVATT.BNUBBB
			TAQRAAAQVLGSSGLFNNHGLOVOOCOORNI.SI.HEVMCMET LOE
1			AGVSVPKGIVAKSPDEAYAIAKKLGSKDVVIKAOVI.AGGDGVOM
1			I FESGLAGGVKIVFSPEEAKAVSSOMTCKKI, FTKOTCEVCDIONO
	İ		V D V CERKY PRREYY FAITMERS FOG PVI, I G S H G C V N I E D V N E
1			I PEALIKEPIDIEEGIKKEOALOLAOKMOEDDNITUEGA A DAMELYE
!	1		DISDELKIDATMIEINPMVEDSDGAVT,CMDAKINEDGMGAVDOV
1	<u> </u>		KIPDLQDWTQEDERDKDAAKANLNYIGIDGWIGGIAMGAGIAMA
			TMDIIKLHGGTPANFLDVGGGATVHQVTEAFKLITSDKKVLAIL
			VNIFGGIMRCDVIAQGIVMAVKDLEIKIPVVVRLQGTRVDDAKA
L	<u> </u>		LIADSGLKILACDDLDEAARMVVKLSEIVTLAKQAHVDVKFQLP
6406	1036	167	HPROMRGEDTPEAPPYSSGRYDSIKTEVSGCPEDLTVGRAPTAD
1			DDDDDHDDHEDNDKMNDSEGMDPERLKAFNMFVRLFVDENLDRM
			VPISKQPKEKIQAIIESCSRQFPEFQERARKRIRTYLKSCRRMK
			KNGMEMTRPTPPHLTSAMAENILAAACESETRKAAKRMRLEIYQ
			55QDEPIALDKQHSRDSAAITHSTYSI,PASSYSODDIVANCET N
1 1	}		1 ISINGIGALSSNLQPPASLOTGNHSNGESGEAPALAGDDADGEN
6407	492		CRAALGSGMGRGKQRPVMERGCT.TA
""	432	150	VGLCLAVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGV
1 1			SWIQQRAGSAPRYLLYYRSEEDHHRPADIDDDEGAAVDGAIDIAG
6408	1458	903	VLITSPVQPEDDADYYCSVGYGFSP
1 ' 1		203	RGCITSSQAWRLFGGVTRGFNMRIEKCYFCSGPIYPGHGMMFVR
1 1	į		NDCKVFRFCKSKCHKNFKKKRNPRKVRWTKAFRKAAGKELTVDN
1 1			SFEFEKRRNEPIKYQRELWNKTIDAMKRVEBIKQKRQAKFIMNR
	1		LKKNKELQKVQDIKEVKQNIHLIRAPLAGKGKQLEEKMVQQLQE DVDMEDAP
6409	150	446	NTALANLLRCFTCDRLCGGCTAPAPPAHQGIVLQPVMPSCDPGP
] [		•	GPACLPTKTFRSYLPRCHRTYSCVHCRAHLAKHDELISKSFQGS
-		<u> </u>	HGRAYLFNSV
6410	85	607	RGGTAGCVACLGCWGQSSSPKAAFPAGSACLPADSCPCLLFQAC
1 1			AISGUENCITIHPUNIAAGVWMIMNAFILLLCEADECCORTERN
1 1	1		NIVAEKVDRLRSWOKAVFYCGMAVVDTUTGLTI TOTLL CNA TA TO
6411	200		IGVLYGLSALGKKGDAISYARIOOOROOADEEKI.Appri Popi
0411	302	772	RUS IMASS LINEDPEGSRITYVKGDI FACEKTOSI AUGTERFORM
			GAGIAVLEKKKEGGVOELLNOOKKSGEVAVLKPDGPVIVVI INK
] }			RASHAPIYENLQKSLEAMKSHCLKNGVTDLSMPRIGCGLDRIA
6412	61	1700	WENVSAMIEEVFEATDIKITVYTI,
	-	1709	RPVTSFSPLPGSCGGRLGTRTMLGRSLREVSAALKQGQITPTEL
]			CORCLELIKKTKFLNAYITVSEEVALKOAEESEKPVKNGOGIOD
]	!		LDGIPIAVKDNFSTSGIETTCASNMLKGYIPPVNATVAOKIIDO
] ]	1	1	GALLMGKTNLDEFAMGSGSTDGVFGPVKNPWSVSKOVPEVPVOM
( I	į	•	PHSENEDSDWLITGGSSGGSAAAVSAFTCYAALGSDTGGSTRNP
	1	• 1	AAHCGLVGFKPSYGLVSRHGLIPLVNSMDVPGILTRCVDDAAIV
		ļ	LGALAGPDPRDSTTVHEPINKPFMLPSLADVSKLCIGIPKEYLV
	1	ļ	PELSSEVQSLWSKAADLFESEGAKVIEVSLPHTSYSIVCYHVLC
			TSEVASNMARFDGLQYGHRCDIDVSTEAMYAATRREGFNDVVRG
		1	RILSGNFFLLKENYENYFVKAQKVRRLIANDFVNAFNSGVDVLL
ļ .			TPTTLSEAVPYLEFIKEDNRTRSAQDDIFTQAVNMAGLPAVSIP VALSNQGLPIGLQFIGRAFCDQQLLTVAKWFEKQVQFPVIQLQE
		f	LMDDCSAVLENEKLASVSLKQ
_ <del>_</del> _			

SEO	Predicted	Predicted end	Amino acid compat contain
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
Ì	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
6413	2	885	HEPRCAGMAASLWMGDLEPYMDENFISRAFATMGETVMSVKIIR
			NRLTGIPAGYCFVEFADLATAEKCLHKINGKPLPGATPAKRFKL
ł			NYATYGKQPDNSPEYSLFVGDLTPDVDDGMLYEFFVKVYPSCRG
1	1		GKVVLDQTGVSKGYGFVKFTDELEOKRALTECOGAVGLGSKPVR
1			LSVAIPKASRVKPVEYSQMYSYSYNQYYOOYONYYAOWGYDONT
			GSYSYSYPQYGYTQSTMQTYEEVGDDALEDPMPOLDVTEANKEF
			MEQSEELYDALMDCHWQPLDTVSSEIPAMM
6414	1	538	RGGRAALLPWRRFPCCRPRPQPARPSSRATPGPRSPGMATSIGV
1			SFSVGDGVPEAEKNAGEPENTYILRPVFOORFRPSVVKDCTHAV
			LKEELANAEYSPEEMPQLTKHLSENIKDKLKEMGFDRYKMVVOV
	1		VIGEORGEGVFMASRCFWDADTDNYTHDVFMNDSLFCVVAAFGC
		·	FYY
6415	2	1168	FVRQWQSSHRRACGLGCEARAGGGEEPRGRASSVAGWVGAFRAP
	}		FIEAAVAGLGAGSGKRRRGWKMPVHSRGDKKETNHHDEMEVDYA
ł			ENEGSSSEDEDTESSSVSEDGDSSEMDDEDCERRRMECLDEMSN
į	į i		LEKQFTDLKDQLYKERLSQVDAKLQEVIAGKAPEYLEPLATLQE
			NMQIRTKVAGIYRELCLESVKNKYECEIQASRQHCESEKLLLYD
			TVQSELBEKIRRLEEDRHSIDITSELWNDELQSRKKRKDPFWPD
			KKKPGVVSGPYIVYMLQDLDILEDWTTIRKAMATLGPHRVKTEP
			PVKLEKHLHSARSEEGRLYYDGEWYIRGQTICIDKKDECPTSAV ITTINHDEVWFKRPDGSKSKLYISQLQKGKYSIKHS
6416	410	1519	EIAPADLEIPACAPVLLSRATSSTMSVTGGKMAPSLTQEILSHL
1			GLASKTAAWGTLGTLRTFLNFSVDKDAQRLLRAITGQGVDRSAI
	l (		VDVLTNRSREQRQLISRNFQERTQQDLMKSLQAALSGNLERIVM
1			ALLQPTAQFDAQELRTALKASDSAVDVAIEILATRTPPQLQECL
1	1		AVYKHNFQVEAVDGITSETSGILQDLLLALAKGGRDSYSGIIDY
1.			NLAEQDVQALQRAEGPSREETWVPVFTQRNPEHLIRVFDQYQRS
İ			TGQELEEAVQNRFHGDAQVALLGLASVIKNTPLYFADKLHOALO
1			ETEPNYQVLIRILISRCETDLLSIRAEFRKKFGKSLYSSLQDAV
			KGDCQSALLALCRAEDM
6417	1	845	RGESRVLWSELEGEAGGAGGWASSLNARMDNRFATAFVIACVLS
1	ļ		LISTIYMAASIGTDFWYEYRSPVQENSSDLNKSIWDEFISDEAD
	1		EKTYNDALFRYNGTVGLWRRCITIPKNMHWYSPPERTESFDVVT
			KCVSFTLTEQFMEKFVDPGNHNSGIDLLRTYLWRCQFLLPFVSL
			GLMCFGALIGLCACICRSLYPTIATGILHLLAGLCTLGSVSCYV
		İ	AGIELLHQKLELPDNVSGEFGWSFCLACVSAPLQFMASALFIWA
6418	2	662	AHTNRKEYTLMKAYRVA
	"	202	TRTRPRRPPGLGAAVGKAGARSTSTPAGASPAAAYQADPPPPAH
		į	TPAPPPPPPCGGIACHGEPAKFYGYDNLQRQPIFTTQQEAELVQ
1			YPDCKSSSGNIGEDPDHLNQSSSPSQMFPWMRPQAAPGRRRGRQ
[ ]		· .	TYSRFQTLELEKEFLFNPYLTRKRRIEVSHALALTERQVKIWFQ NRRMKWKKENNKDKFPVSRQEVKDGETKKEAQELEEDRAEGLTN
6419	1	973	PGRPRVRNFDLNSKSILQEFFCTRSIQIPANRSKTAMSKCPIFP
! !	ŀ	· · -	MARSISTSGPLDKEDTGRQKLISTGSLPATLQGATDSLGLEWHL
1		İ	PSPDPVTVPYLSPLVVWKELESLLENEGDHAITVADFVDHHPIV
			FWNLVWYFRRLDLPSNLPGLILSSEHCNKYSKIPRHCMSEDSKY
	.		VLIQMLWDNMKLHQDPGQPLYILWNAHTQKYPMVHLLQKSDNSF
1	Í		NQELLKSMVKSIKMNDVYGPMSQILETLNKCPHFKRQRSLYREI
			LFLSLVALGRENIDIDAFDKEYKMAYDRLTPSQVKSTHNCDRPP
<u> </u>			STGVMECRKTFGEPYL
6420	207	1187	RKMIDKNQTCGVGQDSVPYMICLIHILEEWFGVEQLEDYLNFAN
1 1			YLLWVFTPLILLILPYFTIFLLYLTIIFLHIYKRKNVLKEAYSH
1 1			NLWDGARKTVATLWDGHAAVWHGYEVHGMEKIPEDGPALIIFYH
			GAIPIDFYYFMAKIFIHKGRTCRVVADHFVFKIPGFSLLLDVFC
			ALHGPREKCVEILRSGHLLAISPGGVREALISDETYNIVWGHRR
L l		J	GFAQVAIDAKVPIIPMFTQNIREGFRSLGGTRLFRWLYEKFRYP
-			

SEO	Predicted	I Dun di an a 3	
ID	beginning	Predicted end nucleotide	
NO:	nucleotide	location	
1	location	corresponding	1 TAGEMENT ACTO, PEPPENVISION CO.
	corresponding	to first	1 "-" Value Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later Later
İ	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
[	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	<u>L</u>	\=possible nucleotide insertion)
1			FAPMYGGFPVKLRTYLGDPIPYDPQITAEELAEKTKNAVQALID
6421		<u>                                     </u>	MORTPONINSALLERPH
0421	1844	362	WALSLRROPERMSNKLLSPHPHSVVI.RSFFVMACCDAVILDAGD
	1		A ZWODINGSAYFLGSPOLROVGOTTRVDADMAAGT. TY TIPL OF COL
1	1		1 22 TALANTARCHAPEOPVIIRASIRDERGALEOATTABARBARBAR
1			DEBUGEAUGGERGLE PMGLINAL EDER DE LIDET LIVE DE LIDET EN COMPANY DE LIDET LIVE DE LIDET LIVE DE LIDET LIVE DE LIDET LIVE DE LIDET LIDET LIVE DE LIDET LIVE DE LIDET LIVE DE LIDET LIVE DE LIDET LIVE DE LIDET LIVE DE LIDET LIVE DE LIDET LIVE DE LIDET LIVE DE LIDET LIVE DE LIDET LIVE DE LIDET LIVE DE LIDET LIVE DE LIDET LIVE DE LIDET LIVE DE LIDET LIVE DE LIDET LIVE DE LIDET LIVE DE LIDET LIVE DE LIDET LIDET LIVE DE LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LIDET LID
1	1		TELEVIDORDEDPORKLICTOTRIFEDVET. DOCUMENTAL CONTROL
1	1	·	TELEFERGER POIVDMFGTGGGLLEVRACITACECENTRACE AND
			1 TIDDEET HEILIGE FEERMNYLLSWOFT COCCURS TO TOWN
]	1		LICUSMAST LKG1TAAVVINGSVANVCCTI DVVCCTI DVVCCTI DVVCCTI
1	1		1 MAIN INDGIADIVDVLNSPLEGPDOKSEIDVEDAEGED DIVIN
1	·		VOUNNIASE YANEACKRI OAHGRRKDOTTOVDEROVIVE TOTOLOGI
	1		PLCRASLHALVGSPIIWGGEPRAHAMAQVDAWKQLQTFFHKHLG GREGTIPSKV
6422	181	2133	OKEGITESKY
j	]		EGENLSWFQEFWGDIAKEFYWKTPCPGPFLRYNFDVTKGKIFIE
i	1		WMKGATTNICYNVLDRNVHEKKLGDKVAFYWEGNEPGETTQITY HQLLVQVCQFSNVLRKQGIHKGDRVAIYMPMIPELVVAMLACAR
	1		IGALHSIVFAGFSSESLCERILDSSCSLLITTDAFYRGEKLVNL
ı	1		TABLED EALLY ACCOUNTS FOR CONTROL OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF THE CHARLES OF
1	1		1 WOCED AND CET DOMNHEL WOEVCOLCED BRICD Y BURN HELD
Í	1 1		1 1 1 3 G 3 I G K P K G V V H I V G G Y M I Y V A T T F K V V P D P U D V D V D V D V D V D V D V D V D V D
	·		TOWAL IGHS I VI YGPLANGATSVI.FEGT DTVDDVAIDT WCTT DTV
1			VINCILARIALKULMKFGDEPVTKHSPASIOUT.GTUGEPTNDES
1	1		THE THE VICEOUS TO THE WOTER CHMITTI DOMINATED CO.
f	}		*F*FGVAPAILNESGEELEGEAEGVI.VEVODMDCIMDURECERS
i			NEET LEEKKEPGYYVTGDGCORDODGVVWTTGDTDDMT NITGGTT
	1		DO THE VESALVEHEAVAEAAVVGHPHPVKGECI VCEVIII COOK
			FSPKLTEELKKQIREKIGPIATPDYIQNAPGLPKTRSGKIMRRV
6423	614	1237	LRKIAQNDHDLGDMSTVADPSVISHLFSHRCLTIQ
1			ANLKEIPRDLPPETVLLYLDSNQITSIPNEIFKDLHQLRVLNLS KNGIEFIDEHAFKGVAETLQTLDLSDNRIQSVHKNAFNNLKARA
j i			RIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRP
			TAMASAUDADICINEPKKTTDYAMI.VTMPCWETMITT CVTTTITT TO A
6424			ADDITION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF TH
0424	1	1188	KKVSWPVAAMVHCSCVLFRKYGNFTDKLPLETPGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
1	1	]	OCHGGRGGDAMAAHINKW.L.KULKULKUBADADADAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA
1	İ		TWO SKONDWET PARAGET AND ENGRY TO ELINE TO BE THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND T
1 1	]	i	GGREITHE LPLKGOKRITHLDLKLIADVGLVGEDNACKGGLIGG
	ĺ	1	VSHARPATAD YAFTTLKPELGKIMVSDEKOTSVADI DOZ ZBORE
l	ŀ	i	THIRD THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROP
]			DUINDUDI ADELOTKPALLAVNIMOT DONODEDITO ACCORDING
	Į.	I	THE PROPERTY OF CHAIN PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY
6425	1850		PORTUGENDADIAR RULEN LWISDIMSSTEDDS KUN TETEVANTE
	1		LAMEGGGGIPLETLKEESQSRHVLPASFEVNSLQKSNWGFLLTG
		1	LVGGTLVAVYAVATPFVTPALRKVCLPFVPATMKQIENVVKMLR CRRGSLVDIGSGREPIVIAAAVYCETAVOOR
1		1	CRRGSLVDIGSGDGRIVIAAAKKGFTAVGYELNPWLVWYSRYRA
1	1	į.	WREGVHGSAKFYISDLWKVTFSQYSNVVIFGVPQMMLQLEKKLE RELEDDARVIACRFPFPHWTPDHVTGEGIDTVWAYDASTFRGRE
			KRPCTSMHFQLPIQA
6426	30	565	SRGAAVGGMSVAGGEIRGDTGGEDTAAPGRFSFSPEPTLEDIRR
l			LHAEFAAERDWEQFHQPRNLLLALVGEVGELAELFQWKTDGEPG
1		, ,	FQUINDEREQUALIQUELISDVI, TVI, VAI, A A DCDUINT DI NUIT CITATION
[		1	NRRRYPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT
6427	145		-4
/	145	959	AASWGPPHVPKAGKMVSWMICRLVVLVFGMLCPAYASYKAVKTK
	<u>-</u>	1	VIREYVRWMMYWIVFALFMAAEIVTDIFISWFPFYYEIKMAFVL
			The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s

SEQ	Predicted		
ID	beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide location	(A=Alanine, C=Cvsteine, D=Aspartic Acid P-
1,01	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
-			WLLSPYTKGASLLYRKFVHPSLSRHEKEIDAYIVQAKERSYETV
			LSFGKRGLNIAASAAVQAATKSQGALAGRLRSFSMQDLRSISDA
j	į		PAPAYHDPLYLEDQVSHRRPPIGYRAGGLQDSDTEDECWSDTEA
			VPRAPARPREKPLIRSQSLRVVKRKPPVREGTSRSLKVRTRKKT
		<u> </u>	VPSDVDS
6428	1982	444	SGSGGKMEDHQHVPIDIQTSKLLDWLVDRRHCSLKWQSLVLTIR
i	1		EKINAAIQDMPESEEIAQLLSGSYIHYFHCLRILDIJKGTEAST
			KNIFGRYSSQRMKDWQEIIALYEKDNTYLVELSSLLVRNVNYET
			PSLKKQIAKCQQLQQEYSRKEEECOAGAAEMREOFYHSCKOYGT
1			TGENVRGELLALVKDLPSQLAEIGAAAOOSLGEAIDVYOASVGP
!			VCESPTEQVLPMLRFVQKRGNSTVYEWRTGTEPSVVERPHLEEL
1	]		PEQVAEDAIDWGDFGVEAVSEGTDSGISAEAAGIDWGTFPESDS
1	,		KDPGGDGIDWGDDAVALQITVLEAGTQAPEGVARGPDALTLLEY
ł			TETRNQFLDELMELEIFLAQRAVELSEEADVLSVSQFQLAPAIL
			QGQTKEKMVTMVSVLEDLIGKLTSLQLQHLFMILASPRYVDRVT
			EFLQQKLKQSQLLALKKELMVQKQQEALEEQAALEPKLDLLLEK TKELQKLIEADISKRYSGRPVNLMGTSL
6429	3413	3442	EPSSWTAAPRGPLAAHPLEAAVQEDDRRALSFDSRIKVFANGTL
			VVKSVTDKDAGDYLCVARNKVGDDYVVLKVDVVMKPAKIEHKEE
1			NDHKVFYGGDLKVDCVATGLPNPEISWSLPDGSLVNSFMQSDDS
			GGRTKRYVVFNNGTLYFNEVGMREEGDYTCFAENQVGKDEMRVR
			VKVVTAPATIRNKTCLAVQVPYGDVVTVACEAKGEPMPKVTWLS
1			PTNKVIPTSSEKYQIYQDGTLLIQKAQRSDSGNYTCLVPNSAGE
1			DRKTVWIHVNVQPPKINGNPNPITTVREIAAGGSRKLIDCKAFC
1 1			IPTPRVLWAFPEGVVLPAPYYGNRITVHGNGSLDIRSLRKSDSU
i i			QLVCMARNEGGEARLIVQLTVLEPMEKPIFHDPISEKTTAMAGH
			TISLNCSAAGTPTPSLVWVLPNGTDLOSGOOLORFYHKADGMLH
	1		ISGLSSVDAGAYRCVARNAAGHTERLVSLKVGLKPEANKQYHNL
	•		VSIINGETLKLPCTPPGAGQGRFSWTLPNGMHLEGPQTLGRVSL
į l	J		LDNGTLTVREASVFDRGTYVCRMETEYGPSVTSIPVIVIAYPPR
	ľ		ITSEPTPVIYTRPGNTVKLNCMAMGIPKADITWELPDKSHLKAG
1 1			VQARLYGNRFLHPQGSLTIQHATQRDAGFYKCMAKNILGSDSKT TYIHVF
6430	1946	602	
1	ļ	002	RTRVSTGLRRTLLWSEAVGASSTRGDTGIPGSGEGGAGPGGGEG AMLEAMAEPSPEDPPPTLKPETQPPEKRRRTIEDFNKFCSFVLA
1 1	J		YAGYIPPSKEESDWPASGSSSPLRGESAADSDGWDSAPSDLRTI
			QTFVKKAKSSKRRAAQAGPTQPGPPRSTFSRLQAPDSATLLEKM
i !			KLKDSLFDLDGPKVASPLSPTSLTHTSRPPAALTPVPLSQGDLS
i I	•		HPPRKKDRKNRKLGPGAGAGFGVLRRPRPTPGDGEKRSRIKKSK
}	1		KRKLKKAERGDRLPPPGPPQAPPSDTDSEEEEEEEEEEERREMA
]			TVVGGEAPVPVLPTPPEAPRPPATVHPEGVPPADSESKEVGSTE
			TSQDGDASSSEGEMRVMDEDIMVESGDDSWDLITCYCRKPFAGP
	1		PMIECSLCGTWIHLSCAKIKKTNVPDFFYCQKCKELRPEARRLG
6431			GPPKSGEP
0431	3	605	WWNSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR
	ļ		LEEEALRRKERLKALREKTGRKDKEDGEPKTKHLREEEEEGEKH
!	1		RELRLRNYVPEDEDLKKRRVPQAKPVAVEEKVKEOLEAAKPRDV
	j		IEEVDLANLAPRKPDWDLKRDVAKKLEKLKKRTQRAIAELIRER
6432	56	1662	LKGQEDSLASAVDAATEQKTCDSD
	30	1692	GGLGTMGSRIKQNPETTFEVYVEVAYPRTGGTLSDPEVQRQFPE
	Į		DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKQR
l			FGFCRLSSGAKSCFCILSYLPWFEVFYKLLNILADYTTKRQENQ
			WNELLETLHKLPIPDPGVSVHLSVHSYFTVPDTRELPSIPENRN
	İ		LTEYFVAVDVNNMLHLYASMLYERRILIICSKLSTLTACIHGSA
		1	AMLYPMYWQHVYIPVLPPHLLDYCCAPMPYLIGIHLSLMEKVRN
			MALDDVVILNVDTNTLETPFDDLQSLPNDVISSLKNRLKKVSTT

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	I M-Manualle, CECVSERING D-Accounting alia -
1	location	corresponding	Gidlamic Acid, Faphenvialaning C. Classic
i	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
ſ	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence		Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
		<del></del>	TGDGVAPAEL KNOARESCENTION)
Į			TGDGVARAFLKAQAAFFGSYRNALKIEPEEPITFCEEAFVSHYR
	!		SGAMRQFLQNATQLQLFKQFIDGRLDLLNSGEGFSDVFEEEINM
1			GBYAGSDKLYHQWLSTVRKGSGAILNTVKTKANPAMKTVYKFDI
I		İ	AENGCAPTPEEQLPKTAPSPLVEAKDPKLREDRRPITVHFGQVR
			PPRPHVVKRPKSNIAVEGRRTSVPSPEQNTIATPATLHILQKSI THFAAKFPTRGWTSSSH
6433	1524	484	APUTKPKEVEA KOCKOCAL PAGED
ł			APVTKRKEVFAKDSKGSALDAGRDPKRPALPETLCESGWASNTA
ı	1		PTTPPQPGWCLCGKDFKSSCQTPGREKERRLATMHGSCSFLMLL
Į	İ		LPLLLLLVATTGPVGALTDEEKRLMVELHNLYRAQVSPTASDML
ŀ	<b>.</b>		HMRWDEELAAFAKAYARQCVWGHNKERGRRGENLFAITDEGMDV
1	1		PLAMEEWHHEREHYNLSAATCSPGQMCGHYTQVVWAKTERIGCG
İ	1		SHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQCP SGYHCKNSLCEPIGSPEDAQDLPYLVTEAPSFRATEASDSRKMG
			AEGPDKPSVVSGLNSGPGHVWGPLLGLLLLPPLVLAGIF
6434	40	2002	MPQLNFGMADPTQMGGLSMLLLAGEHALGTPEVFSGTCRPDVSE
1			SPELRQKSPLFQFAEISSSTSHSDASTKQCQTSALFQFAEISSN
ĺ			TSQLGGAEPVKRCGKSALFQLAEMCLASEGMKMEESKLIKAKES
	, !		DGGRIKELEKGKEEKEIKMEKTDETRLQKEAEFEKSAKENLRDS
į			KELRNFEALQIDDIMAIKMEDPKEIRKEELEEDHKCSHFPDFSY
	1		SASSKIIISDVPSRKDHMCHPHGIMIIEDPAALNKPEKLKKKKK
	1		KSKMDRHGNDKSTPKKTCKKROSSESDIESUIVTIPAUA KODUG
1	Į J		I TEALGOT PRAKVETSSSGKGSTLDAKDDKKKTIVEDEVISIONER
į.	]		SDIIAESAPPDFISISASKNISGETPEGIKAEDI.TDMPDAIDDG
ļ	[ ]		I DOGGARFEDSDCHRRIETCGSRKSERSCKGALVKTT VEDGMT mg
· I	1		LIKANVDRGKRSSGKGNSSDHEGCWNEESWTFSOSGTSGSVVEVV
ļ			I REKEDULLUSAKLDEEFEKKFNSLPOVSDUTEDBYGUTENDER
1			AKIGNVSSEPIKTSKGSGDKWSNKOLFLDATHDTEATHGERDAM I
			PIEF VAR V KNIPSIFNIPEPTTTARTFGGOPKEKSKENDDVCDGG
6435	2227		DIQUAGIANEEVLWMINLMNNCGGVYLKOLRHTAMTATA
	222/	657	ALQRDAAAAYAHPEYEERFLOEETVSOOTMSTETLOTPDT AV DE
			VVNSQRPLQRQVHLRGRPASOPTVTRGTTVVKAVUGEEDNDTDD
1			QUEFFSGUNGVDLLIEDOLLRHNGLMTSVTRPDAATROCHEMA
1			VISUAMACIAPWSSALPOPSTSDPSTANHACUCDTT OTTOTIONS
1	!		PIRESVLUPSPOVPATTVAHTATOOPAADADDAMCDDERTMEAN
1 1	i	ľ	TIVE VERTIVATUSLICADAPAGRITTE ASSETT, SEPRED TONET
1 1			GRCRDTLSTITGPTTONTYGRNEGAWMKDDIAKDED TUTTONTALE
i i			GNTLVEFRNLENFKQGRWSNSYKLPYSWIGTGHVVYNGAFYYNR
1 1			AFTRNIIKYDLKQRYVAAWAMLHDVAYEEATPWRWQGHSDVDFA
1 1			VDENGLWLIYPALDDEGFSQEVIVLSKLNAADLSTQKETTWRTG
	1	]	LRRNFYGNCFVICGVLYAVDSYNQRNANISYAFDTHTNTQIVPR
6436	1295	341	LLFENEYFYTTQIDYNPKDRLLYAWDNGHQVTYHVIFAY
1 1	1		GACRPPVRQDPDSGPDYEALPAGATVTTHMVAGAVAGILEHCVM
1 1			YPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGL
1 1	1		NVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGC
1 1	ŀ	ļ	VATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAG
, I			AFYRSYTTQLTMNVPFQAIHFMTYEFLQEHFNPQRRYNPSSHVL SGACAGAVAAAATTPLDVCKTLLNTQESLALNSHITGHITGMAS
			AFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLIT
			KRQEEWRAGK
6437	1828		
i f			PPAPAPPASPARHVTRTARGHLEGGSRAPPLLQAVFLQIKNMVK
		1	LIHTLADHGDDVNCCAFSFSLLATCSLDKTIRLYSLRDFTELPH SPLKFHTYAVHCCCFSPSCULLAGGGTGTT
1	1	1	SPLKFHTYAVHCCCFSPSGHILASCSTDGTTVLWNTENGOMLAV
ļ .	ļ	ł.	MEQPSGSPVRVCQFSPDSTCLASGAADGTVVLWNAQSYKLYRCG
		[ ]	SVKDGSLAACAFSPNGSFFVTGSSCGDLTVWDDKMRCLHSEKAH DLGITCCDFSSODVSDCFOCLOFFDY ACCORDANCE
		j :	DLGITCCDFSSQPVSDGEQGLQFFRLASCGQDCQVKIWIVSFTH
			ILGFELKYKSTLSGHCAPVLACAFSHDGQMLVSGSVDKSVIVYD

SEO	Predicted	1 7	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
j	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
İ	sequence		\=possible nucleotide insertion)
			THENILHTLTQHTRYVTTCAFAPHTLLLATGSMDKTVNIWQFD
			LETLCQARSTEHQLKQFTEDWSEEDVSTWLCAQDLKDLVGIFKM
ł	1		NNIDGKELLNLTKESLADDLKIESLGLRSKVLRKIEELRTKVKS
l		İ	LSSGIPDEFICPITRELMKDPVIASDGYSYEKEAMENWDPAKRN
i ·	i		RTSPP
6438	109	901	EVQILRAKMFQTGGLIVFYGLLAQTMAQFGGLPVPLDQTLPLNV
ł	j	1	NPALPLSPTGLAGSLTNALSNGLLSGGLLGILENLPLLDILKPG
Ī	i		GGTSGGLLGGLLGKVTSVIPGLNNIIDIKVTDPQLLELGLVQSP
	!		DGHRLYVTIPLGIKLQVNTPLVGASLLRLAVKLDITAEILAVRD
1			KQERIHLVLGDCTHSPGSLQISLLDGLGPLPIQGLLDSLTGILN
1			KVLPELVQGNVCPLVNEVLRGLDITLVHDIVNMLIHGLQFVIKV
6439	23	412	SIQTASAITTEMASQSQGIQQLLQAEKRAAEKVADARKRKARRL
	1		KQAKEEAQMEVEQYRREREHEFQSKQQAAMGSQGNLSAEVEQAT
1	İ		RRQVQGMQSSQQRNRERVLAQLLGMVCDVRPQVHPNYRISA
6440	3	517	RARWINSDMGDLPGLVRLSIALRIQPNDGPVFYKVDGQRFGQNRT
l .			IKLLTGSSYKVEVKIKPSTLQVENISIGGVLVPLELKSKEPDGD
1			RVVYTGTYDTEGVTPTKSGERQPIQITMPFTDIGTFETVWQVKF
1			YNYHKRDHCQWGSPFSVIEYECKPNETRSLMWVNKESFL
6441	234	1373	KSGGLRRRQRPGRSAAVGEEELPPGMEKFKAAMLLGSVGDALGY
1			RNVCKENSTVGMKIQEELQRSGGLDHLVLSPGEWPVSDNTIMHI
1	i		ATAKALTTDYWCLDDLYREMVRCYVEIVEKLPERRPDPATIEGC
			AQLKPNNYLLAWHTPFNEKGSGFGAATKAMCIGLRYWKPERLET
1			LIEVSVECGRMTHNHPTGFLGSLCTALFVSFAAOGKPLVOWGRD
	i		MLRAVPLAEEYCRKTIRHTAEYQEHWFYFEAKWOFYLEERKISK
	i		DSENKAIFPDNYDAEEREKTYRKWSSEGRGGRRGHDAPMIAYDA
			LLAAGNSWTELCHRAMFHGGESAATGTIAGCLFGLLYGLDLVPK
			GLYQDLEDKEKLEDLGAALYRLSTEEK
6442	34	796	AEDPAGGLAGODTMFARGLKRKCVGHEEDVEGALAGLKTVSSYS
1	ļ		LQRQSLLDMSLVKLQLCHMLVEPNLCRSVLIANTVRQIQEEMTQ
	•		DGTWRTVAPQAAERAPLDRLVSTEILCRAAWGQEGAHPASGLGD
i i			GHTQGPVSDLCPVTSAQAPRHLQSSAWEMDGPRENRGSFHKSLD
			QIFETLETKNPSCMEELFSDVDSPYYDLDTVLTGMMGGARPGPC
6443	2	- ree	EGLEGLAPATPGPSSSCKSDLGELDHVVEILVET
0-1-4.3	4	555	MASPAASSVRPPRPKKEPQTLVIPKNAAEEQKLKLERLMKNPDK
			AVPIPEKMSEWAPRPPPEFVRDVMGSSAGAGSGEFHVYRHLRRR
1			EYQRQDYMDAMAEKQKLDAEFQKRLEKNKIAAEEQTAKRRKKRQ
	ļ		KI.KEKKLLAKKMKLEQKKQEGPGQPKEQGSSSSAEASGTEEEEE
6444	390	899	VPSFTMGR
	330	033	GSTPRGKMRAPIPEPKPGDLIEIFRPFYRHWAIYVGDGYVVHLA
1	1.		PPSEVAGAGAASVMSALTDKAIVKKELLYDVAGSDKYQVNNKHD
			DKYSPLPCSKI IQRAEELVGQEVLYKLTSENCEHFVNELRYGVA
6445	2	753	RSDQVRDVIIAASVAGMGLAAMSLIGVMFSRNKRQKQ AGAAGAAGAARSPRPQAHTKGVRGLPSRRRSPDCGRMELAAGSF
	- 1	, 33	CEECEMEN ON EL CODAL AGRANIOL LUERGOS GEOGRAFIA CARRIED DE CODAL AGRANIOL LUERGOS GEOGRAFIA CARRIED DE COMPANIOL LUERGOS GEOGRAFIA CARRIED DE COMPANIOL LUERGOS GEOGRAFIA CARRIED DE COMPANIOL LUERGOS GEOGRAFIA CARRIED DE COMPANIOL LUERGOS GEOGRAFIA CARRIED DE COMPANIOL LUERGOS GEOGRAFIA CARRIED DE COMPANIOL LUERGOS GEOGRAFIA CARRIED DE COMPANIOL LUERGOS GEOGRAFIA CARRIED DE COMPANIOL LUERGOS GEOGRAFIA CARRIED DE COMPANIOL LUERGOS GEOGRAFIA CARRIED DE COMPANIOL LUERGOS GEOGRAFIA CARRIED DE COMPANIOL LUERGOS GEOGRAFIA CARRIED DE COMPANIOL LUERGOS GEOGRAFIA CARRIED DE COMPANIOL LUERGOS GEOGRAFIA CARRIED DE COMPANIOL LUERGOS GEOGRAFIA CARRIED DE COMPANIOL LUERGOS GEOGRAFIA CARRIED DE COMPANIOL LUERGOS GEOGRAFIA CARRIED DE COMPANIOL LUERGOS GEOGRAFIA CARRIED DE COMPANIOL LUERGOS GEOGRAFIA CARRIED DE COMPANIOL LUERGOS GEOGRAFIA CARRIED DE COMPANIOL LUERGOS GEOGRAFIA CARRIED DE COMPANIOL LUERGOS GEOGRAFIA CARRIED DE COMPANIOL LUERGOS GEOGRAFIA CARRIED DE COMPANIOL LUERGOS GEOGRAFIA CARRIED DE COMPANIOL LUERGOS GEOGRAFIA CARRIED DE COMPANIOL LUERGOS GEOGRAFIA CARRIED DE COMPANIOL LUERGOS CARRIED DE COMPANIOL LUERGOS CARRIED DE COMPANIOL LUERGOS CARRIED DE COMPANIOL LUERGOS CARRIED DE COMPANIOL LUERGOS CARRIED DE COMPANIOL LUERGOS CARRIED DE COMPANIOL LUERGOS CARRIED DE COMPANIOL LUERGOS CARRIED DE COMPANIOL LUERGOS CARRIED DE COMPANIOL LUERGOS CARRIED DE COMPANIOL LUERGOS CARRIED DE COMPANIOL LUERGOS CARRIED DE COMPANIOL LUERGOS CARRIED DE COMPANIOL LUERGOS CARRIED DE COMPANIOL LUERGOS CARRIED DE COMPANIOL LUERGOS CARRIED DE COMPANIOL LUERGOS CARRIED DE COMPANIOL LUERGOS CARRIED DE COMPANIOL LUERGOS CARRIED DE COMPANIOL LUERGOS CARRIED DE COMPANIOL LUERGOS CARRIED DE COMPANIOL LUERGOS CARRIED DE COMPANIOL LUERGOS
1 1	ļ		SEEQFWEACAELQQPALAGADWQLLVETSGISIYRLLDKKTGLY
]	j		EYKVFGVLEDCSPTLLADIYMDSDYRKQWDQYVKELYEQECNGE
	Į.	,	TVVYWEVKYPFPMSNRDYVYLRQRRDLDMEGRKIHVILARSTSM
	1		PQLGERSGVIRVKQYKQSLAIESDGKKGSKVFMYYFDNPGGQIP SWLINWAAKNGVPNFLKDMARACQNYLKKT
6446	1	1651	
	-	1037	RCPTRSPPPDTPGSRGTTAMCSLASGATGGRGAVENEEDLPELS
			DSGDEAAWEDEDDADLPHGKQQTPCLFCNRLFTSAEETFSHCKS
, ł	l	·	EHQFNIDSMVHKHGLEFYGYIKLINFIRLKNPTVEYMNSIYNPV
	1	1	PWEKEEYLKPVLEDDLLLQFDVEDLYEPVSVPFSYPNGLSENTS
[ ]	l		VVEKLKHMEARALSAEAALARAREDLQKMKQFAQDFVMHTDVRT
1		ļ	CSSSTSVIADLQEDEDGVYFSSYGHYGIHEEMLKDKIRTESYRD
	<u>-</u>		FIYONPHIFKDKVVLDVGCGTGILSMFAAKAGAKKVLGVDQSEI

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	A=Aranine, C=CVSteine, D=Aspartic Acid n
	location	corresponding	Gracamic Acid, Paphenvialanine Cacinata
[	corresponding	to first	n=nistidine, I=Isoleucine K-Lucine
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
İ	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	sequence	Dagachee	Couon, /=possible nucleoride deletion
			\=possible nucleotide insertion)
	ĺ		LYQAMDITRLNKLEDTITLIKGKIEEVHLPVEKVDVIISEWMGY
			FLLFESMLDSVLYAKNKYLAKGGSVYPDICTISLVAVSDVNKHA
		ļ	DRIAFWDDVYGFKMSCMKKAVIPEAVVEVLDPKTLISEPCGIKH
l			IDCHTTSISDLEFSSDFTLKITRTSMCTAIAGYFDIYFEKNCHN
			RVVFSTGPQSTKTHWKQTVFLLEKPFSVKAGEALKGKVTVHKNK KDPRSLTVTLTLNNSTQTYGLQ
6447	1554	1068	RIGPAEWHI SCOCHATI CARNOCRAY COMPANY
ł	1		RLGPAEWHLSGPCHATLGAANRGRALGVRAAWRGAPLCORVMMP
			SRTNLATGIPSSKVKYSRLSSTDDGYIDLQFKKTPPKIPYKAIA LATVLFLIGAFLIIIGSLLLSGYISKGGADRAVPVLIIGILVFL
Ĺ <u> </u>			PGFYHLRIAYYASKGYRGYSYDDIPDFDD
6448	74	559	GQVLSHCYHYRSSRWRRGGLSRGRGAGVMALVPYEETTEFGLQK
1			FHKPLATFSFANHTIQIRQDWRHLGVAAVVWDAAIVLSTYLEMG
1	1		AVELRGRSAVELGAGTGLVGIVAALLACRIRYERDNNFLAMLER
6449			QFIVRKVHYDPEKDVHIYEAQKRNQKEDL
6449	597	1876	EYGVCENLRKLEITGVSCRDVYAKLI, HRYRHILGLWORDIGDVO
			GHEWAAADGEFIIGMWAFDHDDHADDDWDERDI ED IRI WEDA'N
	1		ATVECMYGHKGPHHGHIOIVKKDEFSTKCNOTDHUDMCCCDOER
İ	1		FRINCHEEWGRTLEDIFHEHMOELILMKFIYTSOVDNCLTVBDI
1			IMPERRUDUL KPGLFKGTYGSHGLFTVMLSFHCPPADCTVING
	1		DPMIPAGQQTVEIDLRHRIOLPDI.ENORNFNEI.SPIVI.EVPPDV
1	1		ROADQEGGHEAGEGRGROGPRESOPSPAOPRAFAPGVGDDCTDG
	1		EDGGEPGDAVAAAEOPAOCGOGOPFVI.PVCVGCPNEDVDDBCCDM
ſ	1		CFIGIGLIAGHGFTSPERTPGVFILFDEDREGEWILELVERGEV
6450	848	269	SRVQATFRNADAPSPQAFDEMLKNIQSLTS
	1	200	FVPAPRTVSGKRSLPGEWEERGEGEQRTGREFSGNGGRAVEAAR
1	[		MRLLCGLWLWLSLLKVLQAQTPTPLPLPPPPMQSFQGNQFQGEWF
			VLGLAGNSFRPEHRALLNAFTATFELSDDGRFEVWNAMTRGQHC DTWSYVLIPAAQPGQFTVDHRVWTHEQAGRPQDQPAGQELVAAS
		_	RDAGPVHLPGQSSGPLG
6451	232	939	HSPTPPTSPRASTMEDVKLEFPSLPQCKEDABEWTYPMRREMQE
[	1	i	ILPGLELGPYSSAMKSKLPVLOKHGTTHTTCTPONTENNETVDY
i i	ĺ		FQQDFRILVDDIADNPVENIIRFFPMTKEETDGGLOMCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
	1		GNAGISKSAAFVIAYIMETFGMKYRDAFAVVOEDDECINDNEGE
1	·		VILLE TO BE TO SELECT TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE P
6452	1		BRODEGINGVATAONG
	- j	652	RTRGESSNMEPLAAYPLKCSGPRAKVFAVLLSIVLCTVTLFLLQ
1	1		DRF DRPKINSFYAFEVKDAKGRTUST.EKVKGKUST URBURGDGO
1			LIDRNYLGLKELHKEFGPSHFSVLAFPCNOFGEGEDDBCVEVEG
			PARKNIGVTFPIFHKIKILGSEGEPAFRFIUDGGKKEDDWIFTER
6453	827	223	ILVNPEGQVVKFWRPEEPIEVIRPDTAALUPOUTTEVEPPI
l	1	223	HRRWLPGLSMSPRRTLPRPLSLCLSLCLCLCLAAALGSAQSGSC
]		1	WORKER A LOOKER LINE OAHALOEKGALOF PECCENDARY
1 1	1		DPGIYKCVVCGTPLFKSETKFDSGSGWPSFHDVINSEAITFTDD
L1	ł	1	FSYGMHRVETSCSQCGAHLGHIFDDGPRPTGKRYCINSAALSFT PADSSGTAEGGSGVASPAQADKAEL
6454	827	223	HRRWI.PGI.SMS.PD.PMI.DD.P.T.GI.GI.GI.GI
]	į		HRRWLPGLSMSPRRTLPRPLSLCLSLCLCLCLAAALGSAQSGSC RDKKNCKVVFSQQELRKRLTPLQYHVTQEKGTESAFEGEYTHHK
1			DPGIYKCVVCGTDLEVCETVEDCGCCVDCETCHKK
	Į.		DPGIYKCVVCGTPLFKSETKFDSGSGWPSFHDVINSEAITFTDD FSYGMHRVETSCSQCGAHLGHIFDDGPRPTGKRYCINSAALSFT
		J	PADSSGTAEGGSGVASPAQADKAEL
6455	1042	173	RVHLATVSASAAWDALGLPVRSHMQGSTRRMGVMTDVHRRFLQL
1		ļ	LMTHGVLEEWDVKRLQTHCYKVHDRNATVDKLEDFINNINSVLE
		1	SLYIEIKRGVTEDDGRPIYALVNLATTSISKMATDFAENELDLF
		į	RKALELIIDSETGFASSTNILNLVDQLKGKKMRKKEAEQVLQKF
			VQNKWLIEKEGEFTLHGRAILEMEQYIRETYPDAVKICNICHSL
			- Z-I-WITT DAVITCHICHSL

	1 2 2 2	·	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
İ	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
·	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
ł	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
l	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ľ	Ĭ	sequence	Codon, /=possible nucleotide deletion,
	sequence	<u> </u>	\=possible nucleotide insertion)
			LIQGQSCETCGIRMHLPCVAKYFQSNAEPRCPHCNDYWPHEIPK
			VFDPEKERESGVLKSNKKSLRSRQH
6456	2	555	RPQSRSISMWRNSLLQVSSGLRWLRVCAMVDILGERHLVTCKGA
		1	TVEAEAALQNKVVALYFAAARCAPSRDFTPLLCDFYTALVAEAR
1		J	RPAPFEVVFVSADGSSQEMLDFMRELHGAWLALPFHDPYRHELR
1		!	KRYNVTAIPKLVIVKQNGEVITNKGRKQIRERGLACFQDWVEAA
			DIFQNFSV
6457	. 23	892	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV
1			KLFPLPLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET
			IILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIFVFLND
[			IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG
1			DLQQATEFNQWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL
1			TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY
			SFLTLSSQLKPKPVGEENICLDLKS
6458	23	892	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV
			KLFPLPLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET
			IILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIFVFLND
			IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG
			DLQQATEFNQWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL
			TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY
			SFLTLSSQLKPKPVGEENICLDLKS
6459	23	892	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV
			KLFPLPLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET
			IILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIFVFLND
	, i		IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG
ĺ			DLQQATEFNQWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL
			TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY
			SFLTLSSQLKPKPVGEENICLDLKS
6460	23	892	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV
			KLFPLPLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET
Į į			IILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIFVFLND
	·		IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG
			DLQQATEFNQWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL
			TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY
			SFLTLSSQLKPKPVGEENICLDLKS
6461	1653	360	LQQRTLRITAVGQTHPIAWMAWEPSLGAFYGPASFITFVNCMYF
1			LSIFIQLKRHPERKYELKEPTEEQQRLAANENGEINHQDSMSLS
			LISTSALENEHTFHSQLLGASLTLLLYVALWMFGALAVSLYYPL
1			DLVFSFVFGATSLSFSAFFVVHHCVNREDVRLAWIMTCCPGRSS
			YSVQVNVQPPNSNGTNGEAPKCPNSSAESSCTNKSASSFKNSSQ
			GCKLTNLQAAAAQCHANSLPLNSTPQLDNSLTEHSMDNDIKMHV
			APLEVQFRTNVHSSRHHKNRSKGHRASRLTVLREYAYDVPTSVE
			GSVQNGLPKSRLGNNEGHSRSRRAYLAYRERQYNPPQQDSSDAC
			STLPKSSRNFEKPVSTTSKKDALRKPAVVELENQQKSYGLNLAI
			QNGPIKSNGQEGPLLGTDSTGNVRTGLWKHETTV
6462	3	773	SEELDREKKLKEDSPRKTPNKESGVPSLPVSLTSIKEEPKEAKH
	ļ		PDSQSMEESKLKNDDRKTPVNWKDSRGTRVAVSSPMSQHQSYIQ
			YLHAYPYPQMYDPSHPAYRAVSPVLMHSYPGAYLSPGFHYPVYG
			KMSGREETEKVNTSPSVNTKTTTESKALDLLQQHANQYRSKSPA
			PVEKATAEREREAERERDRHSPFGQRHLHTHHHTHVGMGYPLIP
		•	GQYDPFQGLTSAALVASQQVAAQASASGMFPGQRRE
6463	2	350	VILCILGGWIFKNADRSMEKKKGEPRTRAEARPWVDEDLKDSSD
	ľ		LHQAEEDADEWQESEENVEHIPFSHNHYPEKEMVKRSQEFYELL
			NKRRSVRFISNEQVPMEVIDNVIRTAGL
6464			MKKKS VKF ISNEQ V PMEV I DN V I K I AGD

ſ	SEQ	Predicted	Predicted end	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
	ID	beginning	nucleotide	Amino acid segment containing signal peptide
- 1	NO:	nucleotide	location	I MENIGHTHE, CECVSEEINE Debensytic and a
- 1		location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
		corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
		to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
		amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
		residue of	amino acid	WaTruntonhan Variance
ı		amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
		sequence	_	\=possible nucleotide insertion)
- 1				LVEPSKLGRTLTHEHLAMTFDCCYCPPPPCQEAISKEPIVMKNL
- 1			-	YWIQKNAYSHKENLQLNQETEAIKEELLYFKANGGGALVENTTT
			1	GISRDTQTLKRLAEETGVHIISGAGFYVDATHSSETRAMSVEQL
			]	TDVLMNEILHGADGTSIKCGIIGEIGCSWPLTESERKVLQATAH
- 1			İ	AVAQLGCPVIIHPGRSSRAPFOIIRILORAGADICVTIMOULDD
				I I LUCKELLE FAQLICY LEYDLEGTELL HVOLGDOT DAND DONNE
	ì			I TRRVRLLVEEGCEDRILVAHDIHTKTRI MKYGGHGVEHTI TORTI
<b>-</b>	6465	126		PRMLLRGITENVLDKILIENPKOWLTFK
	0105	120	1396	KMTVFFKTLRNHWKKTTAGLCLLTWGGHWLYGKHCDNLLRRAAC
	i			QEAQVEGNQLIPPNAOVKKATVFLNPAACKCKAPTLEEVNAADT
				LHLSGMDVTIVKTDYEGOAKKLIELMENTDVITVAGGDGGTODI
	}			VIGVERRIDEATESKIPIGFIPLGETSSISHTI, FARROWET
				TDATLAIVKGETVPLDVLQIKGEKEQPVFAMTGLRWGSFRDAGV
	1			KVSKYWYLEPLKIKAAHFFSTLKEWPQTHQASISYTGPTERPPN
	[			EPEETPVQRPSLYRRILRRLASYWAQPQDALSQEVSPEVWKDVQ
	1			LSTIELSITTRNNOLDPTSKEDFLNICIEPDTISKGDFITIGSR
L			4	KVRNPKLHVEGTECLQASQCTLLIPEGAGGSFSIDSEEYEAMPV EVKLLPRKLQFFCDPRKREQMLTSPTQ
1	6466	1134	828	VARGTELSQLEKAHPPADMGRRKSKRKPPPKKKMTGTLETQFTC
	l	Ĭ		PPCNHEKSCDVKMDRARNTGVISCTVCLEEFQTPITYLSEPVDV
$\perp$				YSDWIDACEAANQ
	6467	301	2571	GELRVLALAHGELACHAVLTASLISLESPIMDSDMDVERDNING
1	1	į	1	I ACVVVGDNAVGKTRLICARACNATITOVOLLATINDTIMA TOO
1	Ì	ŀ		IRVCQEVLERSRDVVDDVSVSLRLWDTFGDHHKDDDERVGDGDV
	1			VVLCFSIANPNSLHHVKTMWYPETKHFCPPADVITLVCCOLDIDI
1				ADDEAVNKAKRPLARPIKPNEILPPEKCREVAKELGIDVVERGI
ı				VAQFGIKDVFDNAIRAALISRRHLOFWKSHLDNVODDIJ ON DOV
	}			FERPPPP11VVPDPPSSSEECPAHLLEDPLCADVILUI OFFICE
1		1		FARKIILSTSSSKFYDLFLMDISEGELGGDSBDGGTUDBDVOG**
	İ	i		DUANHAHHHHHGRDFLLRAASFDVCESVDFACGSCDAGT DAGE
				SDGILRGNGTGYLPGRGRVLSSWSRAFVSIQEEMAEDPLTYKSR
				LMVVVKMDSSIQPGPFRAVLKYLYTGELDENERDLMHIAHIAEL LEVEDLEMMVANILABLE FANCETEN
1	- 1	ł	1	LEVFDLRMMVANILNNEAFMNQEITKAFHVRRTNRVKECLAKGT FSDVTFILDDGTISAHKPLLISSCDWMAAMFGGPFVESSTREVV
		Į		FPYTSKSCMRAVLEYLYTGMFTSSPDLDDMKLIILANRLCLPHL
				VALTEQYTVTGLMEATQMMVDIDGDVLVFLELAQFHCAYQLADW
1				CLAMICINYNNVCRKFPRDMKAMSPENOEVEEKHDWDDVWVIV
1	ł		Í	EUNIQRAKKEREKEDYLHLKRQPKRRWLFWNSPSSPSSSAAGG
-	6468	3		SPSSSSAVV
		-	1374	DAWAGTNMAALAPVGSPASRGPRLAAGLRLLPMLGLLQLLAEPG
1	Į			DGRVHHLALKDDVRHKVHLNTFGFFKDGVMIANUGGI GI NEDDD
	1	•	1	ADVITGESLDRIKNDGFSSYLDEDVNYCTI,KKOGVGVTT 1 77 5 1
				SKSEVKVKSPPEAGTOLPKIIFSRDEKVIGOGORDMUNDAGAGA
	[	1		QTQKTQDGGKSKRSTVDSKAMGEKSFSVHNNGGAVSFOFFPNTC
1				TDDQEGLYSLYFHKCLGKELPSDKFTFSLDIEITEKNPDSYLSA
1		į	ŀ	GEIPLPKLYISMAFFFFLSGTIWIHILRKRRNDVFKIHWLMAAL
1	1	}		PFTKSLSLVFHAIDYHYISSQGFPIEGWAVVYYITHLLKGALLF ITIALIGTGWAFIKHILSDKDKKIFMIVIPRRVLANVAYIIIES
	ľ			TEFGTTEYGLWKDSLELVDLLGGGALLDWYNYAYIIIES
<u> </u>			į,	TEEGTTEYGLWKDSLFLVDLLCCGAILFPVVWSIRHLQEASATD GKGKFSRAHFVLLSLL
1	6469	3	1374	DAWAGTNMAALAPVGSPASRGPRLAAGLRLLPMLGLLQLLAEPG
	1		1 3	LGRVHHLALKDDVRHKVHLNTFGFFKDGYMVVNVSSLSLNEPED
	l		i i	KDVTIGFSLDRTKNDGFSSYLDEDVNYCILKKQSVSVTLLILDI
				SRSEVRVKSPPEAGTQLPKIIFSRDEKVLGQSQEPNVNPASAGN
			1 5	2TQKTQDGGKSKRSTVDSKAMGEKSFSVHNNGGAVSFOFFFNTC
				TDDQEGLYSLYFHKCLGKELPSDKFTFSLDIEITEKNPDSYLSA
				INTERESTED ILSA

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
İ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ĺ	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
1		1	GEIPLPKLYISMAFFFFLSGTIWIHILRKRRNDVFKTHWIMAAL
			PFTKSLSLVFHAIDYHYISSQGFPIEGWAVVYYITHLLKGALLE
-		ļ	ITIALIGTGWAFIKHILSDKDKKIFMIVIPRRVLANVAYITIES
			TEEGTTEYGLWKDSLFLVDLLCCGAILFPVVWSIRHLQEASATD
6470	2726	1437	GKGKFSRAHFVLLSLL
,	1	1437	AAASGVSSRADAPVLAQSPASAGNGRPSTPRVPGSRRHPSAPRS
1			GPLPREDGCRTPGPQLLPLPGALLRPRTLLSSAAETGRSRHPDT
1	<b>)</b> .		QHPSSGGRCRGGTESPSSAAGRPASMAEAEEDCHSDTVRADDDE ENESPAETDLQAQLQMFRAQWMFELAPGVSSSNLENRPCRAARG
	ļ ·		SLOKTSADTKGKQEQAKEEKARELFLKAVEEEQNGALYEAIKFY
			RRAMQLVPDIEFKITYTRSPDGDGVGNSYIEDNDDDSKMADLLS
1			YFQQQLTFQESVLKLCQPELESSQIHISVLPMEVLMYIFRWVVS
1			SDLDLRSLEQLSLVCRGFYICARDPEIWRLACLKVWGRSCTKLV
	·		PYTSWREMFLERPRVRFDGVYISKTTYIROGEOSLDGFYRAWHO
			VEYYRYIRFFPDGHVMMLTTPEEPQSIVPRLRTR
6471	1750	299	FFFDKMAAGGSGVGGKRSSKSDADSGFLGLRPTSVDPALRRRRR
			GPRNKKRGWRRLAQEPLGLEVDQFLEDVRLOERTSGGLISEADN
	'		EKLFFVDTGSKEKGLTKKRTKVQKKSLLLKKPLRVDLILENTSK
1			VPAPKDVLAHQVPNAKKLRRKEQLWEKLAKQGELPREVRRAQAR
			LLNPSATRAKPGPQDTVERPFYDLWASDNPLDRPLVGQDEFFLE
1			QTKKKGVKRPARLHTKPSQAPAVEVAPAGASYNPSFEDHQTLLS
			AAHEVELQRQKEAEKLERQLALPATEQAATQESTFQELCEGLLE
1 1	ľ		ESDGEGEPGQGEGPEAGDAEVCPTPARLATTEKKTEQORRREKA VHRLRVQQAALRAARLRHQELFRLRGIKAQVALRLAELARRQRR
1			ROARREAEADKPRRLGRLKYQAPDIDVQLSSELTDSLRTLKPEG
			NILRDRFKSFQRRNMIEPRERAKFKRKYKVKLVEKRAFREIQL
6472	3	897	SCGSDRAQWAMEFPFDVDALFPERITVLDQHLRPPARRPGTTTP
1			ARVDLQQQIMTIIDELGKASAKAONLSAPITSASRMOSNRHUUV
1			ILKDSSARPAGKGAIIGFIKVGYKKLFVLDDREAHNEVEPLCIL
1	]		DFYIHESVQRHGHGRELFQYMLQKERVEPHOLAIDRPSOKLLKF
	į		LNKHYNLETTVPQVNNFVIFEGFFAHOHRPPAPSLRATRHSRAA
1	1		AVDPTPAAPARKLPPKRAEGDIKPYSSSDREFLKVAVEPPWPLN
6473	22	912	RAPRRATPPAHPPPRSSSLGNSPERGPLRPFVP
	42	312	SSAVEFVWEGEKMAAEPNKTEIQTLFKRLRAVPTNKACFDCGAK
1 1	Ì		NPSWASITYGVFLCIDCSGVHRSLGVHLSFIRSTELDSNWNWFQ
			LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYREKIRQ LGSAALARHGTDLWIDNMSSAVPNHSPEKKDSDFFTEHTQPPAW
] ]	1	1	DAPATEPSGTQQPAPSTESSGLAQPEHGPNTDLLGTSPKASLEL
1 1	į		KSSIIGKKKPAAAKKGLGAKKGLGAQKVSSQSFSEIERQAQVAE
		ļ	KLREQQAADAKKQAEESMVASMRLAYQELQIDR
6474	3	462	LOROROHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS
			KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKTSRGA
			KGKKEEKQEAGKEGTAPSENGETKAEEIHISRSTVNVSTSRGTP
<del> </del>			PSTLSVKGQIETVRVKGTEN
6475	3	462	LOROROHPAAAPAVPVRCPTFCFTDIVIMPKRKSPENTEGKDGS
		I	KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA
1		1	KGKKEEKQEAGKEGTAPSENGETKAEEIHISRSTVNVSTSRGTP
6476			PSTLSVKGQIETVRVKGTEN
07/6	106	1090	ARAMAQYKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEETIL
		j	KSQVDKRFSAHYDAVEAELKSSTVGLVTLNDMKARQEALVRERE
			RQLAKRQHLEEQRLQQERQREQEQRRERKRKISCLSFALDDLDD
	1	ļ	QADAAEARRAGNLGKNPDVDTSFLPDRDREEEENRLREELRQEW
!			EAQREKVKDEEMEVTFSYWDGSGHRRTVRVRKGNTVQQFLKKAL
	ł	l	QGLRKDFLELRSAGVEQLMFIKEDLILPHYHTFYDFIIARARGK
j			SGPLFSFDVHDDVRLLSDATMEKDESHAGKVVLRSWYEKNKHIF
<del></del>			PASRWEAYDPEKKWDKYTIR

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	I WATER COLUMN TO DE NOTATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY
i	location	corresponding	1 oracamite Acta, repheny(slavius a sa .
ł	corresponding	to first	1 m-miscituine, im/solencine virgini
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
- 1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
i	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
i	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence		Codon, /=possible nucleotide deletion,
6477	227	915	\=possible nucleotide insertion)
			LOGHLMGIMAASRPLSRFWEWGKNIVCVGRNYADHVREMRSAVL
1			SEPVLFLKPSTAYAPEGSPILMPAYTRNLHHELELGVVMGKRCR
ŀ			AVPEAAAMDYVGGYALCLDMTARDVQDECKKKGLPWTLAKSFTA
į	i		SCPVSAFVPKEKIPDPHKLKLWLKVNGELRQEGETSSMIFSIPY
		}	IISYVSKIITLEEGDIILTGTPKGVGPVKENDEIEAGIHGLVSM TFKVEKPEY
6478	2	1495	
			FVSSRILPESLASSEASTLEAMGRKEEDDCSSWKKQTTNIRKTF
1	1		IFMEVLGSGAFSEVFLVKQRLTGKLFALKCIKKSPAFRDSSLEN
	1		EIAVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILE
-	ŀ		RGVYTEKDASLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPE
			ENSKIMITDFGLSKMEQNGIMSTACGTPGYVAPEVLAQKPYSKA
			VDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFW
			DDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDI YPSVSLQIQKNFAKSKWRQAFNAAAVVHHMRKLHMNLHSPGVRP
	1		EVENRPPETQASETSRPSSPEITITEAPVLDHSVALPALTQLPC
1	i		QHGRRPTAPGGRSLNCLVNGSLHISSSLVPMHQGSLAAGPCGCC
	. i		SSCLNIGSKGKSSYCSEPTLLKKANKKONFKSEVMVPVKASGSS
			HCRAGQTGVCLIM
6479	3	949	SCRGPGWHPAGGQAGAMELLSALSLGELALSFSRVPLFPVFDLS
			YFIVSILYLKYEPGAVELSRRIPIASWLCAMLHCFGSYILADLL
	1		LGEPLIDYFSNNSSILLASAVWYLIFFCPLDLFYKCVCFLPVKL
1	1		TE VALUE VICE VICE AND THE THE THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT
i	1		I MISH EQUURGYWAPETNETLHMSFDTKASLVCATLEDT COMPA-
ļ	1 1		DE VOICHOUTE TE TLEMVSCKVFI D'ATHQUQQDEDAT COVERNS
ŀ	1		FGSACGGDHHHDNHGGSHSGGGPGAQHSAMPAKSKEELSEGSRK
6480	192		I MARKAD
"""	192	514	DFMSIYFPIHCPDYLRSAKMTEVMMNTQPMEEIGLSPRKDGLSY
	1		VIETOFOUT DRUCKLIKDRLPSTVVPDTPCEVPCCRI DUBBBBBB
6481	110		VQEDEQDACEETAKENKEO
	110	1131	KSRMDLDVVNMFVIAGGTLAIPILAFVASFLLWPSALIRIYYWY
1	1		WARL DOMOVER VHHEDYOFCYSFROPDOMEDCTI ME HODOS *****
İ	1		THE TO A VERY DEVIAL PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY
	]		VE VECTIALINAR PEHLVGTSMGGOVAGVVA AVVDODVGGT 137 ****
1.		l	ACCOUNT ONCE VORDKELOGSAAVERTDI.TDCDDDDDAGDAG I
1			DIVERVEQUILOGIVING THRINEVERI, DI PINGRY COMPANIO
			THE RICK OF LATINGROUP OF THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE PROPERTY THE P
6482	2517	568	MOVALEK PRETAKTI I DELASVHNTONNEKI.D
1			EPVSKVSQSRRKAGVPTANIEESQAVEAAMANVPWAEVCEKFQA
	•		ALALSRVELHKNPEKEPYKSKYSARALLEEVKALLGPAPEDEDE
]	į.	1	RPEAEDGPGAGDHALGLPAEVVEPEGPVAQRAVRLAVIEFHLGV
1 1	1	1	NHIDTEELSAGEEHLVKCLRLLRRYRLSHDCISLCIQAQNNLGI
1 1	l.		LWSEREEIETAQAYLESSEALYNQYMKEVGSPPLDPTERFLPEE
l í	f	İ	EKLTEQERSKRFEKVYTHNLYYLAQVYQHLEMFEKAAHYCHSTL KROLEHNAYHDIEWATANATI CONTANTANTAN KROLEHNAYHDIEWATANATI CONTANTANTAN KROLEHNAYHDIEWATANATI CONTANTANTAN KROLEHNAYHDIEWATANATI CONTANTANTAN KROLEHNAYHDIEWATANATI CONTANTANTAN KROLEHNAYHDIEWATANATI CONTANTANTAN KROLEHNAYHDIEWATANATI CONTANTANTAN KROLEHNAYHDIEWATANATI CONTANTANTAN KROLEHNAYHDIEWATANATI CONTANTANTAN KROLEHNAYHDIEWATANATI CONTANTANTAN KROLEHNAYHDIEWATANATI CONTANTANTAN KROLEHNAYHDIEWATANATI CONTANTANTAN KROLEHNAYHDIEWATANATI CONTANTANTAN KROLEHNAYHDIEWATANATI CONTANTANTAN KROLEHNAYHDIEWATANATI CONTANTANTAN KROLEHNAYHDIEWATANATI CONTANTANTAN KROLEHNAYHDIEWATANATI CONTANTANTAN KROLEHNAYHDIEWATANATI CONTANTANTAN KROLEHNAYHDIEWATANATI CONTANTANTAN KROLEHNAYHDIEWATANATI CONTANTANTAN KROLEHNAYHDIEWATANATI CONTANTANTAN KROLEHNAYHDIEWATANATI CONTANTANTAN KROLEHNAYHDIEWATANATI CONTANTANTAN KROLEHNAYHDIEWATANATI CONTANTANTAN KROLEHNAYHDIEWATANATI CONTANTANTAN KROLEHNAYHDIEWATANATI CONTANTANTAN KROLEHNAYHDIEWATANATI CONTANTANTAN KROLEHNAYHDIEWATANATI CONTANTANTAN KROLEHNAYHDIEWATANATI CONTANTANTAN KROLEHNAYHDIEWATANATI CONTANTANTAN KROLEHNAYHDIEWATANATI CONTANTANTAN KROLEHNAYHDIEWATAN KROLEHNAYHDIEWATANATI CONTANTANTANTANTANTANTAN KROLEHNAYHDIEWATAN KROLEHNAYHDIEWATANATI CONTANTANTAN ANTANTANTANTANTAN KROLEHNAYHDIEWATANTANTANTANTANTANTANTANTANT
] }		ľ	KRQLEHNAYHPIEWAINAATLSQFYINKLCFMEARHCLSAANVI FGOTGKISATEDTBEARGENDELYNDER
j l			FGQTGKISATEDTPEAEGEVPELYHQRKGEIARCWIKYCLTLMQ NAQLSMQDNIGELDLDKQSELRALRKKELDEEESIRKKAVQFGT
1	Í	1	GELCDAISAVEEKVSYLRPLDFEEARELFLLGQHYVFEAKEFFQ
1	J	1	IDGYVTDHIEVVQDHSALFKGLAFFETDMERRCKMHKRRIAMLE
	1	!	PLTVDLNPQYYLLVNRQIQFEIAHAYYDMMDLKVAIADRLRDPD
1		İ	SHIVKKINNLNKSALKYYQLFLDSLRDPNKVFPEHIGEDVLRPA
ľ		İ	MLAKFRVARLYGKIITADPKKELENLATSLEHYKFIVDYCEKHP
			EAAQEIEVELELSKEMVSLLPTKMERFRTKMALT
6483	3	623	NSHLLCGLRARAPLSANGREARAMEQRLABFRAARKRAGLAAQP
ı	į.		PAASQGAQTPGEKAEAAATLKAAPGWLKRFLVWKPRPASARAQP
1			GLVQEAAQPQGSTSETPWNTAIPLPSCWDQSFLTNITFLKVLLW
		1 1	LVLLGLFVELEFGLAYFVLSLFYWMYVGTRGPEEKKEGEKSAYS
			STATE VESTE INFI VOIRGPEEKKEGEKSAYS

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +=Ct==
	amino acid	sequence	Codon, /=possible nucleotide deletion
L	sequence	<u>i</u>	\=possible nucleotide insertion)
			VFNPGCEAIQGTLTAEOLERELOLRPLAGE
6484	201	965	QLAVKTKMSGLRPGTQVDPEIELFVKAGSDGESIGNCDECORLE
Ĭ.			MILWLKGVKFNVTTVDMTRKPEELKDLAPGTNPPFI,VYNKFI,KT
			DFIKIEEFLEQTLAPPRYPHLSPKYKESFDVGCNLFAKESAVIK
i			NTQKEANKNFEKSLLKEFKRLDDYLNTPLLDETDPDSAFEPPVS
1			RRLFLDGDQLTLADCSLLPKLNIIKVAAKKYRDFDIPAEFSGVW
6485	<del> </del>		RYLHNAYAREEFTHTCPEDKEIENTYANVAKQKS
0405	6	1091	FVDLVRAVEFLPCPDSQKLEKECQSSEESMGSNSMRSILEEDEE
1			DEEPPRVLLYHEPRSFEVGMLVWHKHKKYPFWPAVVKSVRQRDK
ŀ			KASVLYIEGHMNPKMKGFTVSLKSLKHFDCKEKQTLLNQAREDF
			NQDIGWCVSLITDYRVRLGCGSFAGSFLEYYAADISYPVRKSIQ
į		1	QDVLGTKLPQLSKGSPEEPVVGCPLGQRQPCRKMLPDRSRAARD
ļ			RANQKLVEYIGKAKGAESHLRAILKSRKPSRWLQTFLSSSQYVT
	J		CVETYLEDEGQLDLVVKYLQGVYQEVGAKVLQRTNGDRIRFILD VLLPEAIICAISAGDEVDYKTAEEKYIKGPSLSYREKEIFDNQL
			LEERNRRRR
6486	10	581	LVLQAGGAHLSPSRVTQGIYYMLAFSEMPKPPDYSELSDSLTLA
1			GGTGRFSGPLHRAWRMNFRQRMGWIGVGLYLLASAAAFYYVFE
1			ISETYNRLALEHIQQHPEEPLEGTTWTHSLKAQLLSLPFWVWTV
			IFLVPYLQMFLFLYSCTRADPKTVGYCIIPICLAVICNRHQAFV
			KASNQISRLQLIDT
6487	352	863	SFLKPLRGKMSVTLHTDVGDIKIEVFCERTPKTCENFLALCASN
İ			YYNGCIFHRNIKGFMVQTGDPTGTGRGGNSIWGKKFEDEYGEVI.
			KHNVRGVVSMANNGPNTNGSOFFITYGKOPHLDMKYTVFGKVID
6488	878		GLETLDELEKLPVNEKTYRPLNDVHIKDITIHANPFAO
0400	878	241	TALQEFGTSGPPLSLRFALPSGTGRFKPLPGARGPSWPPSPRVP
			MEPPNLYPVKLYVYDLSKGLARRLSPIMLGKQLEGIWHTSIVVH
			KDEFFFGSGGISSCPPGGTLLGPPDSVVDVGSTEVTEEIFLEYL
			SSLGESLFRGEAYNLFEHNCNTFSNEVAQFLTGRKIPSYITDLP
6489	1457	375	SEVLSTPFGQALRPLLDSIQIQPPGGSSVGRPNGQS
·		373	KVAKMATALSEEELDNEDYYSLLNVRREASSEELKAAYRRLCML
			YHPDKHRDPELKSQAERLFNLVHQAYEVLSDPQTRAIYDIYGKR GLEMEGWEVVERRRTPAEIREEFERLQREREERRLQQRTNPKGT
			ISVGVDATDLFDRYDEEYEDVSGSSFPQIEINKMHISQSIEAPL
	}		TATDTAILSGSLSTQNGNGGGSINFALRRVTSAKGWGELEFGAG
			DLQGPLFGLKLFRNLTPRCFVTTNCALQFSSRGIRPGLTTVLAR
ļ			NLDKNTVGYLQWHCSSPLLQVQRPHRNTRACAPEPSFRPFLHVP
1			TWDAECSGARTPSTAWTSAAVKLREACLSGPGSGSHQLLLLTPR
			SKRRTGGG
6490	3	1183	HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH
!	,		KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT
1	į		HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWERIVGESNDKLRG
i	ļ		QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIVE
ľ			APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD
I	ĺ		DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNI.
1	j		GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD
i			NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL
6491	3	1103	KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS
	_	1183	HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH
			KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT
			HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG
		İ	QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE
1			APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD
			DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILA LATKDVRIFTLKDVRVELTSSCCOTTVETT
- 1	ļ		GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCIGIL
		<del></del>	THE TOTAL TOTAL TOTAL TOTAL TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL THE TOTAL TH

SEQ	Drods at a		
ID	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide	Canadanine, Cacysteine, Dalamartic hold n
1.0.	location	location	Grucamic Acid, F=Phenylalanine C-cliedes
1	corresponding	corresponding to first	n=nlStldine, I=Isolencine v=traine
	to first	amino acid	L=Leucine, M=Methionine, N-Asparacine
	amino acid	residue of	Periorine, O=Glutamine, D=Argining
1	residue of	amino acid	S=Serine, T=Threonine V-Valino
İ	amino acid	sequence	W=Tryptophan, Y=Tyrosine, Y=Unknown + Gb
j	sequence	sequence	Codon, /=possible nucleofide deleti
<u> </u>	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	<del> </del>	\=possible nucleotide insertion)
6492	34	2573	KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS
1	1	25/3	1PFLKSCCCCLFDFPPPPLDOVOEEECEVEPVEEUCEPVEEUCE
1		1	FUSVARGESQSEDEOFENDLETDPDNWOOTMEDEUT OF KROOK
ŀ		ł	RRQEVINELFYTERAHVRTLKVLDOVFVODVSDEGTI SDGELDV
	1		1 TESTING TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO THE TESTING TO
		}	PGEENURHAAATECSNOPFALEMIKSROKKDSPFOTETIODA TICK
	1		PUCKEDURDITATOMORPEDENTAL
			AADHCRQILNYVNQAVKEAENKQRLEDYQRRLDTSSLKLSEYPN
l			VEELRNLDLTKRKMIHEGPLVWKVNRDKTIDLYTLLLEDILVLL
1	ĺ		QKQDDRLVLRCHSKILASTADSKHTFSPVIKLSTVLVRQVATDN
]			KALFVISMSDNGAQIYELVAQTVSEKTVWQDLICRMAASVKEQS
1	i .		TKPIPLPQSTPGEGDNDEEDPSKLKEEQHGISVTGLQSPDRDLG LESTLISSKPQSHSLSTSGKSEVRDLFVAERQFAKEQHTDGTLK
			EVGEDYQIAIPDSHLPVSEERWALDALRNLGLLKQLLVQQLGLT
			EKSVQEDWQHFPRYRTASQGPQTDSVIQNSENIKAYHSGEGHMP
1	( i		FRTGTGDIATCYSPRTSTESFAPRDSVGLAPQDSQASNILVMDH
	[		MIMTPEMPTMEPEGGLDDSGEHFFDAREAHSDENPSEGDGAVNK
	j l		BEKDVNLRISGNYLILDGYDDVOESSTDEEVASSI WI ODMOGEN
1	1		AVESTROQQHSPONTHSDGAISPFTPFFI.VOODWCAMEVCCDD-
1	ĺ		QSPSSCADSQSQIMEYIHKIEADLEHLKKVEESYTTI.CORIAGE
6493	557		ALIDARSUKS
1	]	1147	TPARMAYQGSSTSDCMSKTLDSASAHFAASAVVSAPVPSRSEVA
I			LECTION TO ANNUAL STATE OF THE ACTION TO THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF THE TANGET OF TANGET OF THE TANGET OF TANGET OF THE TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TANGET OF TAN
	!		VGHITINALIPALCTSSPOTLPMNNSCI.TNAVUI MNUCURICURA
1	1		VHINTRISAPSPTALKLATVAASMDRVDKUTDSSATSSTADDING
6494	2425	1052	EPERLGLNGIAETTVAMEVT
		1032	AVAGGARPCSTPSSPHRRCRRHRPRPLPRPPAAIMSASAVYVLD
1		i	LKGKVLICRNYRGDVDMSEVEHFMPILMEKEEEGMLSPILAHGG
İ			VRFMWIKHNNLYLVATSKKNACVSLVFSFLYKVVQVFSEYFKEL EEESIRDNFVIIYELLDELMDFGYPQTTDSKILQEYITQEGHKL
	1		ETGAPRPPATVTNAVSWRSEGIKYRKNEVFLDVIBSVNLLVSAN
1			GNVLRSEIVGSIKMRVFLSGMPELRLGLNDKVLFDNTGRGKSKS
}			VELEDVKFHQCVRLSRFENDRTISFIPPDGEFELMSYRLNTHVK
	1		PLIMIES VIERHSHSRIEYMIKAKSOPKDDSTANAKETUTOVON
1			DADSPREKTTVGSVKWVPENSEIVWSTKSFPGGKPVIMPRUEGT
1 1		1	FSVEACUREGREPISVKFEIPYFTTSGIOVDVI.KTIDVGGVORT
6495	2425		PMVKIITQNGDYQLRTO
	2723	1052	AVAGGARPCSTPSSPHRRCRRHRPRPLPRPPAAIMSASAVYVLD
1 1		Ĭ	DAGKVLICRNYRGDVDMSEVEHFMPTIMEKEEEGMI CDIT AUGG
	1	1	VRFMWIKHNNLYLVATSKKNACVSIJVEQELVVJAJOVDOTNEDED
1			EBESIKDNFVIIYELLDELMDFGVPOTTDGKTLOEVIMODGGGG
[	Ì		ELGAPAPEATVINAVSWRSEGIKYRKNIPUDI DUTECTOTI TITONA
j i			GNVLRSEIVGSIKMRVFLSGMPELRLGLNDKVLFDNTGRGKSKS
			VELEDVKFHQCVRLSRFENDRTISFIPPDGEFELMSYRLNTHVK
1	1	1	PLIWIESVIEKHSHSRIEYMIKAKSQFKRRSTANNVEIHIPVPN
			DADSPKFKTTVGSVKWVPENSEIVWSIKSFPGGKEYLMRAHFGL PSVEAEDKEGKPPISVKEEIDVETTGGLAND
		1	PSVEAEDKEGKPPISVKFEIPYFTTSGIQVRYLKIIEKSGYQAL PWVRYITQNGDYQLRTQ
6496	247	559	LRAVSLLPLOIAUPEYSTHELECTMEN COORDINATE
	<b>,</b>		LRAVSLLPLQLVLPEYSIHSLFCIMFLCAQEWLTLGLNVPLLFY
		1	HFWRYFHCPADSSELAYDPPVVMNADTLSYCQKEAWCKLAFYLL SFFYYLYCMIYTLVSS
6497	1053	352	ANTQICRLCPRRHLHPPCGAKMGNGTEEDYNFVFKVVLIGESGV
1		13	GKTNLLSRFTRNEFSHDSRTTIGVEFSTRTVMLGTAAVKAQIWD
- 1			TAGLERYRAITSAYYRGAVGALLVFDLTKHQTYAVVERWLKELY
- !		1	DHAEATIVVMLVGNKSDLSQAREVPTEEARMFAENNGLLFLETS
		1 3	ALDSTNVELAFETVLKEIFAKVSKQRQNSIRTNAITLGSAQAGQ
			THE THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF TH

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ŀ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
, <u>I</u>	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	bequence	\=possible nucleotide insertion)
			EPGPGEKRACCISL
6498	2636	272	SLRLCPWGTHLAGPTTMRLSSLLALLRPALPLILGLSLGCSLSL
"""	2030	212	LEVENT CCECERROCUEN VIER COROLLEGEN DE ROCCERROCUEN VIER VIER COROLLEGEN DE ROCCERROCUEN VIER VIER COROLLEGEN DE ROCCERROCUEN VIER VIER VIER VIER VIER VIER VIER VIER
			LRVSWIGGEGEDPCVEAVGERGGPQNPDSRARLDQSDEDFKPRI VPYYRDPNKPYKKVLRTRYIQTELGSRERLLVAVLTSRATLSTL
			AVAVNRTVAHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLM
			CPTI.DUI.UTUECADVDWEEIMODERIZIOADDI AATACII
1			SETLRHLHTHFGADYDWFFIMQDDTYVQAPRLAALAGHLSINQD
			LYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG
1			DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPE KEGSSAFLSAFAVHPVSEGTLMYRLHKRFSALELERAYSEIEQL
i			QAQIRNLTVLTPEGEAGLSWPVGLPAPFTFHSRFEVLGWDYFTE
j i			OHTFSCADGAPKCPLQGASRADVGDALETALEQLNRRYQPRLRF
			QKQRLLNGYRRFDPARGMEYTLDLLLECVTQRGHRRALARRVSL LRPLSRVEILPMPYVTEATRVQLVLPLLVAEAAAAPAFLEAFAA
			NVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAAELERRY
į l	] .		PGTRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTTVWTRPG
) ]			PEVLNRCRMNAISGWQAFFPVHFQEFNPALSPQRSPPGPPGAGP
			DPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAARARLAG
		,	ELAGQEEEEALEGLEVMDVFLRFSGLHLFRAVEPGLVQKFSLRD
			CSPRLSEELYHRCRLSNLEGLGGRAQLAMALFEQEQANST
6499	3	2040	SCSADTRPSGQAWPTVGLRAAAGAFRTGSPLALGPETPQVACLP
			GHPPVRPQVSGGPGAMPDPAAHLPFFYGSISRAEAEEHLKLAGM
			ADGLFLLRQCLRSLGGYVLSLVHDVRFHHFPIERQLNGTYAIAG
1			GKAHCGPAELCEFYSRDPDGLPCNLRKPCNRPSGLEPOPGVFDC
[ [			LRDAMVRDYVRQTWKLEGEALEQAIISQAPQVEKLIATTAHERM
			PWYHSSLTREEAERKLYSGAQTDGKFLLRPRKEQGTYALSLIYG
1			KTVYHYLISQDKAGKYCIPEGTKFDTLWQLVEYLKLKADGLIYC
1	i i		LKEACPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTLNSDGYT
1			PEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKLFLKRDNL
			LIADIELGCGNFGSVRQGVYRMRKKQIDVAIKVLKQGTEKADTE
1 1			EMMREAQIMHQLDNPYIVRLIGVCQAEALMLVMEMAGGGPLHKF
			LVGKREEIPVSNVAELLHQVSMGMKYLEEKNFVHRDLAARNVLL
1			VNRHYAKISDFGLSKALGADDSYYTARSAGKWPLKWYAPECINF
			RKFSSRSDVWSYGVTMWEALSYGQKPYKKMKGPEVMAFIEQGKR
	[		MECPPECPPELYALMSDCWIYKWEDRPDFLTVEQRMRACYYSLA
			SKVEGPPGSTQKAEAACA
6500	1773	726	TGPTHASADAWGLVRSVTBWCANVRGNPCAAALSCPQAVLDAGK
1 1	ļ		MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHL
1 1			QAPNKEDILKISEDERMELSKSFRVYCIILVKPKDVSLWAAVKE
1			TWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMRKAYKYAFDK
[		_	YRDQYNWFFLARPTTFALIENLKYFLLKKDPSQPFYLGHTIKSG
1		•	DLEYVGMEGGIVLSVESMKRLNSLLNIPEKCPEQGGMIWKISED
[			KQLAVCLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMTYHPN
6501			QVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGPYFQ
1 0301	1	570	LVGMSGGGTETPVGCEAAPGGGSKKRDSLGTAGSAHLIIKDLGE
1			IHSRLLDHRPVIQGETRYFVKEFEEKRGLREMRVLENLKNMIHE
1			TNEHTLPKCRDTMRDSLSQVLQRLQAANDSVCRLQQREQERKKI
į			HSDHLVASEKQHMLQWDNFMKEQPNKRAEVDEEHRKAMERLKEQ
6500			YAEMEKDLAKFSTF
6502	213	1650	AGNKPDPWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE
			KSSEALEFMKRDLTEFTQVVQHDTACTIAATASVVKEKLATEGS
1			SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT
1 1	į		AEPYDGTKARLYSLQSDPATYCNEPDGPPELFDAWLSQFCLEEK
	ĺ	İ	KGEISELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHQLEQ.
			EQARRDALKQRAEQSISEEPGWEEEEEELMGISPISPKEAKVPV
ļ i			AKISTFPEGEPGPQSPCEENLVTSVEPPAEVTPSESSESISLVT QIANPATAPEARVLPKDLSQKLLEASLEEQGLAVDVGETGPSPP

SEO	Predicted	Predicted end	Division
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ľ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
ļ	amino acid	residue of	S=Serine, T=Threonine, V=Valine
ŀ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +-C+
ľ	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotice insertion\
		Í	IHSKPLTPAGHTGGPEPRPPARVETLREEAPTDLRVERLINGDGC
			KSTPSNNGKKGSSTDISEDWEKDFDLDMTEEEVOMAL SKUDDEG
6503	213	1650	EVSGPGGSEGSEPNGPGCESSPOPAOLSPOEGPCSCLP
1	213	1020	AGNKPDPWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE
1			KSSEALEFMKRDLTEFTQVVQHDTACTIAATASVVKEKLATEGS
			SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT
J			AEPYDGTKARLYSLQSDPATYCNEPDGPPELFDAWLSQFCLEEK
			KGEISELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHQLEQ EQARRDALKQRAEQSISEEPGWEEEEELLMGISPISPKEAKVPV
1			AKISTFFEGEPGPQSPCEENLVTSVEPPAEVTPSESSESISLVT
	1		QIANPATAPEARVLPKDLSQKLLEASLEEQGLAVDVGETGPSPP
			IHSKPLTPAGHTGGPEPRPPARVETLREEAPTDLRVFELNSDSG
			KSTPSNNGKKGSSTDISEDWEKDFDLDMTBEEVQMALSKVDASG
			EVSGPGGSEGSEPNGPGCESSPOPAOLSPOEGPCSCLP
6504	2131	1294	GKVCLVAHWVCLSILSPPPAGMKTPNAOFAEGOOTPAAACRATC
1			SANMTKKKVSQKKQRGRPSSQPCRNIVGCRISHGWKFGDFDTTO
			WKGTVLDQVPINPSLYLVKYDGIDCVYGLEI,HRDERVI CI KIT C
			DRVASSHISDANLANTIIGKAVEHMFEGEHGSKDEWDGMULAOA
1			PIMKAWFYITYEKDPVLYMYOLLDDYKEGDIRIMDEGGEGDDWG
			REPGGVVDGLIGKHVEYTKEDGSKRIGMVIHQVEAKPSVYFIKF
6505	2131	1294	DDDFHIYVYDLVKKS
1		2071	GKVCLVAHWVCLSILSPPPAGMKTPNAQEAEGQQTRAAAGRATG
[ [			SANMTKKKVSOKKORGRPSSOPCRNIVGCRISHGWKEGDEPITO WKGTVLDOVPINPSLYLVKYDGIDCVYGLELHRDERVLSLKILS
1			DRVASSHISDANLANTIIGKAVEHMFEGEHGSKDEWRGMVLAQA
1			PIMKAWFYITYEKDPVLYMYQLLDDYKEGDLRIMPESSESPPTE
1 1			REPGGVVDGLIGKHVEYTKEDGSKRIGMVIHQVEAKPSVYFIKF
			DDDFHIAAADTAKK2
6506	1	1350	EVSPPTSCCLTVAVADPGVSEGFRGFGAGCEMPGRGRCPDCGST
[ [			ELVEDSHYSQSQLVCSDCGCVVTEGVLTTTFSDEGNLDEVTVCD
1		ĺ	SIGENEQVSRSQQRGLRRVRDLCRVLOLPPTFEDTAVAVVOOAV
			RHSGIRAARLQKKEVLVGCCVLITCROHNWPI.TMCATCTLIVAR
1 1			LDVFSSTYMQIVKLLGLDVPSLCLAELVKTYCSSFKLFQASPSV
			PAKYVEDKEKMLSRTMQLVELANETWLVTGRHPLPVITAATFLA
1			WQSLQPADRLSCSLARFCKLANVDLPYPASSRLQELLAVLLRMA
	1		EQLAWLRVLRLDKRSVVKHIGDLLQHRQSLVRSAFRDGTABVET REKEPPGWGQGQGEGEVGNNSLGLPQGKRPASPALLLPPCMLKS
1 [	İ		PKRICPVPPVSTVTGDENISDSEIEQYLRTPQEVRDFQRAQAAR
		i	QAATSVPNPP
6507	1878	929	RSHASRLPELPSGCLVLOVOELVOMSGMEATUTTPTHONKDIGA
	}	Ì	ARSVVRRIGTNLPLKPCARASFETI.PNISDT.CT.PDVPDVDVRV AD
į į	ĺ		TAWLAADEEETYARVRSDTRPLRHTWKPSPLIVMORNASVENILD
		1	GSEERLLALKKPALPALSRTTELODELSHLRSOIAKTVAADAAG
]			ASLTPDFLSPGSSNVSSPLPCFGSSFHSTTSFVISDITEFTEUR
		1	VPELPSVPLLCSASPECCKPEHKAACSSSEEDDCVSLSKASSFA
		İ	DMMGILKDFHRMKQSQDLNRSLLKEEDPAVLISEVLRRKFALKF
6508	862		EDISRKGN
	002	342	WEARKRPQRWPSERREVRVPPPHLQRGRSGLEPGTFRKMAAARP
			SLGRVLPGSSVLFLCDMQEKFRHNIAYFPQIVSVAARMLKNTTL
			DLLDRGLQVHVVVDACSSRSQVDRLVALARMRQSGAFLSTSEGL
6509	2	1053	ILQLVGDAVHPQFKEIQKLIKEPAPDSGLLGLFQGQNSLLH
1	=	1033	FVWNPRGGRKRRRQAAVTQAATRASGTFSPRDGTMTQGKLSVAN
}		1	KAPGTEGQQQVHGEKKEAPAVPSAPPSYEEATSGEGMKAGAFPP
ĺ	İ		APTAVPLHPSWAYVDPSSSSSYDNGFPTGDHELFTTPSWDDQKV
		1	RRVFVRKVYTILLIQLLVTLAVVALFTFCDPVKDYVQANPGWYW ASYAVFFATYLTLACCSGPRRHFPWNLILLTVFTLSMAYLTGML
			THI DACCOGERRAT PWNDILLTVFTLSMAYLTGML

SEQ	Predicted	Predicted end	Amino acid someth
ΙD	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
-	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
-	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
	amino acid	residue of	S=Serine, T=Threonine, V=Valine
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +-C+
1	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
			SSYYNTTSVLLCLGITALVCLSVTVFSFQTKFDFTSCQGVLFVL
		1	LMTLFFSGLILAILLPFQYVPWLHAVYAALGAGVFTLFLALDTQ
6510	37	1156	LLMGNRRHSLSPEEYIFGALNIYLDIIYIFTFFLQLFGTNRE
0320	3,	1136	PCALDGCPQRGAVHPLLSSAMGLLAFLKTQFVLHLLVGFVFVVS
			GLVINFVQLCTLALWPVSKQLYRRLNCRLAYSLWSQLVMLLEWW
	1		SCTECTLFTDQATVERFGKEHAVIILNHNFEIDFLCGWTMCERF
1			GVLGSSKVLAKKELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVV EGLRRLSDYPEYMWFLLYCEGTRFTETKHRVSMEVAAAKGLPVL
1	1		KYHLLPRTKGFTTAVKCLRGTVAAVYDVTLNFRGNKNPSLLGIL
1			YGKKYEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIY
1			NQKGMFPGEQFKPARRPWTLLNFLSWATILLSPLFSFVLGVFAS
			GSPLLILTFLGFVGAGNGHCR
6511	2541	1425	GEEQPLAAAPTECLEQVIGGAGDPGTWASFPSPLPGPAPLKGGK
i			TMATNFSDIVKQGYVKMKSRKLGIYRRCWLVFRKSSSKGPOPLR
1	{		KYPDEKSVCLRGCPKVTEISNVKCVTRLPKETKROAVATIFTDD
			SARTFTCDSELEAEEWYKTLSVECLGSRLNDISLGEPDLLADGV
i	l		QCEQTDRFNVFLLPCPNLDVYGECKLOITHENTYLWDTHNDDVK
	1		LVSWPLCSLRRYGRDATRFTFEAGRMCDAGEGLYTFOTOEGEOT
	į į		YQRVHSATLAIAEQHKRVLLEMEKNVRLLNKGTEHVSVDCTDTT
1 :			MLPRSAYWHHITGSQNIAEASSYAGEGYGAAQASSETDLLNRFI
6512	159	807	LLKPKPSQGDSSEAKTPSQ
	1	007	FGKKSTWFPLSRSLRVASGRSCKLGHGGYTGSGPGFGEPRDSGA
			EVPSGSGRATGCERGGVRGARQGRAPGSSIWRKEPRMVCTRKTK TLVSTCVILSGMTNIICLLYVGWVTNYIASVYVRGQEPAPDKKL
1			EEDKGDTLKIIERLDHLENVIKQHIQEAPAKPEEAEAEPFTDSS
			LFAHWGQELSPEGRRVALKQFQYYGYNAYLSDRLPLDRP
6513	2	756	FVSPEPGFSLAQLNLIWQLTDTKQLVHSFAEGQDQGSAYANRTA
i i			LFPDLLAQGNASLRLQRVRVADEGSFTCFVSIRDFGSDAVGLOV
			AAPYSKPSMTLEPNKDLRPGDTVTITCSSYOGYPEAFVFWODGO
1 1	1		GVPLTGNVTTSQMANEQGLFDVHSILRVVLGANGTYSCLVPNDV
1 1			LQQDAHSSVTITPQRSPTGAVEVQVPEDPVVALVGTDATLRCSF
			SPEPGFSLAQLNLIWOLTDTKOLVHSFAEGODOGSAVANDTALE
1 1			PDLLAQGNASLRLQRVRVADEGSFTCFVSIRDFGSAAVSLQVAA
] ]	į		PYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDGQGV
i i			PLTGNVTTSQMANEQGLFDVHSILRVVLGANGTYSCLVRNPVLQ
1			QDAHSSVTITPQRSPTGAVEVQVPEDPVVALVGTDATLRCSFSP EPGFSLAQLNLIWQLTDTRQLVHSFTEGR
6514	985	302	VGIPGPTISSAAEMEDLUDLDEELRYSLATSRAKMGRRAQQESA
			QAENHLNGKNSSLTLTGETSSAKLPRCRQGGWAGDSVKASKFRR
1			KASERIEDFRLRPQSLNGSDYGGDIPIIPDLEEVQEEDFVLQVA
j í	1		APPSIQIKRVMTYRDLDNDLMKYSAIQTLDGEIDLKLLTKVLAP
			EHEVRERNPSWQDDVGWDWDHLFTEVSSEVLTEWDPLQTEKEDP
			AGQARHT
6515	1345	305	GRVGSRRRGAAVPGGCGAGSTQLEVSASASCGALGSADMNPIVV
		İ	VHGGGAGPISKDRKERVHQGMVRAATVGYGILREGGSAVDAVEG
	1		AVVALEDDPEFNAGCGSVLNTNGEVEMDASIMDGKDLSAGAVSA
l			VQCIANPIKLARLVMEKTPHCFLTDQGAAQFAAAMGVPEIPGEK
	ļ		LVTERNKKRLEKEKHEKGAQKTDCQKNLGTVGAVALDCKGNVAY
			ATSTGGIVNKMVGRVGDSPCLGAGGYADNDIGAVSTTGHGESIL
	İ		KVNLARLTLFHIEQGKTVEEAADLSLGYMKSRVKGLGGLIVVSK
6516	1		TGDWVAKWTSTSMPWAAAKDGKLHFGIDPDDTTITDLP
0210	*	1402	FRRLRYLGQDATAAARDLRTRGLQGYCPSATARQQVLVSALQQL
		i	KGRRSEHRNENQEMPYSTNKELILGIMVGTAGISLLLLWYHKVR
		Į.	KPGIAMKLPEFLSLGNTFNSITLQDEIHDDQGTTVIFQERQLQI
		i	LEKLNELLTNMEELKEEIRFLKEAIPKLEEYIQDELGGKITVHK
			ISPOHRARKRRLPTIQSSATSNSSEEAESEGGYITANTDTEEQS

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	I was a diffuse of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contrac
-	location	corresponding	
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	fartoutile, O=Glutamina D=Naginia
l	amino acid	residue of	S=Serine, T=Threonine, V-Valine
	residue of amino acid	amino acid	W=Tryptophan, Y=Tyrosine v=Unknown
	sequence	sequence	Codon, /=possible nucleotide deletide
<del></del>	Sequence		\"POSSIDIE Nucleotide insertion\
	i	l	FPVPKAFNTRVEELNLDVLI.OKVDHI.PMSESCKSEGER
- [	ł	Ì	DOLL ROBIE FUNK PAKAYGOMY FLOT NTO FUNT COMP.
[			THRAFINGICHLWIAVLCGYVSEFEGIONKINVCUT EKRIT 575
1	1		TARREST TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGET TO A TARGE
	_}		QEALHNFLKAEELCPGYSNPNYMYLAKCYTDLEENQNALKFCNL ALLLPTVTKEDKEAQKEMQKIMTSLKR
6517	3	1414	GRVWGGSSSLNAMUVUBGUAERVERVER
1	ľ	İ	GRVWGGSSSLNAMVYVRGHAEDYERWOROGARGWDYAHCLPYFR KAQGHELGASRYRGADGPLRVSRGKTNHPLHCAFLEATQQAGYP
	1		LTEDMNGFQQEGFGWMDMTIHEGKRWSAACAYLHPALSRTNLKA
	1		DASIDVSKVLFEGTRAVGVEYVKNCOQUDAVACVEVITA OGGE TE
-	1	ĺ	A ADDINGS I GNADDLKKLG I PWYCHI, DCYCOM ODYN DEWYSON
1			TACTACT TURSAUKPLRKVCTGLEWI.WVEFGEGAGAGAGAGA
ł	ļ		1 2 2 2 4 FARDIOFHE LPSOVI DHGRUDTOOFA VOURINGE
1			TOWNS TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE P
1			TAGREDUFGSHIOSHKETDAFTDAKADCAVTIDGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
			T T DDE TO V DPUIKVLGVENLRVVDA G IMPOMUCOMI ATA PORTAGE
6518	242	1098	L DIGITALITA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE LA PORTINA DE
1	1		PAWNPGSEPRTRVRPRARSFPLPPPRAPRRRHRLLRAVPGPSR
i	1 1		RHRCRRAPPPPSTMGDAGSERSKAPSLPPRCPCGFWGSSKTMN LCSKCFADFQKKQPDDDSAPSTSNSQSDLFSEETTSDNNNTSIT
	,		TPTLSPSQQPLPTELNVTSPSKEECGPCTDTAHVSLITPTKRSC
1	!!!		O'DOUGHERSPYRRPRLLENTERSEETSDSYOVEDDDGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
ì			1 YOUR VERDOSCRUGIVE CMLHRI DROUDCTEDUMCDGDDD T
6519	3		1 WITH DRIVERS CORTGEGCS
		1113	ERKMALPPSPVHCVAAAAPTATVSEKEPFGKLQLSSRDPPGSLS
	[		I ARRANGE GERGANGE OF A DODOGUCON - I
	ŀ		I TOTAL DEPARTS POSSESSESSESSES ACTIVIDED A CONCERNAL I
1 1			VPPTLLHAQPHHLLLPAAAAASANAKSRRPKEKREKERRHGL
1			GGAREAGGASREENGEVKPLPRDKIKDKIKERDKEKERRHGL VMNEIKKENGEVKILLKSGKEKPKTNIEDLQIKKVKKKKKKKKK
			ENEKRKRPKMYSKSIQTICSGLLTDVEDQAAKGILNDNIKDYVG
1			KNLDTKNYDSKIPENSEFPFVSLKEPRVQNNLKRLDTLEFKQLI
6520			HILLING NGGASVIRCLO
0520	3	1113	ERKMAEPPSPVHCVAAAAPTATVSEKEPEGVI OLGGERERA
1 1			MANATEDANAPRIONGEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
	1		"" TO THE POPULATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PR
1 1	ŀ		**************************************
1 1	ĺ		OCH MITTAGGATSKEENIGEAK DI DADKI KUKI KEEDDKEKEDDKEKEENING
1	f		VMNEIKKENGEVKILLKSGKEKPKTNIEDLQIKKVKKKKKKKKKK ENEKEKPPKMYSKSIOTIGGGIKTNIEDLQIKKVKKKKKKKKKKK
			ENEKRKRPKMYSKSIQTICSGLLTDVEDQAAKGILNDNIKDYVG KNLDTKNYDSKIPENSEFPFVSLKEPRVQNNLKRLDTLEFKQLI
CE33			HIEHQPNGGASVIHCLQ
6521	. 184	1798	KLFKMATDTSQGELVHPKALPLTVGAQLTHADYLCEVHORE
	1	ĺ	TAX TANGET PERSKLAEGEEEK PEDDIGGEPOVO TURBOTER
·	1		TE CALCOCACUPAGE PENERKEENKSSEETVADDADOGGOVERNO 1
1	İ	1	TARL LEGWATUSASOLARAOKOTOMA GGDDDEMDA TI MDA TICA
j			TURGUAS VALKKYLIHKYPSLELEDDOVLIVONT VDDT VDGT
		1	AS A S A S A S A S A S A S A S A S A S
Í		P .	DV DE DAE I RUCEPREASYSLIRKYVSOVVDVI.DUDIDDOT TIOTE
1			PARTY ERGOLDOLI TORGASGI FOLKKSGEKDI I CCCI MENT TIC
}			ALAAMMERA I CSTTALKKYVLENHPGTNSNYOMHI I VVOT OVOT
ł		1	KNGWMEQISGKGFSGTFQLCFPYYPSPGVLFPKKEPDDSRDEDE
		1	DEDESSEEDSEDEEPPPKRRLQKKTPAKSPGKAASVKQRGSKPA PKVSAAQRGKARPLPKKAPPKAKTPAKKTRPSSTVIKKPSGGSS
6522			RREALSARRE
0322	1042		NKWLRPSPRSHRTPESGRVLSLFRLPPPGMALSGSTPAPCWEED
			THE TOTAL DOG TAMPOWEED

SEQ	Predicted	Predicted end	2
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
· '	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ŀ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
			ECLDYYGMLSLHRMFEVVGGQLTECELELLAFLLDEAPGAAGGL
			SRARSGLKLLLELERRGQCDESNLRLLGQLLRVLARHDLLPHLA
J			RKRRRPVSPERYSYGTSSSSKRTEGSCRRRROSSSSANSOOGSP
			PTKRQRRSRGRPSGGARRRRRGPQPHPSSSQSPPDLPLKAK
6523	2	1097	ASCOTRRITAALDSGERIAGRESPIALAMASNENDIVKOGYVKI
	<b>\</b>		RSRKLGIFRRCWLVFKKASSKGPRRLEKFPDEKAAYFRNFHKVT
1			ELHNIKNITRLPRETKKHAVAIIFHDETSKTFACESELEAEEWC
			KHLCMECLGTRLNDISLGEPDLLAAGVQREQNERFNVYLMPTPN
			LDIYGECTMQITHENIYLWDIHNAKVKLVMNPLSSLRRYGRDST
1			WFTFESGRMCDTGEGLFTFQTREGEMIYQKVHSATLAIAEQHER
Ī	}		LMLEMEQKARLQTSLTEPMTLSKSISLPRSAYWHHITRQNSVGE
			IYSLQGNHENRHSDLTGKSCKTSENRFLEENAPLVMYGITHHLF MDTSTCKVVHDLE
6524	2	1097	
	_ · .	2037	ASCQTRRRTAALDSGERIAGRRSPIALAMASNFNDIVKQGYVKI RSRKLGIFRRCWLVFKKASSKGPRRLEKFPDEKAAYFRNFHKVT
1			ELHNIKNITRLPRETKKHAVAIIFHDETSKTFACESELEAEEWC
1	}		KHLCMECLGTRLNDISLGEPDLLAAGVQREQNERFNVYLMPTPN
			LDIYGECTMQITHENIYLWDIHNAKVKLVMWPLSSLRRYGRDST
			WFTFESGRMCDTGEGLFTFQTREGEMIYQKVHSATLAIAEQHER
1	l l		LMLEMEQKARLQTSLTEPMTLSKSISLPRSAYWHHITRQNSVGE
1	· i		IYSLQGNHENRHSDLTGKSCKTSENRFLEENAPLVMYGITHHLF
			MDTSTCKVVHDLE
6525	1	1859	GESPFSEEESIEFNPSSSGRSARTVSSNSFCSDDTGWPSSQSVS
			PVKTPSDAGNSPIGFCPGSDEGFTRKKCTIGMVGEGSIQSSRYK
1			KESKSGLVKPGSEADFSSSSSTGSISAPEVHMSTAGSKRSSSSR
1 .			NRGPHGRSNGASSHKPGSSPSSPREKDLLSMLCRNQLSPVNIHP
1			SYAPSSPSSNSGSYKGSDCSPIMRRSGRYMSCGENHGVRPPNP
			EQYLTPLQQKEVTVRHLKTKLKESERRLHERESEIVELKSQLAR
1 1			MREDWIEEECHRVEAQLALKEARKEIKQLKQVIETMRSSLADKD KGIQKYFVDINIQNKKLESLLQSMEMAHSGSLRDELCLDFPCDS
			PEKSLTLNPPLDTMADGLSLEEQVTGEGADRELLVGDSIANSTD
[ ]	· •		LPDEIVTATTTESGDLELVHSTPGANVLELLPIVMGQEEGSVVV
			ERAVQTDVVPYSPAISELIQSVLQKLQDPCPSSLASPDESEPDS
			MESFPESLSALVVDLTPRNPNSAILLSPVETPYANVDAEVHANR
l			LMRELDFAACVEERLDGVIPLARGGVVRQYWSSSFLVDLLAVAA
1 1	1		PVVPTVLWAFSTQRGGTDPVYNIGALLRGCCVVALHSLRRTAFR
			IKT
6526	2	2034	SGRAGEPEEWRGRQIIDSKETWIPFNSEDSQQLEEAYSSGKGCN
1	ļ		GRVVPTDGGRYDVHLGERMRYAVYWDELASEVRRCTWFYKGDKD
, 1		ı	NKYVPYSESFSQVLEETYMLAVTLDEWKKKLESPNREIIILHNP
	1		KLMVHYQPVAGSDDWGSTPMEQGRPRTVKRGVENISVDIHCGEP
[	1		LQIDHLVFVVHGIGPACDLRFRSIVQCVNDFRSVSLNLLQTHFK
	1		KAQENQQIGRVEFLPVNWHSPLHSTGVDVDLQRITLPSINRLRH
.	ſ		FTNDTILDVFFYNSPTYCQTIVDTVASEMNRIYTLFLQRNPDFK
			GGVSIAGHSLGSLILFDILTNOKDSLGDIDSEKGSLNIVMDQGD
1			TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDRDLQEIGIP LGPRKKILNYFSTRKNSMGIKRPAPQPASGANIPKESEFCSSSN
			TRNGDYLDVGIGQVSVKYPRLIYKPEIFFAFGSPIGMFLTVRGL
1			KRIDPNYRFPTCKGFFNIYHPFDPVAYRIEPMVVPGVEFEPMLI
			PHHKGRKRMHLELREGLTRMSMDLKNNLLGSLRMAWKSFTRAPY
			PALQASETPEETEAEPESTSEKPSDVNTEETSVAVKEEVLPINV
			GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV
			LKEIYQTQGIFLDQPLQ
6527	1	922	GWVPLLSRILPSDACKIYKQGINIRLDTTLIDFTDMKCQRGDLS
	ł	•	FIFNGDAAPSESFVVLDNEQKVYQRIHHEESEMETEEEVDILMS
			SDIYSATLSTKSISFTRAQTGWLFREDKTERVGNFLADFYLVNG
			The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s

SEQ	Predicted	Predicted end	Amino acid come
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
[	location	corresponding	H-Histidine, I-Isoleucine, K-Lysine,
ľ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ŀ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
- 1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
)	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			LVLESRKRREHLSEEDILRNKAIMESLSKGGNIMEQNFEPIRRO
1	1		SLTPPPQNTITWEEYISAENGKAPHLGRELVCKESKKTFKATIA
			MSQEFPLGIELLLNVLEVVAPFKHFNKLREFVQMKLPPGFPVKL
	<u> </u>		DIPVFPTITATVTFQEFRYDEFDGSIFTIPDDVKEDPSPEDDI
6528	1	1073	LTGPAAAEPRCAADAGMKRALGRRKGVWLRLRKILECVICIVIA
1	1	1	IPFLIKLCPGIQAKLIFLNFVRVPYFIDLKKPODOGINUTCHVV
1			LQPEEDVTIGVWHTVPAVWWKNAOGKDOMWYEDALASSUPTITY
			LHGNAGTRGGDHRVELYKVLSSLGYHVVTFDYRGWGDSVGTBER
			RGMTYDALHVFDWIKARSGDNPVYIWGHSIGTGVATMINDDICE
			RETPPDALILES OF TNIREEAKSHOPS VIYRY FOGEOWERI DDT
1			TSSGIKFANDENVKHISCPLLILHAEDDPVVPFQLGRKLYSIAA
			PARSFRDFKVQFVPFHSDLGYRHKYIYKSPELPRILREFLGKSE
6529	363	2215	РЕНОН
ŀ	İ	4217	THIRYNKIGVVKTMSCGNEFVETLKKIGYPKADNLNGEDFDWLF
i	·		EGVEDESFLKWFCGNVNEQNVLSERELEAFSILQKSGKPILEGA
			ALDEALKTCKTSDLKTPRLDDKELEKLEDEVQTLLKLKNLKIQR RNKCQLMASVTSHKSLRLNAKEEEATKKLKQSQGILNAMITKIS
			NELQALTDEVTQLMMFFRHSNLGQGTNPLVFLSQFSLEKYLSQE
			EQSTAALTLYTKKQFFQGIHEVVESSNESQFFNFLKIQTPSICD
1 .			NQEILEERRLEMARLQLAYICAQHQLIHLKASNSSMKSSIKWAE
			ESLHSLTSKAVDKENLDAKISSLTSEIMKLEKEVTQIKDRSLPA
			VVRENAQLLNMPVVKGDFDLOIAKODYVTARORIJITATOT TKOKA
			SFELLQLSYEIELRKHRDIYROLENLVOELSOSNMMLVKOLEMI
			TDPSVSQQINPRNTIDTKDYSTHRLYOVLEGENKKKELELTUCH
1			LEEVAEKLKQNISLVQDQLAVSAOEHSFFLSKRNKDVDMLCDTI
			YQGGNQLLLSDQELTEOPHKVESOLNKI,NHI,I,TDTI,ADVKTKDK
1 1	1		TLANNKLHOMEREFYVYFLKDEDYLKDIVENLETOSKIKAVSIR
6530	128	2986	D 1
1		2300	GAAHHGAIVQVHPLLPGSSTIMIHDLCLVFPAPAKAVVYVSDIQ
1 7		1	ELYIRVVDKVBIGKTVKAYVRVLDLHKKPFLAKYFPFMDLKLRA
1 1			ASPIITLVALDEALDNYTITFLIRGVAIGQTSLTASVTNKAGQR INSAPQQIEVFPPFRLMPRKVTLLIGATMQVTSEGGPQPQSNIL
1		1	FSISNESVALVSAAGLVQGLAIGNGTVSGLVQAVDAETGKVVII
1 1		j	SQDLVQVEVLLLRAVRIRAPIMRMRTGTQMPIYVTGITNHQNPF
1 1			SFGNAVPGLTFHWSVTKRDVLDLRGRHHEASIRLPSQYNFAMNV
		į.	LGRVKGRTGLRAVVKAVDPTSGQLYGLARELSDEIQVQVFEKLQ
1			LLNPEIEAEQILMSPNSYIKLOTNRDGAASTSVRVI DCDEVATOV
1 1			VHVDEKGFLASGSMIGTSTIEVIAOEPFGANOTTTVAVKUEDUS
1	1		YLKVSMSPVLHTQNKEALVAVPLGMTVTFTVHFHDNSGDVBUAU
1 1			SSVLNFATNRDDFVQIGKGPTNNTCVVRTVSVGI.TI.I.PVMDAVU
] ]	1		PGLSDFMPLPVLOAISPELSGAMVVGDVI.CI.ATVI TELECT COM
1 1	1	j,	WSSSANSILHIDPKTGVAVARAVGSVTVYYEVAGHI.DTVVENDI
1 1	İ	1	SVPQKIMARHDHPIQTSFORATASKVIVAVGDRSSMI.pcpcmpm
f l			QREVIQALHPETLISCQSQFKPAVFDFPSODVFTVEPOFDTALC
! !			QYFCSITMHRLTDKQRKHLSMKKTALVVSASLSSSHFSTEQVGA
		1	EVPFSPGLFADQAEILLSNHYTSSEIRVFGAPEVLENLEUKSGS
<b>f</b>		f	PAVLAFAKEKSFGWPSFITYTVGVLDPAAGSOGPLSTTLTEGD
]		-	VTNQAIAIPVTVAFVVDRRGPGPYGASLFQHFLDSYQVMFFTLF
		1.	ALLAGTAVMI LAYHTVCTPRDLAVPAALTPRASPGHSPHYFAAS
6531	845	1425	SPTSPNALPPARKASPPSGLWSPAYASH
		-443	PSASIPPSASPDPVPDIRTCHFCLVEDPSVGCISGSEKCTISSS
	1	1.2	SLCMVITIYYDVKVRFIVRGCGQYISYRCQEKRNTYFAEYWYQA
1		1,	QCCQYDYCNSWSSPQLQSSLPEPHDRPLALPLSDSQIQNFYQAL
			NLSLPLPNFHAGTEPDGLDPMVTLSLNLGLSFAELRRMYLFINS SGLLVLPQAGLLTPHPS
6532	2	954	AAGPPSEVVNQDSLFPEPEPGPAPQVLLGPQGPGLIKGVAPPTL
			THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PERFORM OF THE PE

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
İ	residue of	amino acid	W-Truntonhan V manain V V V
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
ı	sequence		\=possible nucleotide insertion)
			ITDSTGTHLVLTVTNKNAHSPGLSRGSPQQPSSQPGSPAPAPSA
1	1	l	QMDLEHPLQPLFGTPTSLLKKEPPGYEEAMSQQPKQQENGSSSQ
			QMDDLFDILIQSGEISADFKEPPSLPGKEKPSPKTVCWSPLAAQ
ľ	ſ	1	PSPSAELPQAAPPPPGSPSLPGRLEDFLESSTGLPLLTSGHDGP
.1	1		EPLSLIDDLHSQMLSSTAILDHPPSPMDTSELHFVPEPSSTMGL
}		1	DLADGHLDSMDWLELSSGGPVLSLAPLSTTAPSLFSTDFLDGHD
1	1		LQLHWDSCL
6533	1798	373	STISWLARVEPPRRSSGVGAARLRFPGGSRPLRARACVLALAVL
1	1		ALLERNNADSMSAHSMLCERIAIAKELIKRAESLSRSRKGGIEG
			GAKLCSKLKAELKFLQKVEAGKVAIKESHLQSTNLTHLRAIVES
1			AENLEEVVSVLHVFGYTDTLGEKQTLVVDVVANGGHTWVKAIGR
1		]	KAEALHNIWLGRGQYGDKSIIEQAEDFLQASHQQPVQYSNPHII
1			FAFYNSVSSPMAEKLKEMGISVRGDIVAVNALLDHPEELQPSES
1			ESDDEGPELLQVTRVDRENILASVAFPTEIKVDVCKRVNLDITT
			LITYVSALSYGGCHFIPKEKVLTEQAEQERKEQVLPQLEAFMKD
	1	·	KELFACESAVKDFQSILDTLGGPGERERATVLIKRINVVPDQPS
			ERALRLVASSKINSRSLTIFGTGDTLKAITMTANSGFVRAANNQ
			GVKFSVFIHQPRALTESKEALATPLPKDYTTDSEH
6534	47	596	KATRFISAAFVVLNKOGVSPAKLPHTSWSWSLOTLSELESCOLA
	1		EKSLQCFPCSAMLLELIPLLGIHFVLRTARAOSVTOPDIHITVS
ļ			EGASLELRCNYSYGATPYLFWMERTVEEAFILLVCLKPWRVASS
1			LEKKEKEDESFQLLLGSRYNVLKAHCLLPLIRWLTSGDSLLSAQ
			PHCPQGL
6535	250	964	LIKTFFRDVAIQRDLLPKEKNLETLLTLAFLEIDKAFSSHARLS
1	1 1		ADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKT.
	1 I		TIDHTPERKDEKERIKKCGGFVAWNSLGOPHVNGRLAMTRSIGD
			LDLKTSGVIAEPETKRIKLHHADDSFLVLTTDGINFMVNSQEIW
		•	DFVNQCHDPNEAAHAVTEQAIQYGTEDNSTAVVVPFGAWGKYKN
6536	242		SEINFSFSRSFASSGRWA
0550	242	1174	SLVKEMTNQYGILFKQEQAHDDAIWSVAWGTNKKENSETVVTGS
]	1		LDDLVKVWKWRDERLDLQWSLEGHQLGVVSVDISHTLPIAASSS
(	}		LDAHIRLWDLENGKQIKSIDAGPVDAWTLAFSPDSQYLATGTHV
			GKVNIFGVESGKKEYSLDTRGKFILSIAYSPDGKYLASGAIDGI
( )			INIFDIATGKLLHTLEGHAMPIRSLTFSPDSQLLVTASDDGYIK
1			IYDVQHANLAGTLSGHASWVLNVAFCPDDTHFVSSSSDKSVKVW
i i	1		DVGTRTCVHTFFDHQDQVWGVKYNGNGSKIVSVGDDQEIHIYDC
6537	1638	921	= =
] - ]		J 2 4	NRFNPPPTQGPDPSLVYRPDVDPEVAKDKASFRNYTSGPLLDRV
<b>!</b> }	1		FTTYKLMHTHQTVDFVRSKHAQFGGFSYKKMTVMEAVDLLDGLV DESDPDVDFPNSFHAFQTAEGIRKAHPDKDWFHLVGLLHDLGKV
			LALFGEPOWAWGDTERWGCDDON CURRENT TO THE TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTA
1 1			LALFGEPQWAVVGDTFPVGCRPQASVVFCDSTFQDNPDLQDPRY STELGMYQPHCGLDRVLMSWGHDGEARGGQWGGGRWGTVGGGG
<u> </u>			AEAVPAGDTLSPQSTCTR
6538	3345	2412	PYLYDFLDALITCQTAPEEAFIKLDGLAGMLTEQLRRLTKQVQE
j j			ARHNRDDEAIKKAVNEYDETMEKYIPVLMAQAKIYWNLENYPMV
į l			EKIFRKSVEFCNDHDVWKLNVAHVLFMQENKYKEAIGFYEPIVK
			KHYDNILNVSAIVLANLCVSYIMTSQNEKAEELMRKIEKEEEQL
	Ī		SYDDPNRKMYHLCIVNLVIGTLYCAKGNYEFGISRVIKSLEPYN
	]		KKLGTDTWYYAKRCFLSLLENMSKHMIVIHDSVIQECVQFLGHC
	ł		ELYGTNIPAVIEQPLEEERMHVGKNTVTDESRQLKALIYEIIGW
I	İ		NK
6539	218	339	FLGAASPHPHFSSLAPHPDQPEFTPVQDELEAMELWGPGV
6540	3	391	LERLWLLLLRRPEDAMAECPTLGEAVTDHPDRLWAWEKFVYLDE
ļ			KQHAWLPLTIEIKDRLQLRVLLRREDVVLGRPMTPTQIGPSLLP
	1		IMWQLYPDGRYRSSDSSFWRLVYHIKIDGVEDMLLELLPDD
			ZZ

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	Hanistidine, laisoteucine, kabysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
-	amino acid	1	P=Proline, Q=Glutamine, R=Arginine,
		residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u></u>	sequence	L	\=possible nucleotide insertion)
6541	1165	536	RTLVQRRILMLLRKPARGRDLRGRGRGTPRGGRKGLLPTPDEFP
1		l	RFEGGRKPDSWDGNREPGPGHEHFRDTPRPDHPPHDGHSPASRE
į.	1		RSSSLQGMDMASLPPRKRPWHDGPGTSEHREMEAPGGPSEDRGG
	1	Ī	KGRGGPGPAQRVPKSGRSSSLDGEHHDGYHRDEPFGGPPGSGTP
1	ì	i	SRGGRSGSNWGRGSNMNSGPPRRGASRGGRGR
6542	3	3775	SWPRGRGETGGHPGALRTRTMQKSVRYNEGHALYLAFLARKEGT
	<u> </u>	1	VPCEL CVVDA DA CRIMIDINIDA MONTO TORONO DE LA COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPONIDA MONTO DE COMPO
1	[		KRGFLSKKTAEASRWHEKWFALYQNVLFYFEGEQSCRPAGMYLL
			EGCSCERTPAPPRAGAGQGGVRDALDKQYYFTVLFGHEGQKPLE
1			LRCEEEQDGKEWMEAIHQASYADILIEREVLMQKYIHLVQIVET
1			EKIAANQLRHQLEDQDTEIERLKSEIIALNKTKERMRPYQSNQE
1	1		DEDPDIKKIKKVOSFMRGWLCRRKWKTIVQDYICSPHAESMRKR
			NQIVFTMVEAESEYVHQLYILVNGFLRPLRMAASSKKPPISHDD
	]		VSSIFLNSETIMFLHEIFHQGLKARIANWPTLILADLFDILLPM
1	{		LNIYQEFVRNHQYSLQVLANCKQNRDFDKLLKQYEANPACEGRM
	1		LETFLTYPMFQIPRYIITLHELLAHTPHEHVERKSLEFAKSKLE
1			ELSRVMHDEVSDTENIRKNLAIERMIVEGCDILLDTSQTFIRQG
	ŀ		SLIQVPSVERGKLSKVRLGSLSLKKEGERQCFLFTKHFLICTRS
ł	ł		SGGKLHLLKTGGVLSLIDCTLIEEPDASDDDSKGSGQVFGHLDF
			KIVVEPPDRAAFTVVLLAPSRQEKAAWMSDISQCVDNIRCNGLM
			TIVFEENSKVTVPHMIKSDARLHKDDTDICFSKTLNSCKVPQIR
1	1		VACUEDI I EDI EDI DEI GEDEI MERITATENE ANTICI ETERNA NATURA DEI GEDEI MERITATENE ANTICE ETERNA NATURA DEI GEDEI MERITATENE ANTICE ETERNA NATURA DEI GEDEI MERITATENE ANTICE ETERNA NATURA DEI GEDEI MERITATENE ANTICE ETERNA NATURA DEI GEDEI MERITATENE ANTICE ETERNA NATURA DEI GEDEI MERITATENE ANTICE ETERNA NATURA DEI GEDEI MERITATENE ANTICE ETERNA NATURA DEI GEDEI MERITATENE ANTICE ETERNA NATURA DEI GEDEI MERITATENE ANTICE ETERNA NATURA DEI GEDEI MERITATENE ANTICE ETERNA NATURA DEI GEDEI MERITATENE ANTICE ETERNA NATURA DEI GEDEI MERITATENE ANTICE ETERNA DE CONTROL DEI GEDEI MERITATENE ANTICE ETERNA DE CONTROL DEI GEDEI MERITATENE ANTICE ETERNA DE CONTROL DEI GEDEI MERITATENE ANTICE ETERNA DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CO
1	<b>(</b>		YASVERLLERLTDLRFLSIDFLNTFLHTYRIFTTAAVVLGKLSD
1			IYKRPFTSIPVRSLELFFATSQNNRGEHLVDGKSPRLCRKFSSP
	1		PPLAVSRTSSPVRARKLSLTSPLNSKIGALDLTTSSSPTTTTQS
	]		PAASPPPHTGQIPLDLSRGLSSPEQSPGTVEENVDNPRVDLCNK
	1		LKRSIQKAVLESAPADRAGVESSPAADTTELSPCRSPSTPRHLR
			YRQPGGQTADNAHCSVSPASAFAIATAAAGHGSPPGFNNTERTC
			DKEFI IRRTATNRVLNVLRHWVSKHAQDFELNNELKMNVLNLLE
•			EVLRDPDLLPQERKAAANILMALSQDDQDDJHLKLEDIIOMTDC
	i		MKAECFESLSAMELAEQITLLDHVIFRSIPYEEFLGOGWMKLDK
Ī			NERTPYIMKTSQHFNDMSNLVASQIMNYADVSSRANAIEKWVAV
†			ADICRCLHNYNGVLEITSALNRSATYRLKKTWAKVSKOTKALMD
	[		KLQKTVSSEGRFKNLRETLKNCNPPAVPYLGMYLTDLAFIEEGT
			PNFTEEGLVNFSKMRMISHIIREIRQFQQTSYRIDHQPKVAQYL
			LDKDLIIDEDTLYELSLKIEPRLPA
6543	1857	950	FVSGCGRAGIGLSWAMAAEARVSRWYFGGLASCGAACCTHPLDL
}		,,,,	LKVHLOTOOPUVI DATCANI DURTOONI TURTOOTI STEELASCGAACCTHPLDL
			LKVHLQTQQEVKLRMTGMALRVVRTDGILALYSGLSASLCRQMT
			YSLTRFAIYETVRDRVAKGSQGPLPFHEKVLLGSVSGLAGGFVG
ł			TPADLVNVRMQNDVKLPQGQRRNYAHALDGLYRVAREEGLRRLF
1		•	SGATMASSRGALVTVGQLSCYDQAKQLVLSTGYLSDNIFTHFVA
			SFIAGGCATFLCQPLDVLKTRLMNSKGEYQGVFHCAVETAKLGP
<u> </u>			LAFYKGLVPAGIRLIPHTVLTFVFLEQLRKNFGIKVPS
6544	630	79	PSPCFIRSRLDGQPWMAGLEAWLSQNFSLHQPQSRVRVRRASIS
	1		EPSDTDPEPRTLNPSPAGWFVQQHPELELMSSFRERFGRNWLOY
1			RSHLEPSGNPLPATPTTSAPSAPPASSQGPDTAPRPSPPQEEAR
l i	1		GPQESPQKMSEEVRAEPQEEEEEKEGKEEKEEGEMAPLPEAHLG
l i	]		EGKQKECP
6545	176	560	PPHSHAALLPAAMTPLLTLILVVLMGLPLAQALDCHVCAYNGDN
1	·		CFNPMRCPAMVAYCMTTRTYYTPTRMKVSKSCVPRCFETVYDGY
}			CVUNCTUCCOONTI CACCOOT A MESSAGE STRUCTUCTUCTUCTUCTUCTUCTUCTUCTUCTUCTUCTUCTU
6546	1657	264	SKHASTTSCCQYDLCNGTGLATPATLALAPILLATLWGLL
55.46	100/	364	HLLNGLDEVAAFFVADLGAIVRKHFCFLKCLPRVRPFYAVKCNS
1	Ī		SPGVLKVLAQLGLGFSCANKAEMELVQHIGIPASKIICANPCKQ
		ļ	IAQIKYAAKHGIQLLSFDNEMELAKVVKSHPSAKMVLCIATDDS
			HSLSCLSLKFGVSLKSCRHLLENAKKHHVEVVGVSFHIGSGCPD
į į	İ		PQAYAQSIADARLVFEMGTELGHKMHVLDLGGGFPGTEGAKVRF
			EEIASVINSALDLYFPEGCGVDIFAELGRYYVTSAPTVAVSIIA
j !	1	ľ	KKEVLLDQPGREEENGSTSKTIVYHLDEGVYGIFNSVLFDNICP
	<del></del>		E E E E- E- E- E- E- E- E- E

Designing nucleotide location corresponding corresponding to first amino acid amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid sequence   P-Proline, O-Glutamine, R-Arginine, D-Ropertic Acid, E-Proline, D-Ropertic Acid, E-Proline, D-Ropertic Acid, E-Proline, D-Ropertic Acid, E-Proline, D-Ropertic Acid, E-Proline, D-Ropertic Acid, E-Proline, D-Ropertic Acid, E-Proline, D-Ropertic Acid, E-Proline, D-Ropertic Acid, E-Proline, D-Ropertic Acid, E-Proline, D-Ropertic Acid, E-Proline, D-Ropertic Acid, E-Proline, D-Ropertic Acid, E-Proline, D-Ropertic Acid, E-Proline, D-Ropertic Acid, E-Proline, D-Ropertic Acid, E-Proline, D-Ropertic Acid, E-Proline, D-Ropertic Acid, E-Proline, D-Ropertic Acid, E-Proline, D-Ropertic Acid, E-Proline, D-Ropertic Acid, E-Proline, D-Ropertic Acid, E-Proline, D-Ropertic Acid, E-Proline, D-Ropertic Acid, E-Proline, D-Ropertic Acid, E-Proline, D-Ropertic Acid, E-Proline, D-Ropertic Acid, E-Proline, D-Ropertic Acid, E-Proline, D-Ropertic Acid, E-Proline, D-Ropertic Acid, E-Proline, D-Ropertic Acid, E-Proline, D-Ropertic Acid, E-Proline, D-Ropertic Acid, E-Proline, D-Ropertic Acid, E-Proline, D-Ropertic Acid, E-Proline, D-Ropertic Acid, E-Proline, D-Ropertic Acid, E-Proline, D-Ropertic Acid, E-Proline, D-Ropertic Acid, E-Proline, E-Proline, D-Ropertic Acid,	1 Omino			
NO:   nucleotide   corresponding to first amino acid residue of amino acid residue of amino acid sequence   September   Leucine, Membethionine, Neaparagine, Peroline, Occupant, Neaparagine, Peroline, Occupant, Neaparagine, Sequence   Sequence   Security, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York, New York,	1	1	A contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of	Amino acid segment containing signal peptide
Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Corresponding   Correspondin	NO:	nucleotide		Glutamic Acid E-Phonylalania C Cl
Corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence solvente amino acid sequence solvente amino acid sequence solvente amino acid sequence solvente amino acid sequence solvente amino acid sequence solvente amino acid sequence solvente amino acid sequence solvente amino acid sequence solvente amino acid sequence solvente amino acid sequence solvente amino acid sequence solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solvente solven		location	corresponding	H=Histidine T=Teolegoine V=Lycine,
amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid	1		to first	L=Leucine. M=Methionine M-Asnaragine
residue of amino acid sequence since acid sequence solve tryptophan, Y-Tyrooine, X-Unknown, *-stop Codon, /-possible nuclectide deletion, \			amino acid	P=Proline, O=Glutamine, R=Arginine
### ### ### ### ### ### ### ### ### ##			residue of	S=Serine, T=Threonine, V=Valine,
Sequence    Codon, /-possible nucleotide deletion,    -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nu	İ		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *-Stop
Appossible nucleotide insertion		1	sequence	Codon, /=possible nucleotide deletion
TPILOKRSTEOPINSSIMGRAUGHCHAGHAUNDE LVPRIMGATY LVGMSSPHWGTGAHTTVAMSHARROLMAS EQEDDVEGVCKPLSCOMEITDTLC/GFVFTPASIM  1		sequence		\=possible nucleotide insertion)
6547  1 541				TPILQKKPSTEQPLYSSSLWGPAVDGCDCVAEGLWLPQLHVGDW
S41				LVFDNMGAYTVGMGSPFWGTQACHITYAMSRVAWEALRROLMAA
PPLAGARAOPPRICTITYOGFACCLINLIGHORICGELETICRES MDFHACAGOVISCOPERAAVWESLOORAROAPPRINHTLCGA PVHURERGTGSETMOETIERATAPALPHAPAPPLIAARIALAYLL RPLA 6548 2 219 FVSRLSVRDVRFPTFLGGGGADAMHTDPDYSAAYVPIETDAEDG IKSCGTTFTLCKGTEVGELKILSRFONA 6549 73 1490 ETGRVCEDARPACCSSKRRNERABEJTFTSPSSSSPTSSRPA ARAFSKAPARLSRPRACGSSKRRNERABEJTFTSPSSSSPTSSRPA ARAFSKAPARLSRPRACGSSKRRNERABEJTFTSPSSSSPTSSRPA ARAFSKAPARLSRPRACGSSKRRNERABEJTFTSPSSSSPTSSRPA ARAFSKAPARLSRPRARESPPDPGRYTYGELIOARKHKLIKKC SVAAKLMFULTRIRIENDYPGKELIGALKCUKEWFDQLAGHGVQLDPTFS YGGHAPFAKMIDERLITAYPGVVVVRVPTPPGALGHGVQLDPTFS YGGHAPFAKMIDERLITAYPGVVVVRVPTPGALGHGVQLDPTFS YGGHAPFAKMIDERLITAYPGVVVRVPTPGALGHGVQLDPTFS YGGHAPFAKMIDERLITAYPGVANTRGGRKKAVPLARDKHHLA DESHLTRHERPYLDGVVTVESHGRDDVVIVRVPTPGALGHGVVGTDLL MKDDGSFCVCERNANNGFLAFDTRACHLOVGRVVGTMLECST DGRMOSNCSLGGVCMCSLSSDGKGLAJOVSNILADVGTDLL MKDDGSFCVCERNANNGFLAFDTRACHLOVGRVVGTMLECST DGRMOSNCSLGGVCMCSLSSDGKGLAJOVSNILADVGTDLL MKDDGSFCVCERNANNGFLAFDTRACHLOVGRVVGTMLECST DGRMOSNCSLGGVCRACHSCHARDVGTAVGTAVANTAGTDRACHTON PESTPRELLTLALDGGLFWNDOLLANEIKCLT MKDGSFCVCERNANNGFLAFDTRACHLOVGRVVGTWLECST DGRMOSNCSLGGVCCERNANNGFLAFDTRACHLOVGRVGTWLECST DGRMOSNCSLGGVCCERNANNGFLAFDTRACHLOVGRVGTWLECST LICHTALSVALIPHOVLIANE TARGATSCHARGGSVGTACGTSSRGCWYYLKYPFF LYVSLOTHLILLGVUFWYGNVHVSTESKLQATERRAGGLYSG UCCADRVYTYMFNGATHALOSSGVARCHARGSVARAFGLIANSSFR COCQODRVYTYMFHAATILISKCCROGSFCMMINASCDALIPHI NORVETLEVE LAKENTICTKORSSVLIKMVAREGUVECVKTEE LONGGRGGADATURINGFRAGGSTARGCVVKTEE LONGGRGGADATURINGFRAGGSTARGCVVKTEE LONGGRGGADATURINGFRAGGSTARGCVVKTEE LONGGRGGADATURINGFRAGGSTARGCVVKTEELARGLARD ARCSKOTILLABLEKAVLIKKERSGCARGCVVKTEELARGLARD ARCSKOTILLABLEKAVLIKKERSGCARGCVVKTEELARGLARD ARCSKOTILLABLEKAVLIKKERSGCARGCVVKTEELARGLARDHARGTVATATA ANTVULNINCUISIMMVILLARCTGGGSFVUIKAPPSTGVYFFT ASLPRROPSLEEICKKLEAABERRKYGCBELLKRLABKEEHER EVIGATIEENNINFINAACKERAGRS ASLPRROPSLEEICKKLEAABERRKYGCBELLKRLABKEEHER EVIGATIEENNINFINAACKERAGRS ASLPRROPSLEEICKKLEAABERGRYGCVUIKAPSTGVYFFT ASLPRROPSLEEICKKLEAABERRKYGCBELLKRLABKREHER EVIGATIEENNINFINAACKERAGRS ASLPRROPSLEEICKKLEAABERRKYGCBELLKRLABK	6543	<del> </del>		EQEDDVEGVCKPLSCGWEITDTLCVGPVFTPASIM
NDFHACASOVISGOPERAAJWESLQCEARGAPRENHITLICGS	0347	<u> </u>	541	LHSKYLAPALCSQPGMMRCCRRRCCCRQPPHALRPLLLLPLVLL
6548 2 219 FVSRLSVRDVRFPTLGGKGADMHTDDVSAAVUIETDAEDO 6549 73 1490 ETGRVCEDARPACGSRSRRRKEAAPGIPTPSESSSFTSSERA RAPSKAPARLSRPBAEPDPDGKTYOGE I JOARKHKLI INC SSVAAKLWFLTDRRIREDYPOKSILRALKAKCCEELIPRAVVM DEVVLTIEGGMLGGLIRINGELITAY POVVVVVPTPTWOSDSDIT VLRHLEKMCCRLMNRPQAILNCVKFTYGELGAGGVUPLDPTTS YOGGINFAKHILDEGMLGIRINGELITAY POVVVVVVPTPTWOSDSDIT ULRHLEKMCCRLMNRPQAILNCVKFTYGELGAGGVUPLDPTTS YOGGINFAKHIDAEVLEFPMVKNTKSHEGKAVLARDKHHLA DLSHLIRBARYLOKVKESIGBDVENIVVGGRVGTMGRCST DGRMGSNCSLGGVCMMCSLSEGGKQLAIQVSNILIMDVCGIDLI MKDDGSFCVCEANANVGYTAFFTGELAGGGVALIADVSHILMDVCGIDLI MKDDGSFCVCEANANVGYTAFFTGELAGGGVALIADVSHILMDVCGIDLI MKDDGSFCVCEANANVGYTAFFTGELAGGSKGCLAIQVSNILIMDVCGIDLI MKDDGSFCVCEANANVGYTAFFTGELAGGGVASASSSSVDSD FRYSRGGAPDCGIFGMGLAMERIGGSYARAGGSSRGCWYYLKYFF FRYSRGGAPDCGIFGMGLAMERIGGSYARAGGSSRGCWYYLKYFF COCGORUN TYNNORYMARAI ILLSEKGCROATERRAEGISGO LLGLTASGSNLTKELNFTTRAKDAIMOMNINARRDLDRINASSR COCGORUN TYNNORYMARAI ILLSEKGCHOMINASCRALIFALI NGKVKTLEVE IAKSKTICTKOKESVLLINKRVAEEDLVECVKTEE LONGERGLAKEDLGKVAALCLEJELDKRÜKVEKKAPAGENACH NGKVKTLEVE IAKSKTICTKOKESVLLINKRVAEEDLVECVKTEE LONGERGLAKEDLGKVAALCLEJELDKRÜKVEKKAPAGENACH AECSGOTOLIALEEKAVLIREERINLAKELEEKKPEREAGLRADLAG IERVARENSDLORGKLEAGOGLRASGSKOKVYKEKAADARBAKLO AECSGOTOLIALEEKAVLIREERINLAKELEEKKPEREAGLRADLAG LESQRPPAGIDVABSGC  157 748 IOPPDFRINKTANYKEKNELPELVSLFCSCFLADPLINKSSYKYE ADTVULNINCVISIMEVIELINKCTSGGSFEVILKPSPEDGVPEFN ASLPRRPDPSLEEIGKKLEAABERRKYGSAELLHALEKREHER EVIQKAILEENNINFIKMAKKKLAGAMESNKENREHLALAMLERLQ EDKHAAEEVKRNEKLEERASR 10PPDFRINKTLAYKEKKELEFALSGAELKHLAEKREHER EVIQKAILEENNINFIKMAKKLAGAMESNKENREHLAAMLERLQ EDKHAAEEVKRNEKLEERASR 10PPDFRINKTLAYKEKKEERASR 10PPDFRINKTLAYKEKKEERASR 10PPDFRINKTLAYKEKKEERASR 10PPDFRINKTLAYKEKKEERASR 10PPDFRINKTLAYKEKKEERASR 10PPDFRINKTLAYKEKKEERASR 10PPDFRINKTLAYKEKKEERASR 10PPDFRINKTLAYKEKKEERASR 10PPDFRINKTLAYKEKKEERASR 10PPDFRINKTLAYKEKKEERASR 10PPDFRINKTLAYKEKKEERASR 10PPDFRINKTLAYKEKKEERASR 10PPDFRINKTLAYKEKKEERASR 10PPDFRINKTLAYKEKKEERASR 10PPDFRINKTLAYKEKKEERASR 10PPDFRINKTLAYKEKKEERASR 10PPDFRINKTLAYKEKKEERASR 10PPDFRINKTLAYKEKKE				PPLAAAAAGPNRCDTIYQGFAECLIRLGDSMGRGGELETICRSW
6548 2 219 FYSKLSVRDVRFPTFLGGHGADAMHTDFDVSAAVVPIETDAEDG  FKSGLSVRDVRFPTFLGGHGADAMHTDFDVSAAVVPIETDAEDG  6549 73 1490 ETGRVCDARPACGSRSRRKEAPITPSFSSSSFTSSRDA  ARAPSKAPARLSRPRAEEPPDGERYIQEEIIQARKHKLIRVC SSVAKIMFLTDRIRTRDYPOKSILRALKAKCCEEELDFRAVVM  DEVVLTIEGGNLGLRINGELITATPQVVRYPTFWVQSSDIT  VLRHLEKMGCKLAMRPQALINCVNFFTFVLGGGVDLFDTFS  YGGHENFARMIDEAPLEFPMVNRTIGHGKGKAVPLARDKSBDIT  VLRHLEKMGCKLAMRPQALINCVNFFTFVLGGGVDLFDTFS  YGGHENFARMIDEAPLEFPMVNRTIGHGKGKAVPLARDKSHLA  DLSHLTRHEAPYLFGKYVKESIGDVRVIVVGGGVVGTMLRCST  DGRMQSNOSLGGVCMRNSLSEGGKGLAIOVSNILGMDVCGIDLL  MKDDGSFCVCEANANVGFIAPPKACNLDVAGIIADYAASLLPSG  RLTRANSLLSVSTASSTSEPBLIGPRAANDNASSSSVDSD  PESTERELLTKLPGGLFNNNOLLANE KLLVU  FRVSRGGAPGCGIENGKAMAMEGGSYARAGGSSGCGWYYLRYFF  LFVSLOPHILIGUVLFMVYGKVHVSTESNLQATERRAEGLYSG  LFVSLOPHILIGUVLFMVYGKVHVSTESNLQATERRAEGLYSG  LGULASGONLTKELNFTTRAADAILMANARRDLDRINASFR  OCGGREVIYTNNORYMAAIILEKCCEDDFKDMNKSCDALLFPL  NGKVKTLEVEIARSKTICTKDKESVLLNKRVAEEDLVECVKTRE  LGHGFQLAKBOLGKVQALCLFLDKKFFENDLRIMKRSIPRS  LDNLGYNLYHPLGSELASIRRACCHMPSIMSKVEELARSLRAD  IRVNAERSDLOKKULEAGAGGKRAVGKREAQARSRAKQ  ARCSKOTGLALEEKAVLKREERDNLAKSLEEKKFREAGCLRRELAI  RNSALDTCILKKSGOPMBVSRPMGPUDTDASSLEEFKRII  LESQRPPRGIIVAPSSC  6551 157 748 IQPPDFRNMTLAAYKEKMEELPLVSLFCSCFLADPLNKSSYKYE  ADTVOLNNCVISIMEVIELINKCTSGGSFEVILKPPSFDGVPFFN  ASLPRRNPPSLEEIGKKLEAABERRKYDGRALLKHLAEKKEERER  EVIGKAIEENNNTIKAAKEKLAAGKMESNKENREAHLAAMLERLQ  EKOKHABEVRINELKERASR  6552 157 748 IQPPDFRNMTLAAYKEKMEELDVSLFCSCFLADPLNKSSYKYE  ADTVOLNNCVISIMEVIELINKCTSGGSFEVILKPSFSDGVPFFN  ASLPRRNPPSLEEIGKKLEAABERRKYDGRALLKHLAEKKEERER  EVIGKAIEENNFIKAAKEKLAAGKMESNKERBALLAHLAEKKEERER  EVIGKAIEENNFIKAAKEKLAAGKMESNKERBALLAAMLERLQ  GOKHABEVERNNELKEREASR  6552 1607 FWSSMAAHLSYGRVINNLERGARFECFLEGDTS  LYHAAKGLHUOVISIMEVIELINGTTSGGSFEVILKPEGTGOPTS  LYHAAKGLHOVISIMEVIELINGTGGSRFVILKPEGTGOPTS  LYHAAKGLHOVISIMEVIELINGTGGGSFVILKPEGTGOPTS  LYHAAKGLHOVISIMEVIELINGTGGRRVTLIFFTGERNSCHTGGTGNAMM  FNAVGSVLKKKAKLERASR  ORDSLFFFTFTREETSLANDFUNDLITPLATORTGERSFGOVDHMQAA  ROSLAMITSTAELIKOVITSEDFFCOVTAELAGRAFECYNGENDOTS  LYHAAKGLLBOPTORTHE				NDF HACASQVLSGCPEEAAAVWESLQQEARQAPRPNNLHTLCGA
1490   FVSELSVEDVREPTFLIGHGADAMHTDFDVSAAVVPIETDAEDG   1KGCGITFTLGKGTEVGELKILISRFQNA   1490   ETGRVCEDARPACGSERKRRERAEDGIFFSPSSSSTSSRPA   ARAFSKAPARLSRPRAKEGEPEPPDGRYTYGEIIOARKHKLIKMC   SVAAKUMELIDRRIKENDFYDGKEILAKKCCEEBLDPFRAVM   DEVVLTIEGGNIGHEINGELITAYPOVVVRVPTFWQSDSDIT   VLRHLEKMGCHIMMRPGALINCVNFWTFDGELAGIGVPLDPTFS   VGGENFAKMIDBAEVLEFPMVVKTGGHRGKAVFLARDKHILA   DESHLITMEAPYLFGKYVKESIGRDFVGLAGIGVPLDPTFS   VGGENFAKMIDBAEVLEFPMVVKTGGHRGKAVFLARDKHILA   DESHLITMEAPYLFGKYVKESIGRDFVGLAGIGVPLDPTFS   VGGENFAKMIDBAEVLEFPMVVKTEGHRGKAVFLARDKHILA   DESHLITMEAPYLFGKYVKESIGRDFVAKGCSSSVBGD   DESTRELLITKLJGGJFNNNOLLANEIKLIVU   MKDDGSFCVCENANAVGFIAFDKACNLOVAGIIJADYAASLLPSG   RLTRMSLLSVSTASETSEPLGFPASTAVDNMSASSSSVBD   PESTRELLITKLJGGJFNNNOLLANEIKLIVU   TRVSTGARBGTSTEFPLGFPASTAVDNMSASSSSVBD   PESTRELLITKLJGGJFNNNOLLANEIKLIVU   TRVSTGARBGTSTEFPLGFPASTAVDNMSASSSSVBD   PESTRELLITKLJGGJFNNNOLLANEIKLIVU   TRVSTGARBGTSTEFPLGFPASTAVDNMSASSSSVBD   PESTRELLITKLJGGJFNNNOLLANEIKLJVI   TRVSTGARBGTSTEFPLGFPASTAVDNMSASSSSVBD   PESTRELLITKLJGGJFNNNOLLANEIKLJVI   TRVSTGARBGTSTERPLEGLYS   TRVSTGARBGTSGARGGTSKGCWYYLKYFF   LFVSLLQFLITTRADAILMINARGIJCH INASTR   CCGGDRV1YTNNDYMAAIILSEKKRECHLANARGSTRACHTSRAGGTSKGCWYYLKYFF   LFVSLLQFLITTRADAILMINARGIJCH INASTR   CCGGDRV1YTNNDYMAAIILSEKKRECHLANARGTSCALLFFIL   NQKVKTLEVETAKKTCTKKKESVLINKRECHLANGRSCLARD   TRVSARENSDLQRKKLEAQOGLARSQEAKGKVEKEAQARRAKLQ   ARCSROTICALBEKKNI KREDDLAKEGROKVEKEAQARRAKLQ   ARCSROTICALBEKKNI KREDDLAKEGROKVEKEAQARRAKLQ   ARCSROTICALBEKKNI KREDDLAKEGROKVEKEAQARRAKLQ   ARCSROTICALBEKKNI KREDDLAKEGROKVEKEAQARRAKLQ   ARCSROTICALBEKNI KREDDLAKEGROKVEKEAQARRAKLQ   ARCSROTICALBEKNI KREDDLAKEGROKVEKEAQARRAKLQ   ARCSROTICALBEKNI KREDDLAKEGROKVEKEAQARRAKLQ   ARCSROTICALBEKNI KREDDLAKEGROKVEKEAQARRAKLQ   ARCSROTICALBEKNI KREDDLAKEGROKVEKEAQARRAKLQ   ARCSROTICALBEKNI KREDDLAKEGROK KREDALBAMLERLQ   ARCSROTICALBEKNI KREDDLAKEGROK KREDALBAMLERLQ   ARCSROTICALBEKNI KREDDLAKEGROK KREDALBAMLERLQ   ARCSROTICALBEKNI KREDDLAKEGROK KREDAILAMALERLQ   ARCSROTICALBEKNI KREDDLAKEGROK KREDALBAMLERLQ   ARC				PDI.A
1 1490 ETGRVCEDARPACOGRSGRRRRKEAPGIPTPSPSSSSPTSSRPA ARAPSKAPARLSBRARAESPPDGRATYOSE I JOARNAKKLI KWC SSVAAKUWPLITDRIREDVPOKEILRALKAKCCEEELDPRAVUM DEVVLITIEGGNIGGERINGELITATYOVRYPTWUQSDBIT VLERILEGGNIGGERINGELITATYOVRYPTWUQSDBIT VLERILEGGNIGGERINGELITATYOVRYPTWUQSDBIT VLERILEGGNIGGERINGELITATYOVRYPTWUQSDBIT VLERILEGGNIGGERINGELITATYOVRYPTWUQSDBIT VLERILEGGNIGGERINGELITATYOVRYPTWUQSDBIT VLERILEGGNIGGERINGELITATYOVRYPTWUQSDBIT VLERILEGGNIGGERINGELITATYOVRYPTWUQSDBIT VLERILEGGNIGGERINGELITATYOVRYPTWUGSDBIT VLERILEGGNIGGERINGELITATYOVRYPTWUGSDBIT VLERILEGGNIGGERINGELITATYOVRYPTWIGHTGEST DGRMGSNICSLEGGVCRANATVORITAGRATOVRITIGGERINGERINGERINGERINGERINGERINGERINGER	6548	2	219	1
### TOREVCEDARPACGSRSKRRKEARPHISTPSSSSSTSSRRA ARAPSKAPARLSR PRARESPPDOKILGELIONRUKKLIKM SVAAKUWFLIDERITREDYPOKILRALKAKCCEEELDFRAVM DEVVLITLEGONIGLRITAYPOVVUKWTTQELAGHGYPLDTTS YGGHENFAKMIDEARVLEFPMVVKNTRGHEKAVFLARDKHHLA DLSHLIKHEAPVLEGKYVKESHGRKAVFLARDKHHLA DLSHLIKHEAPVLEGKYVKESHGRKAVFLARDKHHLA DLSHLIKHEAPVLEGKYVKESHGRKAVFLARDKHHLA DLSHLIKHEAPVLEGKYVKESHGRUNGULUVGIRUGTUVTMIKCST DGRMOSNCSLGGVGMMCSLSEGGKQLAIOVSNIIGMDVCGIDLL MKDDGSFCVCENANAVGIJABVASLPSG RLTRRHSLISVVSTASETSBELGPPASTAVDNMSASSSSVDSD PSSTREELITKLIPGGLINMOKLIANIKLIVD  FRYSRGAPDCGIEMGLAMEHGGSVARKGSSEGCHVYLRYFF LFYSLIGPLINLGLULIMVYCONVHVSTESNLQATERRABGLYSQ LLGILTASGSNITKELNFTTRAKDALMQWANARRDLDRINASFF QCQDRVIYTNNQRYMAAIILSEKGCROFROMKSCDALLFML NGRVKTLEVETAKERTICTKDKSVLIANKRVABEQLVCCVKTRE LORGERQLAKROLOKVQALCLFIDUKKFENDLRININGSIIPRS LNNLGNTMYPHIGSELASIRRACDHINSLMSKVEELARSLRAD IERVARENSDLOROKLBAQGILASGEAKGKVEKEAQAREAKLQ AECSROTOLALBEENAVIRKERONLAKELEKKKRBEQLEMELAI RNSALDTTIKTKSODMMPVSRPMGPVPNPQPIDPASLEFFKRI LESQRPPAGIPVAPSSG  157 748 10PPDPRINTLAAYKEENKELPLVSLFCSCFLADPLNKSSYKYE ADTVUDLNWCVISDMEVIELNKCTSGGSFEVILKPPSFDOVPFFN ASLPRRNPSLSEIQKKLRABERRKYOGAELKHLAEKREHER EVIQKALBENNNFIKMAKEKLAQKMESNKENRBAHLAAMLERLQ EKOKHALEEVRINKELKERASR 10PEPRINTITAAYKEMKELPLVSLFCSCFLADPLNKSSYKYE ADTVUDLNWCVISDMEVIELINKCTSGGSFEVILKPPSFDOVPFFN ASLPRRNPSLSEIQKKLRABERRKYOGAELKHLAEKREHER EVIQKALBENNNFIKMAKEKLAQKMESNKENRBAHLAAMLERLQ EKOKHALEEVRINKELKERASR 10PEPRINTITAAYKEMKELPLVSLFCSCFLADPLNKSSYKYE ADTVUDLNWCVISDMEVIELINKCTSGGSFEVILKPPSFDOVPFFN ASLPRROPSLEEIOKKLRABERRKYOGAELKHLAEKREHER EVIQKALBENNFIKMAKEKLAQKMESNKENRBAHLAAMLERLQ EKOKHALEEVRINKELKREASR 10PPSRMATLAAYKEMKELPLVSLFCSCFLADPLNKSSYKYE ADTVUDLNKCVISDMEVIELINKCTSGGSFEVILKPPSFDOVPFN ASLPRROPSLEEIOKKLRABERRKYOGAELKHLAEKREHER EVIQKALBENNFIKMAKEKLAQKMESNKENRBAHLAAMLERLQ EKOKHALEEVRINKELKREASR 10PPSRMATLAAYKEURGHERFERLOGT SONSIFPYFONLLLIDENDHITTERSILCEGGELKD EKOKHALEEVRINKELKKEASR 21 1807 FWSKMAALLSTQGGGGCDLDFREAKLOLINSAERLYAZIRDKN NAVOSUVLISKAKAI ISAAFEERNAKTUGEGGGFCTUTYFNOUTYFRETLETUR ONSTERPTOFFONLOGTENSTERPTENSTATURDENDHITTERTERTE	j	_		IKGCGTTETLCCCTEVCELVILGEROWS
ARAFSKAPARLSRPRARESPPDFORRYIGEBI IOARKHKLIKMC SSVARKUWFILTDRRIEDYPOKURLAKKCCESEBLDFRAVUM DEVVLTIEGGNIGIRINGELITAYPOVUVURVPTFWVQSDDIT VLRHLEKMGCRIKMIPQALILACVHTOGELAGHGVPLDDTFS YGGHENFAKHIDEAEVLEFPMVVKNTRGIRGKAVFLARDKHHLA DLSHLIRHEAPFLFQKYVKESHGRDVRIVVQGRVGTMLRGST JORMOSINGSLGGVGWMGSLEGQGKQLAIQVSNILGMDVCGIDLI MKDDGSFCVCEANANVGFIAFDKACHLDVAGILDVGINLIGHDVCGIDLI MKDDGSFCVCEANANVGFIAFDKACHLDVAGILDVGINLIGHDVGIDLI MKDDGSFCVCEANANVGFIAFDKACHLDVAGILDVSNILGMDVCGIDLI MKDDGSFCVCEANANVGFIAFDKACHLDVAGILDVSNILGMDVCGIDLI MKDDGSFCVCEANANVGFIAFDKACHLDVAGILDVSNILGMDVCGIDLI MKDDGSFCVCEANANVGFIAFDKACHLDVAGILADVLASSLSVDD FESTERELITKLPGGINMOLIANSIKLUD FRVSRGOAPDCGIEGGGAMEHGGSPARAGGSSRGCMYVLRYFF LFVSLIOFLIILGLULMVVYGNVHVSTESNLQATERRABGLYSQ LLGLTASQSNLTKEINFTTRAKDALMQMMINARRDLDRINASSRY CQGGDRVIYTNNQRYMAAIILSKCOOFFKDMNKSCDALLFML NQRVKTLEVEIAKEKTICTKDKSSVILLNKRVAERDLLVECVKTRE LCHQERGCLAKRCLQKVQALCLEJLBCKFEDFLINKSSTAVEL LGHGRGLAKRCLQKVQALCLEJLBCKFEDFLINKSSTAVEL ABCSGOTOLALBEKAVLRKERDMLAKELEEKKREAEQLRMELAI RISALDTCIKTKSQPMBVSRPMGPVNDPQDIDDASLEBFRKKI LESQRPPAGIPVAPSG  6551 157 748 10PPDFRIMTLAAVKERMKELPUSLFCSGFLADPLINKSSYXYE ADTVOLNINCVISIMBUVIEINKCISGGSFEVILKPBSFDGVPEFN ASLPRRNPSLBETQKKLEAABERRKYQEABLLKHLAEKREHER EVIQKA IBENNNFIKMAKKLLAKKKRENREAHLAAMLERLQ EKOKHAEEVRINKELKERASR 6552 157 748 10PPDFRIMTLAAYKEKMKELPUSLFCSCFLADPLINKSSYXYE ADTVOLNINCVISIMBUVIEINKCISGGSFEVILKPBSFDGVVPEFN ASLPRRDPSLBEIQKKLEAABERRKYQEABLLKHLAEKREHER EVIQKA IBENNNFIKMAKKLLAKKKRENRERHLAAMLERLQ EKOKHAEEVRINKELKEBASR 6553 2 1807 FWSKGMAAHLSYGREVINVILRESVERREPLERFLDKCAGSKAIVWD EVILTOPFGLIAQYSLLKHEVEKMFTLKGNRLPAADVRNITIFFV RPLELMDI IAENVLSEDRRGPTROPHTHLEVPRILCEQGINKD LCVLGSFIHREBYSLDLIFFDDOMLSHESSGAFKCYCLEGGDOTS LYHAAKGIMTLQALYGTIPQIFGKGECARQVANMIRKREFFTG SQNSIFPVFONLLLIDENNDLITHEAKTURFSEGAFECTLEGGDOTS LYHAAKGIMTLQALYGTIPQIFGKGECARQVANMIRKREFFTG SQNSIFPVFONLLIDENNDLITERAKTURFSEGAFECTLEGODTS LYHAAKGIMTLQALYGTIPQIFGKGECARGVANMIRKREFTG SQNSIFPVFONLLIDLGARAFTGFTGFTGFTGFTGFTGFTGFTGFTGFTGFTGFTGFTGF	6549	73	1490	ETGRUCEDARDA COCREDEDED VERA DOCUMENTO
SSVAAKLWFLTDRRIKEDYPOKELIRALKARCCEEBLDFRAVUM DEVVLTTEGONLGERINGELITAPUVUVURUPTPWOKDSDIT VURHLEKMEGCHANNROAILNCVNKFWTFOBLAGHGUPLDDTFS YGGHENPAKNIDEREVLEFPWANTSCHRIGKAVPLARDKHHLA DLSHLIRHERAPYLFOKYVKESHGRDVRVIVOGRVVGTHLRGST DGRWOSNCSLGGGWENSLSBOGKGLIGVNILGMEVCSIDLL MKDDGSFCVCENNANVGFIAFDKACNLDVAGIILDYAASLLESG RITRANSLLSVYSTASETSEPELGPPASTAVDMMSASSSSVDSD PESTERELITKLPGGLFMNNOLLANE KKLUVD FESTERELITKLPGGLFMNOLLANE KKLUVD FESTERELITKLPGGLFMNOLLANE KKLUVD FESTERELITKLPGGLFMNOLLANE KKLUVD FESTERELITKLPGGLFMNOLLANE KKLUVD FESTERELITKLPGGLFMNOLLANE KKLUVD FESTERELITKLPGGLFMNOLLANE KKLUVD FESTERELITKLPGGLFMNOLLANE KKLUVD FESTERELITKLPGGLFMNOLLANE KKLUVD FESTERELITKLPGGLFMNOLLANE KKLUVD FESTERELITKLPGGLFMNOLLANE KKLUV FENDAMMASSSSVDSD FESTERELITKLPGGLFMNOLLANE KKLUV FENDAMMASSSSVDSD FESTERELITKLPGGLFMNOLLANE KKLUV FENDAMMASSSSVDSD FESTERELITKLPGGLFMNOLLANE FRADELYSQ LLGLTASGSNLTKEINFTTRAKDAIMOMMINARROLDAI FNASFR CCGGDRVITYNNORYMAAI ILSGCRPGDVERNKSCLARELYSQ LLGLTASGSNLTKEINFTTRAKDAIMOMMINARROLDAI FNASFR CCGGDRVITYNNORYMAAI ILSGCRPGDVERFRADELYSCUPECYBOLRANE ACCSROTOLLALEEKAVIL KRENDLANEKVEEKARQURERELAI RNSALDTCIKTKSGOMMPUSNEPSIMSKVVEKARQARRAKLQ ACCSROTOLLALEEKAVIL KRENDLAKKELEREGULRMELAI RNSALDTCIKTKSGOMMPUSNEPOPDPIDPASLEEFKKI LESQRPAGIPVAJPSSG  6551 157 748 10PPDFRINTLAAYKEKNKELPLVSLIFCSGFLADPLINKSSYKYE ATVOLINGVIJSDMSVIJENKTSGOSFEVILKPPSFDGVPEFN ASLPRRDPSLEEIGKKLERASR FVIGKALEEVRINKELKERASR 10PPDFRINTLAAYKEKNKELPUSLIFCSCFLADPLINKSSYKYE ANTVOLINGVIJSDMSVIJENKIKELKPESFDGVPEFN ASLPRRDPSLEEIGKKLEAABERRKYGGAELLKHLAEKREHER EVIÇKAIEENNIFI KMAKEKLAGKMESNKENREAHLAAMLERLQ EKOKHAEEVRINKELKERASR 10PPDFRINTLAAYKEKNKELPPUSLIFCSCFLADPLINKSSYKYE ANTVOLINGVIJSDMSVIJENKELKPERSGLIKHLAEKREHER EVIÇKAIEENNIFI KMAKEKLAGKMESNKENREAHLAAMLERLQ EKOKHAEEVRINKELKERASR 10PPDFRINTLAAYKEKNKELPPUSLIFCSCFLADPLINKSSYKYE ANTVOSYSTKAKI KRAMPERLICHTPUSLTGGOSFEVILKPSFDGVPEFN ASLPRRDPSLEEIGKKLEAABERRKYGGAELLKHLAPKREHG EVIÇKAIEENNIFI KMAKEKLAGKMENKORMEAHLAAMLERLQ EKOKHAEEVRINKELKELASR 10PPDFRINTLAAYKEKNKELPPUSLIFCDOTTSCHAND 11PPDFRINTLAAYKEKNKELPPUSLIFCHOMANMI R	1			ARAFSKAPARI SPERAPEERDDOCRAYTOFF TO ARWEST
DEWYLTIEGONICALRINGLITATYOUVEVETPEWOSDSDIT VERHLERMGCER,MANPROALINCYNFWTFOELAGHGVPLDDTES YGGHENFAKMIDEAEVLEFPMWYKNTRGHRGKAVPLARDKHHLA DLSHLIFHERAYLFOKYWESENDEWYLVWGGRVVGTMLRCST DGRMOSNCSLGGVGMMCSLSEOGKQLAIQVSNILGMEVCGIDLL MKDDGSFCVCEANANGFIAFDKACHLDVGIIADVAASLLPSG RLTRRHSLLSVVSTASETSEEFLGPASTAVDMSASSSSVDSD PESTERELLTKLPGGLFMNNOLLANGIIADVAASLLPSG RLTRRHSLLSVVSTASETSEEFLGPASTAVDMSASSSSVDSD FESTERELLTKLPGGLFMNNOLLANGIIADVAASLLPSG RLTRRHSLLSVVSTASETSEEFLGPASTAVDMSASSSSVDSD FESTERELLTKLPGGLFMNNOLLANGIIADVALARSLLPSG RLTRRHSLLSVVSTASTASTSEELGPASTAVOMSASSSSVDSD FESTERELLTKLPGGLFMNNOLLANGIITAVAASLLPSG RLTRRHSLLSVVSTASTASTASTASTASTASTASTASTASTASTASTASTAS	İ			SSVAAKLWFLTDRRIBEDYPOKETLDALKAKCCEERI DERAKRI
VLRHLEKMGCRLMNRPOALINCVNKFWTFOBLAGHGUPLDDTFS YGGISMPAKNIDEAEVLEFPWIXTKRGHGKAVPLARDKHHLA DLSHLIRHEAPYLFOKYVKESIGRDVRVIVVGGRVVGTMLRCST DGRWOSNCSLGGVGMMCSLSEQGKUJQVSILIGHDVCGIDLL MKDDGSFCVCEANANVGFIAFDKACNLDVAGIIJDYAASLLPSG RLTRRMSLLSVYSTASETSEPELGPPASTAVDMMSASSSSVDSD PESTERELITKLPGGFFMNOLLANEKKLVD FESTERELITKLPGGFFMNOLLANEKKLVD FESTERELITKLPGGFFMNOLLANEKKLVD LFVSLIOFLIILGLULFMYVGMVAYSTESNLQATERRAEGLYSQ LLGLTASGSNLTKELNFTTRAKDAIMOMMINARRDLDRINASFR QCQGDRVIJTNNQRWAAIILSEKQCRDQFKDNNKSCDALLFML NQRVKTLEVIJAKEKTICTKNEKSVLLNKRVABEQLVECVKTRE LONGGRQLAKEQLQKVQALCLPLDKDKFFMDLRNLWRDSIIPRS LDNLGYNLYHDIGSELASIRRACHMPSIMSSKVEELAASLLRAD IERVARENSDLORQKLEAQQGLRASQEAKKVEKBAQAREAKLQ AECSGTOLALEEKAVLRKERDNLAKELEEKKREAQQIRMELAI RNSALDTCIKTKSQPMMPVSRPMGVPURPQPIDPASLEEFKRKI LESQRPPAGIPVAPSSG  6551 157 748 10PPDPRINTLAAVKEKKELPLVSLFCSCFLADPLNKSYXYE ADTVDLNWCVISDMEVIBLINKCTSGQSFEVILKPPSFDCVPFFN ASLPRRPDSLEEIGKKLEAAERRYYQEABLLKHLAEKREHER EVIQKAIEENNNFIKMAKEKLAGMMESNKENREAHLAAMLERLQ EKOKHAEEVYRNKELKERASR 10PPDPRINTLAAVKENKELPUSLFCSCFLADPLNKSSYXYE ADTVDLNWCVISDMEVIBLNKCTSGQSFEVILKPPSFDCVPFFN ASLPRRPDSLEEICKKLEAAERRYYQEABLLKHLAEKREHER EVIQKAIEENNNFIKMAKEKLAQMMESNKENREAHLAAMLERLQ EKOKHAEEVYRNKELKERASR 10PPDPRINTLAAVKENKELPUSLFCSCFLADPLNKSSYXYE ADTVDLNWCVISDMEVIBLNKCTSGQSFEVILKPPSFDCVPFFN ASLPRRPDSLEEICKKLEAAERRYYQEABLLKHLAEKREHER EVIQKAIEENNNFIKMAKEKLAQMMESNKENREAHLAAMLERLQ EKOKHAEEVYRNKELKERASR 10PPDPRINTLAAVKENKELPUSLFCSCFLADPLNKSSYXYE ADTVDLNWCVISDMEVIBLNCTSGQSFFRULKPPSFDCVPFFN ASLFRRPPSLEEICKJCKLEAAERRYYQEABLLKHLAEKREHER EVIQKAIEENNNFIKMAKEKLAQMMESNKENREAHLAAMLERLQ EKOKHAEEVYRNKELKEBASR 2 1807 PWSKMAAHLSYGRVILNVUREAWRELKEPLDKCAGSKATVWD EYLTCPFFGLIQYSLLKPPSTDPHILIPVRRSLLCEQRIKD LGVLGSFHRREYSLDLIPTGDGLLSMESEGAFKECYLEGDQTS LYHAAKGLMTIQALYGTIPQIFCKGECARQVANMMIRMKRFFTC SQNSIFPVFONLLLLDRNVDLIPTLATOLTVEGLIDEITYGIQNS YWGLPPEKFAPKKQGDGRKDLPTEAKKLQUNSBELVABIRDKN NAVGSVJSKKAKI ISAAFEERINAVGEIK KOYSOLDPHWQAA RGSLANHTSIAELIKDVTTSEDFFDKLTVGDFMSGIDTDKNN YIEDCLAQKHSLI KURLPCLQSVCTOSGLKKVULDYYKRELLOT YGYEHILTLHNLEKAGLLKPQCHNIVTITGGGYFFAKTLUNSDLVWE ONPTII	1			DEVVLTIEOGNLGLRINGELITAY PONNNIN PURPHWOCKETT
PGGHENPÄKHIDEAEULEPPMVVKITRGHIGKAVFLARDKHHLA DLSHLIHHEAPHLFQKYVKESHGRDURVITVGGRVVGTMURGST DGRMQSNCSLGGVCMMCSLSEQGKOLAJQVSNILGMDVCGIDLI MKDDGSFCVCEGRANNUPGI APDWACNLDVAGI IADYAASLLESG RLTRMSLLSVVSTASETSEPELGPPASTAVDNMSASSSSVDSD PESTERELLIKLPGGLFNMMQLLANEIKLLVD  6550 2293 922 FRVSRDGAPDCGEGMGLAMGGSYARAGGSSRGCWYYLRYFF LFVSLIOFLIILGLULFMYVGNHVUSTESNLQATERRASGLYSQ LLGLTASGSNITKELMFTTRAKDAIMQMILMARRDLDRINASFR QCQGDRUIYTNNQRYMAAIILSEKQCRODFKDMIKSCDALLFML NQKVKTLEVEIAEKHICTKDKESVLINKRVAERQLVECVKTRE LQHQERQLAKEQLQKVQALCLEIDKDKFEMDLRNLWRDS IIPRS LDNLGYNLHHPLGSELASIRRACDHMPSLMSSKVEELARSLRAD IERVARENSDLOROKKLEAQGGLASGGARGVKEKAQAREAKLQ AECSROTOLALEEKAVLRRERDNLAKELEEKKREAEQLRMELAI RNSALDTCIKTKSQDPMPVSRMGVPVNPQFIDDASLEEFKRKI LESQRPPAGIPVAPSSG 1QPDPBRNWTLAAYKEKMELPLVSLFCSCFLADPLNKSSYKYE ADTVDLNWCVISDMEVIELNKCTSGQSFEVILKPPSFGGVEFFN ASLPRRRDPSLEEIQKKLEAAEERRKYQBAELLKHLAEKREHER EVIQKAIEENNHFIKMAKEKLAQKMESNKEMREAHLAAMLERLQ EKDKHAEEVRKNKELKERASR 1GPDPFNNWTLAAYKEKMKELPUSLFCSCFLADPLNKSSYKYE ADTVDLNWCVISDMEVIELNKCTSGQSFEVILKPPSFDGVPEFN ASLPRRDPSLEEIQKKLEAAEERRKYQGAELLKHLAEKREHER EVIQKAIEENNHFIKMAKEKLAQKMESNKEMREAHLAAMLERLQ EKDKHAEEVRKNKELKERASR 1GPDPFNNWTLAAYKEKMKELPUSLFCSCFLADPLINKSSYKYE ADTVDLNWCVISDMEVIELNKCTSGQSFEVILKPPSFDGVPEFN ASLPRRDPSLEEIQKKLEAAEERRKYQGAELLKHLAEKREHER EVIQKAIEENNHFIKMAKEKLAQKMESNKEMREAHLAAMLERLQ EKDKHAEEVRKNKELKERASR 6553 2 1807 FWSKMAHALISSGRVMINVLREGWRENKENERHLABAMLERLQ EKDKHAEEVRKNKELKEBASR 6553 2 1807 FWSKMAHALISSGRVMINVLREGWRENKENERHLADAUVNIIFFV RPLLIMDIIABNVLSEDBRGDTROPHILPUPRRSLLCEGRLKD LGVLGSFIHREEYSLDLIPFODLLSMESGAFKECYLEGOOTS LYHAAKGMTUQAJYGITPQIFGKGCCARQVANMMIRMKREFTG SQNSIFPVFDNLLLLDRNVDLIPLATOLTUTEGLIDEIYGIQNS VYKLPPEKFAPKKQGGGKDLPTERKKLOINSAEELAEITRDKN NAVGSVLSKKKKAIISAAPETRAKNITYGEIKGDVSQLPHWQAA RGSLANHTSIABLI LKVLRLVCLQSVCNSGKKKVILGPSQLPHWQAA RGSLANHTSIABLI LKVLRLVCLQSVCNSGKKKURDERGIDTKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGKKKILEPSLGID ONPIDISVYYSGYAPLSVRAGQLKGKVLLDYKREILGT GYSCHILTHINBLEKAGLLKGTGGRNYPPTIRKTLRLMMDDVME ONPIDISVYYSGYAPLSVRAGQLLSRFORKSIEEVLRILEGDF	1			VLRHLEKMGCRLMNRPQAILNCVNKFWTFOELAGHGVDLDDTES
DLSHLIHEAPYLFOKYVKESHGRUVXIVVGGRVVGTMLRGST DGRMGNGNGSIGGVGMMGSLGKOLAIOVSINLGMDVGGIDLL MKDDGSFCVCEANANVGPIAFDKACNLDVAGIIADYAASLLPSG RLTRRMSLLSVVSTASBTSEEPELGPPASTAVDNMSASSSSVDSD PESTERELLIKLPGGLFNMOLLAMBIKLLVD  6550  2293  922  FRVSRDGAPDCGIEGMGLAMENGGSVARAGGSSRGCWYYLRYFF LFVSLIOFLIILGLVLFMVVHVSTESNLOATRRNABGLVSQ LLGLTASGSNLTKELHFTTRAKDAIMOMALNARRDLDRINASFR OCGBRVIYTHNORYMAAIILSKQCRDFKDMNKSCDALLFML NGKVKTLEVEIAKEKTICTKDKESVLLNKRVAEEGLVECVKREE LORIGEROLAKEGLOKVOALCLEIDKNFMDLRINLWRDSIIPRS  MALDTGIKTNORYMAAIILSGELASTRACDHMPSIMSSKVEELARSLRAD IERVARENSDLORGKLEAGOGGRASGEAKGKVEKEAGAREAKLQ AECSRGTGIGALEKAVLRRENDLAKELEEKKREAEQLIMELAI RNSALDTGIKTKSOPMMPVSRPMGPVPNPQPIDPASLEEFKRKI LESQRPPAGIPVAPSSG  6551  157  748  10PPDPRINTLAAYKEKMELPLVSLFCSCFLADPLNKSSYKYE ADTVOLNMCVISDMEVIELNKCTSGGSFFVILKPPSFDGVPEFN ASLPRRDPSLESIOKKLEABERRYOGBELLKHLAEKKHERE EVIGKAIEENNNFIKMAKEKLAGKMESNKENREAHLAAMLERLQ EDKHAEEVKKNKELKEBASR  6552  157  748  10PPDPRINTLAAYKEKMELPLVSLFCSCFLADPLNKSSYKYE ADTVOLNMCVISDMEVIELNKCTSGGSFFVILKPPSFDGVPEFN ASLPRRPDSLEEIOKKLEABERRYOGBELLKHLAEKREHER EVIGKAIEENNNFIKMAKEKLAGKMESNKENREAHLAAMLERLQ EDKHAEEVKRNKELKEBASR  6553  2  1807  FVWSKWAAHLSYGRVULNVLREAVREKKEPLPVSLFCSCFLADPLNKSSYKYE ADTVOLNMCVISDMEVIELNKCTSGGSFEVILKPPSFDGVPEFN ASLPRRPDSLEEDIGKKLEABERRKYQGBELKHLAEKREHER EVIGKAIEENNNFIKMAKEKLAGKMESNKENREAHLAAMLERLQ EDKHAEEVKRNKELKEBASR  6553  2  1807  FVWSKWAAHLSYGRVULNVLREAVREKMERHERPFDRSLCECOFLKD LGVLGSFHREEYSLDLIPFDGDLLSMESGGAFKCVLEGDQTS LVHAAKGLMTLQALYSTLKEHEVEKMFTLKGNLLPADDVNN ITFFV PROLLIAMILLARNVLSEDREGKGCARQVANNMIRMKREFTG SQNSIFPVFDRLLLLDRNVDLLTPLATTOLTYEGGLDEIYGIQNS VVKLPPEKFAPKKGGGGGKDLPTEAKKLQUNSAEELYAEIRDKN YAKLGPEKFAPKKGGGGGKDLPTEAKKLQUNSAEELYAEIRDKN YAKLGPEKFAPKKGGGGGKDLPTEAKKLUNSAEELYAEIRDKN YAKLGPEKFAPKKGGGGGKDLPTEAKKLUNSAEELYAEIRDKN YAKLGPEKFAPKKGGGGGKDLPTEAKKLUNSAEELYAEIRDKN YAKLGPEKFAPKKGGGGGKDLPTEAKKLUNSAEELYAEIRDKN YAKLGPEKFAPKKGGGGGKDLPTEAKKLUNSAEELYAEIRDKN YAKLGPEKFAPKKGGGGGKDLPTEAKKLUNSAEELYAEIRDKN YAKLGPEKFAPKKGGGGKALKVLOLGSVCNSGLKGVCLDYKREILGT YGYEHILTLINLEKAGGLKKGTGGRNNYPTIRKTLELMMDDVME ONPTIDIS	1			YGGHENFAKMIDEAEVLEFPMVVKNTRGHRGKAVFLARDKHHI.A
DGRMQSNCSLGGVCMMCSLSEQGKQLAIQUSNILGMDVCGIDLL   MKDDGSFCVCERANNAYGINEACKLDUAG IIADYAASLLPSG   RLTRRMSLLSVSTASETSEPELGPPASTAVDNMSASSSVDSD    PESTERELLTKLPGGLFNNMQLLANEIKLLVD    FERVSROGAPDCGIECMGLAWHENGSSVARAGGSSRGCWYYLRYFF    LFVSLIQFLIILGLULFMYVGNHVUSTENLQATERRASGLYSQ    LLGLTASGSNILKELMFTTRAKDAIMQMAINARRDLDRINASFR    CCGGDRV1YTNNORYMAAIILSEKQCRDQFKDMINSCDALLFML    NQKVKTLEVEIAKEKTICTKOKSSVLLNKRVAEEQLVECVKTRE    LORGERQLAKEQLQKVQALCLPLDKDKFFMDLRNLMRDSI IPRS    LDNLGYNLYHPLGSELASIRRACDHMPSIMSSKVEELARSLRAD    IERVARENSDLOROKLEAQGLASGAGAKQVKEKAQAREAKLQ    AECSROTOLALEEKAVLRKERDNLAKELEEKKREAEQLRMELAI    RNSALDTCIKTKSQPMMVSRFMGFVPNPQFIDASLEEFKRKI    LESQRPPAGIPVAPSG    ATVOLNWCVISMEVIELNKKTSGQSFFVILKPPSFDGVPEFN    ASLPRRDPSLEEIQKKLEAAEERRKYQGAELLKHLAEKREHER    EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ    EKDKHAEEVRKNKELKERASA    ASTANLANGKELKERASA    ASTANLANGKELKERASA    ASTANLANGKELKERASA    ASTANLANGKELKERASA    ASLPRRDPSLEEIQKKLEAAEERRKYQGAELLKHLAEKREHER    EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ    ASLPRRDPSLEEIQKKLEAAEERRKYQGAELLKHLAEKREHER    EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ    EKDKHAEEVRKNKELKERASA    ASLPRRDPSLEEIQKKLEAAEERRKYQGAELLKHLAEKREHER    EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ    EKDKHAEEVRKNELKERASA    ASLPRRDPSLEEIQKKLEAAEERRKYQGAELLKHLAEKREHER    EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ    EKDKHAEEVRKNELKERASA    ASSANLANGSGRVUINVLREAVERELEFELDKCAGSKAIVWD    EYLTGFFGLIAQYSILKEHEVEKMFTLKGNRLPAADWNIIFFV    PRELEIMDIIAENVLSEDRREGTREDFHILFVPRRSLLCEGRLKD    LOVLOSF HREEYSLDLIFFDGULISMESGAFKECVLEGDOTS    SUNSIFPUDDILLLDRNVDLLTPLATQLTYEGLIDEIYGIQNS    YVKLPPEKFARKGGDGKDLPTEAKKLQINSAEELYAEIRDKN    YVKLPPEKFARKKGGDGKDLPTEAKKLQINSAEELYAEIRDKN    YVKLPPEKFARKKGGDGKDLPTEAKKLQINSAEELYAEIRDKN    YVKLPPEKFARKKGGDGKDLPTEAKKLQINSAEELYAEIRDKN    VYKLPPEKFARKKGGDGKDLPTEAKKLQINSAEELYAEIRDKN    VYKLPPEKFARKKGGDGKDLPTEAKKLQINSAEELYAEIRDKN    VYKLPPEKFARKKGGDGKDLPTEAKLLQINSAEELYAEIRDKN    VYKLPPEKFARKGGDGKOLPTEAKLLQINSTENSSIETOKRILPGTNICHTENDANTATURGERTOGNORSIETOKATURGUNDANTATURGERTOGNOR				DLSHLIRHEAPYLFQKYVKESHGRDVRVIVVGGRVVGTMLRCST
MKDDGSFCVCEANANVGFIAFDKACNLDVAGIIADYAASLLPSG RETERRMELISVVSTASTSTSEPELGPPASTAVDNMSASSSSVDSD PESTERRLITKLPGGLFNMNQLLANEIKLVD  FRVSRDGAPDCGTEUMGLAMEHGGSSRGCMYYLRYFF LFVSLQFLIILGLULEWVGNVWSTESNLQATERRAEGLYSQ LLGLTASGSNLTKEINFTTRAKDAIMGMWIMARRDLDRINASFR CCGGRVIYTMNQRYMAAIILSEKQCRDQFKDMNKSCDALLFML NQKVKTLEVEIAKEKTICTKDKESVLLNKRVAEEQLVECVKTRE LQHQERQLAREQLQKVQALCLPLDKDKFEMDLRTHWNSIPPRS LDNLGYNLYMPLGSELLSIRACHMPSLMSSKVEELARSLRAD LERVARENSDLQRCKLEAQQGLRASQEAKQKVEKEAQAREAKLQ AECSROTQLALEEKAVIRKERDLAKELEEKKREAEQLRMELAI RNSALDTCIKTKSQPMMPVSRPMGPVDNPOPIDPASLEEFKRKI LESQRPPAGIPVAPSG  6551 157 748 IQPPDPRNNTLAAYKEMKELPLVSLFGSCFLADPLNKSSYKYE ADTVDLNWCVISDMEVIELNKCTSGQSFEVILKPSFDGVPEFN ASLPRRRDPSLEEIQKKLEAAGERRKYQEAELLKHLAEKREHER EVIQKAIEENNNFIKMAKELAQAMESNKENREAHLAAMLERLQ EDCKHAAEVKNNELKERASR 1QPFDPRNNTLAAYKEMKELPLVSLFGSCFLADPLNKSSYKYE ADTVDLNWCVISDMEVIELNKCTSGQSFEVILKPSFDGVPEFN ASLPRRRDPSLEEIQKKLEAAERRKYQEAELLKHLAEKREHER EVIQKAIEENNFIKMAKEKLAQAMESNKENREAHLAAMLERLQ EDCKHAEEVRNNELKREASR 1QFDPDPRNNTLAAYKEMKELPLVSLFGSCFLADPLNKSSYKYE ADTVDLNWCVISDMEVIELNKCTSGQSFEVILKPSFDGVPEFN ASLPRRRDPSLEEIQKKLBAAEERRKYQEAELLKHLAEKREHER EVIQKAIEENNFIKMAKEKLAQAMESNKENREAHLAAMLERLQ ECKHAEEVRNNFIKMAKEKLAQAMESNKENREAHLAAMLERLQ EKDKHAEEVRKNKELKEEASR 6553 2 1807 FWSKMAAHLSYGRVWLNVLREAWFELREFLDKCAGSKAIVWD EYLICHGAFIELDYSLLGTGYSLLCHURGNSTAFVUD LYHAAKGLMTLQALYGTIPQIFGKBCARQVANMMIKRKEFTG SQNSIFPVEDNILLLDRNVDLLTPLATOLTYEGLIDEIYGIQNS YKKLPPEKFRAPKKQGGGKDLPTEAKKLQINSAEELYAEIRDKN FNAVGSVLSKKAKIISAAFERRINATVGEIRGFWSGIDTDKVNN YLEDCLAQKHSLIKVLRILVCLQSVCNSGLKKKVLDYYKREILQT YGYEHILTLHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVME ONPTDISVYSGYAPLSVALAQLLESFGGRSIEEVUR LLPGPFFF EERQPLPTGLOKKROPGLIKVLTGFFGRSIEEVUR LLPGPFFF EERQPLPTGLOKKROPGLIKVLTGFFARKSLEFLINDDOWNE ONPTDISVYSGYAPLSVALAQLLESFGGRSIEEVUR LLPGPFFF EERQPLPTGLOKKROPGLIKVLTGFFARKSLEFLINDDOWNE ONPTDISVYSGYAPLSVALAQLLESFGGRSIEEVUR LLPGFFFF	1			DGRMQSNCSLGGVGMMCSLSEOGKOLAIOVSNILGMDVCGIDLI,
RETERRALESVESTASETSEELEGPASTAVDNMSASSSSVDSD PESTERELITELDEGGEPMMOLLANE IRLLUD  FRUSDGAPDCGIECMGLAMEHGGSYARAGGSSRGCWYYLRYFF LFVSLIQPLIILGLULFMVYGNVHVSTESNLQATERRAEGLYSQ LLGLTASGSNLTKELNFTKADAIMCMMUMARREDLDEINASFR QCQGDRVIYTNNORYMAAIILSEKQCROFKDMKKSCDALLFML NOKNKTLEVEIAREKTITUKKESVLLNKRVAEEQLVECVKTRE LQHGERQLAKEQLQKVQALCLPLDKDKYEMDLERNLKRESIIPRS LDNLGYNLYHPLGSELASIRRACDHMPSLMSSKVEELARSLRAD IERVARENSDLORKCHEAQOQLRASQEAKGKVEKFAQAREAKLQ AECSROTOLALEEKAVLRKERDNLAKELEEKKRRAEQLRMELAI RNSALDTCIKTKSCOMMPVSRPMGPVPPPOPIDPASLEEFKRKI LESQRPPAGIPVAPSG  157 748 1QPPDFRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVDLNWCVISDMEVIELHKCTSGQSFEVILKPPSFDGVVEFN ASLPRRRDPSLEEIQKKLEAAEERRKYGEAELLKHLAEKREHER EVIQKAIEENNNFIKMAKEKLAGKMESNKENREAHLAAMLERLQ EKDKHAEEVKKNELKERASR 1QPPDPRNMTLAAYKEKMKELPLUSLFCSCFLADPLNKSSYKYE ADTVDLNWCVISDMEVIELNKCTSGQSFEVILKPSPSGVVEFN ASLPRRRDPSLEEIQKKLEAAEERRKYGEAELLKHLAEKREHER EVIQKAIEENNNFIKMAKEKLAGKMESNKENREAHLAAMLERLQ EKDKHAEEVKKNELKERASR 1GPPDPRNMTLAAYKEKMKELPLUSLFCSCFLADPLNKSSYKYE ADTVDLNWCVISSMEVIELNKCTSGQSFEVILKPSPSGVVFFN ASLPRRRDPSLEEIOKKLEAAEERRKYGEAELLKHLAEKREHER EVIQKAIEENNNFIKMAKEKLAGKMESNKENREAHLAAMLERLQ EKDKHAEEVKRKELKERASR 6553 2 1807 FWSKMAAHLSYGRVNINVLREAVRRELREFLDKAGSKAIVWD EKILTGFFGLIAGYSLLKEHEVEKMFTLKGNRCDAMMTRKREFTG SQNSIFPVEDNILLLDRNVDLLTPLATOLTYEGLIDEIYGIGNS YVKLPPEKKPREVSLDLIFFDGGBLISMESGAFKECYLEGDOTS LYHAAKGLMTLQALYGTIDJIFGGKECARKQUAMMTRKREFTG SQNSIFPVEDNILLLDRNVDLLTPLATOLTYEGLIDEIYGIGNS YVKLPPEKFAPKKQGDGKDLPTEAKKLQLMSAEBLYAEIRDKN PNAVGSVLSKKAKIISAAFEERRNATVGEIKGFVSQLPHMQAA RGSLANHTSIABLIKDVTTSEDFFCDKLTVGGEFMSGIDTDKVNN YIEDOLAGKHSLIKVLRUCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLHNLEKAGLLKPQTGGNNYPTIRKTRLMMDDVME ONPTDISVYYSGYAPLSVALAQLLSRFGWRSIEEVLRILPGPHF				MKDDGSFCVCEANANVGFIAFDKACNLDVAGIIADYAASI.t.psg
FRYSRDGAPDCGIEGMGLAMEHGGSYARAGGSSRGCWYYLRYFF LFYSLIOFLIILGUVLFMYYGNYHVSTESNLQATERRAEGLYSQ LLGLTASQSNLTKELNFTTRAKDAIMQMMINARRDLDRINASFR QCQGDRYIYTHNORYMAAIILEBKQCRDOFKDMNKSCDALLFML NOKVKTLEVELTAKERITCKKESVULINKRVAEEQLVECVKTRE LQHQERQLAKEQLQKVQALCLPLDKKFEMDLRNLWRDSIIPRS LDNLGYMLYHPLGSELASIRRAD IERVARRINSDLQROKLEAQOGLRASGGEAKQKVEKEAGAREAKLQ AEGSROTOLALEEKAVLRKERDNLAKELEEKKREAEQLREELAI RNSALDTCIKTKSOPMMPVSRMGPVPNPOPIDPASLEEFKRKI LESQRPPAGIPVAPSSG 157 748 1OPPDPRNMTLAAVKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVDLNWCVISDMEVIELINKCTSGQSFEVILKPPSFDGVYEFN ASLPRRRDPSLEEICKKLEAABERRRYQEAELLKHLAEKREHER EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKOKHAEEVKNKELEEKEASR ADTVDLNWCVISDMEVIELINKCTSGGSFEVILKPPSFDGVYEFP ASLPRRRDPSLEEIOKKLEAABERRRYQEAELLKHLAEKREHER EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKOKHAEEVKNKELBEASR ADTVDLNWCVISDMEVIELINKCTSGGSFEVILKPPSFDGVYEFP ASLPRRRDPSLEEIOKKLEAABERRRYQEAELLKHLAEKREHER EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKOKHAEEVKNKELKEEASR EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKOKHAEEVKNKELKEEASR EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKOKHAEEVKNKELKEEASR SPHALBIMDIJABANLSYGRVINDVLREAVRRELREFLDKCAGSKAIVMD EYLTGPFGLIAQYSLKKHEVEKMFTLKGNLPAADVKNIIFFV RPRLEIMDIJAGVSLKKHEVEKMFTLKGNLPAADVKNIIFFV SQNSIFPVEDNLLLLDRONDULTPLATOLTVEGLDEIGGONS YVKLPPEKREAPKKQGGGKDLPTEAKKJOLNSAEELYAEIRDKN FNAVGSVLSKKAKIISAAFEERHNAKTVGEIKQFVSQLPHMQAA RGSLANHTSIAELIKDVTTSEDFFDKLTVEGEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRUVLCLOSVCNSGLKOKVLDYYKREILQT YGYEHILTIHNEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE NAVGSVLSKKAKIISAAFEERHNAKTVGEIKGFVSQLPHMQAA RGSLANHTSIAELIKDVTTSEDFFDKLTVEGEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRUVLCLOSVCNSGLKOKVLDYYKREILQT YGYEHILTIHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE EERQPLPTGLQKKRQFURGVURFREIKDGT FERQPLPTGLQKKRQFGRUNVPTIRKTLRLWMDDVNE EERQPLPTGLQKKRQFURGVILAURFLSOIL				RLTRRMSLLSVVSTASETSEPELGPPASTAVDNMSASSSSVDSD
LEGURA SENDA PULL PROPERTING ALL  PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PROPERTING ALL PR	6550	2293		PESTERELLTKLPGGLFNMNQLLANEIKLLVD
LLGLTASGSNITKELMFTTRAKDAIMOMMINARRDLDRINASFR  OCGGGRUYTYTNNORYMAAIILSEKQCRDQFKDMNKSCDALLFML  NQKVKTLEVEIAKEKTICTKDKESVLLINKRVABEQLVECVKTRE  LOHGERQLAKERDLGVKVQALCLFLDKDKFEMDLRNLWRDSIIPRS  LDNLGYMLYPHJGSIASIRRACDHMPSLMSKVEELARSLRAD  IERVARENSDLQROKLEAQQGLRASQEAKQKVEKEAQAREAKLQ  AECSROTOLIALBEKAVILKERERDNLAKELEEKKREAEQLRMELAI  RNSALDTCIIKTKSQPMMPVSRPMGPVPNPQPIDPASLEEFKRKI  LESQRPPAGIPVAPSSG  157 748 IQPPDFRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE  ADTVUDLUNUCVISDMEVIELINKCTSGQSFEVILKPPSFDGVPEFN  ASLPRRDPSLEEIQKKLEAAEERRKYQEAELLKHLAEKREHER  EVIQKAIEENNNFIKMAKEKLAQKMESNKERREAHLAAMLERLQ  EKDKHAEEVKNNELKKERASR  10PPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE  ADTVUDLNWCVISDMEVIELINKCTSGQSFEVILKPPSFDGVPEFN  ASLPRRRDPSLEEIQKKLEAAEERRKYQEAELLKHLAEKREHER  EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ  EKDKHAEEVVRNKELKERASR  10PPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE  ADTVUDLNWCVISDMEVIELINKCTSGQSFEVILKPPSFDGVPEFN  ASLPRRRDPSLEEIQKKLEAAEERRKYQEAELLKHLAEKREHER  EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ  EKDKHAEEVVRNKELKEEASR  1807 FVWSKMAAHLSYGRVNLNVLREAVRRELREFLDKCAGSKAIVWD  EXLTGPFGLIAQYSLLKEHEVEKMFTLKGNRLPAADVKNIIFFV  RPPLELMDILBANVLSEDRREFTRDFHILFVPRRSLLCEQRIKD  LGVLGSFIHREYSLDLIPFFDGULEMSEKGAFKECYLEGDQTS  LYHAAKGLMTLQALYGTIPQIFGKGECARQVANMMIRNKREFTG  SQNSIFPVFDNLLLLDRNVDLLTPLATOLTYEGLIDEITYGIONS  YNKLPPEKFAPKKQGGGKÜLPTEAKKLQINSAEELYABIRDKN  YNAVGSVLSKKAKIISAAFEERNAKTVGEIKQFVSQLPHMQAA  RGSLANHTSIABLIKDVTTSEDFFOKLTVEQEFMSGIDTDKVNN  YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT  YGYEHLLTLINLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE  QNPTDISYVYSGYAPLSVRLAQLLSRFGMRSIEEVLRILDGTHF  EERQPLPTGLQKKRGPGENRVTLIFFLGGYTFFELIALIFFLSOL	0330	2293	922	FRVSRDGAPDCGIEQMGLAMEHGGSYARAGGSSRGCWYYLRYFF
OCCGORTYTYTHOGYMMAILISEKQCROOFKDMINSCOALLFML NOKVKTLEVEIAKEKTICTKOKESVILINKRVAEEQLVECVKTRE LQHQERQLAKEQLQKVQALCLPLDKDKFEMDLRNLWRDSIIPRS LDNLGYNLYHPLGSELASIRRACDHMPSLMSSKVEELARSLRAD IBRVARENSDLOROKLEAQQGLRASQEAKQKVEKEAQAREAKLQ AECSROTQLALEEKAVLRKERDNLAKELEEKKREAEQLRMELAI RNSALDTCIKTKSQPMMPVSRPMGPVPNPQPIDPASLEEFKRKI LESQRPPAGIPVAPSSG  157 748 IQPPDRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVDLNWCVISDMEVIELINKCTSGQSFEVILKPPSFDGVPEFN ASLPRRDPSLEEIQKKLEAAEERRKYQEAELKHLAEKREHER EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAAEEVRNKELKERASR  10PPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVDLNWCVISDMEVIELINKCTSGQSFEVILKPPSFDGVPEFN ASLPRRDPSLEEIQKKLEAAERRKYQEAELLKHLAEKREHER EVIQKAIEENNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAAEEVRNKELKEEASR  6553 2 1807 FVWSKMAAHLSYGRVNLNVLREAVRELREFLDKCAGSKAIVWD EYLIGAIEENNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVRNKELKEEASR  6553 2 1807 FVWSKMAAHLSYGRVNLNVLREAVRELREFLDKCAGSKAIVWD EYLIGFFGLIAQYSLLKEHEVEKMFTLKGNRLPAADVKNIIFFV RPRLBIMDIIABNJEADREGPTRDPHILFVPRRSLLCEQRLKD LGVLGSFIHREEYSLDLIPFDGDLLSMESEGAFKECYLEGDOTS LYHAAKGLMTLQALYGTIPQIFGKGECARQVANMMIRMKREFTG SQNSIFPVFONLLLLDRNVDLLTPLATQLTYEGLIDEIYGIQNS VVKLPPEKFAPKKQGDGGKDLPTEAKKLQLNSAEBLYAEIROKN FNAVGSVLSKKAKIISAAFEERHMAKTVGEIKQFVSQLPHMQAA RGSLANHTSIAELIKDVTTSEDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLINLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIEEVLRILPGPHF	1	1		LIVSLIGHTILGLVLFMVYGNVHVSTESNLQATERRAEGLYSQ
NOKYKTLEVEIAKEKTICTKDKESVILINKRVAEEQLVECVKTRE LOHGEROLAKEQLOKVQALCLPLDKDKKFEMDLRNLWRDSIIPRS LDNLGYNLYHPIGSELASIRRACDHMPSLMSSKVEELARSLRAD IERVARENSDLORQKLEAQQGLRASGEAKGKVEKRAQAREAKLQ AECSROTQLALBEKVIRKERDNLAKELEEKKREAEQLRMELAI RNSALDTCIKTKSQPMMPVSRPMGPVPNPQPIDPASLEEFKRKI LESQRPPAGIPVAPSSG  10PPDPRIMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVDLNWCVISDMEVIELNKCTSGQSFEVILKPPSFDGVPFEN ASLPRRDPSLEEIQKKLEAABERRRYGEAELLKHLAEKREHER EVIQKALEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVRKNKELKEASR  6552 157 748 10PPDPRIMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVDLUNCVISDMEVIELNKCTSGQSFEVILKPPSFDGVPFEN ASLPRRDPSLEEIQKKLEAABERRKYGEAELLKHLAEKREHER EVIQKALEENNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVRNKELKEEASR ASLPRRDPSLEEIQKKLEAABERRKYGEAELLKHLAEKREHER EVIQKALEENNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVRNKELKEEASR  6553 2 1807 FVWSKMAAHLSYGRVNLINVLREAVRRELREFLDKCAGSKAIVWD EYLTGPFGLIAQYSLLKEHEVEKMFTLKGNRLPAADVKNIIFFV RPRLBLMDIIAENVLSEDRRGPTRDFHILFVPRRSLLCEQRILKD LGVLGSFIHREEYSLDLIFPGDDLLSMESEGAFKECVLEGDOTS LYHAAKGLMTLQALYGTIPQIFGKGECARQVAMMMIRMKREFTG SQNSIFPVFDNLLLLDRNVDLLTPLATQLTYEGLIDEIYGGIONS YVKLPPEKFAPKKQGDGGKDLPTEAKKLQLINSAEBLYAEIRDKN FNAVGSVLSKKAKIISAFFERNAKTVGEIKQFVSQLPHMQAA RGSLANHTSIAELIKDVTTSEDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLINLEKAGLLKPQTGGRNNYPTIRKTLRIMMDDVNE QNPTDISYVYSGYAPLSVRLAQLLSRFGWRSIEEVLRILPGPHFF EERQPLPTGLQKKRQFGENRVTLIFFLGGVTFAELALRILSOL	1 1	,		OCOCODRATATIONAL ALLICONO CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTR
LONGYROLAKÇÜÇÜKVQALCLEPLÜKÜKFEMDLENLENGI IPRS LINLIGYNILYHPLGSELASIRRACDHMPSLMSSKVEELARSLRAD IERVARENSDLOROKLEAQOGLRASQEAKQKVEKEAQAREAKLQ AECSROTOLALEEKAVLEKERDNILAKELEEKKREAEQILRMELAI RNSALDTCIKTKSOPMMPVSRPMGPVPNPQPIDPASLEEFKRKI LESQRPPAGIPVAPSSG  157 748 10PPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVDLNWCVISDMEVIELINKCTSGQSFEVILKPPSFFDSVPEFN ASLPRRDPSLEEIQKKLEAAERREKYQEAELLKHLAEKREHER EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKOKHAEEVRKNKELKERASR 10PPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVDLNWCVISDMEVIELINKCTSGQSFEVILKPPSFDSVPEFN ASLPRRDPSLEEIQKKLEAAERREKYQEAELLKHLAEKREHER EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKOKHAEEVRKNKELKEEASR 6553 2 1807 FVWSKMAAHLSYGRVNILNVLREAVRRELREFLDKCAGSKAIVWD EYLTGPFGLIAQYSLLKEHEVEKMFTLKGRILPAADVKNIIFFV RPRLBIMDIIAENVLSEDRRGPTRDPHILFVPRSLLCEQRIKD LGVLGSFIHREEYSLDLIPFDGDLLSMESEGAFKECYLEGDOTS LYHAAKGIMTUQALYGTIPQIFGKGECARQVANMMIRMKREFTG SQNSIFPVFDNLLLLDRNVDLLTPLATOLTYEGLIDEIYGIONS YVKLPPEKFAPKKQGDGGKDLPTEAKKLQINSAEELYAEIRDKN FNAVGSVLSKKAKIISAAFEERHNAKTVGEIKQFVSQLPHMQAA RGSLANHTSIABLIKVURLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLINNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE QNPTDISYVYSGYAPLSVRLAQLLSRFGWRSIEBEVLRILDCPHF EERQPLPTGLQKKRQPGENRYVTLIFFLGGTTFAETAALFILSOL	1			NOKVKTLEVETAKEKTI CTVDVECHI I NOVA PROTESTA
LDNLGYNLYHPLGSELAS IRRACDHMPSIMS SKVEELARSLRAD IERVARENSDLQRQKLEAQQEKRASQEAKQKVEKEAQAREAKLQ AECSROTQLALEEKAVLEKERDNLAKELEEKKREAEQLRMELAI RNSALDTCI KTKSQPMPVSRPMGPVPNPQPIDPASLEEFKRKI LESQRPPAGIPVAPSSG  10PPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVDLNWCVISDMEVIELNKCTSGQSFEVILKPPSFFGVPEFN ASLPRRADPSLEEIQKKLEAAERRKYQEAELLKHLAEKREHER EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVRKNKELKERASR  10PPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVDLINWCVISDMEVIELNKCTSGQSFEVILKPPSFDGVPEFN ASLPRRADPSLEEIQKKLEAAERRKYQEAELLKHLAEKREHER EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVRKNKELKEBASR  6553  2 1807 FVWSKMAAHLSYGRVNLNVLREAVRRELREFLDKCAGSKAIVWD EYLTGFFGLIAQYSLLKEHEVEKMFTLKGNRLPAADVKNIIFFV RPRLELMDIIAENVLSEDRRGPTRDFHILFVPRRSLLCEQRLKD LGVLGSFIHREFYSLDLIFFDGDLLSMESEGAFKECYLEGDOTS LYHAAGSLMTLQALYGTIPQIFGKGECARQVANMMIRMKRFTG SQNSIFPVFDNLLLLDRNVDLLTPLATOLTTEGLIDEIYGIQNS YVKLPPEKFAPKKQGDGGKDLPTEAKKLQLNSAEELYAEIRDKN FNAVGSVLSKKAKIISAAFEERHNAKTVGEIKQFVSQLPHMQAA RGSLANHTSIAELIKDVTTSEDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLINNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIEEVURILPGPHF EERQPLPTGLQKKRQPGENRVYTLIFLEGGTFFAELTREFISOL	1 1			LOHOEROLAKEOLOKWOALCLELDVDVEEMDLDVLWEEQLVECVKTRE
IERVARENSDLQROKLEAQQGLRASGEAKOKVEKEAQAREAKLQ AECSROTQLALEEKAVLRKERDNLAKELEEKKREAEQLRMELAI RNSALDTCIKTKSOPMMPVSRPMGPVPNPQPIDPASLEEFKRKI LESQRPPAGIPVAPSSG 1QPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVOLNNCVISDMEVIELNKCTSGQSFEVILKPPSFDGVPEFN ASLPRRRDPSLEEIQKKLEAAEERRKYQEAELLKHLAEKREHER EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVKNKKLKEFASR 1QPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVOLNNCVISDMEVIELNKCTSGQSFEVILKPPSFDGVPEFN ASLPRRRDPSLEEIQKKLEAAEERRKYQEAELLKHLAEKREHER EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVRKNKELKEEASR 6553 2 1807 FVWSKMAAHLSYGRVINNVLREAVRELREFLDKCAGSKAIVWD EYLTGPFGLIAQYSLLKEHEVEKMFTLKGNRLPAADVKNIIFFV RPRLELMDIIAENVLSEDRRGPTRDPHILFVPRRSLLCEQRLKD LGVLGSFIHREYSLDLIPFDGDLLSMESBGAFKECYLEGDOTS LYHAAKGLMTLQALYGTIPQIFGKGECARQVANNMIRMKREFTG SQNSIFPVFDNLLLIDRNVDLLTPLATOLTYEGLIDEIYGIQNS YVKLPPEKFAPKKQGDGGKDLPTEAKKLQLNSAELYAEIRDKN FNAVGSVLSKKAKIISAAFEERNAKTVGEIKQFVSQLPHMQAA RGSLAMHTSIABILKDVTTSEDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTIHNLEKAGLIKPQTGGRNNYTIIRKTLRLWMDDVNE QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIEEVLRILPGPHF EERQPLPTGLQKKRQFGENRVTLIFFLGGVTFAEIAALRFLSOL	1 1			LDNLGYNLYHPI.GSELASIPPACDUMDGI MCCVUEEL ADGI DE
AECSROTQLALEEKAVI.RKERDNILAKELEEKKREAEQLRMELAI RNSALDTCIKTKSQPMMPVSRPMGPVPNPQPIDPASLEEFKRXI LESQRPPAGIPVAPSSG  1QPPDPRNMTLAAYKEKMKELPIVSLFCSCFLADPLNKSSYKYE ADTVOLINMCVISDMEVIEINKCTSGQSFEVILKPPSFDGVPEFN ASLPRRRDPSLEEIQKKLEAAEERKYQEAELLKHLAEKREHER EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVRKNKELKERASR  1QPPDPRNMTLAAYKEKMKELPIVSLFCSCFLADPLNKSSYKYE ADTVOLINWCVISDMEVIEINKCTSGQSFEVILKPPSFDGVPEFN ASLPRRDPSLEEIQKKLEABERRKYQEAELLKHLAEKREHER EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVRKNKELKEEASR  6553  2 1807  FVWSKMAAHLSYGRVULVVLREAVRRELREFLDKCAGSKAIVWD EYLTGPFGLIAQYSLLKEHEVEKMFTLKGNRLPAADVKNIIFFV RPRLEIMDIIAENVLSEDRRGPTRDFHILFVPRRSLLCEQRLKD LGVLGSFIHREEYSLDLIPFDGDLISMESEGAFKECYLEGDOTS LYHAAKGLMTLQALYGTIPQIFGKGECARQVAMMYIRKREFTG SQNSIFPVFDNLLLLDRNVDLLTPLATOLTYEGLIDEIYGIQNS YVKLPPEKFAPKKGGDGGKDLPTEAKKLQLNSAEELYAEIRDKN FNAVGSVLSKKAKIISAAFEERHNAKTVGEIKQFVSQLPHMQAA RGSLANHTSIAELIKDVTTSEDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHLITHNLEKAGLLKPQTGGRNNYPTIRKTLRLMMDDVNE QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIEEVLRILPGPHF EERQPLPTGLOKKRQPGENRVTTLIFFLGGVTFAEIAAHRFLSOL				IERVARENSDLOROKLEAOOGLRASOEAKOKVEKEAOADEAVIO
RNSALDTCIKTKSQPMMPVSRPMGPVPNPQPIDPASLEEFKRXI LESQRPPAGIPVAPSSG 1GPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVDLNWCVISDMEVIELNKCTSGQSFEVILKPPSFDGVPEFN ASLPRRPDPSLEEIQKKLEAAEBRRKYQEAELLKHLAEKREHER EVIQKAIEENNNFILMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVYKNKELKEEASR 1GPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVDLNWCVISDMEVIELNKCTSGQSFEVILKPPSFDGVPEFN ASLPRRRDPSLEEIQKKLEAAEBRRKYQEAELLKHLAEKREHER EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVYKNKELKEEASR 6553 2 1807 FVWSKMAAHLSYGRVNLNVLREAVRRELREFLDKCAGSKAIVWD EYLTGPFGLIAQYSLLKEHEVEKMFTLKGNRLPAADVKNIIFFV RPRLBLMDIIAENVLSEDRRGPTRDFHILFVPRRSLLCECRLKD LGVLGSFIHREYSLDLIPFDGDLLSMESEGAFKECYLEGDQTS LYHAAKGLMTLQALYGTIPQIFGKGECARQVANMMIRMKREFTG SQNSIFPVFDNLLLLDRNVDLLTPLATOLTYEGLIDEIYGIQNS YVKLPPEKFAPKKQGDGKDLPTEAKKLQLNSAEELYAEIRDKN FNAVGSVLSKKAKIISAAFEERHNAKTVGEIKQFVSQLPHMQAA RGSLANHTSIAELIKDVTTSEDFFDKLTVECEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHLTLHNLEKAGLLKPQTGGRNNYPTIRKTLRLMMDDVNE QNPTDISYVSGYAPLSVRLAQLLSRFGWRSIEEVLRILPGPHF EERQPLPTGLQKKRQPGENRVTTLIFFLGGVTFAEIAALRFLSOL				AECSROTQLALEEKAVLRKERDNLAKELEEKKREAEOLRMELAT
LESQRPPAGIPVAPSG  1QPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVOLNWCVISDMEVIELNKCTSGQSFEVILKPPSFDGVPEFN ASLPRRDPSLEEIQKKLEAAEERRKYQEAELLKHLAEKREHER EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKCKHAEEVRKNKELKEEASR  157 748 1QPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVOLNWCVISDMEVIELNKCTSGQSFEVILKPPSFDGVPEFN ASLPRRPPSLEEIQKKLEAAEERRKYQEAELLKHLAEKREHER EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKCKHAEEVRKNKELKEEASR  6553 2 1807 FVWSKMAAHLSYGRVNLNVLREAVRRELREFLDKCAGSKAIVWD EYLTGPFGLIAQYSLLKEHEVEKMFTLKGNRLPAADVKNIIFFV RPRLELMDIIAENVLSEDRRGPTRDFHILFVPRRSLLCEQRLKD LGVLGSFIHREEYSLDLIPFDGDLLSMESEGAFKECYLEGQCTS LYHAAKGLMTLQALYGTIPQIFGKGECARQVANMMIRMKREFTG SQNSIFPVFDNLLLLDRNVDLLTPLATOLTYEGLIDEIYGIQNS YVKLPPEKFAPKKQGDGGKDLPTEAKKLQLNSAEELYAEIRDKN FNAVGSVLSKKAKIISAAFEERHNAKTVGEIKQFVSQLPHMQAA RGGSLANHTSIAELIKDVTTSEDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHLITLHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE ONPTDISYVYSGYAPLSVRLAQLLSRPGWRSIEEVLRILPGPHF EERQPLPTGLQKKRQPGENRYTLIFFLGGVTFAELAALRFLSOL	1	j		RNSALDTCIKTKSQPMMPVSRPMGPVPNPOPIDPASLEEFKRKI
ADTVOLVMCV1SDMEV1ELNKCTSGQSFEV1LKPPSFDGVPEFN ASLPRRDPSLEE1QKKLEAAEERRKYQEAELLKHLAEKREHER EVIQKA1EENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVKNKELKEFASR  1QPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVOLVMCV1SDMEV1BLNKCTSGQSFEV1LKPPSFDGVPEFN ASLPRRDPSLEE1QKKLEAAEERRKYQEAELLKHLAEKREHER EVIQKA1EENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVRNKELKEEASR  6553 2 1807 FVWSKMAAHLSYGRVNLNVLREAVREELREFLDKCAGSKAIVWD EYLTGPFGLIAQYSLLKEHEVEKMFTLKGNRLPAADVKN11FFV RPRLBLMD11AENVLSEDRRGPTRDFHILFVPRRSILCEQRLKD LGVLGSFIHREEYSLDL1PFDGDLLSMESEGAFKECYLEGDQTS LYHAAKGLMTLQALYGTIPQ1FGKGECARQVANMMIRMKREFTG SQNS1FPVFDNLLLLDRNVDLLTPLATQLTYEGLIDE1YGIQNS YVKLPPEEKPAPKKQGDGGKDLPTEAKKLQLNSAEBLYAEIRDKN FNAVGSVLSKKAKI1SAAFEERHNATTVGEIKQFVSQLPHMQAA RGSLANHTSIAELIKDVTTSEDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLHNLEKAGLLKPQTGGRNNYPTIRRTLRLWMDDVNE QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIBEVLRILPGPHF EERQPLPTGLQKKRQEGENRVTLIFFLGGVTFAELAALRFLSOL		<u> </u>		LESQRPPAGIPVAPSSG
ADTVDLNWCVISDMEVIELNKCTSGQSFEVILKPPSFDGVPEFN ASLPRRRDPSLEEIQKKLEABERRKYQEAELLKHLAEKREHER EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVRKNKELKEEASR  1QPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVDLNWCVISDMEVIELNKCTSGQSFEVILKPPSFDGVPEFN ASLPRRRDPSLEEIQKKLEAAEERRKYQEAELLKHLAEKREHER EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVRKNKELKEEASR  2 1807 FVWSKMAAHLSYGRVNLNVLREAVRRELREFLDKCAGSKAIVWD EYLTGPFGLIAQYSLLKEHEVEKMFTLKGNRLPAADVKNIIFFV RPRLBLMDIIABNVLSEDRRGPTRDFHILFVPRRSLLCEQRLKD LGVLGSFIHREBYSLDLIPFDGDLLSMESEGAFKECYLEGDQTS LYHAAKGLMTLQALYGTIPQIFGKGECARQVANMMIRMKREFTG SQNSIFPVFDNLLLLDRNVDLLTPLATQLTYEGLIDEIYGIQNS YVKLPPEKFAPKKQGDGGKDLPTEAKKLQLNSAEBLYAEIRDKN FNAVGSVLSKKAKIISAAFEERHNAKTVGEIKQFVSQLPHMQAA RGSLANHTSIAELIKDVTTSEDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVME QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIEEVLRILPGPHF EERQPLPTGLQKKRQPGENRVTLIFFLGGVTFAEIAALRFLSOL	6551	157	748	IQPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE
ASLPRRDPSLEEIQKKLEAAERRKYQEAELLKHLAEKREHER EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVRKNKELKEFASR  1QPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVDLNWCVISDMEVIBLNKCTSGQSFEVILKPPSFDGVPEFN ASLPRRDPSLEEIQKKLEAAEERRKYQEAELLKHLAEKREHER EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVRKNKELKEEASR  2 1807 PVWSKMAAHLSYGRVNLNVLREAVRRELREFLDKCAGSKAIVWD EYLTGPFGLIAQYSLLKEHEVEKMFTLKGNRLPAADVKNIIFFV RPRLELMDIIAENVLSEDRRGPTRDFHILFVPRRSLLCEQRLKD LGVLGSFIHREEYSLDLIPFDGDLLSMESEGAFKECYLEGDQTS LYHAAKGLMTLQALYGTIPQIFGKGECARQVANMMIRMKREFTG SQNSIFPVFDNLLLLDRNVDLLTPLATQLTYEGLIDEIYGIQNS YVKLPPEKFAPKKQGDGGKDLPTEAKKLQLNSAEBLYAEIRDKN FNAVGSVLSKKAKIISAAFEERHNAKTVGEIKQFVSQLPHMQAA RGSLANHTSIAELIKDVTTSEDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE QNPTDISYYYSGYAPLSVRLAQLLSRPGWRSIEEVLRILPGPHF EERQPLPTGLQKKRQPGENRVTLIFFLGGVTFAEIAALRFLSOL	l i	i		ADTVDLNWCVISDMEVIELNKCTSGOSFEVILKPPSFDGVPFFN
EKDKHAEEVRKNKELKEFASR  157 748 1QPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVDLNWCVISDMEVIBLNKCTSGQSFEVILKPPSFDGVPEFN ASLPRRRDPSLEEIQKKLEAAEERRKYQEAELLKHLAEKREHER EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVRKNKELKEEASR  6553 2 1807 FVWSKMAAHLSYGRVNLNVLREAVRRELREFLDKCAGSKAIVWD EYLTGPFGLIAQYSLLKEHEVEKMFTLKGNRLPAADVKNIIPFV RPRLELMDIIAENVLSEDRRGPTRDFHILFVPRRSLLCEQRLKD LGVLGSFIHREEYSLDLIPFDGDLLSMESEGAFKECYLEGDQTS LYHAAKGLMTLQALYGTIPQIFGKGECARQVANMMIRMKREFTG SQNSIFPVFDNLLLLDRNVDLLTPLATQLTYEGLIDEIYGIQNS YVKLPPEKFAPKKQGDGGKDLPTEAKKLQLNSAEELYAEIROKN FNAVGSVLSKKAKIISAAFEERHNAKTVGEIKQFVSQLPHMQAA RGSLANHTSIAELIKDVTTSEDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIEEVLRILPGPHF EERQPLPTGLQKKRQPGENRVTLIFFLGGVTFAEIAALRFLSOL	1 1	ľ		ASLPRRRDPSLEEIQKKLEAAEERRKYOEAELLKHLAFKFFHFF
157 748 IQPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVDLNWCVISDMEVIBLNKCTSGQSFEVILKPPSFDGVPEFN ASLPRRDPSLEEIQKKLEAAEERRKYQEAELLKHLAEKREHER EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVRKNKELKEEASR  6553 2 1807 FVWSKMAAHLSYGRVNLNVLREAVRRELREFLDKCAGSKAIVWD EYLTGPFGLIAQYSLLKEHEVEKMFTLKGNRLPAADVKNIIFFV RPRLBLMDIIAENVLSEDRRGPTRDFHILFVPRRSLLCEQRLKD LGVLGSFIHREEYSLDLIFFDGDLLSMESEGAFKECYLEGDQTS LYHAAKGLMTLQALYGTIPQIFGKGECARQVANMMIRMKREFTG SQNSIFPVFDNLLLLDRNVDLLTPLATQLTYEGLIDEIYGIQNS YVKLPPEKFAPKKQGDGGKDLPTEAKKLQLNSAEBLYAEIRDKN FNAVGSVLSKKAKIISAAFEERHNAKTVGEIKQFVSQLPHMQAA RGSLANHTSIAELIKDVTTSEDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIEEVLRILPGPHF EERQPLPTGLQKKRQPGENRVTLIFFLGGVTFAEIAALRFLSOL	1 1			EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLO
ADTVDLINGCVISDMEVIBLINKCTSGQSFEVILKPPSFDGVPEFN ASLPRRRDPSLEEIQKKLEAAEERRKYQEAELLKHLAEKREHER EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVRKNKELKEEASR  FVWSKMAAHLSYGRVNLNVLREAVRRELREFLDKCAGSKAIVWD EYLTGPFGLIAQYSLLKEHEVEKMFTLKGNRLPAADVKNIIFFV RPRLBLMDIIAENVLSEDRRGPTRDFHILFVPRRSLLCEQRLKD LGVLGSFIHREEYSLDLIPFDGDLLSMESEGAFKECYLEGDQTS LYHAAKGLMTLQALYGTIPQIFGKGECARQVANMMIRMKREFTG SQNSIFPVFDNLLLLDRNVDLLTPLATOLTYEGLIDEIYGIQNS YVKLPPEKFAPKKQGDGGKDLPTEAKKLQLNSAEBLYAEIROKN FNAVGSVLSKKAKIISAAFEERHNAKTVGEIKQFVSQLPHMQAA RGSLANHTSIAELIKOVTTSEDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIEEVLRILPGPHF EERQPLPTGLQKKRQPGENRVTLIFFLGGVTFFAETAALRFLSOL	6552	157	740	
ASLPRRDPSLEEIQKKLEAAEERRKYQEAELLKHLAEKREHER EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVRKNKELKEEASR  6553  2 1807 FVWSKMAAHLSYGRVNLNVLREAVRRELREFLDKCAGSKAIVWD EYLTGPFGLIAQYSLLKEHEVEKMFTLKGNRLPAADVKNIIFFV RPRLBLMDIIAENVLSEDRRGPTRDFHILFVPRRSLLCEQRLKD LGVLGSFIHREEYSLDLIFFDGDLLSMESEGAFKECYLEGDQTS LYHAAKGLMTLQALYGTIPQIFGKGECARQVANMMIRMKREFTG SQNSIFPVFDNLLLLDRNVDLLTPLATQLTYEGLIDEIYGIQNS YVKLPPEKFAPKKQGDGGKDLPTEAKKLQLNSAEBLYAEIRDKN FNAVGSVLSKKAKIISAAFEERHNAKTVGEIKQFVSQLPHMQAA RGSLANHTSIAELIKDVTTSEDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIEEVLRILPGPHF EERQPLPTGLQKKRQPGENRVTLIFFLGGVTFAEIAALRFLSOL		13,	/48	TOPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE
EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ EKDKHAEEVRKNKELKEEASR  6553  2 1807  FVWSKMAAHLSYGRVNLNVLREAVRRELREFLDKCAGSKAIVWD EYLTGPFGLIAQYSLLKEHEVEKMFTLKGNRLPAADVKNIIFFV RPRLELMDIIAENVLSEDRRGPTRDFHILFVPRRSLLCEQRLKD LGVLGSFIHREEYSLDLIPFDGDLLSMESEGAFKECYLEGDQTS LYHAAKGLMTLQALYGTIPQIFGKGECARQVANMMIRMKREFTG SQNSIFPVFDNLLLLDRNVDLLTPLATQLTYEGLIDEIYGIQNS YVKLPPEKFAPKKQGDGGKDLPTEAKKLQLNSAEELYAEIRDKN FNAVGSVLSKKAKIISAAFEERHNAKTVGEIKQFVSQLPHMQAA RGSLANHTSIAELIKDVTTSEDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIEEVLRILPGPHF EERQPLPTGLQKKRQPGENRVTLIFFLGGVTFAEIAALRFLSOL	į l		ļ	ACI DED DE COMEVIELNICTS GOSFEVILICA PER DE DE COMET DE LA
6553  2 1807 FVWSKMAAHLSYGRVNLNVLREAVRRELREFLDKCAGSKAIVWD EYLTGPFGLIAQYSLLKEHEVEKMFTLKGNRLPAADVKNIIFFV RPRLEMDIIAENVLSEDRRGPTRDFHILFVPRRSLLCEQRLKD LGVLGSFIHREEYSLDLIPFDGDLLSMESEGAFKECYLEGDQTS LYHAAKGLMTLQALYGTIPQIFGKGECARQVANMMIRMKREFTG SQNSIFPVFDNLLLLDRNVDLLTPLATQLTYEGLIDEIYGIQNS YVKLPPEKFAPKKQGDGGKDLPTEAKKLQLNSAEBLYAEIRDKN FNAVGSVLSKKAKIISAAFEERHNAKTVGEIKQFVSQLPHMQAA RGSLANHTSIAELIKDVTTSEDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIEEVLRILPGPHF EERQPLPTGLQKKRQPGENRVTLIFFLGGVTFAEIAALRFLSOL			İ	ASLPRAKUPSLEETQKKLEAAEERRKYQEAELLKHLAEKREHER
FVWSKMAAHLSYGRVNLNVLREAVRRELREFLDKCAGSKAIVWD EYLTGPFGLIAQYSLLKEHEVEKMFTLKGNRLPAADVKNIIFFV RPRLBLMDIIAENVLSEDRRGPTRDFHILFVPRRSLLCEQRLKD LGVLGSFIHREEYSLDLIPFDGDLLSMESEGAFKECYLEGDQTS LYHAAKGLMTLQALYGTIPQIFGKGECARQVANMMIRMKREFTG SQNSIFPVFDNLLLLDRNVDLLTPLATQLTYEGLIDEIYGIQNS YVKLPPEKFAPKKQGDGGKDLPTEAKKLQLNSAEBLYAEIRDKN FNAVGSVLSKKAKIISAAFEERHNAKTVGEIKQFVSQLPHMQAA RGSLANHTSIAELIKDVTTSEDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIBEVLRILPGPHF EERQPLPTGLQKKRQPGENRVTLIFFLGGVTFAEIAALRFLSOI.				EKTIKHA FEURKNYEL KERA CR
EYLTGPFGLIAQYSLLKEHEVEKMFTLKGNRLPAADVKNIIFFV RPRLBLMDIIAENVLSEDRRGPTRDFHILFVPRRSLLCEQRLKD LGVLGSFIHREEYSLDLIPFDGDLLSMESEGAFKECYLEGDQTS LYHAAKGLMTLQALYGTIPQIFGKGECARQVANMMIRMKREFTG SQNSIFPVFDNLLLLDRNVDLLTPLATQLTYEGLIDEIYGIQNS YVKLPPEKFAPKKQGDGGKDLPTEAKKLQLNSAEBLYAEIRDKN FNAVGSVLSKKAKIISAAFEERHNAKTVGEIKQFVSQLPHMQAA RGSLANHTSIAELIKDVTTSEDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIBEVLRILPGPHF EERQPLPTGLQKKRQPGENRVTLIFFLGGVTFAEIAALRFLSOI.	6553	2	1807	FVWSKMAAHI, SVCDVNI, NVI, DEALTHOUSE DEEL DVC
RPRLELMDIIAENVLSEDRRGPTRDFHILFVPRRSLLCEQRLKD LGVLGSFIHREEYSLDLIPFDGDLLSMESEGAFKECYLEGDQTS LYHAAKGLMTLQALYGTIPQIFGKGECARQVANMMIRMKREFTG SQNSIFPVFDNLLLLDRNVDLLTPLATQLTYEGLIDEIYGIQNS YVKLPPEKFAPKKQGDGGKDLPTEAKKLQLNSAEBLYAEIRDKN FNAVGSVLSKKAKIISAAFEERHNAKTVGEIKQFVSQLPHMQAA RGSLANHTSIAELIKDVTTSEDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIBEVLRILPGPHF EERQPLPTGLQKKRQPGENRVTLIFFLGGVTFAELAALRFLSOL	<b>f</b>	1		EYLTGPFGLTAOVGLLKEUFVEWWEET POURT DARROWS
LGVLGSFIHREEYSLDLIPFDGDLLSMESEGAFKECYLEGDQTS LYHAAKGLMTLQALYGTIPQIFGKGECARQVANMMIRMKREFTG SQNSIFPVFDNLLLLDRNVDLLTPLATQLTYEGLIDEIYGIQNS YVKLPPEKFAPKKQGDGGKDLPTEAKKLQLNSAEBLYAEIRDKN FNAVGSVLSKKAKIISAAFEERHNAKTVGEIKQFVSQLPHMQAA RGSLANHTSIAELIKDVTTSEDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIBEVLRILPGPHF EERQPLPTGLQKKRQPGENRVTLIFFLGGVTFAELAALRFLSOL				RPRLELMDI IAENVI SEDREGDTEDDEUTI EUDDROTT ODGET
LYHAAKGLMTLQALYGTIPQIFGKGECARQVANMMIRMKREFTG SQNSIFPVFDNLLLLDRNVDLLTPLATQLTYEGLIDEIYGIQNS YVKLPPEKFAPKKQGDGGKDLPTEAKKLQLNSAEBLYAEIRDKN FNAVGSVLSKKAKIISAAFEERHNAKTVGEIKQFVSQLPHMQAA RGSLANHTSIAELIKDVTTSEDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIBEVLRILPGPHF EERQPLPTGLQKKRQPGENRVTLIFFLGGVTFAEIAALRFLSOL				LGVLGSFIHREEYSLDI.TPFDCDI.T.CMEGEGAEVECUT ECCO.
SQNSIFPVFDNLLLLDRNVDLLTPLATQLTYEGLIDEIYGIQNS YVKLPPEKFAPKKQGDGGKDLPTEAKKLQLNSAEELYAEIRDKN FNAVGSVLSKKAKIISAAFEERHNAKTVGEIKQFVSQLPHMQAA RGSLANHTSIAELIKDVTTSEDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIEEVLRILPGPHF EERQPLPTGLQKKRQPGENRVTLIFFLGGVTFAEIAALRFLSOI.				LYHAAKGLMTLOALYGTIPOIFGKGFCAPOVANMMIDMVD
YVKLPPEKFAPKKQGDGGKDLPTEAKKLQLNSAEBLYAEIRDKN FNAVGSVLSKKAKIISAAFEERHNAKTVGEIKQFVSQLPHMQAA RGSLANHTSIAELIKDVTTSEDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIEBEVLRILPGPHF EERQPLPTGLQKKRQPGENRVTLIFFLGGVTFAEIAALRFLSOI.		Í		SQNSIFPVFDNLLLLDRNVDLLTPLATOLTVEGLTDETVGTG
FNAVGSVLSKKAKI ISAAFEERHNAKTVGEIKQFVSQLPHMQAA RGSLANHTSIAELIKOVTTSEDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIEEVLRILPGPHF EERQPLPTGLQKKRQPGENRVTLIFFLGGVTFAEIAALRFLSOI.	·	ľ		YVKLPPEKFAPKKQGDGGKDLPTEAKKLOLNSAERI.VAFTDDVA
RGSLANHTSIAELIKDVTTSEDFFDKLTVEQEFMSGIDTDKVNN YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIBEVLRILPGPHF EERQPLPTGLQKKRQPGENRVTLIFFLGGVTFAEIAALRFLSOL				FNAVGSVLSKKAKI ISAAFEERHNAKTVGEIKOFVSOLDHMON N
YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT YGYEHILTLHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIBEVLRILPGPHF EERQPLPTGLQKKRQPGENRVTLIFFLGGVTFAEIAALRFLSOI		1	J	RGSLANHTSIAELIKDVTTSEDFFDKLTVEOEFMSGIDTDKVAM
YGYEHILTLHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIBEVLRILPGPHF EERQPLPTGLQKKRQPGENRVTLIFFLGGVTFAEIAALRFLSOI.	[ [	1	Ì	YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILOT
QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIBEVLRILPGPHF EERQPLPTGLQKKRQPGENRVTLIFFLGGVTFAEIAALRFLSOI	ļ Ē			YGYEHILTLHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE
EERQPLPTGLQKKRQPGENRVTL1FFLGGVTFAE1AALRFLSOL	•			QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIEEVLRILPGPHF
PDCCADACT & MOVE & SAVOMANT POR A COMPANY	1	į	ļ	EERQPLPTGLQKKRQPGENRVTLIFFLGGVTFAEIAALRFLSOL
EDGGIE I V LATIKLMNGTSWI EALMEKPF				EDGGTEYVIATTKLMNGTSWIEALMEKPF

SEO	Predicted	1 5 - 3 /	
ID	beginning	Predicted end	
NO:	nucleotide	nucleotide	[ Water and Called Day on the first and the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the called the
	location	location	Ordinate Acid, Frenchylalaning C.o.
	corresponding	corresponding	I I THE TABLE THE TELESION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF
1	to first	to first	D=DeuCine, M=Methionine N-lengaries
ľ	amino acid	amino acid	F=FLOTING, O=Glutamine P-Argining
	residue of	residue of	S=Serine, T=Threonine V=V=line
l l	amino acid	amino acid	W=Tryptophan, Y=Tyrosine v=II-l-
1		sequence	(Codoli, /=possible nucleotide dolonia-
6554	sequence		( \=Possible nucleotide insertion)
0334	119	1244	FEMGSQVSVESGALHVVIVGGGFGGTAASOLOALNURBUKTUSK
1			1005FIRM VAALKASVETGFAKKTFTSVSVTEVDMEDOOT INGTE
- 1	· i		I DIGIVATIVADA GEAL PESHLI LATGSTGD PDGV ENTEVA COOR TO
- [	-		AYEDMVRQVQRSRFIVVVGGGSAGVEMAAEIKTEYPEKEVTLIH
- 1	Į.	j	SQVALADKELLPSVRQEVKEILLRKGVQLLLSERVSNLEELPLN
Í	į.	1	EYREYIKVQTDKGTEVATNLVILCTGIKINSSAYRKAFESRLAS
	1	1	SGALRVNEHLQVEGHSNVYAIGDCADVRTPKMAYLAGLHANIAV
ŀ			ANIVNSVKQRPLQAYKPGALTFLLSMGRNDGVGQISGFYVGRLM
			VRLTKSRDLFVSTSWKTMRQSPP
6555	1552	498	IHMALLRKINQVLLFLLIVTLCVILYKKVHKGTVPKNDADDESE
Ì	ľ		TPEELEEIPVVICAAAGRMGATMAAINSIYSNTDANILFYVVG
ŀ	1		LRNTLTRIRKWIEHSKLREINFKIVEFNPMGLKGKIRPDSSRPE
1		1	LLQPLNFVRFYLPLLIHQHEKVIYLDDDVIVQGDIQELYDTTLA
-	1	1	LGHAAAFSDDCDLPSAQDINRLVGLQNTYMGYLDYRKKAIKDLG
	1	1	ISPSTCSFNPGVIVANMTEWKHQRITKQLEKWMQKNVEENLYSS
1	ļ		SLGGGVATSPMLIVFHGKYSTINPLWHIRHLGWNPDARYSEHFL
			QEAKLLHWNGRHKPWDFPSVHNDLWESWFVPDPAGIFKLNHHS
6556	241	1449	ASLCKGCFFVTHVLVIILPSLQSPPTFGFLLDIDGVLVRGHRVI
1			PAALKAFRRLVNSQGQLRVPVVFVTNAGNILQHSKAQELSALLG
İ	1	1	CEVDADQVILSHSPMKLFSEYHEKRMLVSGQGPVMENAQGLGFR
ľ	ľ	1	NVVTVDELRMAFPLLDMVDLERRLKTTPLPRNDFPRIEGVLLLG
	1	}	EPVRWETSLQLIMDVLLSNGSPGAGLATPPYPHLPVLASNMDLL
1	ļ	1	WMAEAKMPRFGHGTFLLCLETIYQKVTGKELRYEGLMGKPSILT
	i	f	YQYAEDLIRRQAERRGWAAPIRKLYAVGDNPMSDVYGANLFHQY
İ			LQKATHDGAPELGAGGTRQQQPSASQSCISILVCTGVYNPRNPQ
			STEPVLGGGEPPFHGHRDLCFSPGLMEASHVVNDVNEAVQLVFR
			KEGWALE
6557	2598	1534	RMCGRTSCHLPRDVLTRACAYQDRRGQQRLPEWRDPDKYCPSYN
			KSPQSNSPVLLSRLHFEKDADSSERI IAPMRWGLVPSWFKESDP
			SKLQFNTTNCRSDTVMEKRSFKVPLGKGRRCVVLADGFYEWQRC
			QGTNQRQPYFIYFPQIKTEKSGSIGAADSPENWEKVWDNWRLLT
1 1			MAGIFDCWEPPEGGDVLYSYTIITVDSCKGLSDIHHRMPAILDG
			EEAVSKWLDFGEVSTQEALKLIHPTENITFHAVSSVVNNSRNNT
	i		PECLAPVDLVVKKELRASGSSQRMLQWLATKSPKKEDSKTPQKE
1 1			ESDVPQWSSQFLQKSPLPTKRGTAGLLEQWLKREKEEEPVAKRP
6558			YSQ
0558	21	1138	FHGRRRGGRKMELGSCLEGGREAAEEEGEPEVKKRRLLCVEFAS
1			VASCDAAVAQCFLAENDWEMERALNSYFEPPVEESALERRPETI
1	ļ		SEPKTYVDLTNEETTDSTTSKISPSEDTQQENGSMFSLITWNID
1	ł		GLDLNNLSERARGVCSYLALYSPDVIFLQEVIPPYYSYLKKRSS
, ,	f		NYEIITGHEEGYFTAIMLKKSRVKLKSQEIIPFPSTKMMRNLLC
1 !		1	VHVNVSGNELCLMTSHLESTRGHAAERMNQLKMVLKKMQEAPES
1	1		ATVIFAGDTNLRDREVTRCGGLPNNIVDVWEFLGKPKHCQYTWD
1	ì		TOMNSNLGITAACKLRFDRIFFRAAAEEGHIIPRSLDLLGLEKL
F 655			DCGRFPSDHWGLLCNLDIIL
6559	3	364	GPELSGLPTRPKKLKANQTPIAMDCCASRSCSVPTGPATTICSS
1	ļ		DKSCRCGVCLPSTCPHTVWLLEPTCCDNCPPPCHIPQPCVPTCF
6560			LLNSCQPTPGLETLNLTTFTQPCCEPCLPRGC
6560	3	1435	TATSGGIWLRRKWRCHWPRPLPQSCVGTEGGLQVRDTSSRIAKG
			GVDHTKMSLHGASGGHERSRDRRRSSDRSRDSSHERTESQLTPC
1		ĺ	IRNVTSPTRQHHVEREKDHSSSRPSSPRPQKASPNGSISSAGNS
			SRNSSQSSSDGSCKTAGEMVFVYENAKEGARNIRTSERVTLIVD
1		. 1	NTRFVVDPSIFTAQPNTMLGRMFGSGREHNFTRPNEKGEYEVAE
! !		ĺ	GIGSTVFRAILDYYKTGIIRCPDGISIPELREACDYLCISFEYS
	1	ļ	TIKCRDLSALMHELSNDGARRQFEFYLEEMILPLMVASAQSGER
			ECHIVVLTDDDVVDWDEEYPPQMGEEYSQIIYSTKLYRFFKYIE
			THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY O

SEQ	Predicted	Predicted end	I mino poid agency
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=pcssible nucleotide insertion)
1		i	NRDVAKSVLKERGLKKIRLGIEGYPTYKEKVKKRPGGRPEVIYN
			YVQRPFIRMSWEKEEGKSRHVDFOCVKSKSITNLAAAADIPOD
6561	3	1006	QLVVMHPTPQVDELDILPIHPPSGNSDLDPDAQNPML
0301	) 3	1086	PGRRFRRKESSSSRWFPADCLLGLRGPASSLLSPEPSPSWPSHS
		]	PCPMAALTDLSFMYRWFKNCNLVGNLSEKYVFITGCDSGFGNLL
		 	AKQLVDRGMQVLAACFTEEGSQKLQRDTSYRLQTTLLDVTKSES
1	İ		IKAAAQWVRDKVGEQGLWALVNNAGVGLPSGPNEWLTKDDFVKV
	}		INVNLVGLIEVTLHMLPMVKRARGRVVNMSSSGGRVAVIGGGYC VSKFGVEAFSDSIRRELYYFGVKVCIIEPGNYRTAILGKENLES
ı			RMRKLWERLPQETRDSYGEDYFRIYTDKLKNIMQVAEPRVRDVI
			NSMEHAIVSRSPRIRYNPGLDAKLLYIPLAKLPTPVTDFILSRY
			LPRPADSV
6562	1	1562	MSTLYDIRAHKAQLLRFFASSDSNKALEQRRTLHTPKLEHLDRV
İ			LYEWFLGKRSEGVPVSGPMLIEKAKDFYEQMQLTEPCVFSGGWL
1			WRFKARHGIKKLDASSEKQSADHQAAEQFCAFFRSLAAEHGLSA
			EQVYNADETGLFWRCLPNPTPEGGAVPGPKOGKDRI.TVI.MCANA
1			TGSHRLKPLAIGKCSGPRAFKGIQHLPVAYKAOGNAWVDKEIFS
}			DWFHHIFVPSVREHFRTIGLPEDSKAVLLLDSSRAHPOEAELVS
1	1	•	SNVFTIFLPASVASLVQPMEQGIRRDFMRNFINPPVPLQGPHAR
			YNMNDAIFSVACAWNAVPSHVFRRAWRKLWPSVAFAEGSSSEEE
			LEAECFPVKPHNKSFAHILELVKEGSSCPGQLRQRQAASWGVAG
			REAEGGRPPAATSPAEVVWSSEKTPKADQDGRGDPGEGEEVAWE
			QAAVAFDAVLRFAERQPCFSAQEVGQLRALRAVFRSQQQVRRRR GALGAVVKVEALQEGPGGCGATAQSPLPCSSTAGDN
6563	1319	2694	LARPAQPVLLREPEGAGPPVPAGHLVHHLQGGHLRERAHPDLEA
			HEHPLPCDQMFWRQMGGHLRMVEANSRGVVWGIGYDHTAWVYTG
1			GYGGGCFQGLASSTSNIYTQSDVKCVHIYENQRWNPVTGYTSRG
i i			LPTDRYMWSDASGLQECTKAGTKPPSLQWAWVSDWFVDFSVPGG
1 1			TDQEGWQYASDFPASYHGSKTMKDFVRRRCWARKCKLVTSGPWL
1			EVPPIALRDVSIIPESPGAEGSGHSIALWAVSDKGDVLCRLGVS
	i		ELNPAGSSWLHVGTDQPFASISIGACYQVWAVARDGSAFYRGSV
] }			YPSQPAGDCWYHIPSPPRQRLKQVSAGOTSVYALDENGNI,WYRO
] [	1		GITPSYPQGSSWEHVSNNVCRVSVGPLDQVWVIANKVQGSHSLS
1 1			RGTVCHRTGVQPHEPKGHGWDYGIGGGWDHISVRANATRAPRSS
6564	1	975	SQEQEPSAPPEAHGPVCC
1	_	573	APGSCALWSYCGRGWSRAMRGCQLLGLRSSWPGDLLSARLLSQE
1 1			KRAAETHFGPETVSEEEKGGKVYQVFESVAKKYDVMNDMMSLGI HRVWKDLLLWKMHPLPGTQLLDVAGGTGDIAFRFLNYVQSQHQR
]			KQKRQLRAQQNLSWEEIAKEYQNEEDSLGGSRVVVCDINKEMLK
!!			VGKQKALAQGYRAGLAWVLGDAEELPFDDDKFDIYTIAFGIRNV
1 1	Í		THIDQALQEAHRVLKPGGRFLCLEFSQVNNPLISRLYDLYSFQV
] ]			IPVLGEVIAGDWKSYQYLVESIRRFPSQEEFKDMIEDAGFHKVT
<u> </u>			YESLTSGIVAIHSGFKL
6565	1464	999	RSAVANGLTKRRMGLKLNGRYISLILAVQIAYLVQAVRAAGKCD
			AVFKGFSDCLLKLGDSMANYPQGLDDKTNIKTVCTYWEDFHSCT
j .		İ	VTALTDCQEGAKDMWDKLRKESKNLNIQGSLFELCGSGNGAAGS
6566			LLPAFPVLLVSLSAALATWLSF
6366	3	1385	KYESAQPGGTQPEPGLGARMATHKALVMCLGLPLFLFPGAWAQG
	•		HVPPGCSQGLNPLYYNLCDRSGAWGIVLEAVAGAGIVTTFVLTI
	1		ILVASLPFVQDTKKRSLLGTQVFFLLGTLGLFCLVFACVEKPDF
	1		STCASRRFLFGVLFAICFSCLAAHVFALNFLARKNHGPRGWVIF
			TVALLLTLVEVIINTEWLIITLVRGSGEGGPQGNSSAGWAVASP
ĺ	· · · · · · · · · · · · · · · · · · ·	ł	CAIANMDFVMALIYVMLLLLGAFLGAWPALCGRYKRWRKHGVFV
	1	į	LLTTATSVAIWVVWIVMYTYGNKQHNSPTWDDPTLAIALAANAW
			AFVLFYVIPEVSQVTKSSPEQSYQGDMYPTRGVGYETILKEQKG
	<del></del>	<u></u>	QSMFVENKAFSMDEPVAAKRPVSPYSGYNGQLLTSVYQPTEMAL

6573	767	275	CEEK GGGGGESQSFRAQDGTRTPATDCLMYLQGPRKLMTQGGYDMVQK LFLDFFRRRLSQRPTAEELEQRNILKPRNEQEEQEEKREIKRRL
			EFANMQQQREEDRMAKVQENEEKRLQLQNALTQKLEEMLRQRED LEQVRQELYQEEQAEIYKSKLKEEAEKKLRKQKEMKQDFEEQMA LKELVLQAAKEEEENFRKTMLAKFAEDDRIELMNAQKQRMKQLE HRRAVEKLIEERRQQFLADKQRELEEWQLQQRRQGFINAIIEEE RLKLLKEHATNLLGYLPKGVFKKEDDIDLLGEEFRKVYQQRSEI
		F.	QRKQFLRLLQNEQFELDMEEAIQKAEENKRLKELQLKQEEKLAM ELAKLKHESLKDEKMRQQVRENSIELRELEKKLKAAYMNKERAA QIAEKDAIKYEQMKRDAEIAKTMMEEHKRIIKEENAAEDKRNKA KAQYLDLEKQLEEQEKKKQEAYEQLLKEKLMIDEIVRKIYEED QLEKQQKLEKMNAMRRYIEEFQKEQALWRKKKREEMEEENRKII
6572	49	1646	TPERAQPGALLGAAGCCVCGGRNWPRSHERGYFSSAKMGSKRRN LSCSERHQKLVDENYCKKLHVQALKNVNSOIRNOMYONENDRY
03,1	169	656	APDMNRKKLQKLTDTLTKNCKHLFRGFDKDNDGCVNVLEWIHGL SLFLRGSLEEKMKYCFEVFDLNGDGFISKEEMFHMLKNSLLKQP SEEDPDEGIKDLVEITLKKMDHDHDGKLSFADYELAVREETLLL EAFGPCLPDPKSQMEFEAQVFKDPNEFNDM
6571	169		PASRKMGSKALPAPIPLHPSLQLTNYSFLQAVNTFPATVDHLQG LYGLSAVQTMHMNHWTLGYPNVHEITRSTITEMAAAQGLVDARF PFPALPFTTHLFHPKQGAIAHVLPALHKORPRFDFANLAVAATQ EDPPKMGDLSKLSPGLGSPISGLSKLTPDRKPSRGRLPSKTKKE FICKFCGRHFTKSYNLLIHERTHTDERPYTCDICHKAFRRQDHL RDHRYIHSKEKPFKCQECGKGFCQSRTLAVHKTLHMQTSSPTAA SSAAKCSGETVICGGT
6570	330	1304	PL  ARLPRLTFLREGFLYVLLSHWVFVGAPRPPASDSWKKGLVBGAD
			RMSWLFPLTKSASSSAAGSPGGLTSLQQQKQRLIESLRNSHSSI AEIQKDVEYRLPFTINNLTININILLPPQFPQEKPVISVYPPIR HHLMDKQGVYVTSPLVNNFTMHSDLGKIIQSLLDEFWKNPPVLA PTSTAFPYLYSNPSGMSPYASQGFPFLPPYPPQEANRSITSLSV ADTVSSSTTSHTTAKPAAPSFGVLSNLPLPIPTVDASIPTSONG FGYKMPDVPDAFPELSELSVSQLTDMNEQEEVLLEQFLTLPQLK QIITDKDDLVKSIEELARKNLLLEPSLEAKRQTVLDKYELLTQM KSTFEKKMQRQHELSESCSASALOARLKVAAHFAFFEDNIAED
6569	205	1532	NVADHYGVYKPLFEAVGGSGGKTLEDVFYEREVQMNVLAFNQF HYGVFYAYVKLKEQEIRNIVWIAECISQRHRTKINSYIPIL RRRGPQRLGHGRPTPLLCRWRTAGPSHWEKQARAFQGLRPVDPR
			LEGAELYFNVDHGYLEGLVRGCKASLLTQQDYINLVQCETLEDL KIHLQTTDYGNFLANHTNPLTVSKIDTEMRKRLCGEFEYFRNHS LEPLSTFLTYMTCSYMIDNVILLMNGALQKKSVKEILGKCHPLG RFTEMEAVNIAETPSDLFNAILIETPLAPFFQDCMSENALDELN IELLRNKLYKSYLEAFYKFCKNHGDVTAEVMCPILEFEADRRAF IITLNSFGTELSKEDRETLYPTFGKLYPEGLRLLAQAEDFDQMK
6568	3	1183	ALLSLGIAYYVSGVLPFVENQPBLVH  HASDRLLVLPDNYSHFSQASANLQGPSRTTELFHPTLASISSPM LEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDHCHVLEGARLVENVDH
			TKRSNLKAYACSIHHIRTMSYVFVNDSSQTNVPLLQACIDGDFN YSKRLLESGFDPNIRDSRGRTGLHLAAARGNVDICQLLHKFGAD LLATDYQGNTALHLCGHVDTIQFLVSNGLKIDICNHQGATPLVL AKRRGVNKDVIRLLESLEEQEVKGFNRGTHSKLETMQTAESESA MESHSLLNPNLQQGEGVLSSFRTTWQEFVEDLGFWRVLLLIFVI
6567	125	863	MHKVPSEGAYDIILPRATANSQVMGSANSTLRAEDMYSAQSHQA ATPPKDGKNSQVFRNPYVWD
	amino acid sequence	sequence	Codon, /=possible nucleotide deletion,     \=possible nucleotide insertion
	amino acid residue of	residue of amino acid	S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Imknown +uch-
	corresponding to first	to first amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
NO:	nucleotide location	location corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
ID	beginning	Predicted end nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid R

SEO	Predictod	T nume 32	
ID	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid E-
1.0.	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine
	corresponding	corresponding	H=H1stidine, I=Isoleucine, K=Lvsine
1	to first	to first amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
ì	residue of		S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion,
	Deque		\=possible nucleotide insertion)
6574	204	1159	LTAADKVSRGECWRVGGRTVCWVSLGSPLGSV
""	204	1129	LESSVPVSVGVFWACGVSWTGAAGLQDGALSDTMARNAEKAMTA
1	ſ		LARFRQAQLEEGKVKERRPFLASECTELPKAEKWRRQIIGEISK
[	j		KVAQIQNAGLGEFRIRDLNDEINKLLREKGHWEVRIKELGGPDY
}	1		GKVGPKMLDHEGKEVPGNRGYKYFGAAKDLPGVRELFEKEPLPP
			PRKTRAELMKAIDFEYYGYLDEDDGVIVPLEQEYEKKLRAELVE
	i		KWKAEREARLARGEKEEEEEEEEEINIYAVTEEESDEEGSQEKG
			GDDSQQKFIAHVPVPSQQEIEEALVRRKKMELLQKYASETLQAQ
6575	117	820	SEEARRLLGY
	]	620	SPALASQSGGITEEKMLEPQENGVIDLPDYEHVEDETFPPFPPP
			ASPERQDGEGTEPDEESGNGAPVPVPPKRTVKRNIPKLDAQRLI
1			SERGLPALRHVFDKAKFKGKGHEAEDLKMLIRHMEHWAHRLFPK
1			LQFEDFIDRVEYLGSKKEVQTCLKRIRLDLPILHEDFVSNNDEV
			AENNEHDVTSTELDPFLTNLSESEMFASELSISLTEEQQQRIER NKQLALERRQAKLP
6576	1	1060	
1 1		2000	PEPQALVGQKRGALRLLVARLVLTVSAPAEVRRRVLRPVLSWMD
1	i		RETRALADSHFRGLGVDVPGVGQAPGRVAFVSEPGAFSYADFVR
i l		-	GFLLPNLPCVFSSAFTQGWGSRRRWVTPAGRPDFDHLLRTYGDV VVPVANCGVQEYNSNPKEHMTLRDYITYWKEYIQAGYSSPRGCL
1	i		YLKDWHLCRDFPVEDVFTLPVYFSSDWLNEFWDALDVDDYRFVY
	ļ		AGPAGSWSPFHADIFRSFSWSVNVCGRKKWLLFPPGOEEALRDR
1 1			HGNLPYDVTSPALCDTHLHPRNQLAGPPLEITQEAGEMVFVPSG
1			WHHQVHNLVMCCFSCPLSGAFLQEDGSTTSPLSQPELGWNGVAH
			G
6577	2271	987	SDRMASDDFDIVIEAMLEAPYKKEEDEQQRKEVKKDYPSNTTSS
1 1	ľ		TSNSGNETSGSSTIGETSNRSRDRDRYRRRNSRSRSPGRQCRHR
1	]		SRSWDRRHGSESRSRDHRREDRVHYRSPPLATGYRYGHSKSPHF
1 1	i		REKSPVREPVDNLSPEERDARTVFCMQLAARIRPRDLEDFFSAV
1			GKVRDVRIISDRNSRRSKGIAYVEFCEIQSVPLAIGLTGQRLLG
1 1	i		VPIIVQASQAEKNRLAAMANNLQKGNGGPMRLYVGSLHFNITED
	i		MLRGIFEPFGKIDNIVLMKDSDTGRSKGYGFITFSDSECARRAL
1 1			EQLNGFELAGRPMRVGHVTERLDGGTDITFPDGDOFIDLGSAGG
1 i			RFQLMAKLAEGAGIQLPSTAAAAAAAAAAAAAI.OLNGAVPI.Ga
h (530 +			LNPAALTALSPALNLASQCLQLSSLFTPOTM
6578	377	1489	PSSSATMNRAPLKRATILHMALTGASDPSAEAEANGEKPFLLRA
1			LQIALVVSLYWVTSISMVFLNKYLLDSPSLRLDTPIFVTFYOCI.
1			VTTLLCKGLSALAACCPGAVDFPSLRLDLRVARSVLPLSVVFTC
) I			MITFNNLCLKYVGVAFYNVGRSLTTVFNVLLSYLLLKOTTSFVh
			LTCGIIIGGFWLGVDQEGAEGTLSWLGTVFGVLASLCVSI.NAI
1	ļ	ľ	YTTKVLPAVDGSIWRLTFYNNVNACILFLPLLLLLGELOALPDE
	1		AQLGSAHFWGMMTLGGLFGFAIGYVTGLOIKFTSPLTHNVSGTA
			KACAQTVLAVLYYEETKSFLWWTSNMMVLGGSSAYTWVRGWEMK
6579	2	73.	KTPEEPSPKDSEKSAMGV
	-	711	RPPRVWYPELRELSAAAPRWSHRTAPGIMVFYFTSSSVNSSAYT
			IYMGKDKYENEDLIKHGWPEDIWFHVDKLSSAHVYLRLHKGENT
] {		]	EDIPKEVLMDCAHLVKANSIQGCKMNNVNVVYTPWSNLKKTADM
] ]		1	DVGQIGFHRQKDVKIVTVEKKVNEILNRLEKTKVERFPDLAAEK
[		ł	ECRDREERNEKKAQIQEMKKREKEEMKKKREMDELRSYSSLMKV
6580	62	3 - 3	ENMSSNQDGNDSDEFM
	32	1571	LVALKNWKPKGTNIPAPQSPVFGEAVSGVYMMTKVLGMAPVLGP
		İ	RPPQEQVGPLMVKVEEKEEKGKYLPSLEMFRORFROFGVHDTDC
			PREALSQLRVLCCEWLRPEIHTKEOILELLVLEOFITTI.PORTA
	Ì	ŀ	AWVQEHCPESAEEAVTLLEDLERELDEPGHOVSTPPNEOKPVWE
	1	1	KISSSGTAKESPSSMQPQPLETSHKYESWGPLYIOESGEEGERA
		1	QDPRKVRDCRLSTQHEESADEOKGSEAEGLKGDIISVIIANKPE
<u> </u>			ASLERQCVNLENEKGTKPPLQEAGSKKGRESVPTKPTPGERRYI

SEO	Predicted	I Dwodd of	
ID	beginning	Predicted end	
NO:	nucleotide	nucleotide	\A=Alanine, C=Cvsteine
	location	location	Glucamic Acid, F=Phenylalanine G-Glucino
1	corresponding	corresponding to first	n=nlstidine, l=Isoleucine K=Lveine
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	sequence	1	Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
		<del>                                     </del>	CAECGKAFSNSSNLTKHRRTHTGEKPYVCTKCGKAFSHSSNLTL
	-		HYRTHLVDRPYDCKCGKAFGQSSDLLKHQRMHTEEAPYQCKDCG
ļ	1		KAFSGKGSLIRHYRIHTGEKPYQCNECGKSFSQHAGLSSHQRLH
			TGEKPYKCKECGKAFNHSSNFNKHHRIHTGEKPYWCHHCGKTFC
			SKSNLSKHQRVHTGEGEAP
6581	228	476	RVFLKDLSSTPMASNNTASIAOARKLVEOLKMEANIDRIKVSKA
6582	110		AADLMAYCEAHAKEDPLLTPVPASENPFREKKFFCAII.
6582	1428	718	CFTTKTHCSPVSVPYLSPLVLRKELESLLENEGDCVIHTSSRIN
		1	QHPIIFWTLVWYFRRLDLPSNLPGLILTSEHCNEGVOLPIGGIG
1		i	QDSKLVYIQLLWDNINLHOEPREPLYVSWRNFNSEKKGGILGPE
1	}		QQETSTLVETIRQSIQHNNVLKPINLLSOOMKPGMKPOPSIVE
1			ILFLSLVSLGRENIDIEAFDNEYGIAYNSLSSEILERLOKTDAP
6583	487	41	PSASVEWCRKCFGAPLI
	107	41	RIFSMTSGRLRWRCTWRPATALWSASLRLGTSSMHPSPRSISLP
	1		LSMMLSPLPSNTRGLSPTALFRSPDSEHATSCPRLHLWRCRAPL
L	İ		RSPSPLGRLQVLPRSPLHVHTHNSGKEVLGLQVQRSRSGTGPAC SQAGSGAVQGGNWCIF
6584	189	1750	PLPMAALGPSSQNVTEYVVRVPKNTTKKYNIMAFNAADKVNFAT
			WNQARLERDLSNKKIYQEEEMPESGAGSEFNRKLREEARRKKYG
			IVLKEFRPEDQPWLLRVNGKSGRKFKGIKKGGVTENTSYYIFTQ
			CPDGAFEAFPVHNWYNFTPLARHRTLTAEBAEEEWERRNKVLNH
			FS1MQQRRLKDQDQDEDEEEKEKRGRRKASELRTHDLEDDLEMS
			SDASDASGEEGGRVPKAKKKAPLAKGGRKKKKKKGGDDFAFFDC
			DUGDFEGQEVDYMSDGSSSSOEEPESKAKAPOOFEGPKGVDFOC
			DESEESEEKPPEEDKEEEEEKKAPTPOEKKRRKDESEESDESE
			ESDIDSEASSAFFMAKKKTPPKRERKPSGGSSPGNSPDGTDCAE
į i			GGSTSSTLRAAASKLEQGKRVSEMPAAKRIRI,DTGPOSI,SGKST
			PQPPSGKTTPNSGDVQVTEDAVRRYLTRKPMTTKDLLKKEQTEE
6585	. 3	1678	TGLSSEQTVNVLAQILKRLNPERKMINDKMHFSLKE
		1070	GPIRNSRIDDFVGGDPRAEASCSVLHSKPHAMADSRDPASDQMQ
1			HWKEQRAAQKADVI.TTGAGNPVGDKLNVITVGPRGPLLVQDVVF
	1		TDEMAHFDRERIPERVVHAKGAGAFGYFEVTHDITKYSKAKVFE HIGKKTPIAVPESTVAGESGSADTHDITKYSKAKVFE
	İ		HIGKKTPIAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGNWDL VGNNTPIFFIRDPILFPSFIHSQKRNPQTHLKDPDMVWDFWSLR
	1		PESLHQVSFLFSDRGIPDGHRHMNGYGSHTFKLVNANGEAVYCK
1 1	. [		FHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFNAIATGKYPSW
}	ļ		TFYIQVMTFNQAETFPFNPFDLTKVWPHKDYPLIPVGKLVLNRN
	ł		PVNYFAEVEQIAFDPSNMPPGIEASPDKMLOGRLFAVPDTHPHO
1 1			LGPNYLHIPVNCPYRARVANYORDGPMCMODNOGGAPNYVDNCE
1 1	[		GAPEQQPSALEHS I QYSGEVRRFNTANDDNVTOVD A EVENTUL NE
1			EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHTOALL
6586	32		DRINAERPKNAIHTFVQSGSHLAAREKANL
5555	24	804	PLPEQPAESTSTMPVSGTPAPNKKRKSSKLIMELTGGGQESSGL
1 1	f	j	NLGKKISVPRDVMLEELSLLTNRGSKMFKLROMRVEKFTVFNHD
1	1		DVFSDSSMDHFQKFLPTVGGQLGTAGOGFSYSKSNGRGGSQACC
	1	į	SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE
	Ĭ	}	TGSGDQAGGEGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA
6587	75	1117	YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV
1 1	. =		RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY
]			HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF
1 1	İ		POGYOFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA
]			LIFPOLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH
1 1	į	}	LFSQEELVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT
			FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS
LL		1	RTASLTSASSVDGSR?QACTHSESSEGLGQVNHTMEVSC
			AUCTHORSONG TOWN THE ASC

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptopnan, Y=Tyrosine, X=Unknown, *=Stop
į.	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
- 6588	137	501	LGLQAQLLELRINNYQLSDELRKNGVELTSLRQKVAYLDKEFSK
j			AQKALSKSKKAQEVEVLLSENEMLQAKLHSQEEDFRLQNSTLMA
<u> </u>		!	EFSKLCSQMEQLEQENQQLKEGAAGAGVAQAGP
6589	2	1405	RPWGSAMATFSRQEFFQQLLQGCLLPTAQQGLDQTWLLLATCLA
1	-	1	CRLLWRLGLPSYLKHASTVAGGFFSLYHFFOLHMANAVALLST.LC
	1		YLVLFLCRHSSHRGVFLSVTILIYLLMGEMHMVDTVTWHYMDGA
1		i	QMIVAMKAVSLGFDLDRGEVGTVPSPVEFMGYLYFYGTTVFGPW
			ISFHSYLQAVQGRPLSCRWLOKVARSLALALI.CLVLSTCVGDVL
ì	1		FPYFIPLNGDRLLRNKKRKARGTMVRWLRAYESAVSFH-SNYFV
1	1		GFLSEATATLAGAGFTEEKDHLEWDLTVSKPLNVELPRSMVEVV
	1		TSWNLPMSYWLNNYVFKNALRLGTFSAVLVTYAASALLHGESBU
į			LAAVLLSLAFITYVEHVLRKRLARILSACVLSKRCPPDCSHOHP
ļ			LGLGVRALNLLFGALAIFHLAYLGSLFDVDVDDTTEEQGYGMAY
6590	2177		TVHKWSELSWASHWVTFGCWIFYRLIG
	1 -1//	656	VRAYEHVLSLLENVFTPMFCHRDEYFRQLLRGAESPTRNSKLNR
1			GSLSLDDFRNTQKRGESFGISRIGSKIKGVFKSTTMEGAMLPNY
}			GVAEGEDDFIEEGIVVMEDDSPVEAVSTPNTPRNLAAWKISIPY
1			VDFFEDPSSERKEKKERIPVFCIDVERNDRRAVGHEPEHWSVYR RYLEFYVLESKLTEFHGAFPDAQLPSKRIIGPKNYEFLKSKREE
1			FQEYLQKLLQHPELSNSQLLADFLSPNGGETQFLDKILPDVNLG
ł			KIIKSVPGKLMKEKGQHLEPFIMNFINSCESPKPKPSRPELTIL
1			SPTSENNKKLFNDLFKNNANRAENTERKQNQNYFMEVMTVEGVY
1	1		DYLMYVGRVVFQVPDWLHHLLMGTRILFKNTLEMYTDYYLOCKL
	!		EQLFQEHRLVSLITLLRDAIFCENTEPRSLODKOKGA KOTEREM
1			MNYIPDLLVKCIGEETKYESIRLLFDGLQQPVLNKQLTYVLLDI
6591			VIQELFPELNKVQKEVTSVTSWM
6291	2177	656	VRAYEHVLSLLENVFTPMFCHRDEYFRQLLRGAESPTRNSKLNR
	1		GSLSLDDFRNTQKRGESFGISRIGSKIKGVFKSTTMFCAMT DATV
1	1 1		GVAEGEDDFIEEGIVVMEDDSPVEAVSTPNTPRNIADWKIGTDV
1	1		VDFFEDPSSBRKEKKERIPVFCIDVERNDRRAVCHEDRHWSVVD
}	1		RYLEFYVLESKLTEFHGAFPDAQLPSKRIIGPKNYEFLKSKREE
1	1		FQEYLQKLLQHPELSNSQLLADFLSPNGGETQFLDKILPDVNLG
ł	1	·	KIIKSVPGKLMKEKGQHLEPFIMNFINSCESPKPKPSRPELTIL
			SPTSENNKKLFNDLFKNNANRAENTERKONONYFMEVMTVEGVY
l .	1 1		DYLMYVGRVVFQVPDWLHHLLMGTRILFKNTLEMYTDYYLQCKL EQLFQEHRLVSLITLLRDAIFCENTEPRSLQDKQKGAKQTFEEM
1	[		MNYIPDLLVKCIGEETKYESIRLLFDGLQQPVLNKQLTYVLLDI
	<u> </u>		VIQELFPELNKVQKEVTSVTSWM
6592	3	1861	APEFLGSTISSGSMIDANLKLLQEAEQRLKAIVAEKFAIATKEG
1			DLPQVERFFKIFPLLGLHEEGLRKFSEYLCKQVASKAEENLLMV
ŀ	1		LGTDMSDRRAAVIFADTLTLLFEGIARIVETHQPIVETYYGPGR
1	1		LYTLIKYLQVECDRQVEKVVDKFIKORDYHOOFRHVONNIMPNE
	Ī I		TTEKIEPRELDPILTEVTLMNARSELYLRFLKKRISSDERVCDS
		ĺ	MASEEVKQEHQKCLDKLLNNCLLSCTMOELIGLYVTMERYFMPE
			TVNKAVALDTYEKGQLTSSMVDDVFYIVKKCIGRALSSSSTDCL
İ			CAMINLATTELESDFRDVLCNKLRMGFPATTFODIORGVTSAVN
			IMHSSLOQGKPDTKGIESTDEAKMSFLVTLNNVEVCSENISTLK
l			KTLESDCTKLFSQGIGGEQAQAKFDSCLSDLAAVSNKFRDLLQE
1		!	GLTELNSTAIKPQVQPWINSFFSVSHNIEEEEFNDYEANDPWVQ
İ		i	QFILNLEQQMAEFKASLSPVIYDSLTGLMTSLVAVELEKVVLKS
ł	]	1	TFNRLGGLQFDKELRSLIAYLTTVTTWTIRDKFARLSQMATILN
	_.	i	LERVTEILDYWGPNSGPLTWRLTPAEVRQVLALRIDFRSEDIKR
6593	3	1837	LRL
	_		EAFSAGSRRRGLALQRGVLGGLGGYCPCCCRRRGRLLVLLLLVR
		]	RGGEGGGGRGDKRRRQARRQRRPEPAEARGKMADVLSVL
	·		RQYNIQKKEIVVKGDEVIFGEFSWPKNVKTNYVVWGTGKEGQPR

Designing   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresponding to first   corresp	SEQ	Predicted	Drodies	
Mo:			Predicted end	Amino acid segment containing signal peptide
Cocresponding to first aline, I=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}, N=\text{leading}	NO:			(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
to first amino acid residue of amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence se		location		H=Histidine T-Tooleysias V. r. :
amino acid residue of amino acid sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  seq		corresponding		L=Leucine M-Methioning N-A-rows
residue of amino acid sequence   S-Serine, T-Threonine, V-Valle,   S-Serine, X-Threonine, V-Valle,   S-Serine, X-Threonine, V-Valle,   S-Serine, X-Threonine, V-Valle,   S-Serine, X-Threonine, V-Valle,   S-Serine, X-Threonine, V-Valle,   S-Serine, X-Threonine, V-Valle, S-Serine, X-Threonine, V-Valle, S-Serine, X-Threonine, V-Valle, S-Serine, X-Threonine, V-Valle, S-Serine, X-Threonine, V-Valle, S-Serine, X-Threonine, V-Valle, S-Serine, X-Threonine, V-Valle, S-Serine, X-Threonine, V-Valle, S-Serine, X-Threonine, V-Valle, S-Serine, X-Threonine, V-Valle, S-Serine, X-Threonine, V-Valle, S-Serine, X-Threonine, V-Valle, S-Serine, X-Threonine, V-Valle, S-Serine, X-Threonine, V-Valle, S-Serine, X-Threonine, V-Valle, S-Serine, X-Threonine, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle, V-Valle,	- 1	j -	amino acid	P=Proline, O=Glutamine, N=Asparagine,
amino acid sequence decomo, "FTYPTOSINE, X-Unknown, "=\$top codon, 'possible nuclectide deletion, 'possible nuclectide deletion, 'possible nuclectide disertion) 'possible nuclectide disertion' 'possible nuclectide disertion' 'possible nuclectide disertion' 'possible nuclectide disertion' 'possible nuclectide disertion' 'possible nuclectide disertion' 'possible nuclectide disertion' 'possible nuclectide disertion' 'possible nuclectide disertion' 'possible nuclectide disertion' 'possible nuclectide disertion' 'possible nuclectide disertion' 'possible nuclectide disertion' 'possible nuclectide disertion' 'possible nuclectide disertion' 'possible nuclectide disertion' 'possible nuclectide disertion' 'possible nuclectide disertion' 'possible nuclectide disertion' 'possible nuclectide disertion' 'possible nuclectide disertion' 'possible nuclectide disertion' 'possible nuclectide disertion' 'possible nuclectide disertion' 'possible nuclectide disertion' 'possible nuclectide disertion' 'possible nuclectide disertion' 'possible nuclectide disertion' 'possible nuclectide disertion' 'possible nuclectide disertion' 'possible nuclectide disertion' 'possible nuclectide disertion' 'possible nuclectide disertion' 'possible nuclectide disertion' 'possible nuclectide disertion' 'possible nuclectide disertion' 'possible nuclectide disertion' 'possible nuclectide disertion' 'possible nuclear 'possible nuclear 'possible nuclear 'possible nuclear 'possible nuclear 'possible nuclear 'possible nuclear 'possible nuclear 'possible nuclear 'possible nuclear 'possible nuclear 'possible nuclear 'possible nuclear 'possible nuclear 'possible nuclear 'possible nuclear 'possible nuclear 'possible nu	1		residue of	S=Serine, T=Threonine, V=Valine
Sequence    Codon, /-possible nucleotide diestion, /-possible nucleotide insertion	1	•	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +-C+
PSYSTADE FUGICATION	1		sequence	Codon, /=possible nucleotide deletion
EYYTLÖSILFILMINYILSIPYVYERAZENIPYVERPERKÜLLARKERI YLKORGATSASIDBSARGILGORSTOVKARGULARAKERI EEDEKCVALDKERLAARISCHEGI VOTTGURSILSEAMSVEKIAA TAKAKIMAKKRSTI KTÜLDÜD TÄLKORSPYDUVTRÖURSER RIVERTTI LOSTGKARFSKNIT FÄLLÖSVKAREGGAPEORPAPN AAPVOPTLAKTKOPT DANNINGORGAKKEREKSERIDTOKTYIL GATTIKKSTEGASARKTOTRAAQPVOPTBYGAKRGORGANTI III IPAATTSILITMIAMSULDOLKEVYSDEKKIDTÖKKOSSTIP III IPAATTSILITMIAMSULDOLKEVYSDEKKIDTÖKKOGKENETI III IPAATTSILITMIAMSULDOLKEVYSDEKKIDTÖKKOSSTIP III IPAATTSILITMIAMSULDALKEVIDEKUNDUKVAVBVQ GEMOPKOMPHALDOSSVUTJAKKAPHINDEKDENVÄN VARVO GEMOPKOMPHALDOSSVUTJAKKAPHINDEKARATERI OKRULDALSIARRE PERKREMIDEN VARVO DVTULELSYHKRHLORPYVERVENDEN VARVO DVTULELSYHKRHLORPYVERVENDEN VARVO DVTULELSYHKRHLORPYVERVENDEN VARVO DVTULELSYHKRHLORPYVERVENDEN VARVO DVTULELSYHKRHLORPYVERVENDEN VARVO DVTULELSYHKRHLORPYVERVENDEN VARVO DVTULELSYHKRHLORPYVERVENDEN VARVO DVTULELSYHKRHLORPYVERVENDEN VARVO DVTULELSYHKRHLORPYVERVENDEN VARVO DVTULELSYHKRHLORPYVERVENDEN VARVO DVTULELSYHKRHLORPYVERVENDEN VARVO DVTULELSYHKRHLOR VARVO DVTULELSYHKRHLOR VARVO DVTULELSYHKRHLOR VARVO DVTULELSYHKRHLOR VARVO OKCADORA GASSENALINYRAQUELOVALORA AREA BERYGKOLL AREA GENERAL VARVO OKCADORA GASORA NAVALHIGATURA VARVO DVTULEN VARVO OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCADORA OKCA		sequence		\=possible rucleotide insertion)
### PROPRIEST OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS OF THE PROPRESS	- 1	1		EYYTLDSILFLLNNVHLSHPVYVRRAATENIPVVPPPDPKDLIC
EDESCVELDRENLARRESTIKETLODITTALKORSTOCKTOLOPTOUS	1			YLNGEASTSASIDRSAPLEIGLORSTOVKRAADEVI AFAKKEDI
INAKIMAKRSTIKTÜLDDITALKQRSKPYDAEUDYTRITUSTEGEN RYMERTETI LÖGTEKINSKNIF ALLGOVARPPINKKESTEGFK IDGETTATYTH AAPVUPTLERTKOP I PAAYMYNDOERFEKKEETEGFK IDTMATYTH GATKLEVTERAAPVUPTURAAPPYPHOKKESTET III IPAATTSLITMINAKOLLODLIKFYPSDEKKKOGGOENSTI III IPAATTSLITMINAKOLLODLIKFYPSDEKKKOGGOENSTI III INAKOLLODLIKAPPTRAAMTSSLIKKIPPAGA DEPERKYKKILKEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKINGEN PARKI				EDEECVRLDKERLAARLEGHKEGIVOTEOIRSLSEAMSVEKIAA
GRTLKSVTERAARKTOTRAAPPURPUS APPPHORKESETT IIITBAATTSLITMINAKOLLQDLKFVPSDEKKKOGGGENETT IIITBAATTSLITMINAKOLLQDLKFVPSDEKKOGGCENETT IIITBAATTSLITMINAKOLLQDLKFVPSDEKKNOGGCENETYKERDEKKOGGKENET  EFPGREFREGSOASPLCATCGFALLKARTSLEKKENEPGKOL ARKHEEPREKOLLGKKKILIMALHAGGLEKKENALIERE (KONDA) ARKHEEPREKOKLGKKKILIMALHAGGLEKKENALIERE (KONDA) ARKHEEPREKOKLGKKKILIMALHAGGLEKKENALIERE (KONDA) ARKHEEPREKOKLGKKILIMALHAGGEROGCKRIHFRANDAKKOLL ARKHEEPREKOKLGKKILIMALHAGGEROGCKENALIPERROGCENET (KONDA) ARKHEEPREKOKLGKKILIMALHAGGEROGCKENALIPERROGCENET (KONDA) ARKHEEPREKOKLGKKILIMALHAGGEROGCKENALIPERROGCENALIPERROLLUT (KONDA) ARKHEEPREKOKLGKKILIMALHAGGEROGCKENALIPERROGCENGALIPERROLLUT (KONDA) ARKHEEPREKOKLGKKILIMALAGGEROGCKENALIPERROLLUT (KONDA) ARKHEEPREKOKLGKKILIMALAGGEROGCKENALIPERROLLUT (KONDA) ARKHEEPREKOKLGKKILIMALAGGEROGCKENALIPERROLLUT (KONDA) ARKHEEPREKOKLGKKILIMALAGGEROGCKENALIPERROLLUT (KONDA) ARKHEEPREKOKLGKKILIMALAGGEROGCKENALIPERROLLUT (KONDA) ARKHEEPREKOKLGKKILIMALAGGEROGCKENALIPERROLLUT (KONDA) ARKHEEPREKOKLGKKILIMALAGGEROGCKENALIPERROLLUT (KONDA) ARKHEEPREKOKLGKKILIMALAGGEROGCKENALIPERROLLUT (KONDA) ARKHEEPREKOKLGKKILIMALAGGEROGCKENALIPERROLLUT (KONDA) ARKHEEPREKOKLGKKILIMALAGGEROGCKENALIPERROLLUT (KONDA) ARKHEEPREKOKLGKKILIMALAGGEROGCKENALIPERROLLUT (KONDA) ARKHEEPREKOKLGKKILIMALAGGEROGCKENALIPERROLLUT (KONDA) ARKHEEPREKOKLGKKILIMALAGGEROGCKENALIPERROLLUT (KONDA) ARKHEEPREKOKLGKKILIMALAGGEROGCKENALIPERROLLUT (KONDA) ARKHEEPREKOKLGKKILIMALAGGEROGCKENALIPERROLLUT (KONDA) ARKHEEPREKOKLIMALIPERROLLUT (KONDA) ARKHEEPREKOKLIMAT (KONDA) ARKHEEPREKOKLIMAT (KONDA) ARKHEEPREKOKLIMAT (KONDA) ARKHEEPREK				1 KAKIMAKKRSTIKTDLDDDITALKORSFVDAEVDVTDDTVCDD
GRTLKSVTEGASARKTQTPÄAGPVPRPVSQARPPPROKKGSRTPT IIIIPÄÄTTSLTMINADDLIQOLKPEDKKKGGCGENETL IQRRKDOMQSGTAISVTVPYRVDQPLKIMPODMORVAVPVQ GPÄMOFKGWPHLIPDSSPVIJFÄKKHKLYDEVBLIDPNUCKS DVTVLELSYHKRHLDRPVFLRVWETLDRYWKHKSHLRP EPPGRFRFGSOASPLCATCGFALLRHKHYDEVBLIDPNUCKS DVTVLELSYHKRHLDRPVFLRVWETLDRYWKHKSHLRP EPPGRFRFGSOASPLCATCGFALLRHKHYDEVBLIDPNUCKS NISKKYCGGSEINTLKRALEVPKQUVNAGCHIQLAQSIREE ARKMEBERREKOKLORKTELIMDAIHKQKSLQFKKTMDAKKNYK QKCHOKDEABOAVESABLVAPKQGEKLPVALATSKIAVEDSOK ARMIHIGTLDKVREERGSBHIKACGA FAGGCGRINFFRNALMI HYNOLSQOCVITSDENIKQVKKSLEMCSIQRIBTSVANGTSGDI PAPI HYLENFYSSGRANVAPGKATGPHARRGPLIPTSSGRDD PAPI HYLENFYSSGRANVAPGKATGPHARRGPLIPTSSGRDD WYSJUDDYSLLIVQ GREDNOFTISRGGKASDAVAPGKATGPHARRGPLIPTSSGRDD WYSJUDDYSLLIVQ GRENCYIDDCAKIFCHISDDIDPKNTLCLOVMLPNEYPOTAR GERCYIDDCAKIFCHISDDIDPKNTLCLOVMLPNEYPOTAR PIYQLAMAPHIKQGERADLANSLEETIY GDIGSILYLWVEKIRD VLIGKSGMTEPGPDVKKKTEEBUVECSDDI ILAQPESSVKALD FOISETRTEVEVEELP PIHGIPTIDRSTFGAHLAVVCPKQV KMVLSKLYENKKIASATHNIYAYRIY CEPKOTFLQDCEDDGGTA AGGRLHHMEILMVKNVMVVVSRNYGGILLGDRSKHANAAA AGGRLHHMEILMVKNVMVVVSRNYGGILLACOPESSVKALD FDISTTREVEVEELP PIHGIPTITRRSTFGAHLAVVCPKQV KMVLSKLYENKKIASATHNIYAYRIY CEPKOTFLQDCEDDGGTA AGGRLHHMEILMVKNVMVVVSRNYGGILLACOPESSVKALD FDISTTREVEVEELP PIHGIPTITRRSTFGAHLAVVCPKQV KMVLSKLYENKKIASATHNIYAYRIY CEPKOTFLQDCEDDGGTA AGGRLHHMEILMVKNVMVVVSRNYGGILLACOPESSVKALD FDISTTREVEVEELP PIHGIPTITRRSTFGAHLAVVCPKQV KMVLSKLYENKKIASATHNIYAYRIY CEPKOTFLQDCEDDGGTA AGGRLHHMEILMVKNVMVVVSRNYGGILLACOPESSVKALD FDISTTREVEVEELP PIHGIPTITRRSTFGAHLAVVCPKQV KMVLSKLYENKKIASATHNIYAYRIY CEPKOTFLQDCEDDGGTA AGGRLHHMEILMVKNVMVVVSRNYGGILLACOPESSVKALD FDISTTREVEVEELP PIHGIPTITRGSTFGAHLAPVCPKQV KMVLSKLYENKKIASATHNIYAYRIY CEPKOTFLQDCEDDGGTA AGGRLHHMEILMVKNVMVVSRNYGGILLACOPESSVKALD FDISTTREVEVEELPFIHGGESTLIKGRNKVKURDKRHE LKKKNIEWLDKSKSSFLIMMRRPEBRGKLIYQMVGRSCNNSV FTLYBLINGGDTDESFFLOGESDICHABITITVS DGPRRQVLIAGTCLPLLLTHLRALQALQGGHABGIT LVEKNYTTNSPEBSSKALGNKKKVRIGKRHE LKKKNIEWLDKSKSSFLIMMRRPEBRGKLIYQMVGRSCNNSV FTLYBLITGGDTTDESFFLODEATLIRALQALGOPPTSVTPDD SKOLOS  LKRKGNIEWLDKSKSSFLIMMRRPEBRGKLIYQMVGRSCNNSV	ł	ł	}	RVWRTRTTILQSTGKNFSKNIFAILQSVKAREEGRAPEQRPAPN
1 11 1074 TSLITMLNAKOLLOPICK-VS-DBEKKRGCCREMETI. 1 1076 GPAMOFKGMPHLLPDGSPUDIFAKIKAFHLKYDEVADVUVAPVO GPAMOFKGMPHLLPDGSPUDIFAKIKAFHLKYDEVADVUVAPVO GPAMOFKGMPHLLPDGSPUDIFAKIKAFHLKYDEVALDVUVAPVO GPAMOFKGMPHLLPDGSPUDIFAKIKAFHLKYDEVALDVUVAPVO GPAMOFKGMPHLLPDGSPUDIFAKIKAFHLKYDEVALDVUVAPVO GPAMOFKGMPHLLPDGSPUDIFAKIKAFHLKYDEVALDVUVAPVO DILSTIGVDHI TOHLINGKNICKEFERLERAAIERFYKGULPKSL  DILSTIGVDHI TOHLINGKNICKEFERLERAAIERFYKGULPKSL  AKMEBEREKQKLARKKELIMDAHKKOKSLOFKKTIDAKKNYL  AKMEHIGTILDVREEWGSBHIKACEAFEAGGESINFFRNALMI, HVNOLSQCVTSDEMYSDVKSLEMEGSIQBIBSFYVORKTGOI  PPAP IMYENFYSSOKNAVPAGKATOPNLARRGSLPIPKSSPDDD  NSSLVDDYSLLYQ  PPAP IMYENFYSSOKNAVPAGKATOPNLARRGSLPIPKSSPDDD  NSSLVDDYSLLYQ  PPAP IMYENFYSSOKNAVPAGKATOPNLARRGSLPIPKSSPDDD  NSSLVDDYSLLYQ  PPAP IMYENFYSSOKNAVPAGKATOPNLARRGSLPIPKSSPDDD  NSSLVDDYSLLYQ  PPAP IMYENFYSSOKNAVPAGKATOPNLARRGSLPIPKSSPDDD  NSSLVDDYSLLYQ  RYNALYDESQCEKKARSOPNLSVLOTONNYNARRGRLEPIPKSSPDDD  NSSLVDDYSLLYQ  CKSPHLIPSGOGEKRAR-PPRGELESSPULAVSVPAPTIVLSLG  VCSMPLHSGOGEKRAR-PPRGELESSPULAVSVPAPTIVLSLG  GSPTGGLFHTPPPTPPBQDKEDFSSFOLLVEVALGRARAEMELOK  CODPSSLDLHTPIPLUSENDQ  6596  2 1026 PPLEVRRYGGRELJGGRSRGHMAEGDAGSDQRONEEIBAMAATY  GEBWCVIDDCAKIRCINCISCBSLDTHAWSKIRD  VLIQKSOMTEBGPDVKKKTEBEDVECEDDLILACOPESSVKADD  FDISETRITEVEVEELPP IHOGIPTITAGSSLDAHAVYCPKOV  KMVLSKLYENKKIASATHNI VANIYCEDKOTFJOALDEDGETA  AGGRLHHMETLANKVMVVVSRWYGGLILGPBRFKHINNCANN  ILVEKNYTINSFEBSSKALKKNKVKDKKNKEH  PRIPVREMYGRRELOGRSRGHMAEGDAGSDQRONEEIBAMAATY  GEBWCVIDDCAKIRCINCISCBSHDAKSKOFKOKKNEH  PRIPVREMYGRRELOGRSRGHMAEGDAGSDQRONEEIBAMAATY  GEBWCVIDDCAKIRCINCISCBSHDAKKVKRUKKOKANEH  PRIPVREMYTGRELOGRSRGHMAEGDAGSDQRONEEIBAMAATY  GEBWCVIDDCAKIRCINCISCBSHDAKTARUKKKENEH  PRIPVREMYTGSPESSKALGKNKKVRUKDKRANEG  LRKKGNLEWALDKSKSFILMWRRPEBWGLITOPKKABALOVCPROV  KMVLSKLYENKKLASATINI YAKIYCEDKOTFLOQCEDDGETA  AGGRLHHMETLUNKWAYVVSRWYGGSURSEGGONISV  FTLYSLTINGEDTEDESFFILOPKORLOFKORMEN  BROWNADADAVKLOGRSVELVOIGKOKNEH  PREVRATTMANSFERBEKGLORMKVRUKDKQLAGHERST  THYS BROWNADAVKLOGRSVELVOIGKOKNEH  MENDALADAVKLOGRSVELVOIGKOKARNOR LORDORGEN  SKALOS  SKALOS  FULTOR	{			AAPVUPTERTKQPIPAAYNRYDQERFKGKEETEGFKIDTMGTYH
TORREDOMOSSITATSVTVPTRVDOPERLIMPODMORW OPTVLELSYHKEMPORTUPINOVER OPTVLELSYHKEMPORTUPINOVER OPTVLELSYHKEMPORTUPINOVER OPTVLELSYHKEMPORTUPINOVER OPTVLELSYHKEMPORTUPINOVER OPTVLELSYHKEMPORTUPINOVER OPTVLELSYHKEMPORTUPINOVER OPTVLELSYHKEMPORTUPINOVER OPTVLELSYHKEMPORTUPINOVER OPTVLENDER OF PEPGERPENGSASPICATCGFALLERAPTRAAMTESIFKENDERS OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLENDER OPTVLE		Ì		GWI DASVTEGASARKTQTPAAQPVPRPVSQARPPPNQKKGSRTP
6594  1 1096 EPPGRRRGSGASPLCATGPALLRAPTRAWKHKELEP  EPPGRRRGSGASPLCATGPALLRAPTRAWTHSLEFKONPWSA DILSTIGVENI (JALUNGKIKKLE)  EPPGRRRGSGASPLCATGPALLRAPTRAWTTSLEFKONPWSA DILSTIGVENI (JALUNGKIKKLE) DILSTIGVENI (JALUNGKIKKLE) DILSTIGVENI (JALUNGKIKKLE) ARKMEREPREKKIL, JALUNGKKTELI IMA HUKOSLQFKITHDAKKINYE OKCROKDEAROAVSRAMLVAPKQQEKLEVKLATSKTAVEDSIK ARMIHIGTLOKVREEWQSEHIKACEAPEAQCEGRINFRINALMI. HVNOLSQQCVISDEMIEGVRIKENGIRDIEYEVVORKITGQI PPAPIMYENYISSQKNAVPAGKATGPINLARGPLEIPKSSPDDP  PRAPIMYENYISSQKNAVPAGKATGPINLARGPLEIPKSSPDDD  RYSLVDDYSLLIVQ  RYSLVDDYSLLIVQ GKDNOGTIERRGKASDVALPRGSSPSVLAVSVPAPINVLSIS VCSMPLHSGGGEKPAAPPRRGELESKVLLTGGENILLITRARA GSPTGGLFRTYPPTPPEQDKEDFSSFOLLVEVALQRAAEMELOK OODPSLPLLHTTPILVISENPO CODPSLPLLHTTPILVISENPO CODPSLPLLHTPILVISENPO COPPSLPLLHTPILVISENPO COPPSLPLHTHPILVISENPO COPPSLPLHTHPILVISENPO COPPSLPLHTYPIPTPEDKODKEDFSSFOLLVEVALQRAAEMELOK OODPSLPLHTHPILVISENPO COPPSLPLHTHPILVISENPO COPPSLPLHTHPILVISENPO COPPSLPLHTHPILVISENPO COPPSLPLHTHPILVISENPO COPPSLPLHTHPILVISENPO COPPSLPLHTHPILVISENPO COPPSLPLHTHPILVISENPO COPPSLPLHTHPILVISENPO COPPSLPLHTHPILVISENPO COPPSLPLHTHPILVISENPO COPPSLPLHTHPILVISENPO COPPSLPLHTHPILVISENPO COPPSLPLHTHPILVISENPO COPPSLPLHTHPILVISENPO COPPSLPLHTHPILVISENPO COPPSLPLHTHPILVISENPO COPPSLPLHTHPILVISENPO COPPSLPLHTHPILVISENPO COPPSLPLHTHPILVISENPO COPPSLPLHTHPILVISENPO COPPSLPLHTHPILVISENPO COPPSLPLHTHPILVISENPO COPPSLPLHTHPILVISENPO COPPSLPHTVENTON COPPSCRAMA COPPSLPHTY COPPSCRAMA COPPSLPHT COPPSCRAMA COPPSLPHT COPPSCRAMA COPPSLPHT COPPSCRAMA COPPSLPHT COPPSCRAMA COPPSLPHT COPPSCRAMA COPPSLPHT COPPSCRAMA COPPSLPHT COPPSCRAMA COPPSLPHT COPPSCRAMA COPPSLPHT COPPSCRAMA COPPSLPHT COPPSCRAMA COPPSLPHT COPPSCRAMA COPPSCRAMA COPPSCRAMA COPPSCRAMA COPPSCRAMA COPPSCRAMA COPPSCRAMA COPPSCRAMA COPPSCRAMA COPPSCRAMA COPPSC	ł			TOPPKDOMO OCCUR I CHARLES OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF THE TOPPK OF TH
1 1096 EPFORERYGSUASPEATGREPULRAPTRAAMTESLEKONWAS DILSTIGYDNIIQHLINGRKNCKEFEDFLERRALEERIGKULL NISRKKEPGOSETINTIKRALEVERYGOVDINVAQCHIQLAQSLREE ARKMEEPREKOKLQRKKTELIMDAIHKOKSUQFKKTUDAKKNU OKCHOKLAGSLOPKKTUDAKKNU AYMLHIGTLDKVREEWQSEHIKACEAFEAQCEGRINFERNALMH. HUNQLSQQCVTSDEWYEOVRSLEMCSIGRDIEYEVNORKTIGGI PAPAIWKENYESGOKNAVPAKAGRAHRARGADIEYESSENDO NYSLVDDYSLLVQ  6595 57 781 PLGTWSDDLGEDEGLLSLAGKRERGRILPKESVKILEDMLYLH RYNAYPSEOEKISLEGOTNLSVLQICNWFINARRELPDMLRIND GKDPNOFTISRRGGKASDVALPRASPSVLAVSVPAPTNVLSIS VCSMPLHSQGGEKPAPPPROEILSSPVLAVSVPAPTNVLSIS VCSMPLHSQGGEKPAPPPTPEDDKEDSSVLAVSVPAPTNVLSIS VCSMPLHSQGGEKPAPPPROEILSSPVLAVSVPAPTNVLSIS VCSMPLHSQGGEKPAPPPTPEDDKEDSSVLAVSVPAPTNVLSIS VCSMPLHSQGGEKPAPPPROEDLSSPVLAVSVPAPTNVLSIS VCSMPLHSQGEKPAPPPROEILSSPVLAVSVPAPTNVLSIS VCSMPLHSQGEKPAPPPROEILSSPVLAVSVPAPTNVLSIS VCSMPLHSQGEKPAPPPROEILSSPVLAVSVPAPTNVLSIS VCSMPLHSQGEKPAPPPROEILSSPVLAVSVPAPTNVLSIS VCSMPLHSQGEKPAPPPROEILSSPVLAVSVPAPTNVLSIS VCSMPLHSQGEKPAPPPROEILSSPVLAVSVPAPTNVLSIS VCSMPLHSQGEKPAPPPROEILSSPVLAVSVPAPTNVLSIS VCSMPLHSQGEKPAPPPROEILSSPVLAVSVPAPTNVLSIS VCSMPLHSQGEKPAPPPROEILSSPVLAVSVPAPTNVLSIS VCSMPLHSQGEKPAPPROEILSSPVLAVSVPAPTNVLSIS VCSMPLHSQERDLENSLETITONIGESILVILWVEKID ODDERSTULLANDE TORT TORT TORT TORT TORT TORT TORT TOR	]			GPAWOFKGWPWLI.PDGSPVDTFAKTKAEHI KWDDVDT DDW
### FPGRRRRSGSASPLCATTGPLALIRAPTRAMMTSLEPKONPWSA DILSTIGVENI IQHLMNGRKNCKEPLEPHLARRAN LERYGKOLL NLSRKKPCGGSEINTLKRALEVFKQQVDNVAQCHIQLAQSLREE ARKMEREPTEKOKLORKKTELIMDAITMKSLEVFKTODAKKNYE QKCRDKDEABQAVSRSANLVAPKQQEKLFVKLATSKTAVEDSDK AYMIHIGTLDKVREERQSEHIKACEAFEAQCERINFFRNALMI HVNQLSQQCVTSDEWFEOVRSLEBMCSIGRDIEYFVNQRKTGGI PPAPIMYENYSSQKNAVPACKATGPNLARRGPLPIFKSSPDDD NYSLVDDYSLLVQ PRAPIMYENYSSQKNAVPACKATGPNLARRGPLPIFKSSPDDD NYSLVDDYSLLVQ RYNAVPSEQRKIALGGVNLSVLQICMNFINARRKLLPDMLRRD GKDRNGFTISRRGGKASDVALPRRSSESVLAVSVPAFTNVLSIS. VCSMPLHSGGGKPAPAFPRRGELESSKPLVTTGSTLTLLTRABA GSPTGGLFNTPPITPFDQKKEDSSISVLAVSVPAFTNVLSIS. VCSMPLHSGGGKPAPAFPRRGELESSKPLVTTGSTLTLLTRABA GSPTGGLFNTPPITPFDQKKEDSSISVLAVSVPAFTNVLSIS. VCSMPLHSGGGKPAPAFPRRGELESSKPLVTTGSTLTLLTRABA GSPTGGLFNTPPITPFDQKKEDSSISVLAVSVPAFTNVLSIS. VCSMPLHSGGGKPAPAFPRRGELESSKPLVTTGSTLTLLTRABA GSPTGGLFNTPPITPFDQKKEDSSISVLAVSVPAFTNVLSIS. VCSMPLHSGGGKFAPAFPRRGELESSKPLVTTGSTLTLLTRABA GSPTGGLFNTPPITPFDQKKEDSSISVLAVSVPAFTNVLSIS. VCSMPLHSGGFSGGMAEGDAGSDGKOMEETEAMAATY GEBWCVIDDCAKIFCIRISDDIDPFMTLCLQVMLPMEYPGTAP PIYQLANPHLKGGGFSGGMAEGDAGSDGKOMEETEAMAATY GEBWCVIDDCAKIFCIRISDDIDPFMTLCLQVMLPNEYPGTAP PIYQLANPHLKGGGRSDGKARGMAEGDAGSDGKOMEETEAMAATY GEBWCVIDDCAKIFCIRISDDIDPFMTLCQCEDDGGTA AGGRLLHLME LINVKNVAVVVSKWYGGILLGPBFKHINNCARN ILVEKNYTNSPESSKALGKNKKVRKDKKRMEH PRIVARVYTNSPESSKALGKNKKVRKDKKRMEH VLIQKSOMTEPGPPDVKKKTEEDVECEDDLILAGCPESSVKALD FDISETRTEVEVEELPPIDHGIPITDRSTTGAHLAGVVCPKOV KMVLSKLYENKKIASATHNIYAYTIYCEDKGTILGQCESSUKALD FDISETRTEVEVEELPPIDHGFITDRSTTGAHLAGVVCPKOV KMVLSKLYENKKIASATHNIYAYTIYCEDKGTILGQCESSUKALD VLIGKGMTEPGPPDVKKKVRKDKKKNKDKKKREH  FRANKTYTMANSFESHPROVTPFDFTURGNTGALAAWCSL VLSFCRILHMELINVKNAVVVSKWYGGLLLSPDFKHINNCARN ILVEKKYTNSPESSKALGKNKVRKDKKREH  FRUNKTYTMANSFESHPROVTPFDFTURGNTGALAAWCSL VLSFCRILHMELDKSKSFLIMBRRPEBWGLIJTGMCGLAAWCSL VLSFCRILHMELDKSKSFLIMBRRPEBWGLIJTGMCFESSUKLD LFRAKGNIFFRODTVYCTSDNYMGKFCTLTGRGGTCVFPFI  MEVLAAADTTAMASFEBHKATUMANLAGSUSAMPEKRGEIRR MEVLAAADVKLIGGSVELVDIGKQNLIDGSIPLPPILLGRIG DPKKTVCIYGHLDVQPAALEDGWDSFPFTLVERGCKHGRGST DKGMVAGMINALAAVGCSURVIDANTULLL	<b> </b>			DVTVLELSYHKRHLDRPVFLRVWETI.DDVMUVUVCIII DO
DILSTIGANTIQUILNIGRIKOKCEFEDEHKERAAIEERYGKDLI NISRKAPGOSEINTLKRALEVYKQQUONNAQCHIQLAQSLREE ARKMEERREKQKLQRKKTELIMDAHKKOKSLOPKKTMDAKONYE QKCRNKDEAEGAVSRSANLUNDGOKLFEVKLATSKTAVEDSIK AYMLHIGTLDKVREEMOSEHIKACEAFEAQSCERINFFRRALIKI HYNQLSQOCVTSDEMYBOVYKSLEMCSIQRIEFYNAQRTIGGI PPAPIMYENFYSSOKRAVPBAGKATGPINARRGPLPI KSSPDDP NYSLVDDYSLINYQ NYSLVDDYSLINYQ RYNAYPSEQEKLSLSQTRILSVLQTCINHF INARRALIPDHILRKD RYNAYPSEQEKLSLSQTRILSVLQTCINHF INARRALIPDHILRKD GKDPNOFTISRRGKASDVALPSSPEVLAVSVPAFTNVLSIS VCSMPLHISGGEKPAAPPPRGELESSPELLVYPGSTLTLLTRAEA GSPTGGLFNTPPPTPPEQDKEDFSPFGLLVEVALQRARMELQK CODPSLELLHTPTPLVSENPQ GEEMCVIDDCAKIFCIRISDDIDPKWTLCLQVMLENEYPGTAP PIYQLNAPMLKGGERADISNSLEETYIONIGESILVINWEKIRD VLIQKSQMTEPGFDVKKKTEEDEVESDDILLACQPESSVKALD FDISETTETEVEVEELPFIDHGIPTTDRRSTFQAHLAPVUCPKOV KMVLSKLYENKKLASATINIVAVENKKKKENENH 1LVEKNYTNSPESSKALGKNKKUKKURNENH 1LVEKNYTNSPESSKALGKNKKVKKKKENENH VLIQKSQMTEPGPDVKKKTEEDEVECDDILLACQPESSVKALD FDISETTTEVEVELPFIDHGIPTTDRRSTFGAHLAPVUCPKOV KMVLSKLYENKKLASATINIVAVENKYKOKGILLGPDRFHINNCARN 1LVEKNYTNSPESSKALGKNKKVRKOKKENENH VLIQKSQMTEPGPDVKKKTEEDEVECDDILLACQPESSVKALD FDISETTTEVEVELPPTHGIPTTORRSTFGAHLAPVUCPKOV KMVLSKLYENKKLASATINIVAVENKYKOKGILLGPDRFHINNCARN 1LVEKNYTNSPESSKALGKNKKVRKKKKRENH VLIQKSQMTEPGPDVKKKTEEDEVECDDILLACQPESSVKALD FDISETTTEVEVELPPTHGIPTTORRSTFGAHLAPVUCPKOV KMVLSKLYENKKLASATINIVAVENKYKOKGILLGPDRFHINNCARN 1LVEKNYTNSPESSKALGKNKKVRKKKKRENH VLIQKSQMTEPGPDVKKKTEEDEVECDDILLACQPESSVKALD VLIQKSQMTEPGPDVKKKTEEDEVECDDILLACQPESSVKALD VLIQKSQMTEPGPDVKKKTEEDEVECDDILLACQPESSVKALD VLIQKSQMTEPGPDVKKKTEEDEVECDDILLACQPESSVKALD VLIQKSQMTEPGPDVKKKTEEDEVECDDILLACQPESSVKALD VLIQKSQMTEPGPDVKKKTEEDEVECDDILLACQPESSVKALD VLIQKSQMTEPGPDVKKKTEEDEVECDDILLACQPESSVKALD VLIQKSQMTEPGPDVKKKTEEDEVECDDILLACQPESSVKALD VLIQKSQMTEPGPDVKKKTEEDEVECDDILLACQPESSVKALD VLIQKSQMTEPGPDVKKKTEEDEVECDDILLACQPESSVKALD VLIQKSQMTEPGPDVKKKTEEDEVECDDILLACQPESSVKALD VLIQKSQMTEPGPDVKKKTEEDEVECDDILLACQPESSVKALD VLIQKSQMTEPGPDVKKTEEDEFHGLDEKGLIKPTVEND VLIQKSQMTEPGPDVKKTEEDEFHGLDEKGLIKPTVEND DGPRQVLLLAGTCLPTVTTORSTGAMCST VLIQKGRACH VLIQKSGAMCSTANTAT	6594	1	1096	EFPGRRFRGSOASPLCATCGPALLRADTDAAMTDCLEVCATTOR
NISKKRPGGSEINTLKRALEVPKOQUVNAQCHIQLAGSLREE   ARKMEEPREKQKLQRKKTELINDAIHKQKSLQFKKTDJAKKNYE   OKCRDKDEAEQAVSRSANLVNPKQQEKLFVKLATSKTAVEDSDK   AYMLHICTLDKVREEWGSEHILKCAFEAQECERINFFRRALMI   HYNQLSQCQVTSDEMYEQVRKSLEMCSIQRIDEYFVWQRKIGG    PPAPIMYENFYSSQKBAVPAGKATGFNLARRGPLPFIEVSSPDDP   NYSLVDDYSLLIV    PAPIMYENFYSSQKBAVPAGKATGFNLARRGPLPFIEVSSPDDP    AVSLVDDYSLLIV    OKSPINATION   PIGTIMSDSDLGEDEGLLSAGKKRRGNLPKESVKLEDBLYLH    FYNAMYPSEQEKLSGOTHLSVLOICNMFINARRELPDMLRKD    GKDPNGFTISRRGGKASDVALFGSSPSULAVSVPAPTNVLSLS    GKDPNGFTISRRGGKASDVALFGSSPSULAVSVPAPTNVLSLS    GKDPNGFTISRRGGKASDVALFGSSPSULAVSVPAPTNVLSLS    GKDPNGFTISRRGGKASDVALFGSSPSULAVSVPAPTNVLSLS    GKDPNGFTISRRGGKASDVALFGSSPSULAVSVPAPTNVLSLS    GKDPNGFTISRRGGKASDVALFGSSPSULAVSVPAPTNVLSLS    GKDPNGFTISRRGGKASDVALFGSSPSULAVSVPAPTNVLSLS    GKDPNGFTISRRGGKASDVALFGSSPSULAVSVPAPTNVLSLS    GKDPNGFTISRRGGKASDVALFGSSPSULAVSVPAPTNVLSLS    GKDPNGFTISRRGGKASDVALFGSSPSULAVSVPAPTNVLSLS    GKDPNGFTISRRGGKASDVALFGSSPSULAVSVPAPTNVLSLS    GKDPNGFTISRRGGKASDVALFGSSPSULAVSVPAPTNVLSLS    GKDPNGGKASDVALFGSSPSSPSULAVSVPAPTNVLSLS    GKDPNGGKASTANTANTANTSPSSSVALAD   GEBRCVLDCAKIFGISTSDDLDDPKWTLCLQWULALLAWSKIRD    VLIQKSGMTEPGPDVKKKTEEDLYPIONTELQFOSVVALD    GEBRCVLDCAKIFGISTSDDLDDPKWTLCLQWULDNEYPGTAP    PIGLINAPHIKGGERADLSNSLESITIONIGESILVLWVEKIRD    GEBRCVLDCAKIFGISTSDDLDRFWTLCLQWULDNEYPGTAP    PIGLINAPHIKGGERADLSNSLESITIONIGESILVLWVEKIRD    FULYGRAMPHIKGGERADLSNSLESITIONIGESILVLWVEKIRD    FULYGRAMPHIKGGERADLSNSLESITIONIGESILVLWVEKIRD    FULYGRAMPHIKGGERADLSNSLESITIONIGESILVLWVEKIRD    FULYGRAMPHIKGGERADLSNSLESITIONIGESILVLWVEKIRD    FULYGRAMPHIKGGERADLSNSLESITIONIGESILVLWVEKIRD    FULYGRAMPHIKGGERADLSNSLESITIONIGESILVLWVEKIRD    FULYGRAMPHIKGGERADLSNSLESITIONIGESILVLWVEKIRD    FULYGRAMPHIKGGERADLSNSLESITIONIGESILVLWVEKIRD    FULYGRAMPHIKGGERADLSNSLESITIONICGESILVLWVEKIRD    FULYGRAMPHIKGGERADLSNSLESITIONICGESILVLAWGESILVLW   FULYGRAMPHIKGGERADLSNSLESITIONICGESILVLUNGKGGNILLY   GEBRCVLLDAKSSSFLIMBRRPEWGYKRPKENGTIONICGENALDVKALGKKRPTITORNOTORGGNILBGENGT    FULYGRAMPHIKGGERADLSNSLESITIO	1	1		DILSTIGYDNIIQHLNNGRKNCKEFEDFI.KERAATEERVGVDLI
ARKMEREKQÜÜÜRIKKTELIMDATHIKORSIQPIKKTUDAKINYE  QKCRDKDEAEGOVARSABILINYGQEKLIPVIKLATSKTAVEDSIDK AYMLHICTLOKVREEMOSEHIKACEAFEAGECERINFFRNALML HYNGLSQQCYTSEMYEOVIKSLEMCSIQRIDIEYFYNGKTGGI PPAPTMYENFYSSQKNAVPAGKATGPINARRGPLPIEKSSPDDP NYSLVDDYSLLYQ NYSLVDDYSLLYQ NYSLVDDYSLLYQ RYNSLVDDYSLLYQ RYNSLVDDYSLLYQ RYNSLVDDYSLLYQ RYNSLYDDYSLLYQ LQRAARMELQK COPPSIPERTEVEVERPORTELGERSGHMAEGDAGSDQROMEEIEAMAATY GEEMCVIDDCAKIFCIRISDDIDPKWTLCLQWLENEYPGTAP PIYQLNAPMIKGGERADLSNSLEETYIONIGESILYLWVEKIRD VLIQKSQMTEPEGPDVKKKTEEEDVECDILIACQPESSVKALD FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPRQV KMVLSKLYENKKIASATINIYAYSIYCEDKOTFLQCEDDGETA AGGRLHHAMEILNVKNWVVVYSRYGGILLGPDRFHINNCARN ILVEKNYTINSPEESSKALGKNKKVRKKKKNENE PRIPVYRNYMGRERGGASGGMAEGDAGSDQROMEEIEAMAATY GEEMCVIDDCAKIFCIRISDDIDDFKWTLCLQWMLPNEYPGTAP PIYQLNAPMIKGQERADLSNSLEETYIONIGESILYLWWEKIRD VLIQKSQMTEPEGPDVKKKTEEDVECDDLILACQPESSVKALD FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPRQV KWVLSKLYENKKIASATINIYAYRIYCEDKOTFLQDCEDDGETA AGGRLHHAMEILNVKNWWVVYSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSPEESSKALGKNKKVRKOKKRNEH  FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPRQV KWVLSKLYENKKIASATINIYAYRIYCEDKOTFLQDCEDDGETA AGGRLHHAMEILNVKNWWVVYSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSPEESSKALGKNKKVRKOKKRNEH  FDISETRTEVEVEELPPITHGIPITTORRSTFQAHLAPVVCPRQV VLSFCRIHKQSSMTVMEAGESPLFNNVKLIQRKLFPESIQIVLEE LEKKGRIEBUDGKSSSFLIMBRRPERFGKLIYQWRSGGONISV FTLYELTNGEDTEDEEFHGLDEATLLRALQALQQEHKAEITTVS DGPRRQVLLAGTCLPLLLTSHLSRAPKRRQTGCPPKTGSTVPPD SKGLQS  KMAALTTEFKYDENQDRYIKKLAKWATQOKARNEH MEVAADVKQLGGSVELVDIGKOKLPDGSETLEPILLERIGS DPCKKTVCIYCHLDVQCBALEDGWDSPFTLVERGKLERGST DPKGFVVAGWINALEAVQKTGQEIPPNVKRCEGGMESGSECLDE LIFAKKDTFFKUDDYVCISDNYMLGKKKPCITYGLGRGCYFFIE VECSNKDLHSGVAGGSVHEAMTOLILLMGSSUDKRGNILLBY	]			NLSRKKPCGQSEINTLKRALEVFKOOVDNVAOCHTOLAOSLPEF
QKCRINKBAEQOXPSASNILVAPKQQEKIFYKLATSKTAVEDSINK AYMLHIGTLDKVREEWGSHIFVALKACEAFFAQGERIHFFKRAIML HVNQLSQCVTSDEMYEQVRKSLEMCSIQRDIEYFYWORKTGQI PAPAPMYENTYSSQKNAVPAGKATGPNLARRGPLPIPKSSPDDP PAPAMYENTYSSQKNAVPAGKATGPNLARRGPLPIPKSSPDDP NYSLVDDYSLLYQ  FILTH PLGTMSDSDLGEDEGLLSLAGKRKRRGNLPKESVKILRDWLYLH RYNAYPSEQEKLSLSGQTNLSVLQICNWFINARRRLLPDMLRRD GKDPNQFTISRRGGKASDVALPRGSSSBVLAVSVPAPTRVLSLS VCSMPLHSQGGEKPAPPPRGELESPKPLAVPGSTTLLITRAEA GSPTGGIFNTPPPTPPRQDKEDFSSFQLLVEVALQRAAEMELQK QODPSLPILLTPIPIPLSENDC QODPSLPLLTPIPIPLSSTTLLVEGSTTLLTRAEA GSPTGGIFNTPPTPPPRQDKEDFSSFQLLVEVALQRAAEMELQK QODPSLPLLTPIPIPLSENDC GEWCVIDDCAKIFCIRISDDIDPKMTLCLQVMLDNEYPGTAP PIVQLNAPMIKGGERADLSNSLEEIYIQNIGESILYLWVEKIRD VLIQKSGMTEPGDPVKKKTEEDDVECDDLILACQPESSVKALD FDISETRTTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMVLSKLYENKKTASATHNIYAYRIYCEDKOTFLQDCEDDGETA AGGRLHLMMEILAVKNVMVVVSKWYGGILLGPDRFKHINNCARN ILVEKNYTNSPEESSKALGKNKKVKKDKKCHENEH PRIPVRRYHGRRRLQGRSGSHMAEGDAGSDQRQNEEIEAMAAIY GEBWCVIDDCAKIFCIRISDDIDPKWTLCLQVMLDNEYPGTAP PIVQLNAPMIKGGERADLSNSLEEIYIQNIGESILYLWVEKIRD VLIQKSQMTEPGPDVKKKTEEDEVECEDDLILAQPESSVKALD FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAFVVCPKQV KMVLSKLYENKKIASATHNIYAYRIYCEDKOTFLQDCEDDGETA AGGRLHLMEILNVKNVMVVVSRWGGILLGPDRFKHINNCARN ILVEKNYTNSPEESSKALGKNKVKKOKKOKRNEH FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAFVVCPKQV KMVLSKLYENKKIASATHNIYAYRIYCEDKOTFLQDCEDDGETA AGGRLHLMEILNVKNVMVVVSRWGGILLGPDRFKHINNCARN ILVEKNYTNSPEESSKALGKNKVKKOKKRNEH  FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAFVVCPKQV KMVLSKLYENKKIASATHNIYAYRIYCEDKOTFLQDCEDDGETA AGGRLHLMEILNVKNVMVVVSRWGGILLGPDRFKHINNCARN ILVEKNYTNSPEESSKALGKNKVKVKKOKKRNEH  FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAFVVCPKQV KMVLSKLYENKKIASATHNIYAYRIYCEDKOTFLQDCEDGETA AGGRLHLMEILNVKNVMVVVSRWGGILLGPGRFKHINNCARN ILVEKNYTNSPEESSKALGKNKVKVKOKKRNEH  FDRWAMTTMAMBFEWWQFTYFFFFFTLOPNUTCKQLAAGGSL UNGKTVCITGGDTEDEFHGLOBATLIRALQALQGEHAEILTIVS DGPRRQVLLAGTCIPLLITSHSKRATKRQTQCPPKYGSVTPPD SKGLOS  KMAALTTIPKYJDENOGRYIKKLAGATHONITCHEGKTITAM MEVAAADVKGLGSVELVOIG GKOKLPDGSIPLPPPILLGRLGCYFFTE VECSNKDLHSGVYGGSVHEAMTDLILLHSSLKONITCH				ARKMEEPREKOKLORKKTELIMDAIHKOKSLOFKKTMDAKKNIVE
AYMLIGTLDKYREEWGSEHIKACEAFFAGECBRINFFRNALML HVNOLSQCVTSDEMYSOVRKSLEMCSIQRDIEFYTMQRXTGGI PPAPIMYSNFYSSQKNAVPAGKATGPNLARRGPLPIPKSSPDDP NYSLVDDYSLIJYQ  6595 57 781 PLGTMSDSDLGEDEGLLSLAGKRKRRGNLPKESVKILRDWLYLH RYNAYPSEQEKLSLSGGTNLSVLQICMWFINARRRLIPDMLRKD GKDPNQFTISRRGGKASDVARSSSPSVLAVSVPAPIRVLGLS VCSMPLHSGQGEKPAAPPPRGEIES PKPLVTPGSTITLLTRAEA GSPTGGLFNTPPTPPPDREPSFSSPSVLAVSVPAPIRVLGLS VCSMPLHSGGGEKPAAPPPRGEIES PKPLVTPGSTITLLTRAEA GSPTGGLFNTPPTPPPDREPSFSFOLLVEVALQRAARMELQK QODPSLPLHTPIPLVSENPQ  6596 2 1026 PRLPVRRYHGRRZLQGRSRGHMAEGDAGSDQRONEEIEAMAATY GEEMCVIDDCAKIFCIRISDIDDPKMTLCLQVMLPNEYPGTAP PIYQLNAPMLKGGERADLSNSLEEIVIONIGESILYLWVEKIRD VLIQKSGMTEBGPDVKKKTEDENVEGDDLILACQPESSVKADD FDISETRTEVEVEELPPIDHGIPITDRRSTFOAHLAPVVCPRQV KMVLSKLYENKKLASATHNIYAVRIVYCEMVGTLLGQPESSVKADD FDLYNRYHGRRRLIQGRSRGHMAEGDAGSDQRONEEIEAMAATY GEEMCVIDDCAKIFCIRISDDIDDPKWTLCLQVMLPNEYPGTAP PIYQLNAPMLKQGGRADLSNSLEEIVIONIGESILYLWVEKIRD VLIQKSQMTEPESSKALGKNKKVRKDKRNEH FDLSETRTEVEVEELPPIDHGIPITDRRSTFOAHLAPVVCPRQV KMVLSKLYENKKLASATHNIYARIYLGEMCFTLLQCPESSVKADD FDLSETRTEVEVEELPPIDHGIPITDRRSTFOAHLAPVCPRQV KMVLSKLYENKKLASATHNIYARIYLGEMCFTLLQCPESSVKADD FDLSETRTEVEVEELPPIDHGIPITDRRSTFOAHLAPVCPRQV KMVLSKLYENKKLASATHNIYARIYLGEMCFTLLQCPESSVKADD FDLSETRTEVEVEELPPIDHGIPITDRRSTFOAHLAPVCPRQV KMVLSKLYENKKLASATHNIYARIYLGEMCFTLLQCPESSVKADD FDLSETRTEVEVEELPPIDHGIPITDRRSTFOAHLAPVCPRQV KMVLSKLYENKKLASATHNIYARIYLGEMCFTLLQCPESSVRADD FDLSETRTEVEVEELPPIDHGIPITDRRSTFOAHLAPVCPRQV VLSFCRLHKQSSMTVMEAQESSPLFMNVKLQRKLPVESIQIVLEE LEKKKGNLEHLDRSKSSFLIMRPEBWGKLYRYDVFLOCCODGETA AGGRLHLKEILNNKNWMVVSRWYGGILLGCPRESSFGOMNSV FTLYELTNGEDTEDEEFFIGLDEATLLRALQALQQEKAEIITVS DGPRRQVLLAGTCLPLLLTSHLSRAFRRQTQCPPKYGSVTPPD SKGLQS  VLSFCRLHKQSSMTVMEAQESSPLFMNVKLQRKLPVESIQIVLEE LEKKKGNLEHLDRSKSSFLIMRPEBWGKLYLGVAWYSSRGOMNSV FTLYELTNGEDTEDEEFFIGLDEATLLRALQALQQEKAEIITVS DGPRRQVLLAGTCLPLLLTSHLRARAQAVAYBEGERDER MMEVAAADVKGLGGSVELVDIGKKRPLETRALLGRLCYCFFIE VECSNKDLHSGVYGGSVELVDIGKKRPCTEGMEESGSGGLDE LIFARKDTFFRQVDYVCLSONYWLGKKKPCHTLHPIK				QKCRDKDEAEQAVSRSANLVNPKOOEKLFVKLATSKTAVEDSDK
HVNQLSQCVYSDEMYSQVRKSLEMESIQRDIBYFVNQRKTGGI PAPATMYENTYSSQKNAVPAGKATGPNLARRGPLPIPKSSPDDD PAPIMYENTYSSQKNAVPAGKATGPNLARRGPLPIPKSSPDDD NYSLVDDYSLLYQ  FURMSDSDLGEDGLLSLAGKKKRRGNLPKESVKILRDWLYLH RYNAYPSEQEKLSLSGQTNLSVLQICNWFINARRRLIPDMLRKD GKDPNQFTISRRGGKASDVALPRGSSSPVLAVSVPAPTNVLSLS VCSMPLHSGGGEKPAAPPPRGELESPKPLUTPGSTLTLLTRAEA GSPTGGLFNTPPPTPPBQDKEDFSSFQLLVEVALQRAARMELQK QDPSLPLLHTPIPLVSENPQ  6596  2 1026 PRLPVRRYHGRRILQGRSGCHAAEGDAGSDQRQNEEIEAMAATY GEEMCVIDDCAKIFCIRISDDIDPKMTLCLQVMLPNEYPGTAP PIYQLNAPMLKGGERADLSNSLEEIYIQNIGSILYLWVEKIRD VLIQKSQMTEPGPDVKKKTEEDVECEDDLILACQPESSVKALD FDISETRTEVEVEELPPIHGIPITTRRSTFCAHLAPVUCPKQ KMYLSKLYENKKLASATHNIYAYRIYCEDKQFFLQOCEDDGGTA AGGRLLHLMBILMVKNVNVVVSRWYGGILGPDRFKHINNCARN ILVEKNYTNSPESSKALGKNKVKNKDKKRDEH  6597  2 1026 PRLPVRRYHGRRILQGRSGGMAEGDAGSDQRQNEEIEAMAAIY GEEMCVIDDCAKIFCIRISDDIDDFKMTLCLQVMLPNSPYGTAP PIYQLNAPMLKGGGRADLSNSLEEIYIQNIGSILYLWVEKIRD VLIQKSQMTEPGPDVKKKTEEEDVECEDDLILACQPESSVKALD FDISETRTEVEVELELPPIHGFITDRRSTFCAHLAPVUCPKQV KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLODCEDGGTA AGGRLLHLMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN VLIQKSQMTEPGPDVKKKTEEEDVECEDDLILACQPESSVKALD FDISETRTEVEVELELPPIHGFITDRRSTFCAHLAPVUCPKQV KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLODCEDGGTA AGGRLLHLMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSPEESSKALGKNKKVKDKKRWEH  6598  1099  419 PRVRWATTAMASFEWWQYRFPPFFTLQPNOTTRQKQLAAWGSL UKSKYNTTMAMSFEWWQYRFPPFFTLQPNOTTRQKQLAAWGSL UKSKYNTTMAMSFEWWQYRFPPFFTLQPNOTTRQKQLAAWGSL UKSKYNTTMAMSFEWWQYRFPPFFTLQPNOTTRQKQLAAWGSL UKSKGNLEWLDKSKSSFLIMMRRPEEWGKLIYGWVSRSGONSV FTLYELTNGEDTEDEEFFRGUDGATLLRALQALQGEKREIITVS GDGRRRQVLLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD SKGLQS  MAALTTLFKYTDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSIPLPFILLGRLGS DDKGFVAGWINALBAYQKTGQBIPVNVRFCLEGMESGEGGLDE LIFARKDTFFKUDVQCISONYWGKKKPCLTYSLRGICYFFIE VECSNKDLHSGVYGGSVIEAMTDLILLHSSKUTLHW				AYMLHIGTLDKVREEWOSEHIKACEAFFAOFCERINEFPNALMI
Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Telegrant   Tele	1			HVNQLSQQCVTSDEMYEQVRKSLEMCSIORDIEVFVNORKTGOT
FIGHNSDEDLGEDEGLLSLAGKRKRRGNLPKESVKILRDWLYLH RYNAYPSQEKLSLSGQYNLSVLQLYCMPINARRILEPMLRKD GKDPNQFT1SRRGGKASDVALPRGSSPSVLAVSVRAPTHVLSLS VCSMPLHSGQGEKBAPPPRGELESSKPLLVTPGSTLTILLTRÆR GSPPTGGLENTPPTPTPEDEDLEDFSSFQLLVEVAGRAÆMELOK QODPSLPLLHTPIPLVSENPQ   FOR				PPAPIMYENFYSSQKNAVPAGKATGPNLARRGPLPIPKSSPDDP
RYNAYPSEQEKISLSGQTNISVLQI CNWFINARRILEDMIKHO GKDPNQFTISRRGKASDVALPRGSSESVLAVSVPAPINVLSIS VCSMPLHSGQGEKPAPPRGGIES PKPLVTPGSTLTLITRAEA GSPTGGLFNTPPPTPPEQDKEDFSSFQLLVEVALQRAAEMELQK QQDPSLPLLHTTIPLVSENPQ PRIPVRRYNGRRELGGRSRGHMAEGDAGSDORQNEEIEAMAATY GEEMCVIDDCAKIFCIRISDDIDDPKWTLCLQVMLPNEYPGTAP PIYQLNAPWLKGQERADLSNSLEEIYIQNIGESILYIMVEKIRD VLIQKSGMTERGPDVKKKTEEEDVECEDDILIACOPESSVKALD FDISETRTEVPEVELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMYLSKLYENKKIASATHNIYAYRIYCEDWGTFLQDCEDDGETA AGGRLLHIMEILNVKNWVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSFEESSKALGKNKKVRKDKKRNEH PRIDVRRYHGRRELGGRSGGHMEAGDAGSDQRQNEEIEAMAATY GEEMCVIDDCAKIFCIRISDDIDDFKWTLCLQVMLPNEYPGTAP PIYQLNAPWLKGGERADISNSLEEIYIQNIGESILVIMVEKIRD VLIQKSGMTEFGPDVKKKTEEEDVECEDDLILACOPESSVKALD FDISETRTEVEVERELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA AGGRLHLMEILNVKNWVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSFEESSKALGKNKKVKKDKKRKPH FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA AGGRLHLMEILNVKNWVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSFEESSKALGKNKKVKKDKKRNEH  6598 1099 419 PRVRWATTMAMSFEWPWQYFFPPFFTLQFNVDTRQKQLAAWCSL VLSFCRLHKQSSMTVMEAQESPLFNNVKLQRKLPVESIQIVLEE LRKKGRLEWLDKSKSSFLIMMRFEEWGKLIYQWVSRSGQNNSV FTLYELTNGEDTEDEEFGLDEATLLRALQALQCHKABIITVS DGPRRQVLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD SKGLQS KKAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGETRR MMEVAAADVKQLGSVELVDIGKÇKLPDGSETPLEPILLGRLS DPQKKTVCIYGHLDVQPAALEDGMDSEFFTLVERGOKLHGRGST DDKKFVCGIYGGHNALGEVGGEIPNNWFCLEGMEESSGEGLDE LIFARRDTFFKDVDTVCISDNYWLGKKKPCITYGLRGICYFFTE VECSNKDLHSGVYGGSVHEAMTDLILLMSLUVDKRGNTLIFGTIN EAVAAVTFEEFKLKYDDIDFIEFFAKUPGAOILLHMSKKDTLMW	6595	57	781	
GKDNQFTISRAGASDVALPRGSSESVLAVSVPAPTNVLSLS  VCSMPLHSQGEKPAPPRGELES PEPLVTPGSTLTLLTRAEA GSPTGGLENTPPTPPPQDKEDFSSFQLLVEVALQRAAEMELQK QQDPSLPLLHTPIPLVSENPQ PRLEVRKYHGRRELQGESKGHMAEGDAGSDQRQNEEIEAMAATY GEEMCVIDDCAKIFCIRISDDIDDPKWTLCLQVMLPNEYPGTAP PIYQLNAPWLKQGERADLNSLEEIYIQNIGGSILYLWVEKIRD VLIQKSQMTEPGPDVKKKTEEEDVECEDDIILACOPESSVKALD FDISETRTEVEVEELPFIDHGIPITDRRSTFQAHLAPVVCPKQV KMYLSKLYENKKIASATHNIYAYRIYCEDKOTFLQOCEDDGETA AGGRLLHLMEILNVKNVMVVSRWYGGILLGPPRFKHINNCARN ILVEKNYTNSFEESSKALGKNKKVRKDKKRNEH PRIPVREWHGRRELQGRSGHMAEGDAGSDQRQNEEIEAMAAIY GEEMCVIDDCAKIFCIRISDDIDDPKWTLCLQVMLPNEYPGTAP PIYQLNAPWLKQGERADLSNSLEEIYIQNIGGSILVIWVEKIRD VLIQKSGWTEEGPDVKKKTEEEDVECEDDLILACOPESSVKALD FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMVLSKLYENKKIASATHNIYARIYCEDKQTFLQDCEDDGETA AGGRLHLMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSFEESSKALGKNKKVRKDKKRNEH FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMVLSKLYENKKIASATHNIYARIYCEDKQTFLQDCEDDGETA AGGRLHLMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSFEESSKALGKNKKVRKDKKRNEH  FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMVLSKLYENKKIASATHNIYARIYCEDKQTFLQDCEDDGETA AGGRLHLMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSFEESSKALGKNKKVRKDKRNEH  EKKKGNLEWLDKSKSSFLIMWRFBEWGKLIVGWVSRSGQNNSV FTLYELTNGEDTEDEEFSGLDEATLLRALQALQGEKAEIITVS DGPRRQVLLAGTCLPLLLTSHLSRAFKRQTQCPPKREIITVS DGPRRQVLLAGTCLPLLLTSHLSRAFKRQTQCPPKREIITVS SKGLQS  KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGETRR MMEVAAADVKQLGSVELVDIGKÇKLPDGSETPLEPPILLGRLG DPQKKTVCTYGHLDVQPAALEDGMDSEFFTLVERDGKLHGRGST DDKGPVAGNINALEAVGGEJ PVNVFFCLEGMEESGSGELDE LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFFIE VECSNKDLHSGVYGGSVHEAMTDLILLMSLUVDKGNTLIHPGIN EAVAAVTFEEFKLKYDDIDTIEFFAKUPGAGOILLHMSKKDILMH				PYNAYPSEOFYL SI SCOTTIL SIN OF STREET
VCSMPLHSGQEEMAPPPPREDEESSKPLLVTPGSTLTLLTRREA GSPTGEEMAPPPTPPEDQKEDFSSFQLLVEVALQRAAEMELQK GSPTGEEMATPPPTPPPEQDKEDFSSFQLLVEVALQRAAEMELQK QODPSLPLLHTPIPLVSENPQ   PRLEVRRYHGRRRIQGRSRGHMAEGDAGSDQROMEEIEAMAATY GEEMCVIDDCANIFURISDDIDDPKWTLCLQVMLPNEYPGTAP PIYQLNAPWLKGQERADLSNSLEEIYIONIGESILVLWVEKIRD VL1QKSQMTEPGPDVKKKTEEEDVECEDDLILACQPESSVKALD FDISETRTEVEVEELPIDHGIPITDRRSTFQAHLAPVVCPKQV KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA AGGRLLHLMEILNVKNVMVVVYSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSFEESSKALGKNKKVKKDKKRNEH   PREDVRRYHGRRRLQGRSRGHMAEGDAGSDQRQNEEIEAMAATY GEEMCVIDDCAKIFCIRISDDIDDPKWTLCQVMLPNEYPGTAP PIYQLNAPWLKGQERSGHMAEGDAGSDQRQNEEIEAMAATY GEEMCVIDDCAKIFCIRISDDIDDPKWTLCQVMLPNEYPGTAP PIYQLNAPWLKGQERSTGHMAEGDAGSDQRQNEEIEAMAATY GEEMCVIDDCAKIFCIRISDDIDDPKWTLCQVMLPNEYRGTAP PIYQLNAPWLKGQERSGUNSUFIDIDTROKTCLQVMLPNEYBGTAP FIYGLNAPWLKGRAFTRIDITDRSTFQAHLAPVVCPKQV KMVLSKLYENKIASATHNIYAVRIYCGBKQTFLODCEDDGETA AGGRLHHMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSPESSKALGKNKKVRKDKKRREH AGGRLHHMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSPESSKALGKNKKVRKDKKRREH VLSVKSTFLÜMWLGKKSTLYQWVSRGQNISV VLSFCRILKQSSMTVMEAQESPLFNNVKLQRKLPVESIQIVLEE LRKKGNLEWLDKSKSSFLIMWRPEEEWGKLIYQWVSRGGNISV FFILYELTNGEDTEDEEFHGLDEATLIRAQALQQBHKABIITVS DGPRRQVLLAGTCLPLLLTSHLSRAPKRRQTQCPPKTGSVTPPD SKGLQS  6599 164 1593 KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS DPQKKTVCIYGHDVQPAALEBGWDSEPFTLVERDGKLHGRGST DPQKKTVCIYGHDVQPAALEBGWDSEPFTLVERDGKLHGRGST DPQKKTVCIYGHDVQPAALEBGWDSEPFTLVERDGKLHGRGST DPQKKTVCIYGHDVQPAALEBGESGSEGLDE LIFARKDTFFKUDVYCISDNYMLGKKKPCITYGLRGGCYFFIE VECSNKDLHSGVVGGSVHEAMTDLILLMSHKNTLIHM EAVAAAVTEEHKLYDDFITERSHKLYDDLILLHSHKNTLIHM EAVAAAVTEEHKLYDDFITERSHKLYDDLILLHSHKNTLIHM EAVAAAVTEEHKLYDDFITERSHKLYDDLILLHSHKNTLIHM	1	}		GKDPNOFTISPEGGYASDYAL PROSCOCIA ANGLES
GSPTGGLFNTPPPTPPEGDKEDFSSFQLLVEVALQRAAEMELQK OODPSLPLLHTPT PLVSENPQ PRLPVRRYHGRRRLQGRSGGHMAEGDAGSDORONEEIEAMAAIY GEEMCVIDDCAKIFCIRISDDIDDPKWTLCLQVMLPNEYPGTAP PIYQLNAPWLKGQERADLSNSLEEIYIQNIGESILYLWVEKIRD VLIQKSQMTEPGFDVKKKTEEEDVECEDDLILACQPESSVKALD FDISETRTEVEVEELPPIDHGIPITDRRSTFOAHLAPVVCPKQV KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA AGGRLLHMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYINSPEESSKALGKNKKVRKDKKRNEH PRLPVRRYHGRRRLQGRSRGHMAEGDAGSDQRQNEEIEAMAAIY GEEMCVIDDCAKIFCIRISDDIDDPKWTLCLQVMLPNEYPGTAP PIYQLNAPWLKGGERADLSNSLEEIYIQNIGESILYLWVEKIRD VLIQKSQMTEPGPDVKKKTEEEDVECEDDLILACQPESSVKALD FDISETRTEVEVEELPPIDHGIPITDRSTFOAHLAPVVCPKQV KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA AGGRLLHLMEILNVKNWVVVSRWYGGILLGPDRFKHINNCARN LVVEKNYTNSPEESSKALGKNKKVRDKKRNEH PSTSETTEVEVEELPPIDHGIPITDRSTFOAHLAPVVCPKQV KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA AGGRLLHMEILNVKNWVVVVSRWYGGILLGPDRFKHINNCARN LLVEKNYTNSPEESSKALGKNKKVRDKKRNEH PRVRWATTMAMSFEWPWQYRFPPFFTLQPNVDTRQKQLAAWCSL VLSFCRLHKQSSMTVMEAQESPLENNVKLQRKLPESIQIVLEE LRKKGNLEWLDKSSFLIMWRRPEEWGKLIYQWVSRSGQNNSV FTLYELTNGEDTEDEEFHGLDEATLIRALQALQQEHKAEIITVS DGPRRCVLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD SKGLOS  KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVKGLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSEPFTLVEERDGKLHGRGST DDKGPVAGMINALEAYQKTGQEIPVNVRFCLEGMEEGSSEGLDE LIFARKDTFFKDVDYVCISDNYNLGKKKPCITYGLRGICYFFIE VECSNKDLHSGVYGGSVIEAMTDLILLENGSLVDKRGNILLIGIN EAVAAVTFEEHKLVDDIDFDIEEFFAKDVGAOLLILHSHKKDIMH	1	ĺ		VCSMPLHSGOGEKPAAPFPRGELESCKDLAUTDGGTLUTLUTT
6596 2 1026 PRLPVRRYHGRRZIOGRSGHMAEGDAGSDORONEEIEAMAATY GEEWCVIDDCAKIFCIRISDDIDDPKNTLCLOVMLPNEYBGTAP PIYQLNAPWLKGOERADLSNSLEEIYIQNIGGSILYLWVBKIRD VLIQKSQMTEPGPUKKKTEEEDVECEDDLILACQPESSVKALD FDISETRTEVEVEELPPIDHGIPITDRRSTFOAHLAPVVCPKQV KMYLSKLYENKKLASATHNIYAYRIYCEDKGTFLQDCEDDGETA AGGRLLHLMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSPEESSKALGKNKKVRKDKKRNEH  6597 2 1026 PRLPVRRYHGRRZLQGRSGHMAEGDAGSDQRQNEEIEAMAATY GEEWCVIDDCAKIFCIRISDDIDDPKWTLCLQVMLPNEYPGTAP PIYQLNAPWLKGQERADLSNSLEEIYIQNIGESILYLWVEKIRD VLIQKSQMTEPGPDVKKKTEEDVECEDDLILACQPESSVKALD FFILSETRTEVEVELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA AGGRLLHLMEILNVKNWVVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSPEESSKALGKNKKVRKDKKRNEH  6598 1099 419 PRVRWATTMAMSFEWFWQYRFPPFFTLQPNVDTRQKQLAAWCSL VLSFCRLHKQSSMTVMEAQESPLFMNVKLQRKLPVESIQIVLEE LRKKGRLEWLDKSKSSFLIMWRRPEEWGKLIYQWVSRSGQNNSV VLSFCRLHKQSSMTVMEAQESPLFMNVKLQRKLPVESIQIVLEE LRKKGRLEWLDKSKSSFLIMWRRPEEWGKLIYQWVSRSGGNNSV FTLYELTNGEDTEDEEFHGLDEATLIRALQALQQEHKAEIITVS DGPRRQVILLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD SKGLQS  KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGST DDKGFVAGMINALEAYQKTGQEIPVNVRFCLEGMEESGSEGLDE LIFARKDTFFKDVDYVCISDNYNLGKKKPCITYGLRGICYFFIE VECSNKDLHSGVYGGSVILEAMTDLILLMGSLVDKKGNILIIGIN EAVAAVTFEEHKLYDDIDFDIEEFFAKDVGAOLILHSHKKDTIMH	{			GSPTGGLFNTPPPTPPEODKEDFSSFOLLVEVALOPAREMETOR
6597 2 1026 PRLPVRRYHGRRZLQGRSRGHMAEGDAGSDQRONEEIEAMAAIY GEEWCVIDDCAKIFCIRISDILDPKWTLCLQVMLPNEYBGTAP PIYQLNAPWLKGGGRADLSNSLEEIYIQNIGESILYLWVEKIRD VLIQKSQMTEPGPDVKKKTEEDVECEDDLILACQPESSVKALD FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMVLSKLYENKKLASATHNIYAYRIYCEDKQTFLQDCEDDGETA AGGRLLHLMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYINSPESSKALGKNKKVRKDKKRNEH PRIPVRRYHGRRZLQGRSRGHMAEGDAGSDQRQNEEIEAMAAIY GEEWCVIDDCAKIFCIRISDIDDPKMTLCLQVMLPNEYPGTAP PIYQLNAPWLKGGGRADLSNSLEEIYIQNIGESILYLWVEKIRD VLIQKSQMTEPGPDVKKKTEEDVBCCDDLILACQPESSVKALD FDISETRTEVEVELELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA AGGRLLHLMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSPESSKALGKNKKVRKDKKRNEH PREVRWATTMAMSFEWPWQYRFPPFFTLQPNVDTRQKQLAAWCSL VLSFCRLHKQSSMTVMAQGSPLENNVKLQRKLPVESTQIVLEE LRKKGNLEWLDKSKSSFLIMWRRPEBWGKLIYQWVSRSGQNNSV FTLYELTNGEDTEDEEFHGLDEATLLRALQALQGEHKAEIITVS DGPRRQVLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD SKGLQS KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVKGLGGSVELVDIGKGKLPDGSEIPLPPILLGRLGS DPKKYNCIYGHLDVQPAALEDGWDSEPFTLVERDGKHHRGSST DDKGPVAGWINALEAYQKTGQEIPUNVRFCLEGMEESGSGGLDE LIFARKDTFFKDVDYVCISDNYNLGKKKPCITYGLRGICYFFIE VECSNKDLHSGVYGSVERAMTDLILLENGSLVDKKRILLIGIIN EAVAAVTFEEHKLYDDIDFDIEEFFAKDVGAOLILHSHKKDIJMH	CE06			QQDPSLPLLHTPIPLVSENPQ
GEEWCVIDDCAKIFCIRISDDIDDPKWTLCLQVMLPNEYPGTAP PIYQLNAPWLKQQERADLSNSLEEIYIQNIGESILYLWVEKIRD VLIQKSQMTEPGPDVKKKTEEDDVECEDDLILACQCPSSVKALD FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA AGGRLLHLMEILNVKNWVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSPEESSKALGKNKKVRKDKKKRNEH PIYQLNAPWLKGQERADLSNSLEEIYIQNIGESILYLWVEKIRD VLIQKSQMTEPGPDVKKKTEEEDVECEDDLILACQPESSVKALD FPIYQLNAPWLKGGGRADLSNSLEEIYILONGESILYLWVEKIRD VLIQKSQMTEPGPDVKKKTEEEDVECEDDLILACQPESSVKALD FPISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMVLSKLYENKKLASATHNIYAYRIYCEDKQTFLQDCEDDGETA AGGRLLHLMEILNVKNWVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSPEESSKALGKNKKVRKDKKRNEH PRVRWATTMAMSFEWPWQYRFPPFFTLQPNVDTRQKQLAAWCSL VLSFCRLHKQSSMTVMEAQESPLFNNVKLQRKLPVESIQIVLEE LRKKGNLEWLDKSKSSFLIMWRRPEEWGKLIYQWVSRSGQNNSV FTLYELTNGEDTEDEEFHGLDEATLLRALQALQCHKAEIITVS DGPRRQVLLAGTCLPLLLTSHLSRAPKRRQTQCPPKTGSVTPPD SKGLQS  KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS DPQKKTVCIYGHLDVQPALEDGWDSEPFTLVERDGKLHRGGST DDKGPVAGWINALEAYQKTGQEIPVNVRFCLEGMEESGSEGLDE LIFARRDTFFKDVDYVCISDNYMLGKKKPCTTYGLRGICYFFIE VECSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILITGIIN EAVAAVTFEEHKLYDDIDFDIEEFAKDVGAOILLHEHKKDTIMM	6596	2	1026	PRLPVRRYHGRRRLOGRSRGHMAEGDAGSDORONEETEAMAATV
PTYQLMAPWLKQQERADLSNSLEETYIQNIGESILYLMVEKIRD VLIQKSQMTEBGPDVKKKTEEDVECEDDLILACQPESSVKALD FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMYLSKLYEMKKIASATHNIVAYRIYCEDKQTFLQDCEDDGETA AGGRLHHMEILNVKNVMVVVVSWYGGILLGPDRFKHNNCARN ILVEKNYTNSPEESSKALGKNKKVRKKKREH PRIDVRRYHGRRRLQGRSRGHMAEGDAGSDQRQNEEIEAMAAIY GEEWCVIDDCAKIFCIRISDDIDDFKWTLCLQVMLPNEYPGTAP PIYQLNAPMLKQQERADLSNSLEEIYIQNIGESILYLWVEKIRD VLIQKSQMTEPGPDVKKKTEEDVECEDDLILACQPESSVKALD FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMYLSKLYENKKIASATHNIYAYRIYCEDKQTFKQDCEDGETA AGGRLHHMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSPEESSKALGKNKKVRKDKKNREH  6598 1099 419 PRVRWATTMAMSFEWPWQYRFPPFFTLQPNVDTRQKQLAAWGSL VLSFCRHKQSSMTVMEAQESPLFNNVKLQRKLPVESIQIVLEE LRKKGNLEWLDKSKSSFLIMWRRPEEWGKLIYQWVSRSGQNNSV FTLYELINGEDTEDEEFHGLDEATLLRALQALQQEHKAEIITVS DGPRRQVLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD SKGLQS  KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAAVCQLGSVELVDIGKQKLPDGSEIPLPPILLGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGST DDKGPVAGWINALEAYQKTGQGIPVNVRFCLEGMEESGSECIDE LIFARKDTFFKDVDYVCTSDNYWLGKKKPCITYGLRGICYFFIE VECSNKDLHSGVYGGSVHEAMTDLILLMGSLUDKRGNILIPGIN EAVAAAVTFEEHKLYDDIDFDIEEFAKDVQAOILLHSKKNILMH EAVAAAVTFEEHKLYDDIDFDIEEFAKDVQAOILHSKNILMH				GEEWCVIDDCAKIFCIRISDDIDDPKWTLCLOVMLDNEVDGTAR
FDISETRTEVEVEELPFIDHGIPTDRRSTFQAHLAPVVCPKQV KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA AGGRLIHLMEILNVKNVMVVVSKWYGGILLGPDRFKHINNCARN ILVEKNYTNSPEESSKALGKNKKVRKDKRNEH  6597 2 1026 PRIPVRYHGRRLQGRSRGHMAEGDAGSDQRQNEEIEAMAAIY GEEWCVIDDCAKIFCIRISDIDDPKWTLCLQVMLPNEYPGTAP PIYQLNAPWLKQGERADLSNSLEEIYIQNIGESILYLWVEKIRD VLIQKSQMTEPGPDVKKKTEEDVECEDDLILACQPESSVKALD VLIQKSQMTEPGPDVKKKTEEDVECEDDLILACQPESSVKALD FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA AGGRLIHLMEILNVKNVMVVVSRWYGGILLGPDRFKKINNCARN ILVEKNYTNSPEESSKALGKNKKVRKDKKRNEH  6598 1099 419 PRVRWATTMAMSFEWPWQYRFPPFFTLQPNVDTRQKQLAAWCSL VLSFCRIHKQSSMTVMEAQESPLFNNVKLQRKLPVESIQIVLEE LRKKGNLEWLDKSKSSFLIMWRRPEEWGKLIYQWVSRSGQNNSV FTLYELTNGEDTEDEFHGLDEATLLRALQALQQEHKAEIITVS DGPRRQVLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD SKGLQS  KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGST DDKGPVAGWINALEAYQKTGQEIPVNVRFCLEGMEESGSEGLDE LIFARKDTFFRDVDYVCISDNYNLGKKKPCITTGLRGICYFFIE VECSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTFEEHKLYDDIDFDIEEFAKDVGAOILLHSHKKDTIMH				PIYQLNAPWLKGQERADLSNSLEEIYIONIGESTLVLWURKIRD
AGGRLHHMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN  ILVEKNYTNSFEESSKALGKNKKVRKKKREH  PRLPVRRYHGRRRLQGRSRGHMAEGDAGSDQRQNEEIEAMAAIY GEEWCVIDDCAKIFCIRISDDIDDPKWTLCLQVMLPNEYPGTAP PIYQLNAPWLKGQERADLSNSLEEIYIQNIGESILYLWVEKIRD VLIQKSQMTEFGPDVKKKTEEEDVECEDDLILACOPESSVKALD FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KWVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA AGGRLHHMEILNVKNVWVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSPEESSKALGKNKKVRKDKKRNEH  PRVRWATTMAMSFEWPWQYRFPPFFTLQPNVDTRQKQLAAWCSL VLSFCRLHKQSSMTVMEAQESPLFNNVKLQRKLPVESIQIVLEE LRKKGNLEWLDKSKSSFLIMWRRPEEWGKLIYQWVSRSGQNNSV FTLYELTNGEDTEDEEFHGLDEATLLRALQALQQEHKAEIITVS DGPRRQVLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD SKGLQS  KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGST DDKGPVAGWINALEAYQKTGQEIPVNVRFCLEGMEESGSEGLDE LIFARKDTFFKDVDTVCISDNYNLGKKKPCITYGLRGICYFFIE VECSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILLIPGIN EAVAAVTREEHKLYDDIDFDIESFAKDVGAQILLHSHKKDTIMH	1			VLIQKSQMTEPGPDVKKKTEEEDVECEDDLILACQPESSVKALD
AGGRLIHLMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN  ILVEKNYTNSPEESSKALGKNKKVRKDKRREH  PRIPVRRYHGRRIGGRSRGHMAEGDAGSDQRQNEEIEAMAAIY GEEWCVIDDCAKIFCIRISDDIDDPKWTLCLQVMLPNEYPGTAP PIYQLNAPWLKGQERADLSNSLEEIYIQNIGESILYLWVEKIRD VLIQKSQMTEPGPDVKKKTEEEDVECEDDLILACOPESSVKALD FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KNVLSKLYENKKLASATHNIVAYRIYCEDKQTFLQDCEDDGETA AGGRLIHLMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSPEESSKALGKNKKVRKDKKRNEH  PRVWMATTMAMSFEWPWQYRFPPFFTLQPNVDTRQKQLAAWCSL VLSFCRLHKQSSMTVMEAQESPLFNNVKLQRKLPVESIQIVLEE LRKKGNLEWLDKSKSSFLIMWRPEEWGKLIYQWVSRSGQNNSV FTLYELTNGEDTEDEEFHGLDEATLLRALQALQQEHKAEIITVS DGPRRQVLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD SKGLQS  KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGST DDKGPVAGWINALEAYQKTGQEIPVNVRFCLEGMEESGSEGLDE LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGGRGICYFFIE VECSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTFEEHKLYDDIDFDIEEFAKDVGAOILLHSHKKDILMH				PDISETRIEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV
6597 2 1026 PRLPVRRYHGRRLQGRSRGHMAEGDAGSDQRQNEEIEAMAAIY GEEWCVIDDCAKIFCIRISDDIDDPKWTLCLQVML?NEYPGTAP PIYQLNAPWLKGQERADLSNSLEEIYIQNIGESILYLWVEKIRD VLIQKSQMTEPGPDVKKKTEEEDVECEDDLILACQPESSVKALD FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDGGETA AGGRLHLMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSPEESSKALGKNKKVRKKKRNEH  6598 1099 419 PRVRWATTMAMSFEWPWQYRFPPFTLQPNVDTRQKQLAAWCSL VLSFCRLHKQSSMTVMEAQESPLFNNVKLQRKLPVESIQIVLEE LRKKGNLEWLDKSKSSFLIMWRRPEEWGKLIYQWVSRSGQNNSV FTLYELTNGEDTEDEEFHGLDEATILIRALQALQQEHKAEIITVS DGPRRQVLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD SKGLQS  KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGST DDKGPVAGWINALEAYQKTGQEIPVNVRFCLEGMEESGSEGLDE LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIE VECSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTFEEHKLYDDIDFDIEEFAKDVGAOLLHSHKKDILMH	1 1			AGGRILLIMETIAN MATTER PROPERTY AGGRILLIA MATTER PROPERTY AGGRILLIA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATTER PROPERTY AGGRILLA MATT
PREDVRRYHGRRRLQGRSRGHMAEGDAGSDQRQNEEIEAMAAIY  GEEWCVIDDCAKIFCIRISDDIDDPKWTLCLQVML?NEYPGTAP PIYQLNAPWLKGQERADLSNSLEEIYIQNIGESILYIWVEKIRD VLIQKSQMTEPGPPDVKKKTEEEDVECEDDLILACQPESSVKALD FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA AGGRLLHLMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSPEESSKALGKNKKVRKDKKRNEH  PRVRWATTMAMSFEWPWQYRFPPFFTLQPNVDTRQKQLAAWCSL VLSFCRLHKQSSMTVMEAQESPLFNNVKLQRKLPVESIQIVLEE LRKKGNLEWLDKSKSSFLIMWRRPEEWGKLIYQWVSRSGQNNSV FTLYELTNGEDTEDEEFHGLDEATLLRALQALQQEHKAEIITVS DGPRRQVLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD SKGLQS  KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGST DDKGPVAGMINALEAYQKTGQEIPVNVRFCLEGMEESGSEGLDE LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIE VECSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTFEEHKLYDDIDFDIEEFAKDVGAOLLHSHKKDTI.MH				ILVEKNYTNSPERSONAL CKNYKURKDYKONEN
GEEWCVIDDCAKIFCIRISDDIDDFKWTLCLQVMLPNEYPGTAP PIYQLNAPWLKGQERADLSNSLEEIYIQNIGESILYLWVEKIRD VLIQKSQMTEPGPDVKKKTEEEDVECEDDLILACQPESSVKALD FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAFVVCPKQV KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA AGGRLHLMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSPEESSKALGKNKKVRKDKKRNEH  PRVRWATTMAMSFEWPWQYRFPPFFTLQPNVDTRQKQLAAWCSL VLSFCRLHKQSSMTVMEAQESPLFNNVKLQRKLPVESIQIVLEE LRKKGNLEWLDKSKSSFLIMWRRPEEWGKLIYQWVSRSGQNNSV FTLYELTNGEDTEDEEFHGLDEATLLRALQALQQEHKAEIITVS DGPRRQVLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD SKGLQS  KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGST DDKGPVAGWINALEAYQKTGQEIPVNVRFCLEGMEESGSEGLDE LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIE VECSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTEEEHKLYDDIDFDIEEFAKDVGAOILLHSHKKDILMH	6597	2	1026	PRI.PVRRVHCRDDI.CCDCDCUMA ECDA CCDCDC
FIYQLNAPWLKGQERADLSNSLEEIYIQNIGESILYLWVEKIRD VLIQKSQMTEPGPDVKKKTEEDVECEDDLILACOPESSVKALD FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMYLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA AGGRLLHLMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSPEESSKALGKNKKVRKDKKRNEH PRVRWATTMAMSFEWPWQYRFPPFFTLQPNVDTRQKQLAAWCSL VLSFCRLHKQSSMTVMEAQESPLFNNVKLQRKLPVESIQIVLEE LRKKGNLEWLDKSKSSFLIMWRRPEEWGKLIYQWVSRSGQNNSV FTLYELTNGEDTEDEEFHGLDEATLLRALQALQQEHKAEIITVS DGPRRQVLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD SKGLQS  KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGST DDKGPVAGWINALEAYQKTGQEIPVNVRFCLEGMEESGSEGLDE LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGRGICYFFIE VECSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTEEEHKLYDDIDFDIEEFAKDVGAOILLHSHKKDILMH				GEEWCVIDDCAKIFCIFISDDIDDDKWTT CTOVAL CONTROL
VLIQKSQMTEPGPDVKKKTEEEDVECEDDLILACQPESSVKALD FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA AGGRLLHLMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSPEESSKALGKNKKVRKDKKRNEH PRVRWATTMAMSFEWPWQYRFPPFFTLQPNVDTRQKQLAAWCSL VLSFCRLHKQSSMTVMEAQESPLFNNVKLQRKLPVESIQIVLEE LRKKGNLEWLDKSKSSFLIMWRRPEEWGKLIYQWVSRSGQNNSV FTLYELTNGEDTEDEEFHGLDEATLLRALQALQQEHKAEIITVS DGPRRQVLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD SKGLQS  KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGST DDKGPVAGWINALEAYQKTGQEIPVNVRFCLEGMEESGSEGLDE LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIE VECSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTEEEHKLYDDIDFDIEEFAKDVGAOILLHSHKKDTIMH	1	ł		PIYQLNAPWLKGOERADLSNSLEEIYIONIGESILVIUUREVID
FOISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA AGGRLHHMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSPEESSKALGKNKKVRKDKKRNEH PRVRWATTMAMSFEWPWQYRFPPFFTLQPNVDTRQKQLAAWCSL VLSFCRLHKQSSMTVMEAQESPLFNNVKLQRKLPVESIQIVLEE LRKKGNLEWLDKSKSSFLIMWRRPEEWGKLIYQWVSRSGQNNSV FTLYELTNGEDTEDEEFHGLDEATLLRALQALQQEHKAEIITVS DGPRRQVLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD SKGLQS  KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGST DDKGPVAGWINALEAYQKTGQEIPVNVRFCLEGMEESGSEGLDE LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIE VECSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTEEEHKLYDDIDFDIEEFAKDVGAOILLHSHKKDILMH	]			VLIQKSQMTEPGPDVKKKTEEEDVECEDDITIACOPESSVKALD
6598 1099 419 PRVRWATTMAMSFEWPWQYRFPPFTLQDQCEDDGETA AGGRILHLMEILINVKNVMVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSPEESSKALGKNKKVRKDKKRNEH PRVRWATTMAMSFEWPWQYRFPPFTLQPNVDTRQKQLAAWCSL VLSFCRLHKQSSMTVMEAQESPLFNNVKLQRKLPVESIQIVLEE LRKKGNLEWLDKSKSSFLIMWRRPEEWGKLIYQWVSRSGQNNSV FTLYELTNGEDTEDEEFHGLDEATLLRALQALQQEHKAEIITVS DGPRRQVLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD SKGLQS  KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGST DDKGPVAGWINALEAYQKTGQEIPVNVRFCLEGMEESGSEGLDE LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIE VECSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTEEEHKLYDDIDFDIEEFAKDVGAOILLHSHKKDTIMH	i j	i		FDISETRTEVEVEELPPIDHGIPITDRRSTFOAHIADING PKON
AGGRLIHLMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN ILVEKNYTNSPEESSKALGKNKKVRKDKKRNEH  PRVRWATTMAMSFEWPWQYRFPPFFTLQPNVDTRQKQLAAWCSL VLSPCRLHKQSSMTVMEAQESPLFNNVKLQRKLPVESIQIVLEE LRKKGNLEWLDKSKSSFLIMWRRPEEWGKLIYQWVSRSGQNNSV FTLYELTNGEDTEDEEFHGLDEATLLRALQALQQEHKAEIITVS DGPRRQVLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD SKGLQS  KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGST DDKGPVAGWINALEAYQKTGQEIPVNVFCLEGMEESGSEGLDE LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIE VECSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTEEEHKLYDDIDFDIEEFAKDVGAOILLHSHKKDTIMH	1		ĺ	KMVLSKLYENKKIASATHNIYAYRIYCEDKOTFLODCEDDGETA
6598 1099 419 PRVRWATTMAMSFEWPWQYRFPPFFTLQPNVDTRQKQLAAWCSL VLSPCRLHKQSSMTVMEAQESPLFNNVKLQRKLPVESIQIVLEE LRKKGNLEWLDKSKSSFLIMWRRPEEWGKLIYQWVSRSGQNNSV FTLYELTINGEDTEDEEFHGLDEATLLRALQALQQEHKAEIITVS DGPRRQVLLAGTCLPLLTSHLSRAFKRRQTQCPPKTGSVTPPD SKGLQS  KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGST DDKGPVAGWINALEAYQKTGQEIPVNVFCLEGMEESGSEGLDE LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIE VECSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTEEEHKLYDDIDFDIEEFAKDVGAOILLHSHKKDTIMH	; I			AGGRLLHLMEILNVKNVMVVVSRWYGGILLGDDDFKHTNMCADN
PRVWARTTMAMSFEWPWQYRFPPFTLQPNVDTRQKQLAAWCSL VLSFCRLHKQSSMTVMEAQESPLFNNVKLQRKLPVESIQIVLEE LRKKGNLEWLDKSKSSFLIMWRRPEEWGKLIYQWVSRSGQNNSV FTLYELTNGEDTEDEEFHGLDEATLLRALQALQQEHKAEIITVS DGPRRQVLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD SKGLQS  KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGST DDKGPVAGWINALEAYQKTGQEIPVNVRFCLEGMEESGSEGLDE LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIE VECSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTEEEHKLYDDIDFDIEEFAKDVGAOILLHSHKKDILMH	6598	1000		TLVEKNYTNSPEESSKALGKNKKVRKDKKRNEH
VLSFCRLHKQSSMTVMEAQESPLFNNVKLQRKLPVESIQIVLEE LRKKGNLEWLDKSKSSFLIMWRRPEEWGKLIYQWVSRSGQNNSV FTLYELTINGEDTEDEEFHGLDEATLLRALQALQQEHKAEIITVS DGPRRQVLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD SKGLQS  KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGST DDKGPVAGWINALEAYQKTGQEIPVNVRFCLEGMEESGSEGLDE LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIE VECSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTEEEHKLYDDIDFDIEEFAKDVGAOILLHSHKKDTIMH			419	PRVRWATTMAMSFEWPWQYRFPPFFTLQPNVDTRQKQLAAWCSL
FTLYELTNGEDTEDEEFHGLDEATLLRALQALQQEHKAEIITVS DGPRRQVLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD SKGLQS  KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGST DDKGPVAGWINALEAYQKTGQEIPVNVRFCLEGMEESGSEGLDE LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIE VECSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTEEEHKLYDDIDFDIEEFAKDVGAOILLHSHKKDTIMH	1		}	VLSFCKLHKQSSMTVMEAQESPLFNNVKLQRKLPVESIQIVLEE
DGPRRQVLLAGTCLPLLTSHLSRAFKRRQTQCPPKTGSVTPPD SKGLQS  KMALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGST DDKGPVAGWINALEAYQKTGQEIPVNVRFCLEGMEEGSEGLDE LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIE VECSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTEEHKLYDDIDFDIEEFAKDVGAOILLHSHKKDTIMH			[	ETLYELTHGEDTERRETION DESCRIPTION DESCRIPTION DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT DE L'ACCOUNT
6599  164  1593  KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR  MMEVAAADVKQLGGSVELVDIGKQKLIPDGSEIPLPPILLGRLGS  DPQKKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGST  DDKGPVAGWINALEAYQKTGQEIPVNVFFCLEGMEESGSEGLDE  LIFARKDTFFKDVDYVCISDNYNLGKKKPCITYGLRGICYFFIE  VECSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN  EAVAAVTEEHKLYDDIDFDIEEFAKDVGAOILLHSHKKDILMH	, ,	1		DGPPPOVIL ACTOL DE LE MONTO CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CO
KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR  MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS DPQKKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGST DDKGPVAGWINALEAYQKTGQEIPVNVRFCLEGMEESGSEGLDE LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIE VECSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTEEHKLYDDIDFDIEEFAKDVGAOILLHSHKKDILMH	[	į	]	SKGLOS
MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS DPQKKTVCIYGHLDVQPAALEGWDSEPFTLVERDGKLHGRGST DDKGPVAGWINALEAYQKTGQEIPVNVFCLEGMEESGSEGLDE LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIE VECSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTFEEHKLYDDIDFDIEEFAKDVGAOILLHSHKKDTIMH	6599	164	1593	
DPQKKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGST DDKGPVAGWINALEAYQKTGQEIPVNVRFCLEGMEESGSEGLDE LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIE VECSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTFEEHKLYDDIDFDIEEFAKDVGAOILLHSHKKDTIMH		į	-	MMEVAAADVKOLGGSVELVDIGKOKI DDGGETDI BETTI
DDKGPVAGWINALEAYQKTGQEIPVNVRFCLEGMEESGSEGLDE LIFARKDTFFKDVDYVCISDNYNLGKKKPCITYGLRGICYFFIE VECSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTEEHKLYDDIDFDIEEFAKDVGAOILLHSHKKDTIMH	[	1	1	DPQKKTVCIYGHLDVOPAALEDGWDGEDETLUEBBOOKITGE
LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIE  VECSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN  EAVAAVTEEHKLYDDIDFDIEEFAKDVGAOILLHSHKKDTIMH		I	1	DDKGPVAGWINALEAYOKTGOEIPVNVRFCLFCMFFCCCCCT
VECSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN EAVAAVTEEHKLYDDIDFDIEEFAKDVGAOILLHSHKKDTI.MH		1	į	LIFARKDTFFKDVDYVCISDNYWLGKKKPCITVGLEGICVERTE
EAVAAVTEEHKLYDDIDFDIEEFAKDVGAOILIHSHKKDTI.MH				VECSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILTEGIN
RWRYPSLSLHGIEGAFSGSGAKTVIPRKVVGKFSIRLVPNMTPF				EAVAAVTEEHKLYDDIDFDIEEFAKDVGAOILLHSHKKDTI.MH
	LL			RWRYPSLSLHGIEGAFSGSGAKTVIPRKVVGKFSIRLVPNMTPE

Deginning   nucleotide   location   corresponding   contion   corresponding   contion   corresponding   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   continue   cont	SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
Incledited   Cocation   Corresponding to first   Samina acid   residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Residue of   Resid	,	· ·	1	(A=Alanine, C=Cysteine, D=Aspartic Acid B
corresponding to first shino acid sequence corresponding to first shino acid sequence control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of	NO:			Glutamic Acid. F=Phenylalanine G-Glucina
to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequenc		location	corresponding	H=Histidine, I=Isoleucine, K=Ivsine
amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
smino acid   residue of			1	P=Proline, Q=Glutamine, R=Arginine.
sequence    Codon, /=possible nucleotide deletion, /=possible nucleotide dinsertion	j			S=Serine, T=Threonine, V=Valine,
Sequence   N=possible nucleotide insertion   N=possible nucleotide insertion   VegOvPSVLEWRABLUSPDERVYMEDRAWVSDESHPHYL   AGREAMRYVFOVEDUTERGS: PVTLEQATGROWNLEPVGS ADDEBLISORER   NEW POSSIBLE NUCLEAR   AGREAMRYVFOVEDUTERGS: PVTLEY   NEW POSSIBLE NUCLEAR   AGREAMRYVFOVEDUTERGS: PVTLEY   NEW POSSIBLE NUCLEAR   AGREAMRYVFOVEDUTERGS: PVTLEY   NEW POSSIBLE NUCLEAR   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY   AGREAMRY	1	1		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
### AGRAMKTY-POPEDITEEGES FYTLIFOEATGENWALLPVG AGRAMKTY-POPEDITEEGES FYTLIFOEATGENWALLPVG ADDGAHSONELLBRYNY1EGTRALAAVLYSVSQLKO  POPELFRVANBESGLEDLELBLD-TYPETRENTEGOLTVLEND AALSALCOLLASAADPOTROPAAVLTRRENTEMBELLALDEE LKSLITALOBETEHCVSLESLALDERTERTRENTEMBELLALDEE LKSLITALOBETEHCVSLESLALDEATFERTRENTEMBELLALDEE LKSLITALOBETEHCVSLESLALDEATFERTRENTEMBELLALDET LGEVGSFGLLFYSLATITTMAPTLSTEDVLENDPOLLDLL OHSTHSPHSPEREMGLLLLSVVTTRPPAROPHHRELLELLENET LGEVGSFGLLFYSLATITTMAPTLSTEDVLENDPOLLDLL OHSTHSPHSPEREMGLLLSVVTTRPAPAPTLSEVLTPCLEVAR NVALGRATE IR ILCCLTFLVKVKK KALLKNRILATLANPELLARDE LGEVGSFGLLFYSLATITTALOCACOKI  ***ENTITWODPRKAMSQPLAHMALHEAVSSTPVPORSNAVSODHLVM** NVALGRATE IR INCOMPRESENTALORGENSTATEOLOGOCKAL RICHTODPRKAMSQPLAHMALHEAVSSTPVPORSNAVSODHLVM** NNOHOGOCAM SPTISSOONPTON PAGIMSPHTTLOCACOKIAL RICHTODPRKAMSQPLAHMALHEAVSSTPVPORSNAVSODHLVM** NNOHOGOCAM SPTISSOONPTON PAGIMSPHTTLOCACOKIAL RICHTODPRKAMSQPLAHMALDEPLACOKIALDES NPHTTPEBPTLSVNUTBEMDTGENAGOTPMNI TNOPOTREPDFLOCIACT NVOLGTLESELD FLYENDVSSALMSS SPPLTITOOCACOKIAL RICHTODPRKAMSQPLANDS SPRUTTIOOCACOKIAL NISTMALLCTBROADCOVSTOMILTYMSSPALLEDITOCACOKIAL NISTMALLCTBROADCOVSTOMILTYMSSPALLEDITOCACOKIAL NISTMALLCTBROADCOVSTOMILTYMSSPALLEDITOCACOKIA NISTMALLCTBROADCOVSTOMILTYMSSPALLEDITOLTAHVLKO GKTLAFTSVULTHAVANCHLA LOCENTHALDO APERIVVENTAS PEDDVILLE PRIVYPENSINGELIEVI KAPITKABNF REVUGENTAS PEDDVILLE PRIVYPENSINGELIEVI KAPITKABNF REVUGENTAS PEDDVILLE PRIVYPENSINGELIEVI KAPITKABNF REVUGENTAS PEDDVILLE PRIVYPENSINGELIEVI KAPITKABNF NISTMALLCTBROADCOVSTOMILTYMSSPALLEDITOLTAHVLKO GKTLAFTSVULTHAVANCHLA LOCENTHALDO APERIVVENTAS PEDDVILLE PRIVYPENSINGELIEVI KAPITKABNF REVUGENTAS PEDDVILLE PRIVYPENSINGELIEVI KAPITKABNF REVUGENTAS PEDDVILLE PRIVYPENSINGELIEVI KAPITKABNF REVUGENTAS PEDDVILLE PRIVYPENSINGELIEVI KAPITKABNF REVUGENTAS PEDDVILLE PRIVYPENSINGELIEVI KAPITKABNF REVUGENTAS PEDDVILLE PRIVYPENSINGELIEVI KAPITKABNF REVUGENTAS PEDDVILLE PRIVYPENSINGELIEVI KAPITKABNF REVUGENTAS PEDDVILLE PRIVYPENSINGELIEVI KAPITKABNF REVUGENTAS PEDDVILLE PRIVYPENSINGELIEVI KAPITKABNF REVUGENTAS PED			sequence	Codon, /=possible nucleotide deletion,
AGRRAMKTYFGVEPDITEGGS:PYTLIFGEATGKNYNILIPUGS ADDGAHSORREKNRYNIEGTKALAALYYSYGLKÖ  PORLFRVAMMESAGLEGULKELLIPDITERIRKATGOLYILEND AALSALCULJASADPQIRGPAVUTRRENTRATGOLYILEND AALSALCULJASADPQIRGPAVUTRRENTRATGOLYILEND AALSALCULJASADPQIRGPAVUTRRENTRATGOLYILEND ALSALCULJASADPQIRGPAVUTRRENTRATGOLYILEND AUSTHSPHISPERMIGLLISESPYVITTYINTRENTLABORES LKSLILITALQRETEHCVSLSIAQLSATIFFKEGLEAPPQLLQLL GUSTHSPHISPERMIGLLISESPYVITTYINTRENTLABORES LKSLILITALQRETEHCVSLSIAQLSATIFFKEGLEAPPQLLQLL GUSTHSPHISPERMIGLLISESPYVITTYINTRENTLAADPORT NILIFIDENAKAGRALGRADHAUPKLIMMO TLIPIDENAKAGRALGRADHAUPKLIMMO TLIPIDENAKAGRALGRADHAUPKLIMMO TLIPIDENAKAGRADHAUPKUTALAANPPHPHC GC GC  FRAARAFPPAVLRRERAAAGAGEMTHAPJASTYPQSKNAVSQPNIJVM NHONQQXAPSTLSQQNIPPYONPPAGRAMSPRALITQQQQQOKK RLORIOMBRITINSSSPPLINGSPYTISREGOSTDSGLGLGCYSV PTTPEDPLSNIPDENTSHTONGSPYTISREGOSTDSGLGLGCYSV PTTPEDPLSNIPDENTSHTONGSPYTISREGOSTDSGLGLGCYSV PTTPEDPLSNIPPDMITTENSAGPTHANGSPYTISREGOSTDSGLGLGCYSV PTTPEDPLSNIPPDMITTENSAGPKAYCHAUPKAGALCKAUPTEPLDLCLEGT NVDLGTLESEDLIPLFINDSSALNESSPFLTVL APPANDERTHAAAACHAUPKAGAGRACHAUPKAGAGAGAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAACHAUPKAGAAC		sequence		\=possible nucleotide insertion)
6600 2 934 PORLINGYNYIEGITMILAYLIVENGIGU  FORLFYVANAESACEGLIKELLIPTERIRATEGIOTVLEAP AALSALCDLLASAADPQIROPAAVLTRREINRATEGIOTVLEAP AALSALCDLLASAADPQIROPAAVLTRREINRATEGIOTVLEAP AALSALCDLLASAADPQIROPAAVLTRREINRATEGIOTVLEAP AALSALCDLLASAADPQIROPAAVLTRREINRATEGIOTVLEAP AALSALCDLLASAADPQIROPAAVLTRREINTRRIGELABACCEAL LEGYGSFGLLIPSIRTITTMAPTISTEDHARIVEKILMAMO TLIF IDEAKACCALERIDELLESEVYTTYTISEVITPCLEVAR RVALGNAIR IRILCCLIFTLVKVKSKALLKIRLLATLAAHPFPLO GC.  6601 529 1420 PRAAARAPPAVLERDRRAATAPOAGEMTLIGGPLAGDRYELNITE KITTWODPRKAMNOPLINHINLIPAVSSTPUPOGRMAUSOPNILUM NOHOGOCMA PSTLEGOMPHSTONPAGINENALTOCOCOXIL RLOR IOMEREI IRRIGEELMIRORAALCROLPMEAETLAPVOADV NPPTMTPDMS ITMNSSPPTINOPAGINENALTOCOCOXIL RLOR IOMEREI IRRIGEELMIRORAACCIPMINENATITOCOCOXIL RLOR IOMEREI IRRIGEELMIRORAACCIPMININDOCTREPDELOCLOCT NVOLIGTLISEBELT PLENDVESALMISSEPTING PHASEATITOCOCOXIL REGULARITY OF THE STANDENCH PROPINGE PHASEATITOCOCOXIL REGULARITY OF THE STANDENCH PROPINGE PHASEATITOCOCOXIL REGULARITY OF THE STANDENCH PROPINGE PHASEATITOCOCOXIL REGULARITY OF THE STANDENCH PROPINGE PHASEATITOCOCOXIL REGULARITY OF THE STANDENCH PROPINGE PHASEATITOCOCOXIL PROPINCE PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHASEATITICA PHA	Į	1		VVGEQVTSYLTKKFAELRSPNEFKVYMGHGGKPWVSDFSHPHYL
ALSALCALULASAADPOI ROPARUTARIAGENES LKSI.LITALQRETEHCVSI.SIAQISATITRIKEGILAMPQLI.QLI.  GHSHISHIS PEREMGILLISUVVUS REPORIBRILLICIAET LGEVGSFGILFYS.RTI.TTMAPYI.STEDUPLARRILVPKI.IMAM TILFI IDERAKACEALEALISUSVVUS REPORIBRILLICIAET LGEVGSFGILFYS.RTI.TTMAPYI.STEDUPLARRILVPKI.IMAM TILFI IDERAKACEALEALISUSVVUS REPORIBRILLISEVLTPCILEVAR NVALGNATH IRILCCLTFLVKVKS.KALLKNRLLATLAAHPFPHC GC GC 6601 529 1420 PEAANRAPPEAVILERDERAATAPEADEMTLIGFI.AGRYFI.NHIE KITTMODPIKAMOPLINHMILHPAVSSTYPUPGSMAVSQPHLIWN NHOHOQCMA.PSTLSQOMHSTONPFAGLMSKINALTTQQQOOKL RLONIOMBER IRMROSELMRIGHALICRQLSMRANDRITTANSOP PILMSENSTRIALTDQOOKL RLONIOMBER IRMROSELMRIGHALICRQLSMRANDRITTANSOP PILMSENSTRIALTDQOOKL NPPTMTPDNRS ITMNSSD PFILMSQPHYRSERSTDSGIGIGGCSY PTTPEDFI.SNVDERDTGERMAGTIPMAINPQOTRYPI.HTE ANDIGTILES BEEL IPLENDVSSALMKSSEPTATSHTQSILREVI LGAVKYARNP ERVIGNRITIVASAAPGKVI CENKVEBEHTMAIGTHHGUTATLIVD NISTMALLCTERGAPOVSVDINITYMSPAKIGEDIVITAHVI.KQ GKTLAFTSVDJALITYMSAAPGKVI CENKVEBEHTMAIGTHHGUTATLIVD NISTMALLCTERGAPOVSVDINITYMSPAKIGEDIVITAHVI.KQ GKTLAFTSVDJALITYMSPAKIGEDIVITAHVI.KQ GKTLAFTSVDJALITYMSPAKIGGONICALIANIAQINDI HQVKILDVMLKGLFKVLEDSRTVLTAADVLYDDOFDEKIKK ASHVVENTAFFODVULR FPI.LIVHYYFHANSININLIIRINGISFC NCHOVENGGPRSTILSIM  6604 3 688 TSTARQRGGERMSFGRGGGGGGGGGGGGRGGRGGGGGGGGGGGGGGGGGG	ĺ	t		ADDGAHSONEYI NEVNYI ECTYMI AAVI VEVGOT KO
AALSALCDLLASAADPOIROPRAVLTRRRINTRYRRIAABORES  LKRSILITALQRESTHCVSSLIAQUSANTYRSEGLAMPOPLIQLL  OHSTHSPHSPEREMGLILLSVVVTSRPEAFQPHERELBLINET  LGEVGSFGLIPYSIRRITTMAPYLSTEUDRAHUPKILIMAMO  TLIF IDEAKACEALEALDELLESEVVTTPYLSEVLTPCLEVAR  RVALGNAIR IRILCCLITFLVKVKS KALLKNRLATLAAHPSPHO  GC  GC  GC  FRAARRPPBAVLERDERATTADEAGEMENLLASTLAAHPSPHO  RTTMODPBRAMNOPLNHMNLHPAVSSTTVPQRSMAVSGPNLVM  NHONOQCMAPSTLSQOMPTONPPRASMAVSGPNLVM  NHONOQCMAPSTLSQOMPTONPPRASMAVSGPNLVM  NHONOQCMAPSTLSQOMPTONPPRASMAVSGPNLVM  NPETMIPDMRSITINSSDPTLNGGPYHSREGSTDSGLGGCYSV  PTTPEDFLSKNIDEBUTGERMGRALCKGLEMERETLARVOQAAV  NPETMIPDMRSITINSSDPTLNGGPYHSREGSTDSGLGGCYSV  PTTPEDFLSKNIDEBUTGERMGRALCKGLEMERETLARVOQAAV  NPETMIPDMRSITINSSDPTLNGGPYHSREGSTDSGLGGCYSV  NISTMALLCTBROAPOVSWANTYMSPENGUTSKEVITAAVTKARNP  ERVLGRITLVSAAPGKVICEMKVEBEHTNAIGTLHGGLITATLVO  NISTMALLCTBROAPOVSWANTYMSPENGUTSKEVITAAVTKARNP  ERVLGRITLVSAAPGKVICEMKVEBEHTNAIGTLHGGLITATLVO  NISTMALLCTBROAPOVSWANTYMSPENGUTSKEPVILAAVTKARNP  ERVLGRITLVSAAPGKVICEMKVEBEHTNAIGTLHGGLITATLVO  NISTMALLCTBROAPOVSWANTYMSPENGUTSKEPVILAAVTKARNP  ERVLGRITLVSAAPGKVICEMKVEBEHTNAIGTLHGGLITATLVO  NISTMALLCTBROAPOVSWANTYMSPENGUTSKIPTGVICE  GKTLAFTSVUDLTNKATGKLIAQCKHTKHLGG  GKTLAFTSVUDLTNKATGKLIAQCKHTKHLGG  GKTLAFTSVUDLTNKATGKLIAQCKGPTKHLGGNIFTKANG  AFSHVVENTAPFGLGGRGGGGGGGGGGNINGGGGGNIFTKGGG  GKOGGGNERGGGRGGGGGGGGGGGGGGNINGGGGGNIFTKGGG  GGGGGGGNGGGGGGGGGGGGGGGGGGGGGGGGG	6600	2	934	PGRI-FVAAMESACI-FOLLDELLI BOTERIDDATEOTOTIV DA D
LKSLILTALQRETEHCVSLIAQUSATIFREGGLEMPQLIADLE  ORSTHSFHS PREMGLILLSVVVYSRPERPGHERILLLIADET LGEVGSFGLLFYSLRTILTMAPYLSTEDUPLARRIUVEKLIMAMO TLIF IDERARCEALEALBLESEVVYITSEVLTFCLEVAR NVALGRATRIRILCCLTFLVKVKSKALLKNRLLATLAAHPPPHC GC  6601 529 1420 PRAARRAPPAVLERDERAATAPGAGEMPTLIGFLAGVERPLHTE RICHTOMPER INTROSEMPTIONEP AGIMSKENALTTOQOOOKL RICHTOMPORT SITUMS OF PHARCE PHISEOSTEP OF PHARCE PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF PHISEOSTEP OF	ļ			AALSALCDLLASAADPOIROFAAVI.TRRRINTRWDDI.AARODEG
OHSTHSPHSPEREMOLILLISVVTGRPEACPHERLIRLINAMO TILIPIDEARACEALEALDELLISSEVPVITPYLSEVLIRMONDATILIPIDEARACEALEALDELLISSEVPVITPYLSEVLIRTCLEVAR RVALGMINIRIRICCLTFLVKVKK KALLKRILLATLAAHPFPHC GC PRAARARPPPAVLRRDERAATAPAGAGEMTLIGGLAGDYFLAHIE KITTWODPEKAMNOPLHHMMLIPAVSGTPVPORSMAVSOPHLVM NHOHOCOMA PSTLSQOHHPYONP FAGLMSVPNALITQOOQOOKL RLOPIOMERERIRMQEEMMGRAALGCOLPMBATLAPVORAV NPPTMTFDMRSITINNSSDPFLNGGVHSREGSTHSGLGLGCYSV PTTPEDFLSNVDEMDTGBRAGGTVBNINPOOTRFPDELDCLGGT NVDLGTLSSEDLIPLENDVESDTGBRAGGTVBNINPOOTRFPDELDCLGGT NVDLGTLSSEDLIPLENDVESDTGBRAGGTVBNINPOOTRFPDELDCLGGT NVDLGTLSSEDLIPLENDVESDTGBRAGGTVBNINPOOTRFPDELDCLGGT NVDLGTLSSEDLIPLENDVESDTGBRAGGTVBNINPOOTRFPDELDCLGGT NVDLGTLSSEDLIPLENDVESDTAMSTORLINFOOTRFPDELDCLGGT NVDLGTLSSEDLIPLENDVESDTAMSTORLINFOOTRFPDELDCLGGT NVDLGTLSSEDLIPLENDVESDTAMSTORLINFOOTRFPDELDCLGGT NVDLGTLSSEDLIPLENDVESDTAMSTORLINFOOTRFPDELDCLGGT NVDLGTLSSEDLIPLENDVESDTAMSTORLINFOOTRFPDELDCLGGT NVDLGTLSSEDLIPLENDVESDTAMSTORLINFOOTRFPDELDCLGGT NVDLGTLSSEDLIPLENDVESDTAMSTORLINFOOTRFPDELDCLGGT SCHAMBERT STANDARGEN STANDARGEN SPECTALLONG NVSLATAFTSVDLTINNATGKLIAGGRTKHLGN HSTMALLCTERGAGPOSVDMMITTMSPAKLGBDLUTAFLKJEND HOOVELLDUNKGLFKVLEDSSTULTAADULPDGPPPODERKO GKATGTLRTSLDPSLEITKMFBVKRRSDLLASINLAQLINDI HOOVELLDUNKGLFKVLEDSSTULTAADULPDGPPPODERKO AFSHVVENTAPFGDVULRFPRIVHYYPDHSNMINLLIRMGISFC NCTIOVNNOCHBISPILLSIM SCHAMBINGSPERKINGCDGGGGGGTGGGSGSHIFFGGG GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1			LKSLILTALORETEHCVSLSLAOLSATIFRKEGLEAWPOLLOLI.
LGEWGSFGLLFYSLRTLTTMAPYLSTEDVPLARMLUPKLINAMO TLIFIDERACGADEADELLSSEVSTYPTSEVLTFCLSVAR NVALGNAIRIRILCCLTFLVKVKSKALLKNRLLATLAAHPFPHC GC GC GC GC FRAARRAPPPAVLREDERATADGAGEMTILIGELAGRYFLNHIE KITTWODPRKAMNQPLNHMNLHPAVSTTPVQRSMAVSQPMLWN NHQHQQCMAPSTLSQQNHPTQNFFAGLMSWPNALTTQQOQOOKL RLGRIQMBEREIRRGSELMRQBEALGKQDWBEATLAPVQAAW NPFHMTPOMPRSITHNSSDPFLKNGGFYBISRGSSTDSGLGLGGYSV PTTPEDFLSNVDEMDTGEMAGGTPMNINPQOTFPDFLDCLPGT NVDLIGTLESEDLIPLENDVESALNSSEPLTWL LLDPPALPKFVLAGSFKAGKPSTMTSWIGSLRSVIAWTKARNP ERVLGKITLVSAAPGKVICGMKVEEBHTNAIGTLHGGLTATLVD NISTMALLCTERGAPGVSUMMITTMSPAKIGSDVIATATLVD NISTMALLCTERGAPGVSUMMITTMSPAKIGSDVIATATLVD NISTMALLCTERGAPGVSUMMITTMSPAKIGSDVIATATLVD NISTMALLCTERGAPGVSUMMITTMSPAKIGSDVIATATLVD NISTMALLCTERGAPGVSUMMITTMSPAKIGSDVIATATLVD NISTMALLCTREGAPGVSUMMITTMSPAKIGSDVIATATLVD NISTMALLCTREGAPGVSUMMITTMSPAKIGSDVIATATLVD NISTMALLCTREGAPGVSUMMITTMSPAKIGSDVIATATLVD NISTMALLCTREGAPGVSUMMITTMSPAKIGSDVIATATLVD NISTMALLCTREGAPGVSUMMITTMSPAKIGSDVIATATLVD NISTMALLCTREGAPGVSUMMITTMSPAKIGSDVIATATLVD NISTMALLCTREGAPGVSUMMITTMSPAKIGSDVIATATLVD NISTMALLCTREGAPGVSUMMITTMSPAKIGSDVIATATLVD NISTMALLCTREGAPGVSUMMITTMSPAKIGSDVIATATUK NISTMALLCTREGAPGVSUMMITTMSPAKIGSDVIATATUK NISTMALLCTREGAPGVSUMMITTMSPAKIGSDVIATATUK NISTMALLCTREGAPGVSUMMITTMSPAKIGSDVIATATUK NISTMALLCTREGAPGVSUMMITTMSPAKIGSDVIATATUK NISTMALLCTREGAPGVSUMMITTMSPAKIGSDVIATATUK NISTMALLCTREGAPGVSUMMITTMSPAKIGSTSNIATATUK NISTMALLCTREGAPGVSUMMITTMSPAKIGSDLAKIKON NISTMALLCTREGAPGVSUMMITTMSPAKIGSDLAKIKON NISTMALLCTREGAPGVSUMMITTMSPAKIGSDLAKIKON NISTMALLCTREGAPGVSUMMITTMSPAKIGSDLAKIKON NISTMALLCTREGAPGVSUMMITTMSPAKIGSDLAKIKON NISTMALMSPAKIKON NISTMALLCTREGAPGVSUMMITTMSPAKIGSDVAKIKON NISTMALLCTREGAPGVSUMMITTMSPAKIGSDVAKIKON NISTMALLCTREGAPGVSUMMITTMSPAKIGSDVAKIKON NISTMALLCTREGAPGVSUMMITTMSPAKICH NISTMALCTREGAPGVSUMMITTMSPAKICH NISTMALCTREGAPGVSUMMITTMSPAKICH NISTMALCTREGAPGVSUMMITTMSPAKICH NISTMALCTREGAPGVSUMMITTMSPAKICH NISTMALCTREGAPGVSUMMITTMSPAKICH NISTMALCTREGAPGVSUMMITTMSPAKICH NISTMALCTREGAPGVSUMMITTMSPAKICH NISTMALTCHAMITTMSPAKICH NISTMALTCHAMITTMSPAKICH NISTMAL	İ	ļ		QHSTHSPHSPEREMGLLLLSVVVTSRPEAFOPHHRELLRLLNET
TLIPIDEARACEALEALDELLESEVPVITPYLSEVLTECLEVAR RVALGANIRIRICCLTFL/KVKK KALLKRILATLAAHPFPHC GC GC PRAARAPPPAVLREDERAATARGAGEWTLHGFLAGRYFLNHIE KITTWQDPRKAMNQPLNHMNLHPAVSSTEVPQRSMAVSQPHLWM NHQHQQARAPSTLSQQNHPTQNFPAGMSWPNALTTQQQQOKL RLGRIGMBRERIRRNGSELMRGBALGCLOPMBAETLAPYQDAAV NPPTMTPDNESITNNSEDPFLAGGPYHSRGSTDSGLGLGCYSV PTTPEDFLSINVDEMDTGEMAGGPYMINTPQOTFPPDFLOLDGT NVDLGTLESEDLIPLFNDUESJALNSSEPFLTWL LLDPPALPFVLAGSPKAGKPSTMTSDSLREVIKAWTKARNF ERVLGKITLVSAAPGKVICEMKVBEEHTNALTGLINGLTAALVD NISTMALLCTERGAPGVSVMMITTYSVALKGBUVITAAVLKQ GKTLAFTSVDLTNKATGKLIAQGRITKHLGN PVGFSSLAARTGLGHLPFLHALAGSRGLEMDLLQFLAFIFVLLL SCMGATGTLRTSLDPSLEITYKMPEVKRRRQLLALANLAQLNDI HQQYKILDUMKGLFKVLEDSKTVLTAADVLPPDFPCDFELKDK AFSHVVENTAFFGGVVLRPFRVTHYPYPHNSNMRLLIRMGISFC NCTAVVENGPHSPILSLM FYSTORGERMSFRGGGRGGFRRGGGGGFRGGGSSSNHFRGGG GGGGGNTRGGGRGGFRGGGGGFRGGGGGFRGGGGGGFRGGGGGGGG				LGEVGSPGLLFYSLRTLTTMAPYLSTEDVPLARMLVPKLIMAMO
6601 529 1420 FRAARRAPPPAVLRRDREAATAPGAGEMTLHGPLAQRYFLNHIE KITTWODPRKANNQELNHMINLHPAVSSTPVPQRSWANSOPNLVM NHGHQCQMAPSTLSQONHPTONIPGMSMYPNALTTCQQQQGKL RLQRIQMERERIRMRQEELMRQEAALCRQLPMEASTLAPVQAAV NPPTMTPDMRSITINNSSDPTLNGGPYHSREOSTDSGLGLGCYSV PTTPEDPLSNVDEMDTGENAGQTPHSNDSLAFTLAPVQAAV NPPTMTPDMRSITINNSSDPTLNGGPYHSREOSTDSGLGLGCYSV PTTPEDPLSNVDEMDTGENAGQTPHSNDSLAFVLKAWTKARNP ERVLGKITLVSAAPGKVICEMKVEEBHTNAIGTLHGGLTATLVD NISTMALLCTRERGAGVSVDMITYSPAKLGEBLYVLTAHVLKG GKKTAFTSVDLTNKATGKLIAQGRHTKHLGN 6603 79 660 PVGPSSLAARTGGLHPPLHRLGSRCHAVDLLQELAFI,FVLLI SGMATGTLTTSLDDSLEIYKMPEVKRREQLLALKNLAQLNDI SGMATGTLTTSLDDSLEIYKMPEVKRREQLLALKNLAQLNDI HQQYKILDVMLKGLFKVUEDSRTVLTAADVLDGFFPQDEKLKD AFSHVVENTAFFGDVLRFFRIVHYFDENSNWELLTMGISFC NCGVSNOGPHSFILSIM 6604 3 688 TSTAQRGGERNSFRGGGRGGFNRGGSGNFFRGGG GGGGGNFRGGGRGGFGGRGGGFFGGGGGGFFGGRG GGGGGNFRGGGRGGFGGRGGGGFFGGGGGGFFGGRG GGFGGGGG GGGGNFRGGGRGGGGGGGGGG				TLIPIDEAKACEALEALDELLESEVPVITPYLSEVLTFCLEVAR
S29				
KITTWODPRRANDPLNIMMLEPASSTEVPORSMASOPHLWN NHORQCMAPSTLSQONIPTONP AGLMSPPNALTTQQQQQKL RLORI QOMERER IRMGEELIMEQRACCHLPMEASTLAPVQAAV NPPTMTPDMRS TINNSSDPTLNGGPYHSROSTDSGLGLGCYSV PTTPEDPLSNVDEMTGENAGCTIPEN TOPQOTREPDELDCLPGT NVDLGTLESEDLI PLENDVESALMKSEPPLITUL  6602 127 617 LLDFPALPKFVLAQSFKAGKPSTHTSHTQSLREVI KAPTKANF ERVLGKITLVSAAPGKVI CEMKVEEBHTNAI GETLHGGLTATLVDI NISTMALLCTERGABGUSVDMNITTYMSPAKLGEDI VITIAHVIKQ GKTLAFTSVDLINKATGKLIAQGMTHAIGTTHAIGT LTHGGLTATLVDI NISTMALLCTERGABGUSVDMNITTYMSPAKLGEDI VITIAHVIKQ GKTLAFTSVDLINKATGKLIAQGMTHAIGTUTTAHVIKQ GKTLAFTSVDLINKATGKLIAQGMTHAIGTUTTAHVIKQ GKTLAFTSVDLINKATGKLIAQGMTHAIGTUTTAHVIKQ GKTLAFTSVDLINKATGKIAQGMTHAIGTUTTAHVIKQ GKTLAFTSVDLINKATGKIAQGMTHAIGTUTTAHVIKQ GKTLAFTSVDLINKATGKIAGGMTHAIGTUTTAHVIKQ GKTLAFTSVDLINKATGKIAGGMTHAIGTUTTAHVIKQ GKTLAFTSVDLINKATGKATGKIAGGMTHAIGTUTTAHVIKQ GKTAGTLSTSDLESITKAMPKREDILLAIXALQLINDI HQQYKILDVMLKGLEKVLEDSRTVLTAADVLDGFPFPQDEKKD AFSHVVENTAFFQDVVLRFPRIVLTAADVLDGFPPPQGEKKD AFSHVVENTAFFQDVVLRFPRIVLTYADVLDGFPPPQGEKKD AFSHVVENTAFFQDVVLRFPRIVLTYADVLDGFPPPQGEKKD GGGGGGGRTGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	6503	E 20	1400	1 = - ,
NHORIQCMARSTLSQONHTQNPFAGLNSMYNNALTTOQQOQOKL RLQRIQMERSIRMQSELMRQCBALCRQLFMEASTLAPVQAAV NPPTMTPDMRSITNNSSDPFLNGGPYNNSTPGSTDSGLGLGCYSV PTTPEDPLSNYDBMDYGBNAGGPYNNSTPGSTDSGLGLGCYSV PTTPEDPLSNYDBMDYGBNAGGPYNNSTPGSTBGGLGLGCYSV NVDLGTLESEDLIPLFNDVESALNKSEPFLTWL  6602  127 617 LLDFPALPKFVLAQSFKAGKPSTMYSMTGSLREVIKAMTGANF FRVLGKITLVSAAPGKVLGEMKVEEHTNALGTLHGGLTATLVD NISTMALLCTERGAPGVSVDMNITTMSPARLGEDIVITAHVLKQ GKTLAFTSVDLTNKATGKLLAGGRTKHLGN 6603 79 660 PVGPSSLAARTGLGHLPFLHRLASSEGLDMDLLDFLAFIFVLLI CGMALATTSVDLTNKATGKLLAGGRTKHLGN AFSHVVENTAFFSDVVLRFPRIVHYYPDHSNNMLLIRMGISFC NCYGVPNQGHBSJISLSM GGGGGGNFRIGGGGGFNRGGGGGGNRGGSSNHFRGGG GGGGGNFRIGGGGGFGRGGGGFNRGGGGGGNRGGSSNHFRGGG GGGGGNFRIGGGGGFRRGGRGFNRGGGGGFNRGDGGPPERVVLLGEFL HPCEDDIVCKCTTDENKVPYFNAPVYLENKEQIGKVDEJFGUR GPPRGGRGGRGGGRGGGGGGGGGGGRGGGGGGGGGG	9801	529	1420	PRAAARAPPPAVLRRDRRAATAPGAGEMTLHGPLAQRYFLNHIE
RLORI OMERRI IMROGEDIMOGLAMICA PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO PUMP TO				NUOUCOCMA RETU SCONUMENTA SE MENERAL TERRESONALIZADO DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DEL COMPANIA DE LA COMPANIA DE LA COMPANIA DEL COMPANIA DE LA COMPANIA DE LA COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DEL C
MPPTMTPDMRSITNNSSDPFLNGGPHRSEGSTBSGLGLGCYSV PTTPEDPLSNVUEMTGRBAGCTPWNINPQOTRPFDFIDCLPGT NVDLGTLESSDLIPLENDVESALNKSEPFLTWL  6602  127 617 LLDFPALPKPVLAGSFKAGKPSTMTSMTSLREVIKAMTGANFE ERVLGKITLVSAAPGKVICEMKVEEHTNAIGTLHGGLTATLVD NISTMALLCTERGAPGVSVDMNITTMSPARLGEDIVITAHVLKQ GKTLAFTSVDLTNKATGKLIAGGNTKHLGN  6603 79 660 PVGPSSLAARTGLGHLPFLHRLASSRGLDMDLLQFLAFLFVLLL SGMGATGTLRTSLDBSLBIYKMFEVKRERGLLALKALAGLNDI HQGYKILDVHLKGLFKVLEDSSTVLTAADVLPDGPFQDEKLKN AFSHVVENTAFFGDVVLRFPRIVHYYPDHNSNMNLLIRWGISFC NCTGVPNQGHBSJISLM GGGGGRNFRGGGRGGFRGGGGGGFNRGGSSNHFRGGG GGGGGRNFRGGGRGFRGGRGGGFNRGGGGGFNRGGSSNHFRGGG GGGGGNFRGGGRGFRGGRGGGGGGGGGGGGGGFNRGGSSNHFRGGG GGFRGGH  6604 3 688 TSTAQRGGGRGFGGGGGGGGGGGGGGGGGGGGGGGNUEMDLIGFEL HPCEDDIVCKCTTDENKVYFINAPVYLENKEQIGKVDLEIFGQLR DFYFSVKLSENNKASSFKKLQKFYIDPYKLLPLQFFLPRPPGEK GPPRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG				RLORIOMERERIEMPOEELMPORA ALCROLEMEA EST A DIVOA AL
PTTPEDFLSNYDEMDTGENAGGIPMNINPOGTREPDELDCHGT	1			NPPTMTPDMRSITNNSSDPFLNGGPYHSREOSTDSGIGLGCVCV
6602 127 617 LLDPPALDKYPLAGSPKAGESTMTSMTGSLREVIKAMTKARNF ERVLGKITLVSAAPGKVICEMKVEEHTNAIGTLHGGLTATLVD NISTMALLCTERGAPGVSVDMNITYMSPAKLGEDIVITAHVLKQ GKTLAFTSVDLTNKATGKLIAQCRHTKHLGN  6603 79 660 PVGPSSLAARTGLGHLDFLHRLASSRGLDMDLLQFLAFLFVLLL SGMGATGTLHRSTLDPSLEIVKKMFEKKREDLLALGVLAQLNDI HQQYKILDVMLKGLFKVLEDSRTVLTAADVLPDGPPPQDEKLKD AFSHVVENTAFFGDVVLRFPRIVHYYFDHNSMNNLLIRMGISFC NQTGVPNQGPHSJILSIM 6604 3 688 TSTAQRGGGRRGFRGGGRGGFNRGGSSNHFRGGG GGGGMFRGGGRGFGGRGGGGGFRNGGDQDGPPERVVLLGEFL HPCEDDIVCKCTTDENKVPYFNAPVYLENKEQIGKVDEJFGQLR DFYFSVKLSENNKASSFKKLQKFYIDPYKLLPLQRFLPRPPGEK GPPRGGRGGRGGGGGGGGGGGGGGGGGGGGGGGGGGGG				PTTPEDFLSNVDEMDTGENAGOTPMNINPOOTRFPDFLDCLPGT
6602  127 617 LLDPPADPKPVLAGS PKAGKPSTMTSMTQSLREVI KAMTKARNF ERVLGKITLVSAAPGKVI CEMKVEEEHTNAIGTLHIGGLTATLUD NI STMALLCTERGAPGVSVDMNITYMSPAKIGEDIVITAHVLKQ GKTLAFTSVDLTNKATGKLIAQQRHTKHLGN 6603 79 660 PVGPSSLAARTGJGHDFILBIKLASSKGLDMDLLQFLAFI,FVLLL SGMGATGTLRTSLDPSLEI YKKMFEVKRREQLLALKNLAQLNDI HQQYKILDVMLKGLFKVLEDSRTVLAADVLPEDGFPQDEKLKD AFSHVVENTAFFGDVVLRFPRIVHYYPDHNSNMNLIRMGISFC NCTGVPNQGPHSPILSIM 6604 3 688 TSTAQRGGERGMFFRGGGGGGFNRGGGGGGFNRGGSSNHFRGGG GGGGGNFRGGGRGGFRGGGGGGFNRGGSSNHFRGGG GGGGGNFRGGGRGGFRGGGGGGFRGGGGGGFRGGGGGGGFRGGGGGG				NVDLGTLESEDLIPLFNDVESALNKSEPFLTWL
ERVLGKTLUSAABGKVICEMKUEEHTMAIGTLHGGLTATLUD NISTMALLCETERGABGWSVDMNITYMSPAKIGEDIVITAHVUKQ GKTLAFTSVDITNKATGKLIAQGRHTKHLGN  6603  79 660 PVGPSSLARTGLGHLPFLHRLASSRGLDMDLLQFLAFLFVLLL SGMATGLISTSLDPSLEJ YKKMEFUKRREDLIALANLAQLNDI HQYKILDVMLKGLFKVLEDSRTVLTAADVLPDGFPPQDEKLKD AFSHVVENTJAFGDVVLRFPRIVHYYFDHNSNMNLLIRWGISFC NCTGVFNQGPHSPILSIM  6604 3 688 TSTAQRGGERMSFRGGGRGGFRRGGGGGFNRGGSSNHFRGGG GGGGGMFRGGGGGGGFRGGGGGGFNRGGGSGNHFRGGG GGGGGGFRGGGGGGGGGGGGGGGGGGGGGGGGG	6602	127	617	LLDFPALPKFVLAQSPKAGKPSTMTSMTQSLREVIKAMTKARNF
GKTLAFTSVDLINKATGKLIAGGRHTKHLGN  6603  79  660  PVGPSSLAARTGLGHLPFLHRLASSRGLDMDLLQFLAFI,FVLLL SGMGATGTLRTSLDPSLEIYKMFBVGRREQLLAIKNLAQLNDI HQQYKILDVMLKGLFKVLEDSRTVLTAADVLPDGPFPGDEKLKD AFSHVVENTAFFGDUVLRFPRIVHYYPDHNSNWNLLIRWGISFC NCTGVFNQGPHSPILSLM  6604  3  688  TSTAQROGGERMSFRGGGRGGFNKGQDGGPFRKGGSSNHFRGGG GGGGGFRGGGRGGFNKGQDQGPPERVVLLGEFL HPCEDDIVCKCTTDENKVPYFNAPVYLENKEQIGKVDEIFFGGLR DFYFSVKLSENMKASSFKKLQKFYIDPYKLLPLQRFLPRPDEK GPPRGGRGGRGGRGGGGGGGGGGGGGGGGGGGGGGGGG	İ			ERVLGKITLVSAAPGKVICEMKVEEEHTNAIGTLHGGLTATLVD
6603 79 660 PVGPSLAARTGLGHLPFLHRLASSRGLDMDLQFLAFLFVLLL SGMGATGTLRTSLDPSLEIYKKMFEVKRREQLLALKNLAQLNDI HQQYKILDVMLKGLFKVLEDSRTVLTAADVLPDGEPFQDEKLKD AFSHVVENTAFFGDVVLRFPRIVHYYPDHNSNWNLLIRWGISFC NCTGVFNQGPHSPILSLM  6604 3 688 TSTAQRGGGERMSFRGGGRGGFNRGGGGGFNRGGSSNHFRGGG GGGGGGFRGGGRGFRGGGRGFNRGQDQGPPERVVLLGEFL HPCEDDIVCKCTTDENKVPYFNAPVYLENKEQIGKVDELFGQLR DFYFSVKLSEMMKASSFKKLQKFYIDPYKLLPLQRFLPFPDGEK GPPRGGRGGRGGRGGGRGGGRGGGRGGGGGGGGGGGGG	1			NISTMALLCTERGAPGVSVDMNITYMSPAKLGEDIVITAHVLKQ
SGMGATGTRRTSLDPSLETYKKMFEVGRREQLLALKNLAQLNDI HQQYKILDVMLKGLFKVLEDSRTVLTAADVLPDGFFPQDEKLKD AFSHVVENTAFFGDUVLRFPRIVHYYFDHNSNWNLLIRWGISFC NCTGVFNQGPHSPILSLM  6604  3 688 TSTAQROGGERMSFRGGGRGGFNKGQDQGPPERVVLLGEFL HPCEDDIVCKCTTDENKVPYFNAPVYLENKEQIGKVDEIFFQGLR GGGGGFRFGGGRGGFGGGGGGGGGFRGGRGGFNKGQDGPPERVVLLGEFL HPCEDDIVCKCTTDENKVPYFNAPVYLENKEQIGKVDEIFFQGLR GFPRGGGRGGFGGGGGGGGGGGGGGGGGGGGGGGGGGG	6603	70	660	GKTLAFTSVDLTNKATGKLIAQGRHTKHLGN
HQQYKILDVMLKGLFKVLEDSRTVLTAADVLPDGPFPGDEKLKD AFSHVVENTAFFGDVVLFFPRIVHYYFDHNSNWNLLIRWGISFC NQTGVFNQGPHSPILSLM  6604 3 688 TSTAQRQGERMSFRGGGGGFNRGGSSNHFRGGG GGGGGGNFRGGGRGFNKGQDQGPPERVVLLGEFL HPCEDDIVCKCTTDENKVPYFNAPVYLENKEQIGKVDEIFGGLR DFYFSVKLSENMKASSFKKLQKFYIDPYKLLPLQRFLPRPPGEK GPPRGGRGGRGGRGGGRGGGGGGGGGGGGGGGGGGGGG	0003	/ 9	660	PVGPSSLAARTGLGHLPFLHRLASSRGLDMDLLQFLAFI,FVLLL
AFSHVVENTAFFGDVULRFPRIVHYYFDHNSNWNLLIRWGISFC NCTGVFNQGPHSPILSLM  6604  3 688 TSTAQRQGGERMSFRGGGRGGFNRGGSGNHFRGGG GGGGGNFRGGGGGFNRGGGGGFNRGGSSNHFRGGG GGGGGNFRGGGRGFRGGGRGGFNRGQDQGPPERVVLLGEFL HPCEDDIVCKCTTDENKVPYFNAPVYLENKEQIGKVDEIFGGLR DFYFSVKLSENNKASSFKKLQKFYIPPYKLLPLQRFPPPGEK GPPRGGRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG				HOOVELLDAMING ENTIT EDGETTI EN ARIE DOGETORES EN
NCTGVFNGGPHSPILSIM	1			AFSHVVENTAFFGDWURFERTUHVVEDUNGNUNG TEMOTOFF
6604  3 688 TSTAQRQGGERMSFRGGGRGGFNRGGGSGNHFRGGG GGGGGNFRGGGGGGGFNRGQDQGPPERVULLGEFL HPCEDDIVCKCTTDENKVPYFNAPVYLENKEQIGKVDEIFGQLR DFYFSVKLSENMKASSFKKLQKFYIDPYKLLPLQFFLPRPGEK GPPRGGRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG				
GGGGGFRRGGGRGGGRGGFRKGQDQGPPERVVLLGEFL HPCEDDIVCKCTTDENKVPYFNAPVYLENKEQIGKVDEIFGQLR DFYFSVKLSEMKASSFKKLQKPYIDPYKLLPLQRFLPRPPGEK GPPRGGRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	6604	3	688	
HPCEDDIVCKCTTDENKVPYTENAPVYLENKEQIGKVDEIFGQLR DFYFSVKLSENMKASSFKKLQKFYIDPYKLLPLQRFLPRPPGEK GPPRGGRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG				GGGGGGNFRGGGRGGFGGGGGGGFNKGQDQGPPERVVLLGEFL
GPPRGGRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG				HPCEDDIVCKCTTDENKVPYFNAPVYLENKEQIGKVDEIFGOLR
GGFRGGH  VHKRYPGL VKVVRNQKREGLIRARIEGWKVATGQVTGFFDAHVEFTAGWAEP VLSRIQENRKRVILPSIDNIKQDNFEVQRYENSAHGYSWELWCM YISPPKDWWDAGDPSLPIRTPAMIGGSFVVNRKFFGEIGLLDPG MDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIERKKKPYNGNI GFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENPGIDIGDVSER RALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGELRNNKAKDVC LDQGPLENHTAILYPCHGWGPQLARYTKEGFHLGALGTTTLLP DTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQNGAIMNKGTG RCLEVENRGLAGIDLILRSCTGQRWTIKNSIK GCLEVENRGLAGIDLILRSCTGQRWTIKNSIK GISFQGRGGAGPGVPTRTQVFAAMGAVMGTFSSLQTKQRRFSKD				DFYFSVKLSENMKASSFKKLQKFYIDPYKLLPLQRFLPRPPGEK
6605 7 848 SGSRRGAMRAAGVGLVDCHCHLSAPDFDRDLDDVLEKAKKANVV ALVAVAEHSGEFEKIMQLSERYNGFVLPCLGVHPVQGLPPEDQR SVTLKDLDVALPIIENYKDRLLAIGEVGLDFSPRFAGTGBQKEE QRQVLIRQIQLAKRLNLPVNVHSRSAGRPTINLLQEQGAEKVLL HAFDGRPSVAMEGVRAGYFFSIPPSIIRSGQQKLVKQLPLTSIC LETDSPALGPEKQVRNEPWNISISABYIAQVKGISVEEVIEVTT QNALKLFPKLRHLLQK  FVEIRPRAEVANLSAHSASPIQDAVLKRLSLLEDIVYRQLNGLS KSLGLIEGYGGRGKGGLPATLSPAEEKAKGPHEKYGYNSYLSE KISLDRSIPDVRPTKCKELKYSKDLPQISIIFIFVNEALSVILR SVHSAVNHTPTHLLKEIILVDDNSDEEELKVPLBEYVHKRYPGL VKVVRNQKREGLIRARIEGWKVATGQVTGFFDAHVEFTAGWAEP VLSRIQENRKRVILPSIDNIKQDNFEVQRYENSAHGYSWELWCM YISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKFFGEIGLLDPG MDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIERKKRYNSNI GFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENPGIDIGDVSER RALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGELRNNKAKDVC LDQGPLENHTAILYPCHGWGPQLARYTKEGFLHLGALGTTTLLP DTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQNGAIMNKGTG RCLEVENRGLAGIDLILRSCTGQRWTIKNSIK  6607 137 986 VPACAGLKKEARSLLASPPRLINTKLQASCRALFSPPIQSRQTT GISFQGRGGAGPGVPTRTQVFAAMGAVMGTFSSLQTKQRRPSKD				
ALVAVAEHSGEFEKTMQLSERYNGFVLPCLGUHPVQGLP PEDQR SVTLKDLDVALPIIENYKDRLLAIGEVGLDFSPRFAGTGEQKEE ORQVLIRQIQLAKRLNLPVNVHSRSAGRPTINLLQEQGAEKVLL HAFDGRPSVAMEGVRAGYFFSIPPSIIRSGQOKLVKQLPLTSIC LETDS PALGPEKQVRNEPWNISISABYIAQVKGISVEEVIBVTT QNALKLFPKLRHLLQK  6606 2 1682 FVEIRPRAEVANLSAHSASPIQDAVLKRLSLLEDIVYRQLNGLS KSLGLIEGYGGRGKGGLPATLSPAEEEKAKGPHEKYGYNSYLSE KISLDRSIPDYRPTKCKELKYSKDLPQISIIFIFVNEALSVILR SVHSAVNHTPTHLLKEIILVDDNSDEEELKVPLEEYVHKRYPGL VKVVRNQKREGLIRARIEGWKVATGQVTGFFDAHVEFTAGWAEP VLSRIQENRKRVILPSIDNIKQDNFEVQRYENSAHGYSWELWCM YISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKFFGEIGLLDPG MDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIERKKPYNSNI GFYTKRNALRVAEDWMDDYKSHVYIAWNLPLENPGIDIGDVSER RALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGELRNNKAKDVC LDQGPLENHTAILYPCHGWGPQLARYTKEGFLHLGALGTTTLLP DTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQNGAIMNKGTG RCLEVENRGLAGIDLILRSCTGQRWTIKNSIK 6607 137 986 VPACAGLKKEARSLLASPPRLLNTKLQASCRALFSPPIQSRQTT GISFQGRGGAGPGVPTRTQVFAAMGAVMGTFSSLQTKQRRPSKD	6605	7	040	
SVTLKDLDVALPIIENYKDRLLAIGEVGLDFSPRFAGTGBQKEE QRQVLIRQIQLAKRLNLPVNVHSRSAGRPTINLLQEQGAEKVLL HAFDGRPSVAMEGVRAGYFFSIPSIIRSGQQKLVKQLPLTSIC LETDS PALGPEKQVRNEPWNISISABYIAQVKGISVEEVIBVTT QNALKLFPKLRHLLQK  FVEIRPRAEVANLSAHSASPIQDAVLKRLSLLEDIVYRQLNGLS KSLGLIEGYGGRGKGGLPATLSPAEEEKAKGPHEKYGYNSYLSE KISLDRSIPDYRPTKCKELKYSKDLPQISIIFIFVNEALSVILR SVHSAVNHTPTHLLKEIILVDDNSDEEELKVPLEEYYHKRYPGL VKVVRNQKREGLIRARIEGWKVATGQVTGFFDAHVEFTAGWAEP VLSRIQENRKRVILPSIDNIKQDNFEVQRYENSAHGYSWELWCM YISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKFFGEIGLLDPG MDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIERKKKPYNSNI GFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENPGIDIGDVSER RALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGELRNNKAKDVC LDQGPLENHTAILYPCHGWGPQLARYTKEGFLHLGALGTTTLLP DTRCLVVDNSKSRLPQLLDCDKVKSSLYKRWNFIQNGAIMNKGTG RCLEVENRGLAGIDLILRSCTGQRWTIKNSIK  6607 137 986 VPACAGLKKEARSLLASPPRLLNTKLQASCRALFSPPIQSRQTT GISFQGRGGAGPGVPTRTQVFAAMGAVMGTFSSLQTKQRRPSKD	5555	•	040	ALVAVAEHSGEEEKIMOI SEERVIGERA DOI GHIDUGAY DEBEN
QRQVLIRQIQLAKRLNLPVNVHSRSAGRPTINLLQEQGAEKVLL HAFDGRPSVAMEGVRAGYFFSIPPSIIRSGQOKLVKQLPLTSIC LETDSPALGPEKQVRNEPWNISISABYIAQVKGISVEEVIBVTT QNALKLFPKLRHLLQK  6606 2 1682 FVEIRPRÆVANLSAHSASPIQDAVLKRLSLLEDIVYRQLNGLS KSLGLIEGYGGRGKGGLPATLSPAEEEKAKGPHEKYGYNSYLSE KISLDRSIPDYRPTKCKELKYSKDLPQISIIFIFVNEALSVILR SVHSAVNHTPTHLLKEIILVDDNSDEEELKVPLEEYVHKRYPGL VKVVRNQKREGLIRARIEGWKVATGOVTGFFDAHVEFTAGWAEP VLSRIQENRKRVILPSIDNIKQDNFEVQRYENSAHGYSWELWCM YISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKFFGEIGLLDPG MDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIERKKKPYNSNI GFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENPGIDIGDVSER RALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGELRNNKAKDVC LDQGPLENHTAILYPCHGWGPQLARYTKEGFLHLGALGTTTLLP DTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQNGAIMNKGTG RCLEVENRGLAGIDLILRSCTGQRWTIKNSIK  6607 137 986 VPACAGLKKEARSLLASPPRILNTKLQASCRALFSPPIQSRQTT GISFQGRGGAGPGVPTRTQVPAAMGAVMGTFSSLQTKQRRPSKD				SVTLKDLDVALPI I FNVKDPLLA I GEVGL DEGDE FACEGEOVER
HAFDGRPSVAMEGVRAGYFFSIPPSIIRSGQQKLVKQLPLTSIC LETDS PALGPEKQVRNEPWNISISABYIAQVKGISVEEVIEVTT QNALKLFPKLRHLLQK  FVEIRPRAEVANLSAHSASPIQDAVLKRLSLLEDIVYRQLNGLS KSLGLIEGYGGRGKGGLPATLSPAEEEKAKGPHEKYGYNSYLSE KISLDRSIPDYRPTKCKELKYSKDLPQISIIFIFVNEALSVILR SVHSAVNHTPTHLLKEIILVDDNSDEEELKVPLEEYVHKRYPGL VKVVRNQKREGLIRARIEGWKVATGQVTGFFDAHVEFTAGWAEP VLSRIQENRKRVILPSIDNIKQDNFEVQRYENSAHGYSWELWCM YISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKFFGEIGLLDPG MDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIERKKKPYNSNI GFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENPGIDIGDVSER RALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGELRNNKAKDVC LDQGPLENHTAILYPCHGWGPQLARYTKEGFLHLGALGTTTLLP DTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQNGAIMNKGTG RCLEVENRGLAGIDLIRSCTGQRWTIKNSIK  6607 137 986 VPACAGLKKEARSLLASPPRLLNTKLQASCRALFSPPIQSRQTT GISFQGRGGAGPGVPTRTQVPAAMGAVMGTFSSLQTKQRRPSKD				OROVLIROIOLAKRINI.PVNVHSRSAGRPTINI.LOFOCARVULL
LETDS PALGPEKQVRNEPWNISISABYIAQVKGISVEEVIEVTT QNALKLFPKLRHLLQK  FVEIRPRAEVANLSAHSASPIQDAVLKRLSLLEDIVYRQLNGLS KSLGLIEGYGGRGKGGLPATLSPAEEEKAKGPHEKYGYNSYLSE KISLDRSIPDYRPTKCKELKYSKDLPQISIIFIFVNEALSVILR SVHSAVNHTPTHLLKEIILVDDNSDEEELKVPLBEYVHKRYPGL VKVVRNQKREGLIRARIEGWKVATGQVTGFFDAHVEFTAGWAEP VLSRIQENRKRVILPSIDNIKQDNFEVQRYENSAHGYSWELWCM YISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKFFGEIGLLDPG MDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIERKKKPYNSNI GFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENPGIDIGDVSER RALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGELRNNKAKDVC LDQGPLENHTAILYPCHGWGPQLARYTKEGFLHLGALGTTTLLP DTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQNGAIMNKGTG RCLEVENRGLAGIDLILRSCTGQRWTIKNSIK  6607 137 986 VPACAGLKKEARSLLASPPRLLNTKLQASCRALFSPPIQSROTT GISFQGRGGAGPGVPTRTQVPAAMGAVMGTFSSLQTKQRRPSKD	į			HAFDGRPSVAMEGVRAGYFFSIPPSIIRSGOOKLVKOLPI.TSIC
FVEIRPRAEVANLSAHSASPIQDAVLKRLSLLEDIVYRQLNGLS KSLGLIEGYGGRGKGGLPATLSPAEEEKAKGPHEKYGYNSYLSE KISLDRSIPDYRPTKCKELKYSKDLPQISIIFIFVNEALSVILR SVHSAVNHTPTHLLKEIILVDDNSDEEELKVPLEEYVHKRYPGL VKVVRNQKREGLIRARIEGWKVATGQVTGFFDAHVEFTAGWAEP VLSRIQENRKRVILPSIDNIKQDNFEVQRYENSAHGYSWELWCM YISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKFFGEIGLLDPG MDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIERKKKPYNSNI GFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENPGIDIGDVSER RALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGELRNNKAKDVC LDQGPLENHTAILYPCHGWGPQLARYTKEGFLHLGALGTTTLLP DTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQNGAIMNKGTG RCLEVENRGLAGIDLILRSCTGQRWTIKNSIK  6607 137 986 VPACAGLKKEARSLLASPPRLLNTKLQASCRALFSPPIQSRQTT GISFQGRGGAGPGVPTRTQVPAAMGAVMGTFSSLQTKQRRPSKD	! [	1		LETDSPALGPEKQVRNEPWNISISABYIAQVKGISVEEVIRVTT
KSLGLIEGYGGRKGGLPATLSPAEEEKAKGPHEKYGYNSYLSE KISLDRSIPDYRPTKCKELKYSKDLPQISIIFIFVNEALSVILR SVHSAVNHTPTHLLKEIILVDDNSDEEELKVPLEEYVHKRYPGL VKVVRNQKREGLIRARIEGWKVATGQVTGFFDAHVEFTAGWAEP VLSRIQENRKRVILPSIDNIKQDNFEVQRYENSAHGYSWELWCM YISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKFFGEIGLLDPG MDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIERKKKPYNSNI GFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENPGIDIGDVSER RALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGELRNNKAKDVC LDQGPLENHTAILYPCHGWGPQLARYTKEGFLHLGALGTTTLLP DTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQNGAIMNKGTG RCLEVENRGLAGIDLILRSCTGQRWTIKNSIK  6607 137 986 VPACAGLKKEARSLLASPPRLLNTKLQASCRALFSPPIQSROTT GISFQGRGGAGPGVPTRTQVPAAMGAVMGTFSSLQTKQRRPSKD				QNALKLFPKLRHLLQK
KSLGLIEGYGGRGKGGLPATLSPAEEEKAKGPHEKYGYNSYLSE KISLDRSIPDYRPTKCKELKYSKDLPQISIIFIFVNEALSVILR SVHSAVNHTPTHLLKEIILVDDNSDEEELKVPLEEYVHKRYPGL VKVVRNQKREGLIRARIEGWKVATGQVTGFFDAHVEFTAGWAEP VLSRIQENRKRVILPSIDNIKQDNFEVQRYENSAHGYSWELWCM YISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKFFGEIGLLDPG MDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIERKKKPYNSNI GFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENFGIDIGDVSER RALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGELRNNKAKDVC LDQGPLENHTAILYPCHGWGPQLARYTKEGFLHLGALGTTTLLP DTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQNGAIMNKGTG RCLEVENRGLAGIDLILRSCTGQRWTIKNSIK  6607 137 986 VPACAGLKKEARSLLASPPRLLNTKLQASCRALFSPPIQSROTT GISFQGRGGAGPGVPTRTQVPAAMGAVMGTFSSLQTKQRRPSKD	6606	2	1682	FVEIR PRAEVANLSAHSAS PIQDAVLKRLSLLEDIVYRQLNGLS
SVHSAVNHTPTHLLKEIILVDDNSDEEELKVPLEEYVHKRYPGL VKVVRNQKREGLIRARIEGWKVATGQVTGFFDAHVEFTAGWAEP VLSRIQENRKRVILPSIDNIKQDNFEVQRYENSAHGYSWELWCM YISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKFFGEIGLLDPG MDVYGGENIELGIKVWLCGGSMEVLPGSRVAHIERKKKPYNSNI GFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENPGIDIGDVSER RALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGELRNNKAKDVC LDQGPLENHTAILYPCHGWGPQLARYTKEGFLHLGALGTTTLLP DTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQNGAIMNKGTG RCLEVENRGLAGIDLILRSCTGQRWTIKNSIK  6607 137 986 VPACAGLKKEARSLLASPPRLLNTKLQASCRALFSPPIQSRQTT GISFQGRGGAGPGVPTRTQVPAAMGAVMGTFSSLQTKQRRPSKD	] ]	]		KSLGLIEGYGGRGKGGLPATLSPAEEEKAKGPHEKYGYNSYLSE
VKVVRNQKREGLIRARIEGWKVATGQVTGFFDAHVEFTAGWAEP  VLSRIQENRKRVILPSIDNIKQDNFEVQRYENSAHGYSWELWCM  YISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKFFGEIGLLDPG  MDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIERKKKPYNSNI  GFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENPGIDIGDVSER  RALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGELRNNKAKDVC  LDQGPLENHTAILYPCHGWGPQLARYTKEGFLHLGALGTTTLLP  DTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQNGAIMNKGTG  RCLEVENRGLAGIDLILRSCTGQRWTIKNSIK  6607  137  986  VPACAGLKKEARSLLASPPRLLNTKLQASCRALFSPPIQSROTT  GISFQGRGGAGPGVPTRTQVFAAMGAVMGTFSSLQTKQRRPSKD		j		ALBUDKSIPUYKPTKCKELKYSKDLPQISIFIFVNEALSVILR
VLSRIQENRKRVILPSIDNIKQDNFEVQRYENSAHGYSWELWCM YISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKFFGEIGLLDPG MDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIERKKKPYNSNI GFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENPGIDIGDVSER RALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGELRNNKAKDVC LDQGPLENHTAILYPCHGWGPQLARYTKEGFLHLGALGTTTLLP DTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQNGAIMNKGTG RCLEVENRGLAGIDLILRSCTGQRWTIKNSIK  6607 137 986 VPACAGLKKEARSLLASPPRLLNTKLQASCRALFSPPIQSRQTT GISFQGRGGAGPGVPTRTQVFAAMGAVMGTFSSLQTKQRRPSKD	]	İ		
YISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKFFGEIGLLDPG MDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIERKKKPYNSNI GFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENPGIDIGDVSER RALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGELRNNKAKDVC LDQGPLENHTAILYPCHGWGPQLARYTKEGFLHLGALGTTTLLP DTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQNGAIMNKGTG RCLEVENRGLAGIDLILRSCTGQRWTIKNSIK  6607 137 986 VPACAGLKKEARSLLASPPRLLNTKLQASCRALFSPPIQSRQTT GISFQGRGGAGPGVPTRTQVPAAMGAVMGTFSSLQTKQRRPSKD				
MDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIERKKKPYNSNI GFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENPGIDIGDVSER RALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGELRNNKAKDVC LDQGPLENHTAILYPCHGWGPQLARYTKEGFLHLGALGTTTLLP DTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQNGAIMNKGTG RCLEVENRGLAGIDLILRSCTGQRWTIKNSIK  6607 137 986 VPACAGLKKEARSLLASPPRLLNTKLQASCRALFSPPIQSRQTT GISFQGRGGAGPGVPTRTQVPAAMGAVMGTFSSLQTKQRRPSKD		ļ		YISPPKDWWDAGDPSLPIRTPAMTGCSFVVNRKFRGETGTT DDG
GFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENFGIDIGDVSER RALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGELRNNKAKDVC LDQGPLENHTAILYPCHGWGPQLARYTKEGFLHLGALGTTTLLP DTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQNGAIMNKGTG RCLEVENRGLAGIDLILRSCTGQRWTIKNSIK  6607 137 986 VPACAGLKKEARSLLASPPRLLNTKLQASCRALFSPPIQSRQTT GISFQGRGGAGPGVPTRTQVPAAMGAVMGTFSSLQTKQRRPSKD	Į	Ì		MDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIERKKK>VNGNT
RALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGELRNNKAKDVC LDQGPLENHTAILYPCHGWGPQLARYTKEGFLHLGALGTTTLLP DTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQNGAIMNKGTG RCLEVENRGLAGIDLILRSCTGQRWTIKNSIK  6607 137 986 VPACAGLKKEARSLLASPPRLLNTKLQASCRALFSPPIQSRQTT GISFQGRGGAGPGVPTRTQVFAAMGAVMGTFSSLQTKQRRPSKD	]			GFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENPGIDIGDVSER
DTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQNGAIMNKGTG RCLEVENRGLAGIDLILRSCTGQRWTIKNSIK  6607 137 986 VPACAGLKKEARSLLASPPRLLNTKLQASCRALFSPPIQSRQTT GISFQGRGGAGPGVPTRTQVFAAMGAVMGTFSSLQTKQRRPSKD		Ì		RALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGELRNNKAKDVC
DTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQNGAIMNKGTG RCLEVENRGLAGIDLILRSCTGQRWTIKNSIK  6607 137 986 VPACAGLKKEARSLLASPPRLLNTKLQASCRALFSPPIQSRQTT GISFQGRGGAGPGVPTRTQVFAAMGAVMGTFSSLQTKQRRPSKD				LDQGPLENHTAILYPCHGWGPQLARYTKEGFLHLGALGTTTLLP
986 VPACAGLKKEARSLLASPPRLLNTKLQASCRALFSPPIQSRQTT GISFQGRGGAGPGVPTRTQVFAAMGAVMGTFSSLQTKQRRPSKD		ļ	· ·	DTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQNGAIMNKGTG
GISFQGRGGAGPGVPTRTQVFAAMGAVMGTFSSLQTKQRRPSKD	6607			RCLEVENRGLAGIDLILRSCTGQRWTIKNSIK
	1000/	137	986	VPACAGLKKEARSLLASPPRLLNTKLQASCRALFSPPIQSRQTT
KIEDELEMTMVCHRPEGLEQUEAQTNFTKRELQVLYRGFKNECP				
				KLEDEDEMTMVCHRPEGLEQLEAQTNFTKRELQVLYRGFKNECP

SEQ	Predicted	Predicted end	D
ID	beginning	nuclcotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, O=Glutamine, R=Arginine
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine Y=Unknown + G
- {	amino acid	sequence	Codon, /=possible nucleotide deletion
<b> </b>	sequence		\=Possible nucleotide insertion\
1			SGVVNEDTFKQIYAQFFPHGDASTYAHYI,FNAFDTTOTGSVVEE
ł			DFVTALSILLRGTVHEKLRWTFNLYDINKDGVTNOFFMMDIWA
		1	1 TYDMNGKYTYPVLKEDTPROHVDVFFOKMDKNKDGTVTI DEELE
6608	224	1140	SCQEDDNIMRSLQLFQNVM
	1	1 1110	RPCFSSPTGLCPRLSYPMILLQHAVLPPPKQPSPSPPMSVATRS
			TGTLQLPPQKPFGQEASLPLAGEEELSKGGEQDCALEELCKPLY
			CKLCNVTLNSAQQAQAHYQGKNHGKKLRNYYAANSCPPPARMSN VVEPAATFVVPVPPQMGSFKPGGRVILATENDYCKLCDASFSSP
	1		AVAQAHYQGKNHAKRLRLAEAQSNSFSESSELGQRRARKEGNEF
ļ	l	į	KMMPNRRNMYTVQNNSGPYFNPRSRQRIPRDLAMCVTPSGQFYC
			SMCNVGAGEEMEFRQHLESKQHKSKVSEQRYRNEMENLGYV
6609	1	443	FRLRCRRFRVAGGRLAGAGLRESRVPAPEORLSALTILEMEAVE
			PAAEPGNFQLSPAEPRGPLASPVRAAPRAPCDAAEMSELNTVTC
1	1		PATNQAAGQEEKGKAGNVKKAEEEEEIDIDLTAPETEKAALATO
6610	319	0.04	GKFRRFQKRKKDPSS
1 0010	319	881	GRKSLCNLHIPIRFPLTYPDMYMGMMCTAKKCGIRFQPPAIILI
	1		YESELKGKIRQRIMPVRNFSKFSDCTRAAFOLKMNDDUKGVI EO
1	1		VSLRQLEKLFSFLRGYLSGQSLAETMEQIQRETTIDPEEDLNKL
			DDKELAKRKSIMDELFEKNQKKKDDPNFVYDIEVEFPQDDQLQS CGWDTESADEF
6611	978	212	PGCSGAGSRVWWLPALRHLAMGSTESSEGRRVSFGVDEEERVRV
1			LQGVRLSENVVNRMKEPSSPPPAPTSSTFGLQDGNLRAPHKEST
	i i		LPRSGSSGGQQPSGMKEGVKRYEQEHAAIQDKLFQVAKREREAA
Į.			TKHSKASLPTGEGSISHEEQKSVRLARELESREAELRRRDTFYK
			EQLERIERKNAEMYKLSSEOFHEAASKMESTIKDDDVEDVCCCI
6612	1704		QAQILHCYRDRPHEVLLCSDLVKAYORCVSAAHKG
0012	1724	992	VSTHASALSRTOGOPOROPRAAASGAGAGTAGGGGSGGAEGEVM
			STEAURVODSPSTSGGSSDGDORESVOOEDERROVORKERKE
			SSKTAAKLSTSAKRIOKELAEITLDPPPNCSAGDYGDNTVEWDG
1			TILGPPGSVYEGGVFFLDITFSPDYPFKPPKVTFRTRIYHCNIN
1 1			SQGVICLDILKDNWSPALTISKVLLSICSLLTDCNPADPLVGSI ATQYMTNRAEHDRMARQWTKRYAT
6613	130	748	ELELSSNMPEQSNDYRVAVFGAGGVGKSSLVLRFVKGTFRESYI
			PTVEDTYRQVISCDKSICTLQITDTTGSHQFPAMQRLSISKGHA
1		į	FILVYSITSRQSLEELKPIYEQICEIKGDVESIPIMLVGNKCDE
			SPSKEVQSSEAEALARTWKCAFMETSAKINHNVKELFOFTINI F
6614			KRRTVSLQIDGKKSKQQKRKEKLKGKCVIM
0014	3	1191	SSAAEAMRVLVRRCWGPPLAHGARRGRPSPOWRALARI GWRDCD
1			DSRVREKPPWRVLFFGTDOFAREALRALHAARENKEEELTDVLE
1 1			VVTMPSPSPKGLPVKQYAVOSOLPVYEWPDVGSGEVDVGVAGE
1 1	ĺ		GRELNEALILKPPYGILNVHPSCLPRWRGPAPVIHTVIHGDTVT
		1	GVIIMQIRPKRFDVGPILKOETVPVPPKSTAKELRAVI.SPICAM
1		ł	MLISVLKNLPESLSNGRQQPMEGATYAPKISAGTSCIKWEEQTS
1 1			EQIFRLYRAIGNIIPLQTLWMANTIKLLDLVEVNSSVLADPKLT
	İ	İ	GQALIPGSVIYHKQSQILLVYCKDGWIGVRSVMLKKSLTATDFY MGYLHPWYQKNSQAQPSQCRFQTLRLPTKKKQKKTVAMQQCIE
6615	832	35	GRVGAGASAMSELPGDVRAFLREHPSLRLQTDARKVRCILTGHE
] [		l	LPCRLPELQVYTRGKKYQRLVRASPAFDYAEFEPHIVPSTKNPH
			QLFCKLTLRHINKCPEHVLRHTQGRRYQRALCKYEECQKQGVEY
		1	VPACLVHRRRREDOMDGDGPRPREAFWEPTSSDEGGAASDDSM
			TDLIPPELITRKDLGSTEDGDGTDDFLTDKEDEKAKPPPEKATD
		i	EGRRETTVYRGLVQKRGKKQLGSLKKKFKSHHRKPKSFSSCKOS
6616	347		G
0010	347	1886	LLPPCQGARPLSSPPHASEDNLFLFWNCILCAFPHPSPQPLQYP
		<u></u>	VWPLLLVITQIPAPRHLRNRPFSFSRGGLDSFSGSLSTPSICRS

SEQ	Predicted		
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
j	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
			PAWVKMAPWPPKGLVPAVLWGLSLFLNLPGPIWLQPSPPPQSSP
	1		PPQPHPCHTCRGLVDSFNKGLERTIRDNFGGGNTAWEEENLSKY
1			KDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQQEA
	1		PDLFQWLCSDSLKLCCPAGTFGPSCLPCPGGTERPCGGYGQCEG
1			EGTRGGSGHCDCQAGYGGEACGQCGLGYFEAERNASHLVCSACF
ľ			GPCARCSGPEESNCLQCKKGWALHHLKCVDIDECGTEGANCGAD QFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKC
			LDVDECETEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQ
}			IPESAGFFSEMTEDELVVLQQMFFGIIICALATLAAKGDLVFTA
1	-		IFIGAVAAMTGYWLSERSDRVLEGFIKGR
6617	1.18	673	VWMAWQVSLLELEDRLQCPICLEVFKESLMLQCGHSYCKGCLVS
			LSYHLDTKVRCPMCWQAVDGSSSLPNVSLAWVIEALRLPGDPEP
			KVCVHHRNPLSLFCEKDQELICGLCGLLGSHOHHPVTPISTVCS
1			RMKEELAALFSELKQEQKKVDELIAKLVKNRTRIDGSAPSLCPC
6618	548		LGPATFTFL
0010	348	136	DGKVARRAPNSPAFQNDIYPLVSAPRATTAESPWSKVLQNTQCR
			NVPKMTSERSRIPCLSAAAAEGTGKKQQEGRAMATLDRKVPSPE
			AFLGKPWSSWIDAAKLHCSDNVDLEEAGKEGGKSREVMRLNKEA WKYGT
6619	246	842	PASSEVLTAAVMFLLLNCIVAVSQNMGIGKNGDLPRPPLRNEFR
İ			YFQRMTTTSSVEGKQNLVIMGRKTWFSIPEKNRPLKDRINLVLS
ļ		~ *	RELKEPPQGAHFLARSLDDALKLTERPELANKVDMIWIVGGSSV
ł			YKEAMNHLGHLKLFVTRIMQDFESDTFFSEIDLEKYKLLPEYPG
			ILSDVQEGKHIKYKFEVCEKDD
6620	3	1879	NSRVDDFVARARMAAENEASQESALGAYSPVDYMSITSFPRLPE
1			DEPAPAAPLRGRKDEDAFLGDPDTDPDSFLKSARLQRLPSSSSE
ĺ			MGSQDGSPLRETRKDPFSAAAAECSCRQDGLTVIVTACLTFATG
			VTVALVMQIYFGDPQIFQQGAVVTDAARCTSLGIEVLSKQGSSV
i			DAAVAAALCLGIVAPHSSGLGGGGVMLVHDIRRNESHLIDFRES APGALREETLQRSWETKPGLLVGVPGMVKGLHEAHQLYGRLPWS
			QVLAFAAAVAQDGFNVTHDLARALAEQLPPNMSERFRETFLPSG
			RPPLPGSLLHRPDLAEVLDVLGTSGPAAFYAGGNLTLEMVAEAQ
			HAGGVITEEDFSNYSALVEKPVCGVYRGHLVLSPPPPHTGPALI
			SALNILEGFNLTSLVSREQALHWVAETLKIALALASRLGDPVYD
	-		STITESMDDMLSKVEAAYLRGHINDSQAAPAPLLPVYELDGAPT
			AAQVLIMGPDDFIVAMVSSLNQPFGSGLITPSGILLNSQMLDFS
			WPNRTANHSAPSLENSVQPGKRPLSFLLPTVVRPAEGLCGTYLA
			LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG
6621	1	662	VQGITSYQQRLQALRKEKSRDAARSRRGKENFEFYELAKLLPLP
		<del></del>	AAITSQLDKASIIRLTISYLKMRDFANQGDPPWNLRMEGPPPNT
	ĺ		SVKVIGAQRRRSPSALAIEVFEAHLGSHILQSLDGYVFALNQEG
	. 1		KFLYISETVSIYLGLSQVELTGSSVFDYVHPGDHVEMAEQLGMK
	· · · · · · · · · · · · · · · · · · ·		LPPGRGLLSQGTAEDGASSASSSSQSETPEPVVCFPPASDOFLL
6622	2	319	GRASGAQEETEAGGPERARAMEANMPKRKEPGRSLRIKVISMGN
			AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN
6623	1000		IFDMAGHPFFYEVRKPF
0023	1886	189	KALFEKVKKFRLHVEEGDILYAMYVRQTVLKVIKFLIIIAYNSA
			LVSKVQFTVDCNVDIQDMTGYKNFSCNHTMAHLFSKLSFCYLCF
ĺ	ľ		VSIYGLTCLYTLYWLFYRSLRBYSFEYVRQETGFDDIPDVKNDF
ľ			AFMLHMIDQYDPLYSKRFAVFLSEVSENKLKQLNLNNEWTPDKL
i			RQKLQTNAHNRLELPLIMLSGLPDTVFEITELQSLKLEIIKNVM
			IPATIAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKFDD MRELPPWMYGLRNLEELYLVGSLSHDISRNVTLESLRDLKSLKI
į			LSIKSNVSKIPQAVVDVSSHLQKMCIHNDGTKLVMLNNLKKMTN
	_ ·		LTELELVHCDLERIPHAVFSLLSLQELDLKENNLKSIEEIVSFQ

SEO	Predicted	1 December 2	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
j	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
1			HLRKLTVLKLWHNSITYIPEHIKKLTSLERLSFSHNKTEVI.DSH
1			LFLCNKIRYLDLSYNDIRFIPPEIGVLQSLOYFSITCNKVESLP
ı			DELYFCKKLKTLKIGKNSLSVLSPKIGNLLFLSYLDGKGNHFET
6624			LPPELGDCRALKRAGLVVEDALFETLPSDVREOMKTE
6624	218	1786	GSRRGGGSRIPAVSTHVAPGRSVLRPFASGALRLRSLVKALGGC
ŀ			RGRPSGLAHLSQETSHWRAKRSGRACLGDFPGEILRSFIMKCTA
			REWLRVTTVLFMARAIPAMVVPNATLLEKLLEKYMDEDGEWWIA
1			KQRGKRAITDNDMQSILDLHNKLRSQVYPTASNMEYMTWDVELE
}			RSAESWAESCLWEHGPASLLPSIGQNLGAHWGRYRPPTFHVQSW
1		•	YDEVKDFSYPYEHECNPYCPFRCSGPVCTHYTQVVWATSNRIGC
I			AINLCHNMNIWGQIWPKAVYLVCNYSPKGNWWGHAPYKHGRPCS
1			ACPPSFGGGCRENLCYKEGSDRYYPPREEETNEIERQQSQVHDT HVRTRSDDSSRNEVISAQQMSQIVSCEVRLRDQCKGTTCNRYEC
1			PAGCLDSKAKVIGSVHYEMQSSICRAAIHYGIIDNDGGWVDITR
	1		QGRKHYFIKSNRNGIQTIGKYQSANSFIVSKVTVQAVTCETTVE
			QLCPFHKPASHCPRVYCPRKLYASKSTLCSCNWNSSLF
6625	1124	543	PGPRGGGGSLLSTKALGRSRGLGMHPGPSSGGTEGGVPTALRPP
			GPLVPSTSDDNLLKNIELFDKLALRFHGRLLFLKDVLGDEICCW
}	]		SFYGQGRKIAEVCCTSIVYATEKKQTKVEFPEARIFEETLNILI
1	ĺ		YETPRGPDPALLEATGGAAGAGGAGRGEDEENREHRVRRIHVRR
			HITHDERPHGQQIVFKD
6626	3	1498	SAVEFVYTDRFHLILGISVEFLCSLRSDATMESITACLHALQAL
ŧ			LDVPWPRSKIGSDQDSGIELLNVLHRVILTRESPSIOLASLEVV
-			RQIICAAQEHVKEKRRSAEVDDGAAEKETLPEFGEGKDTGGLVP
1			GKSLVFATLELCVCILVRQLPELNPKLTGSPGVKATKPQILLED
			GSRLVSAALVILSELPAVCSPEGSISILPTILYLTIGVLRETAV
1			KLPGGQLSSTVAASLQALKGILSSPMARAEKSRTAWTDLLRSAL
1			TTILDCWDPVDETHQELDEVSLLTAITVFILSTSPEVTTIPCLQ
1 1			KRCIDKFKATLEIKDPVVQIKTYQLLHSIFQYPNPAVSYPYIYS
			LASCIMEKLQEIDKRKPENTAELEIFQEGIKVLETLVTVAEEHH
[ .			RAQLVACLLPILISFLLDENSLGSATSIMRNLHDFALQNLMQIG PQYSSVFKSLVASSPALKARLEAAIKGNQESVKVKIPTSKYTKS
1. 1	· ·		PGKNSSIQLKTSFL
6627	1	697	GIPHLSSRDMTGTPGAVATRDGEAPERSPPCSPSYDLTGKVMLL
	ļ		GDTGVGKTCFLIQFKDGAFLSGTFIATVGIDFRNKVVTVDGVRV
ł	F		KLQIWDTAGQERFRSVTHAYYRDAQALLLLYDITNKSSFDNIRA
			WLTEIHEYAQRDVVIMLLGNKADMSSERVIRSEDGETLAREYGV
i l			PFLETSAKTGMNVELAFLAIAKELKYRAGHQADEPSFQIRDYVE
F 500			SQKKRSSCCSFM
6628	1	1861	QCAEFGGGSGGGGGGGGGGGGGGEENKENERPSAGSKAN
ļ i			KEPGDSLSLEILQIIKESQQQHGLRHGDFORYRGYCSRRORRIR
] ]			KTLNFKMGNRHKFTGKKVTEELLTDNRYLLLVLMDAERAWSYAM
1 1			QLKQEANTEPRKRFHLLSRLRKAVKHAEELERLCESNRVDAKTK
j f			LEAQAYTAYLSGMLRFEHQEWKAAIEAFNKCKTIYEKLASAFTE
}			EQAVLYNORVEEISPNIRYCAYNIGDQSAINELMQMRLRSGGTE
[ ]	1		GLLAEKLEALITOTRAKQAATMSEVEWRGRTVPVKIDKVRIFLL
]	1		GLADNEAAIVQAESEETKERLFESMLSECRDAIQVVREELKPDQ
	1	!	KQRDYILEGEPGKVSNLQYLHSYLTYIKLSTAIKRNENMAKGLQ
	ļ		RALLQQQPEDDSKRSPRPQDLIRLYDIILQNLVELLQLPGLEED
		ł	KAFQKEIGLKTLVFKAYRCFFIAQSYVLVKKWSEALVLYDRVLK
	l		YANEVNSDAGAFKNSLKDLPDVQELITQVRSEKCSLQAAAILDA
	}	ļ	NDAHQTETSSSQVKDNKPLVERFETFCLDPSLVTKQANLVHFPP GFQPIPCKPLFFDLALNHVAFPPLEDKLEQKTKSGLTGYIKGIF
			GFRS GFRS
6629	5653	4549	GATPLGSVGGRTGKMDAATLTYDTLRFAEFEDFPETSEPVWILG
		•	RKYSIFTEKDEILSDVASRLWFTYRKNFPAIGGTGPTSDTGWGC

SEQ	Predicted	I Brodieted and	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	] -	\=possible nucleotide insertion)
		· · · · · · · · · · · · · · · · · · ·	MLRCGQMIFAQALVCRHLGRDWRWTQRKRQPDSYFSVLNAFIDR
			KDSYYSIHQIAQMGVGEGKSIGQWYGPNTVAQVLKKLAVFDTWS
1	1	)	SLAVHIAMONTVVMEEIRRLCRTSVPCAGATAFPADSDRHCNGF
ľ			PAGAEVTNRPSPWRPLVLLIPLRLGLTDINEAYVETLKHCFMMP
			QSLGVIGGKPNSAHYFIGYVGEELIYLDPHTTQPAVEPTDGCFI
]	1		PDESFHCQHPPCRMSIAELDPSIAVVRGGHLSTQAFGAECCLGM
			TRKTFGFLRFFFSMLG
6630	2	423	LVQCGGIRRRSAWGAMPGRHVSRVRALYKRVLQLHRVLPPDLKS
	i		LGDQYVKDEFRRHKTVGSDEAQRFLQEWEVYATALLOOANENRO
Ì	1		NSTGKACFGTFLPEEKLNDFRDEQIGQLQELMQEATKPNRQFSI
			SESMKPKF
6631	2	423	LVQCGGIRRRSAWGAMPGRHVSRVRALYKRVLQLHRVLPPDLKS
			LGDQYVKDEFRRHKTVGSDEAQRFLQEWEVYATALLQQANENRQ
			NSTGKACFGTFLPEEKLNDFRDEQIGQLQELMQEATKPNRQFSI
6632	1273		SESMKPKF
0032	12/3	588	WNSRGRTQRGAAPLAPAAAMKAVVQRVTRASVTVGGEQISAIGR
			GICVLLGISLEDTQKELEHMVRKILNLRVFEDESGKHWSKSVMD
			KQYEILCVSQFTLQCVLKGNKPDFHLAMPTEQAEGFYNSFLEQL
	'		RKTYRPELIKDGKFGAYMQVHIQNDGPVTIELESPAPGTATSDP
]	j		KQLSKLEKQQQRKEKTRAKGPSESSKERNTPRKEDRSASSGAEG DVSSEREP
6633	1145	617	ATGRHEGVPTLEGIIQQLVNGIITPATIPSLGPWGVLHSNPMDY
		027	AWGANGLDAIITQLLNQFENTGPPPADKEKIQALPTVPVTEEHV
			GSGLECPVCKDDYALGERVRQLPCNHLFHDGCIVPWLEQHDSCP
	·	,	VCRKSLTGQNTATNPPGLTGVSFSSSSSSSSSSSSSSNENATSNS
6634	1	1134	CGGIPRKGSGPRRRLPMARLRDCLPRLMLTLRSLLFWSLVYCYC
1			GLCASIHLLKLLWSLGKGPAQTFRRPAREHPPACLSDPSLGTHC
Ì			YVRIKDSGLRFHYVAAGERGKPLMLLLHGFPEFWYSWRYQLREF
			KSEYRVVALDLRGYGETDAPIHRQNYKLDCLITDIKDILDSLGY
	!		SKCVLIGHDWGGMIAWLIAICYPEMVMKLIVINFPHPNVFTEYI
			LRHPAQLLKSSYYYFFQIPWFPEFMFSINDFKVLKHLFTSHSTG
			IGRKGCQLTTEDLEAYIYVFSQPGALSGPINHYRNIFSCLPLKH
			HMVTTPTLLLWGENDAFMEVEMAEVTRFYVKNYFRLTILSEASH
6635 •	1400		WLQQDQPDIVNKLIWTFLKEETRKKD
9932.	1420	470	EMRAGQQLASMLRWTRAWRLPREGLGPHGPSFARVPVAPSSSSG
			GRGGAEPRPLPLSYRLLDGEAALPAVVFLHGLFGSKTNFNSIAK
			ILAQQTGRRVLTVDARNHGDSPHSPDMSYEIMSQDLQDLLPQLG
]	i		LVPCVVVGHSMGGKTAMLLALQRPELVERLIAVDISPVESTGVS
1			HFATYVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL
1 1			LTNLVEVDGRFVWRVNLDALTQHLDKILAFPQRQESYLGPTLFL
			LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI AAIRGFLV
6636	1514	1801	SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE
1 1			QPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD
; !	l		DGGDGVF
6637	2	1501	CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI
			KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT
1	ļ		VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD
] ]			LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG
			DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS
1 1	ļ		CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW
]	!		FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR
[	ŀ	ĺ	DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS
			TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL
	1	į	RSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC
L1			TAETGGIAAVSFPGRASPEPRWHLMGLVSWSYDKTCSHRLSTAF

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine.
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	104	\=possible nucleotide insertion)
			TKVLPFKDWIERNMK
6638	1391	224	GGIPQAGGKMAAPWWRAALCECRRWRGFSTSAVLGRRTPPLGPM
		<del>-</del>	PNSDIDLSNLERLEKYRSFDRYRRRAEQEAQAPHWWRTYREYFG
			EKTDPKEKIDIGLPPPKVSRTQQLLERKQAIQELRANVEEERAA
		į	RLRTASVPLDAVRAEWERTCGPYHKQRLAEYYGLYRDLFHGATF
	1		VPRVPLHVAYAVGEDDLMPVYCGNEVTPTEAAQAPEVTYEAEEG
			SLWTLLLTSLDGHLLEPDAEYLHWLLTNIPGNRVAEGOVTCPYL
I	}	j	PPFPARGSGIHRLAFLLFKQDQPIDFSEDARPSPCYQLAORTFR
			TFDFYKKHQETMTPAGLSFFQCRWDDSVTYIFHQLLDMREPVFE
			FVRPPPYHPKQKRFPHRQPLRYLDRYRDSHEPTYGIY
6639	2046	1268	IGCFIMDGGDDGNLIIKKRFVSEAELDERRKRRQEEWEKVRKPE
	i		DPEECPEEVYDPRSLYERLQEQKDRKQQEYEEQFKFKNMVRGLD
			EDETNFLDEVSRQQELIEKQRREBELKELKEYRNNLKKVGISQE
•			NKKEVEKKLTVKPIETKNKFSQAKLLAGAVKHKSSESGNSVKRL
1	1		KPDPEPDDKNQEPSSCKSLGNTSLSGPSIHCPSAAVCIGILPGL
Ĺ			GAYSGSSDSESSSDSEGTINATGKIVSSIFRTNTFLEAP
6640	117	1043	VLEPPDVSMAESEDRSLRIVLVGKTGSGKSATANTILGEEIFDS
1			RIAAQAVTKNCQKASREWQGRDLLVVDTPGLFDTKESLDTTCKE
i			ISRCIISSCPGPHAIVLVLLLGRYTEEEQKTVALIKAVFGKSAM
	ļ		KHMVILFTRKEELEGQSFHDFIADADVGLKSIVKECGNRCCAFS
1	<u> </u>		NSKKTSKAEKESQVQELVELIEKMVQCNEGAYFSDDIYKDTEER
			LKQREEVLRKIYTDQLNEEIKLVEEDKHKSEEKKEKEIKLLKLK
			YDEKIKNIREEAERNIFKDVFNRIWKMLSEIWHRFLSKCKFYSS
6641	1	894	SAAVGRRSEVRGCAPRPRLRRSARRMDPVPGTDSAPLAGLAWSS
1			ASAPPPRGFSAISCTVEGAPASFGKSFAQKSGYFLCLSSLGSLE
	1		NPQENVVADIQIVVDKSPLPLGFSPVCDPMDSKASVSKKKRMCV
1	1		KLLPLGATDTAVFDVRLSGKTKTVPGYLRIGDMGGFAIWCKKAK
1	1		APRPVPKPRGLSRDMQGLSLDAASQPSKGGLLERTASRLGSRAS
1	i		TLRRNDSIYEASSLYGISAMDGVPFTLHPRFEGKSCSPLAFSAF
6642	22	1296	GDLTIKSLADIEEEYNYGFVVEKTAAARLPPSVS PLEERMMTKMDPNDQAQRDIIFELRRIAFDAESDPSNAPGSGTE
0042		1296	KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV
	!		HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP
			NEGRNDYHPMFFTHDRAFEELFGICIQLLNKTWKEMRATAEDFN
			KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSER
ļ			MSQDDFQSPPIVELREKIOPEILELIKOORLNRLCEGSSFRKIG
1			NRRRQERFWYCRLALNHKVLHYGDLDDNPQGEVTFESLQEKIPV
1			ADIKAIVTGKDCPHMKEKSALKONKEVLELAFSILYDPDETLNF
}			IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTLLSMEMKLRL
1			LDLENIQIPEAPPPIPKEPSSYDFVYHYG
6643	3049	2265	SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHITCRLCSGYLI
1			DATTVTECLHTFCRSCLVKYLEENNTCPTCRIVIHQSHPLQYIG
1			HDRTMQDIVYKLVPGLQEAEMRKQREFYHKLGMEVPGDIKGETC
1			SAKQHLDSHRNGETKADDSSNKEAAEEKPEEDNDYHRSDEQVSI
1			CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNEL
1			DILCNEEILGKDHTLKFVVVTRWRFKKAPLLLHYRPKMDLL
6644	1489	290	FRPLATEPRGSSPVQLVSSTMSVRTLPLLFLNLGGEMLYILDOR
1			LRAQNIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR
1			TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL
1	[		LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ
1			LIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT
j.			EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL
1			KLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF
			LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEEQAALTRPEELSY
1			EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM
L			DEL

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown *-Ston
Ī	amino acid	sequence	Codon, /=possible nucleotide deletion
6645	sequence		\=possible nucleotide insertion)
0045	6530	4646	FVEGLAGYVYKAASEGKVLTLAALLLNRSESDIRYLLGYVSQQG
1			GQRSTPLIIAARNGHAKVVRLLLEHYRVQTQQTGTVRFDGYVID
1			GATALWCAAGAGHFEVVKLLVSHGANVNHTTVTNSTPLRAACFD
1			GRLDIVKYLVENNANISIANKYDNTCLMIAAYKGHTDVVRYLLE
-			QRADPNAKAHCGATALHFAAEAGHIDIVKELIKWRAAIVVNGHG MTPLKVAAESCKADVVELLLSHADCDRRSRIEALELLGASFAND
			RENYDIIKTYHYLYLAMLERFQDGDNILEKEVLPPIHAYGNRTE
			CRNPQELESIRQDRDALHMEGLIVRERILGADNIDVSHPIIYRG
			AVYADNMEFEQCIKLWLHALHLRQKGNRNTHKDLLRFAQVFSQM
1		ı	IHLNETVKAPDIECVLRCSVLEIEQSMNRVKNISDADVHNAMDN
1			YECNLYTFLYLVCISTKTQCSEEDQCKINKOIYNI,IHI,DPRTRE
			GFTLLHLAVNSNTPVDDFHTNDVCSFPNALVTKLLLDCGAFINA
1			VDNEGNSALHIIVQYNRPISDFLTLHSIIISLVEAGAHTDMTNK
			QNKTPLDKSTTGVSEILLKTQMKMSLKCLAARAVRANDINYQDQ
6646	176	890	IPRTLEEFVGFH
1		450	PSSRMNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESY EGREKKGISDVRRTFCLFVTFDLLFVTLLWIIELNVNGGIENTL
ĺ			EKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIAL
1			TTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLD
į			FKVLPQEAEEENRLLIVQDASERAALIPGGLSDGQFYSPPESEA
- 65.17			GSEEAEEKQDSEKPLLEL
6647	176	890	PSSRMNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESY
1			EGREKKGISDVRRTFCLFVTFDLLFVTLLWIIELNVNGGTENTI.
			EKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIAL
	•		TTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLD
			FKVLPQEAEEENRLLIVQDASERAALIPGGLSDGQFYSPPESEA GSEEAEEKQDSEKPLLEL
6648	413	897	RNCWNCFTKYFNSPPEDIDHKDSYLITRSIMAEPDYIEDDNPEL
1 1			IRPQKLINPVKTSRNHQDLHRELLMNQKRGLAPQNKPELQKVME
			KRKRDQVIKQKEEEAQKKKSDLEIELLKROOKLEOLELEKOKLO
			EEQENAPEFVKVKGNLRRTGQEVAQAQES
6649	1357	832	WIPRAAGIRHEVKWDVKEIMSOHNIYVDALLKEFEOFNRRINEV
] [			SKRVRIPLPVSNILWEHCIRLANRTIVEGYANVKKCSNEGRALM
]			QLDFQQFLMKLEKLTDIRPIPDKEFVETYIKAYYLTENDMERWI
6650	32	765	KEHREYSTKQLTNLVNVCLGSHINKKARQKLLAAIDDIDRPKR
		703	LVPLVFSLLVQSCKQVYRSIAMKFVPCLLLVTLSCLGTLGQAPR OKOGSTGFFFFFOTGGPRSGTMFFFGLLGOVTLSCLGTLGQAPR
			QKQGSTGEEFHFQTGGRDSCTMRPSSLGQGAGEVWLRVDCRNTD QTYWCEYRGQPSMCQAFAADPKSYWNQALQELRRLHHACQGAPV
1 1			LRPSVCREAGPQAHMQQVTSSLKGSPEPNQQPEAGTPSLRPKAT
1 1			VKLTEATQLGKDSMEELGKAKPTTRPTAKPTQPGPRPGGNEEAK
			KKAWEHCWKPFQALCAFLISFFRG
6651	3425	1353	AKELLKVGDFSLCAGPYQNTADTMENLSKEPLASFVSESFDISA
		İ	CGIATEHVKIDNSGEGLTAEAGSETLSRDGEVGVNSDMHVFLSG
			DSDLDLLGDCRNPRLDLEDSYTLRGSYTRKKDVPTDGYESSLNE
[ [			HNNNQEDWGCSSWVPGMETSLPPGHWTAAVKKEEKCVPPYVQIR
			DLHGILRTYANFSITKELKDTMRTSHGLRRHPSFSANCGLPSSW
1 1			TSTWQVADDLTQNTLDLEYLRFAHKLKQTIKNGDSQHSASSANV FPKESPTQISIGAFPSTKISEAPFLHPAPRSRSPLLVTVVESDP
	į		RPQGQPRRGYTASSLDSSSSWRERCSHNRDLRNSQRNHTVSFHL
	ļ	1	NKLKYNSTVKESRNDISLILNEYAEFNKVMKNSNQFIFQDKELN
			DVSGEATAQEMYLPFPGRSASYEDIIIDVCTNLHVKLRSVVKEA
] }	1	l	CKSTFLFYLVETEDKSFFVRTKNLLRKGGHTEIEPQHFCQAFHR
]	j	1	ENDTLIIIIRNEDISSHLHQIPSLLKLKHFPSVIFAGVDSPGDV
		1	LDHTYQELFRAGGFVISDDKILEAVTLVQLKEIIKILEKLNGNG
		İ	RWKWLLHYRENKKLKEDERVDSTAHKKNIMLKSFOSANTTELLH
			YHQCDSRSSTKAEILKCLLNLQIQHIDARFAVLLTDKPTIPREV

SEO	Predicted	Predicted end	Amino poid compat
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	<u> </u>		FENNGILVTDVNNFIENIEKIAAPFRSSYW
6652	2	1343	IPGSTISCSCHSRRLRGGSPAPRLSLGAASPRPRPPSLPLPLPL
			PFPLFLPTRPAERAWIRSRRASEWVGKMEVPRLDHALNSPTSPC
	1		EEVIKNLSLEAIQLCDRDGNKSQDSGIAEMEELPVPHNIKISNI
İ	]		TCDSFKISWEMDSKSKDRITHYFIDLNKKENKNSNKFKHKDVPT
1	f		KLVAKAVPLPMTVRGHWFLSPRTEYTVAVQTASKQVDGDYVVSE
1			WSEIIEFCTADYSKVHLTQLLEKAEVIAGRMLKFSVFYRNQHKE
	•		YFDYVREHHGNAMQPSVKDNSGSHGSPISGKLEGIFFSCSTEFN
			TGKPPQDSPYGRYRFEIAAEKLFNPNTNLYFGDFYCMYTAYHYV
			ILVIAPVGSPGDEFCKQRLPQLNSKDNKFLTCTEEDGVLVYHHA
			QDVILEVIYTDPVDLSLGTVAEITGHQLMSLSTANAKKDPSCKT
l i			CNISVGR
6653	170	1910	FFLEPRLRPFPASRARFVPARTRPSPLHPCCFCFEGGGSMLSPQ
	ļ		RVAAAASRGADDAMESSKPGPVQVVLVQKDQHSFELDEKALASI
			LLQDHIRDLDVVVVSVAGAFRKGKSFILDFMLRYLYSQKESGHS
			NWLGDPEEPLTGFSWRGGSDPETTGIQIWSEVFTVEKPGGKKVA
ŀ			VVLMDTQGAFDSQSTVKDCATIFALSTMTSSVQIYNLSQNIQED
1			DLQQLQLFTEYGRLAMDEIFQKPFQTLMPLVRDWSFPYEYSYGL
			QGGMAFLDKRLQVKEHQHEEIQNVRNHIHSCFSDVTCFLLPHPG
			LQVATSPDFDGKLKDIAGEFKEQLQALIPYVLNPSKLMEKEING
			SKVTCRGLLEYFKAYIKIYQGEDLPHPKSMLQATAEAYNLAAAA
	l		SAKDIYYNNMEEVCGGEKPYLSPDILEEKHCEFKQLALDHFKKT
] ]			KKMGGKDFSFRYQQELEEEIKELYENFCKHNGSKNVFSTFRTPA
			VLFTGIVALYIASGLTGFIGLEVVAQLFNCMVGLLLIALLTWGY
			IRYSGQYRELGGAIDFGAAYVLEQASSHIGNSTQATVRDAVVGR
			PSMDKKAQ
6654	1	705	RTSLSPSQCSSFNLAMASAGMQILGVVLTLLGWVNGLVSCALPM
1			WKVTAFIGNSIVVAQVVWEGLWMSCVVQSTGOMOCKVYDSLLAL
1 1			PODLQAARALCVIALLVALFGLLVYLAGAKCTTCVEEKDSKARL
1 1			VLTSGIVFVISGVLTLIPVCWTAHAVIRDFYNPLVAEAOKRELG
1			ASLYLGWAASGLLLLGGGLLCCTCPSGGSQGPSHYMARYSTSAP
			AISRGPSEYPTKNYV
6655	341	16	KDAYMFKKGLLALALVFSLPVFAAEHWIDVRVPEQYQQEHVQGA
	1		INIPLKEVKERIATAVPDKNDTVKVYCNAGRQSGQAKEILSEMG
			YTHVENAGGLKDIAMPKVKG
6656	2	1212	TELPPRPANLAIQPPLSPLRALAPLPEKPGAVPPPQKRMAKVAK
	į		DLNPGVKKMSLGQLQSARGVACLGCKGTCSGFEPHSWRKICKSC
<u> </u>	[		KCSQEDHCLTSDLEDDRKIGRLLMDSKYSTLTARVKGGDGIRIY
			KRNRMIMTNPIATGKDPTFDTITYEWAPPGVTQKLGLQYMELIP
			KEKQPVTGTEGAFYRRRQLMHQLPIYDQDPSRCRGLLENELKLM
}	. }	ł	EEFVKQYKSEALGVGEVALPGQGGLPKEEGKQQEKPEGAETTAA
	f	ļ	TINGSLSDPSKEVEYVCELCKGAAPPDSPVVYSDRAGYNKOWHP
			TCFVCAKCSEPLVDLIYFWKDGAPWCGRHYCESLRPRCSGCDEI
	1		IFAEDYQRVEDLAWHRKHFVCEGCEQLLSGRAYIVTKGQLLCPT
6657	830		CSKSKRS
1 ,,, 1	030	2120	LLTCQERAGDCLLSASTMKEVVYWSPKKVADWLLENAMPEYCEP
1			LEHFTGQDLINLTQEDFKKPPLCRVSSDNGQRLLDMIETLKMEH
1 1			HLEAHKNGHANGHLNIGVDIPTPDGSFSIKIKPNGMPNGYRKEM
			IKIPMPELERSQYPMEWGKTFLAFLYALSCFVLTTVMISVVHER
( l	1	1	VPPKEVQPPLPDTFFDHFNRVQWAFSICEINGMILVGLWLIQWL
[ [	ļ	j	LLKYKSIISRRFFCIVGTLYLYRCITMYVTTLPVPGMHFNCSPK
ļ İ			LFGDWEAQLRRIMKLIAGGGLSITGSHNMCGDYLYSGHTVMLTL
	1		TYLFIKEYSPRRLWWYHWICWLLSVVGIFCILLAHDHYTVDVVV
[ [	İ	!	AYYITTRLFWWYHTMANQQVLKEASQMNLLARVWWYRPFQYFEK
6658	36		NVQGIVPRSYHWPFPWPVVHLSRQVKYSRLVNDT
7070	35	855	HCCALGAPGSPYRGLYFSSAAPCTAPRKAKHQSTLEGLTKRMLM

			•
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cvsteine, D=Aspartic Acid B
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine
}	location	corresponding	H=H1Stidine, I=Isoleucine, K=Lysine
-	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
ı	amino acid	residue of	S=Serine, T=Threonine, V=Valine
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown *=Ctop
ĺ	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
ł	1		FDPVPVKQEAMDPVSVSYPSNYMESMKPNKYGVTVSTDI DEVER
	j		QTPEGLSHGIQMEPVDLTVNKRSSPPSAGNSPSSI,KFDSGUDDA
ļ			SPGLSMPSSSPPIKKYSPPSPGVOPFGVPLSMPPVMAAALSPUG
			IRSPGILPVIQPVVVQPVPFMYTSHLOOPLMVST.SFFMFNCSSS
		ì	MQVPVIESYEKPISQKKIKIEPGIEPQRTDYYPEEMSPPLMNSV
6659			SPPQALLQE
6639	18	523	EPQRGDCETWFQNCSLPKFVCFFCWGFWLWRAHSMSNLHSLPGL
1			RGLTSISRNQLQCTNAMRVINNYORRWKNONTFI.I.ATEANUANU
			CGNPTITCPHNRTLNNCHHSGVQVPLMYCNLTTPSPONISMCPV
6660			AQTPANMFYIVACDNRDQRRDPPQYPVVPVHLHTTT
0000	514	1707	CAASLDCRHHLCEPDMKLVWPSAKLLOAAAGASARACDSVTSMV
}	1		LPLLLEQFHKHSQSSQRRTILEMLLGFLKLOOKWSYEDKDOPPI
	ł		NGFKDQLCSLVFMALTDPSTOLOLVGIRTLTVICAOPDLLSVPD
			LELAVGHLYRLSFLKEDSQSCRVAALEASGTLAAT, YPVAFSSHI.
1	ł		VPKLAEELRVGESNLTNGDEPTQCSRHLCCLOALSAVSTHDSTV
İ			KETLPLLLQHLWQVNRGNMVAOSSDVIAVCOSLROMARKCOODR
			ESCWYFHQTAIPCLLALAVQASMPEKEPSVLRKVLLEDEVLAAM
j			VSVIGTATTHLSPELAAQSVTHIVPLFLDGNVSFLPENSFPSRF
i			QPFQDGSSGQRRLIALLMAFVCSLPRNVSEHIWEVLLFNLDKVT
6661	179	430	PG
	]	430	GVHAASGTLSATWLAEAKMFDSLAKAGKYLGQAAKLMIGMPDYD
6662	185	423	NYVEHMRVNHPDQTPMTYEEFFRERQDARYGGKGGARCC
i -	""	443	RSLPKPAPAQPASIHCARFSGVTPPTAKTAMSDGNTAFNALMYC
6663	3	1005	GPKADDGNIFSACAPASSAVKASVSVAQPGQAVIP
}		1005	RPVLSSRVDDFVPPLPETSGRRKKLERMYSVDRVSDDIPIRTWF
1			PKENLFSFQTASTTMQAISNFRKHLRMVGSRRVKAQTFAERRER
1			SFSRSWSDPTPMKADTSHDSRDSSDLQSSHCTLDEAFEDLDWDT
1			EKGLEAVACDTEGFVPPKVMLISSKVPKAEYIPTIIRRDDPSII
			PILYDHEHATFEDILEEIERKLNVYHKGAKIWKMLIFCQGGPGH
1 1			LYLLKNKVATFAKVEKEEDMIHFWKRLSRLMSKVNPEPNVIHIM GCYILGNPNGEKLFQNLRTLMTPYRVTFESPLELSAQGKQMIET
1			YFDFRLYRLWKSRQHSKLLDFDDVL
6664	58	968	PRLLRLPRSVVVMDSPWDELALAFSRTSMPPFFDIAHYLVSVMA
i l			VKRQPGAAALAWKNPISSWFTAMLHCFGGGILSCLLLAEPPLKF
1	i		LANHTNILLASSIWYITFFCPHDLVSQGYSYLPVQLLASGMKEV
!!!			TRTWKIVGGVTHANSYYKNGWIVMIAIGWARGAGGTIITNFERL
	1		VKGDWKPEGDEWLKMSYPAKVTLLGSVIFTFQHTQHLAISKHNL
i i			MPLYTIFIVATKITMMTTQTSTMTFAPFEDTLSWMLFGWQQPFS
			SCEKKSEAKSPSNGVGSLASKPVDVASDNVKKKHTKKNE
6665	171	1278	DERRLACRQVVTQQRSELYPGFQKRQRFLPKAGEEAAAQGGRHL
]			PGRWLGPGCTQNPCSVHTATGPEPRKLPLLPPDSPNSGYPKEPA
[		İ	ALCPGIPSPCRMTHQDLSITAKLINGGVAGLVGVTCVFPIDLAK
l t			TRLQNQHGKAMYKGMIDCLMKTARAEGFFGMYRGAAVNLTLVTP
[			EKAIKLAANDFFRRLLMEDGMQRNLKMEMLAGCGAGMCQVVVTC
j i			PMEMLKIQLQDAGRLAVHHQGSASAPSTSRSYTTGSASTHRRPS
	)		ATLIAWELLRTQGLAGLYRGLGATLLRDIPFSIIYFPLFANLNN
1	ŀ		LGFNELAGKASFAHSFVSGCVAGSIAAVAVTPLDVLKTRIQTLK
			KGLGEDMYSGITDCAR
6666	498	2868	MTTFLPVPQMMAGFSFGTFGNPPMESPSAWQTIHQPFIVSCLTL
		İ	WSPGCWPQPIQKEGVGLWDIRKPQSSLLRYGGNLSLQSAMSVRF
1			NSNGTQLLALRRRLPPVLYDIHSRLPVFQFDNQVYFNSCTMKSC
	į	ł	CFAGDRDQYILSGSDDFNLYMWRIPADPEAGGIGRVVNGAFMVL
1		l	KGHRSIVNQVRFNPHTYMICSSGVEKIIKIWSPYKQPGCTGDLD
j	f		GRIEDDSRCLYTHEEYISLVLNSGSGLSHDYANQSVQEDPRMMA
1			FFDSLVRREIEGWSSDSDSDLSESTILOLHAGVSERSGYTDSEC
			SASLPRSPPPTVDESADNAFHLGPLRVTTINTVASTPPTPTCED
			THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY O

SEQ	Predicted	Predicted end	L Amino Colinario
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Ston
i	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence		\=possible nucleotide insertion)
			AASRQQRLSALRRYQDKRLLALSNESDSEENVCEVELDTDLFPR
1		ĺ	PRSPSPEDESSSSSSSSSSEDEEELNERRASTWQRNAMRRRQKT
			TREDKPSAPIKPTNTYIGEDNYDYPQIKVDDLSSSPTSSPERST
1			STLEIQPSRASPTSDIESVERKIYKAYKWLRYSYISYSNNKDGE
1			TSLVTGEADEGRAGTSHKDNPAPSSSKEACLNIAMAQRNQDLPP
j	j		EGCSKDTFKEETPRTPSNGPGHEHSSHAWAEVPEGTSQDTGNSG
	İ		SVEHPFETKKLNGKALSSRAEEPPSPPVPKASGSTLNSGSGNCP RTQSDDSEERSLETICANHNNGRLHPRPPHPHNNGQNLGELEVV
			AYSSPGHSDTDRDNSSLTGTLLHKDCCGSEMACETPNAGTREDP
1			TDTPATDSSRAVHGHSGLKRQRIELEDTDSENSSSEKKLKT
6667	171	1310	ABEVERLAAMRSDSLVPGTHTPPIRRRSKFANLGRIFKPWKWRK
	1		KKSEKFKHTSAALERKISMRQSREELIKRGVLKEIYDKDGELSI
			SNEEDSLENGQSLSSSQLSLPALSEMEPVPMPRDPCSYEVLOPS
			DIMDGPDPGAPVKLPCLPVKLSPPLPPKKVMICMPVGGPDLSLV
İ			SYTAQKSGQQGVAQHHHTVLPSQIQHQLQYGSHGQHLPSTTGSL
			PMHPSGCRMIDELNKTLAMTMQRLESSEQRVPCSTSYHSSGLHS
[			GDGVTKAGPMGLPEIRQVPTVVIECDDNKENVPHESDYEDSSCL
l			YTREEEEEEBDEDDDSSLYTSSLAMKVCRKDSLAIKPSNRPSKR
6668	714	358	ELEEKNILPRQTDEERLELRQQIGTKL TLAVATGPALTLRCHVCTSSSNCKHSVVCFASSRFCKTTNTVEP
	,	330	LRGNLVKKDCAESCTPSYTLQGQVSSGTSSTQCCQEDLCNEKLH
I			NAAPTRTALAHSALSIGLALSILAVILAPSI
6669	459	1207	KDEETRKDYDYMLDHPEEYYSHYYHYYSRRLAPKVDVRVVILVS
ĺ			VCAISVFQFFSWWNSYNKAISYLATVPKYRIQATEIAKQQGLLK
İ			KAKEKGKNKKSKEEIRDEEENIIKNIIKSKIDIKGGYOKPOICD
			LLLFQIILAPFHLCSYIVWYCRWIYNFNIKGKEYGEEERLYIIR
			KSMKMSKSQFDSLEDHQKETFLKRELWIKENYEVYKQEQEEELK
6670	184		KKLANDPRWKRYRRWMKNEGPGRLTFVDD
0070	104	594	VARI*GEAAKMSSEPPPPYPGGPTAPLLEEKSGAPPTPGRSSPA
1			VMQPPPGMPLPPADIGPPPYEPPGHPMPQPGFIPPHMSADGTYM PPGFYPPPGPHPPMGYYPPGPYTPGPYPGPGHTATVLVPSGAA
· .			TTVTV
6671	1	763	LPAEKPRSAPNMAGGRCGPQLTALLAAWIAAVAATAGPEEAALP
}	}		PEQSRVQPMTASNWTLVMEGEWMLKFYAPWCPSCQQTDSEWEAF
			AKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGIFRR
			YRGPGIFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFS
] [			ISGKIWHLHNYFTVTLGIPAWCSYVFFVIATLVFGLSMDLVL*V
6672	304		ISQCNWDPPYRHVS*/RPSTNLGVHTAHTSEHLRL
00/2	304	1089	APGSKPVQFMDFEGKTSFGMSVFNLSNAIMGSGILGLAYAMAHT
			GVIFFLALLCIALLSSYSIHLLLTCAGIAGIRAYEQLGQRAFG
			PAGKVVVATVICLHNVGAMSSYLFIIKSELPLVIGTFLYMDPEG
			DWFLKGNLLIIIVSVLIILPLALMKHLGYLGYTSGLSLTCMLFF LVSVIYKKFQLGLCYRATMKQQWESEALVGTPQPRDSTAAVKAQ
ļ	]		MFHS*LTGVLTQWPIMAFAFVCHPGGAGPSITELCRAFQAQD
6673	1116	1963	LQIQTHHTHHGARVTHLGSHQLLANAGTMLCRQQSSSMAPAFSO
	.		SVTCGPSPCVRKQESATKCLHIGACGSDLWARGWEQG*G*GLNV
			WLCPCVAFHRGARPQAEEGGARWNSLVSSPWIPPNP*HSSIGAE
		-	NAVPRP*QG*KVNPSGQERQS\WVLPLPVPGEPLKLPGLPG*NK
	•		SFSRV/SGSKGKWILPRQLM*AS*R\TPRFVPGTQWVPITW/PL
	1	j	ITWH*SAPTPPLKACPAPRESDPCSSCLSCPCVTQHPRFSDTGW
			FGAGHCHSSCDFTRKGAAGGPG
6674	1	440	LEFDYMCQYDYVEVRDGDNRDGQIIKRVCGNERPAPIQSIGSSL
	]		HVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSY
			KCACLAGYTGQRCENLLEERNCSDPG/WPSQWVPENNRGPWAYQ
LJ			PTPC*IGTRVAFFLT

	7	
	ý	ੈ. ਹੈ

SEQ Predicted beginning nucleotide nucleotide location corresponding to first amino acid amino acid segment containing signal procession of the first amino acid residue of amino acid sequence Predicted end nucleotide nucleotide location corresponding to first amino acid residue of amino acid sequence Predicted end nucleotide sequence Amino acid segment containing signal procession procession of the first amino acid segment containing signal procession procession or calculation (A=Alanine, C=Cysteine, D=Aspartic Acid Glutamic Acid, F=Phenylalanine, G=Glyc H=Histidine, I=Isoleucine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, **Codon, /=possible nucleotide insertion)	d. E=
No: nucleotide location corresponding to first amino acid residue of amino acid sequence location corresponding to first amino acid residue of amino acid sequence location corresponding to first amino acid residue of amino acid sequence location corresponding to first amino acid residue of amino acid sequence location location corresponding to first amino acid residue of amino acid sequence location location corresponding to first amino acid sequence location (Blutamic Acid, F=Phenylalanine, G=Glyc H=Histidine, I=Isoleucine, N=Asparagine, P=Proline, Q=Glutamine, G=Glyc H=Histidine, I=Isoleucine, N=Asparagine, P=Proline, Q=Glutamine, G=Glyc H=Histidine, I=Isoleucine, N=Asparagine, P=Proline, Q=Glutamine, G=Glyc H=Histidine, I=Isoleucine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, G=Glyc H=Histidine, I=Isoleucine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, G=Glyc H=Histidine, I=Isoleucine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, G=Glyc H=Histidine, I=Isoleucine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, G=Glyc H=Histidine, I=Isoleucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, G=Glyc H=Histidine, I=Isoleucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, G=Glyc H=Histidine, I=Isoleucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, G=Glyc H=Histidine, I=Isoleucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, G=Glyc H=Histidine, I=Isoleucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, G=Glyc H=Histidine, I=Isoleucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, G=Glyc H=Histidine, I=Isoleucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, G=Glyc H=Histidine, I=Isoleucine, M=Methionine, M=Methionine, M=Methionine, M=Methionine, M=Methionine, M=Methionine, M=Methionine, M=Methionine, M=Methionine, M=Methionine, M=Methionine, M=Methionine, M=Methionine, M=Methionine, M=Methionine, M=Methionine, M=Methionine, M=Methionine, M=Methionine, M=Methionine, M=Methionine, M=Methionine, M=Methionine, M=Methionine, M=Methionine,	d, E= ine,
location corresponding to first amino acid residue of amino acid amino acid amino acid sequence corresponding to first amino acid residue of amino acid sequence corresponding to first amino acid residue of amino acid sequence corresponding to first amino acid sequence corresponding to first L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, ** (Codon, /=possible nucleotide deletion, N=possible nucleotide insertion)	ine,
corresponding to first amino acid residue of amino acid amino acid amino acid amino acid sequence corresponding to first amino acid residue of amino acid sequence corresponding to first amino acid w=Tryptophan, Y=Tyrosine, X=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, N=Asparagine, N=Asparagine, N=Asparagine, N=Asparagine, N=Asparagine, N=Asparagine, N=Asparagine, N=Asparagine, N=Asparagine, N=Asparagine, N=Asparagine, N=Asparagine,	
amino acid residue of amino acid residue of amino acid sequence amino acid sequence amino acid sequence amino acid sequence amino acid sequence \[ P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, ** (Codon, /=possible nucleotide deletion, N=possible nucleotide insertion)	
amino acid residue of sequence   S=Serine, T=Threonine, V=Valine, w=Tryptophan, Y=Tyrosine, X=Unknown, *: Codon, /=possible nucleotide deletion, sequence   \=possible nucleotide insertion)	
residue of amino acid W=Tryptophan, Y=Tyrosine, X=Unknown, *: amino acid sequence Codon, /=possible nucleotide deletion, sequence \=possible nucleotide insertion)	
amino acid sequence   Codon, /=possible nucleotide deletion,   \=possible nucleotide insertion)	
sequence   \=possible nucleotide insertion)	=Stop
, , product induction	
6675 277 1678 GNWPTERMAFLDNPTIILAHIROSHVTSDDTGMCFMVI	
- CANTELLICATE DON'T LITTLE TO A LAND TO THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTRO	IDHDVD
LEKIHPPSMPGDSGSEIQGSVGAQSVDITSSI	NDFGIR
RRSNTAQRLERLRKERQNQIKCKNIQWKERNSKQSAQEI	KSLFE
KKSLKEKPPISGKQSILSVRLEQCPLQLNNPFNEYSKFI GTTATKKIDVYLPLHSSQDRLLPMTVVTMASARVQDLIQ	JGKGHV
YTSEGREPKLNDNVSAYCLHIAEDDGEVDTDFPPLDSNI	FILCMO
GFSTLALVEKYSSPGLTSKESLFVRINAAHGFSLIQVD:	PIHKE
KEILLKAVKRRKGSQKVSGSRADGVFEEDSQIDIATVQI	1.T.KAJM
HYKSFKVSMIHRLRFTTDVQL/GCALFPGVLRKRAAPVI	MESSH
ADTWRQEQIGCCGAACAALRS*DSHKC*EGISGDKVEII	CLRPS
KASTKFWIKQKPISIDSDLLCAC\DLAEE	DMLAAC
6676 277 1678 GNWPTERMAFLDNPTIILAHIRQSHVTSDDTGMCEMVLI	. D. I. D
LEKIHPPSMPGDSGSEIQGSNGETQGYVYAQSVDITSSV	DECT-
RRSNTAQRLERLRKERQNQIKCKNIQWKERNSKQSAQEI	DEGIR
KKSLKEKPPISGKQSILSVRLEQCPLQLNNPFNEYSKFI	MADEE
GTTATKKIDVYLPLHSSQDRLLPMTVVTMASARVQDLIG	T TOWO
YTSEGREPKLNDNVSAYCLHIAEDDGEVDTDFPPLDSNE	TITCMÓ
GFSTLALVEKYSSPGLTSKESLFVRINAAHGFSLIQVDN	LATUVE
KEILLKAVKRRKGSQKVSGSRADGVFEEDSQIDIATVQD	TVALCULT
HYKSFKVSMIHRLRFTTDVQL/GCALFPGVLRKRAAPVI	MIDSSE
ADTWRQEQIGCCGAACAALRS*DSHKC*EGISGDKVEID	יבאועבט
KASTKFWIKQKPISIDSDLLCAC\DLAEE	T VIIIQ
6677 277 1678 GNWPTERMAFLDNPTIILAHIRQSHVTSDDTGMCEMVLI	DHDVD
LEKIHPPSMPGDSGSEIQGSNGETQGYVYAQSVDITSSW	DECTE
RRSNTAQRLERLRKERQNQIKCKNIQWKERNSKQSAQEI	KSLEE
KKSLKEKPPISGKQSILSVRLEOCPLOLNNPFNEYSKFD	GKCHV
GTTATKKIDVYLPLHSSQDRLLPMTVVTMASARVODLIG	LICWO
YTSEGREPKLNDNVSAYCLHIAEDDGEVDTDFPPLDSNE	PIHKF
GFSTLALVEKYSSPGLTSKESLFVRINAAHGFSLIOVDN	TKVTM
KEILLKAVKRRKGSQKVSGSRADGVFEEDSOIDIATVOD	MLSSH
HYKSFKVSMIHRLRFTTDVQL/GCALFPGVLRKRAAPVD	CLRPS
ADTWRQEQIGCCGAACAALRS*DSHKC*EGISGDKVEID	PVTNQ
KASTKFWIKQKPISIUSDLLCAC\DLAEE	
6678 221 865 GPSNQSSGSLSLIVTGCSSYWS*INDTCTILRVLSSNFG	RQ*LR
PFPCSQLPMSQGCLWHLDCCCPWVPYIPGQQWRKGRQRM	RN*OS
LLGSDQESVGLEDLCVFVNFLLHVLLGLFP*PHELFLLP	VVDLG
FLFPLLLQGGCHCLVLPANLVSQAPQIGKLSCRLQTHDL	EGSRN
HHPLFLVVGRWDAVKHLETVQSGLASLGFVGQHTSHGPP	
- I DELFACORIFF DOQUARS POURWART DERSES	FVSDL
SSYCNKEVYNKENLFNSLNYD/SCSQEEKEGHAE*QNQN	S\DFH
QEKWIYVHKGSTKERHGYCTLGEAFNRLDFSTAILDSRR:	FNYVV
RLLELIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQN	ITLIR
ELLQTLYTSLCTLVKRVGKSVLVGNINMWVYRMETILHW	<b>DOOLM</b>
ITATMINAMATANAA	SGLF
NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTEE	SISEE
NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTEE  6680 1498 2951 PLCTLPLMPSALPGWAGERWEKQWPLA/PGPGTWQTPVG	
NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTEE:  6680 1498 2951 PLCTLPLMPSALPGWAGERWEKQWPLA/PGPGTWQTPVG: P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSEGAEIOTS:	A*ALP
NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTEE:  6680 1498 2951 PLCTLPLMPSALPGWAGERWEKQWPLA/PGPGTWQTPVG: P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSEGAEIQTS: /NQVSPPQPM*GAEENGDQRGGKEEAGEELHRSSSGLTA;	A*ALP APGF2
NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTEE:  6680 1498 2951 PLCTLPLMPSALPGWAGERWEKQWPLA/PGPGTWQTPVG: P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSEGAEIQTS: /NQVSPPQPM*GAEENGDQRGGKEEAGEELHRSSSGLTA; EVHRNLQTFPGLPSRGGP/GGAGTQGSWAPGEQPP/SPI	A*ALP APGF? LLPAS
NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTEE.  6680 1498 2951 PLCTLPLMPSALFGWAGERWEKQWPLA/PGPGTWQTPVG: P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSEGAEIQTTS; /NQVSPPQPM*GAEENGDQRGGKEEAGEELHRSSSGLTA; EVHRNLQTFPGLPSRGGP/GGAGTQGSWAPGEQPP/SPI MQRSQAGLPGWEAGLVESPTHHIPALRPSGTNATGEAFPS	A*ALP APGF? LLPAS STTCS
NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTEE.  6680  1498  2951  PLCTLPLMPSALFGWAGERWEKQWPLA/PGPGTWQTPVG: P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSEGAEIQTTS; /NQVSPPQPM*GAEENGDQRGKEEAGEELHRSSSGLTA; EVHRNLQTFPGLPSRGGP/GGAGTQGSWAPGEQPP/SPI MQRSQAGLPGWEAGLVESPTHHIPALRPSGTNATGEAFPS SGP\PAPPGFTGLRPGGGSSSGGHG**PGLPVGKV\GALG	A*ALP APGF? LLPAS STTCS GAAOD
NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTEE:  6680 1498 2951 PLCTLPLMPSALPGWAGERWEKQWPLA/PGPGTWQTPVG: P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSEGAEIQTS: /NQVSPPQPM*GAEENGDQRGKEEAGGELHRSSSGLTA; EVHRNLQTFPGLPSRGGP/GGAGTQGSWAPGEQPP/SPI MQRSQAGLPGWEAGLVESPTHHIPALRPSGTNATGEAFP: SGP\PAPPGFTGLRPGGSSSGGHG**PGLPGKV\GALG PQSQGRGPTQGTVGTEMLLSGLGSAKACPAARPAVP*LPS	A*ALP APGF2 LLPAS STTCS GAAQD SDPAS
NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTEE:  6680  1498  2951  PLCTLPLMPSALPGWAGERWEKQWPLA/PGPGTWQTPVG: P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSGAEIQTS; /NQVSPPQPM*GAEENGDQRGKEEAGEELHRSSSGLTA; EVHRNLQTFPGLPSRGGGP/GGAGTQGSWAPGEQPP/SPI MQRSQAGLPGWEAGLVESPTHHIPALRPSGTNATGEAFP: SGP\PAPPGGPTGLRPGGSSSGGHG**PGLPVGKV\GALG PQSQGRGPTQGTVGTEMLLSGLGSAKACPAARPAVP*LPS TIPKKGTRGFGEGPGVLQERNRWVVGRAQGFTSADAAGTI	A*ALP APGF2 LLPAS STTCS SAAQD SDPAS APPGV
NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTEE:  6680  1498  2951  PLCTLPLMPSALPGWAGERWEKQWPLA/PGPGTWQTPVG: P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSEGAEIQTS; /NQVSPPQPM*SALENGDQRGKEEAGEELHRSSSGLTA; EVHRNLQTFPGLPSRGGGP/GGAGTQGSWAPGEQPP/SPI MQRSQAGLPGWEAGLVESPTHHIPALRPSGTNATGEAFP: SGP\PAPPGFTGLRPGGSSSGGHG**PGLPVGKV\GALG PQSQGRGPTQGTVGTEMLLSGLGSAKACPAARPAVP*LPS TIPKKGTRGFGEGPGVLQERNRWVVGRAQGFTSADAAGTI *LPAPLSQPPGATEPQVRACGMAPPSPGTSGRLVAWGRHI	A*ALP APGF2 LLPAS STTCS GAAQD EDPAS APPGV
NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTEE:  6680 1498 2951 PLCTLPLMPSALPGWAGERWEKQWPLA/PGPGTWQTPVG: P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSEGAEIQTS; /NQVSPPQPM*GAEENGDQRGKEEAGEELHRSSSGLTA; EVHRNLQTFPGLPSRGGGP/GGAGTQGSWAPGEQPP/SPI MQRSQAGLPGWEAGLVESPTHHIPALRPSGTNATGEAFP; SGP\PAPPGPTGLRPGGSSSGGHG**PGLPVGKV\GALG PQSQGRGPTQGTVGTEMLLSGLGSAKACPAARPAVP*LPS TIPKKGTRGFGEGPGVLQERNRWVVGRAQGFTSADAAGT; *LPAPLSQPPGATEPQVRACGMAPPSPGTSGRLVAWGRH AQGCPPGAGCWGSQPRGSQRCPRTYTHSPLGHGRAPCPRE	A*ALP APGF? LLPAS STTCS SAAQD SDPAS APPGV PGPQV RCWH*
NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTEE:  6680  1498  2951  PLCTLPLMPSALPGWAGERWEKQWPLA/PGPGTWQTPVG: P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSEGAEIQTS; /NQVSPPQPM*GAEENGDQRGGKEEAGEELHRSSSGLTA; EVHRNLQTFPGLPSRGGGP/GGAGTQGSWAPGEQPP/SPI MQRSQAGLPGWEAGLVESPTHHIPALRPSGTNATGEAFP: SGP\PAPPGFTGLRPGGSSSGGHG**PGLPVGKV\GALG PQSQGRGPTQGTWGTEMLLSGLGSAKACPAARPAVP*LPS TIPKKGTRGFGEGPGVLQERNRWVVGRAQGFTSADAAGTI *LPAPLSQPPGATEPQVRACGMAPPSPGTSGRLVAWGRHI	A*ALP APGF2 LLPAS STTCS SAAQD SDPAS APPGV PGPQV RCWH*

	◀.	
34263	1 V	

SEQ	Predicted	Predicted end	Dmine and
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ł	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
ì	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	bequence	Codon, /=possible nucleotide deletion,
6681	1169	511	\=possible nucleotide insertion)
	1	311	INYIYYNQQQRAFHELK\EKLMSAPALGLPDLTKLFTLHVSERE
ı			KMTVGVLTQTVGPWSRPGAYLSKQLDGVSKGWPPCPRALAATAL
			LAQEADELTLRQNLNRKSPHA\VVTLINTKGHH*LINARLTRYQ
1	1		TLLCENPHKTIEVSNT/LNPATLLLVTESPVKHNCLEVLDSVYS
1	ł		SRPNLRDHP*TSVDWELYVDGSGFANPCKVTLKKETSPAPVTPR
6682	109	1238	S
0002	103	1238	TVLCGAMQVSSLNEVKIYSLSCGKSLPEWLSDRKKRALQKKDVD
Ī	1		VRRRIELIQDFEMPTVCTTIKVSKDGQYILATGTYKPRVRCYDT
}			YQLSLKFERCLDSEVVTFEILSDDYSKIVFLHNDRYTEFHSOSC
ł	ł		FYYKTRIPKFGRDFSYHYPSCDLYFVGASSEVYRLNLEQGRYLN
			PLQTDAAENNVCDINSVHGLFATGTIEGRVECWDPPTPNDVGLL
1			D\AP*TVSQQIQR*TSLPTISALKFN\GALTMAVGTTTGQVLLY
			DLRSDKPLLVKDHQYGLPIKSVHFQDSLDLILSADSRIVKMWNK
	ł .		NSGKIFTSLEPEHDLNDVCLYPNSGMLLTANETPKMGTVYTDUT
6683	109	1000	GPAPRWCSFLDNLTEELEENPESNE
""	109	1238	TVLCGAMQVSSLNEVKIYSLSCGKSLPEWLSDRKKRALQKKDVD
1	ì		VRRRIELIQDFEMPTVCTTIKVSKDGOYILATGTVKBDVBCVDT
ļ	[		YQLSLKFERCLDSEVVTFEILSDDYSKIVFI.HNDDVTFFUCOCC
1	i i		FYYKTRIPKFGRDFSYHYPSCDLYFVGASSEVYRINT.EOGPVIN
	1		PLQTDAAENNVCDINSVHGI.FATGTTEGRVFCWhppTpNpvctt
1			D\AP*TVSQQIQR*TSLPTISALKFN\GALTMAVGTTTGQVLLY
İ			DERSDRPLLVKDHQYGLPIKSVHFODSLDLILSADSRIVKMWNK
1	}		NSGKIFTSLEPEHDLNDVCLYPNSGMLLTANETPKMGIYYIPVL
6684	111	527	GPAPRWCSFLDNLTEELEENPESNE
1	***	321	GLRGGTSRGRAGREPEFAAGVLCVVAGFCQSPCPPGGRGREAPA
			PP\SGRRHA*RPA*WLGGPGGDSGGREEGGS/GELQRAMESKMG
	1		ELPLDINIQEPRWDQSTFLGRARHFFTVTDPRNLLLSGAQLEAS
6685	258	1473	RNIVQNYR
	~333	±4/3	KLLGDNFEGFCNKFELSDSENGSNS*QSPL\FDRLFDPDPQKVL
1 1	!		QGVIDMKNAVIGNNKQKANLIVLGAVPRLLYLLQQETSSTELKT
[ ]	1		ECAVVLGSLAMGTENNVKSLLDCHIIPALLQGLLSPDLKFIEAC
í í			LRCLRTIFTSPVTPEELLYTDATVIPHLMALLSRSRYTQEYICQ
	l		IFSHCCKGPDHQTILFNHGAVQNIAHLLTSLSYKVRMQALKCFS
1 1	j		VLAFENPQVSMTLVNVLVDGELLPQIFVKMLQRDKPIEMQLTSA
	j		KCLTYMCRAGAIRTDDNCIVLKTLPCLVRMCSKERLLEERVEGA
j 1	ł	•	ETLAYLIEPDVELQRIASITDHLIAMLADYFKYPSSVSAITDIK
1			RLDHDLKHAHELRQAAFKLYASLGANDEDIRKKVSLGEGRPPVL TASRQGVTST
6686	310	927	
ļ [			DSVTFDDLAVDFTPKEWTLLDPTQRNLYRDVMLENYKNLATVGY
j [		ł	QLFKPSLISWLEQEESRTVQRGDFQASEWKVQLKTKELALQQDV
] [			LGEPTSGIQMIGSHNGGEVSDVKQCGDVSSEHSCLKTHVRTQN
1 1	1		SENTFECYLYGVDFLTLHKKTSTGEQRSVFSHVWKKPSSLNPDV
6687	181	915	VCQKNRCTRKKKAF*LQLTLGKSFH*SIHT
	~~~	713	EAMLEAPYKKEEDEQQRKEVKKDYPSNTTSSTSNSGNETSGSST
ļ l	1		IGETSNRSRDRDRYRRRNSRSRSPGRQCRHRSRSWDRRHGSESR
	İ		SRDHRREDRVHYRSPPLATGEPVDNLSPEERDARTVFCMQLAAR
	1		IRPRDLEDFFSAVGKVRDVRIISDRNSRRSKGIAYVEFCEIQSV
	1		PLAIGLTGQRLLGVPIIVQASQAEKNRLAAMANNLQKGNGGPMR
6688	1025	1	LYVGSLHFNITEDMLRGIFEPFGKV
	1023	- 1	AEVPNYPRVFHKCPDSCWRFKFQPIQLQPYILLSFSSEKPPISF
! !	}		SEPGLPR/SATARMATAAAPPNSSIDLPSDSGMGFISPAGDSLD
	ļ	j	LPSDGGTGFFSLAGDSSSTRLSSLAFISFSLSSVSVGSSAGTTS
	ļ	ŀ	STSVGSVVAAFTSSSSSSTNRDVAGLDFSTVITSVSGSLVPSPE
			VAVICGSKGAGASGSASCSSRAGKTTEATAASSMPSGTSSFSTC
			TMSELEELFSLFSPAPLLSKLFTSSGSIAICCODSGPSDTGRIS
			VCQLWLADSDTGKLSDCQEVVTVGDSGGLTCPELSLGRM*MSLL

SEO	Predicted	I haddened and	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Į.	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ŀ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
			SSAVIPGYSSSSDSRLNTVPTVDLLCPFQTKSST
6689	640	1299	SSSASYATSATSISDTAFSGSLKLKHGLLSALDSSSRTS*STSS
1			AEDSTFRICSPSVSDTSSDSSGSKDNVLILFSKVSI*SCESLSS
		İ	FFSDSISFCFSSSSFCKR*FVSSKVSONALLSSRLSNGPGGSSK
		İ	QRNSLTARQLAMSL*ATKF*RNACNPNCLSSKKSAL*LSLNORF
<u> </u>			GGSASRKPGNISFNSQKCSALSYCCNFVIKPREVSVSSENYPAF
6690	1	442	GTRGKMAATLGPLGSWQQWRRCLSARDGSRMLLLLLLLGSGOGP
			QQVGAGQTFEYLKREHSLSKPYQGVGTGSSSLWNLMGNAMVMTO
1			YIRLTPDMQSKQGALWNRVPCFLRDWELQVHFKIHGQGKKNL\H
6691			GDGLAIWYTKDRMQP
6697	287	1401	LKTETSEEKARRYKDRPSQLNAVFQEQKKMIQAQESITLEDVAV
ł	ł		DFTWEEWQLLGAAQKDLYRDVMLENYSNLVAVGYQASKPDALFK
ļ			LEQGEQLWTIEDGIHSGACSDIWKVDHVLERLQSESLVNRRKPC
l			HEHDAFENIVHCSKSQFLLGQNHDIFDLRGKSLKSNLTLVNQSK
[t and the second		GYEIKNSVEFTGNGDSFLHANHERLHTAIKFPASQKLISTKSQF
			ISPKHOKTRKLEKHHVCSECGKAFIKKSWLTDHQVMHTGEKPHR
	1		CSLCEKAFSRKFMLTEHQRTHTGEKPYECPECGKAFLKKSRLNI HQKTHTGEKPYICSECGKGFIQKGNLIVHQRIHTGEKPYICNEC
ı	J .		/GKGFIQKTCLIAHQRFHTER
6692	178	939	WIKEGELSLWERFCANIIKAGPMPKHIAFIMDGNRRYAKKCQVE
}	i l		RQEGHSQGFNKLAETLRWCLNLGILEVTVYAFSIENFKRSKSEV
			DGLMDLARQKFSRLMEEKEKLQKHGVCIRVLGDLHLLPLDLQEL
] .		IAQAVQATKNYNKCFLNVCFAYTSRHEISNAVREMAWGVEQGLL
			DPSDISESLLDKCLYTNRSPHPDILIRTSGEVRLSDFLLWQTSH
			SCLVFQPVLWPEYTFWNLFEAILQFOMNHSVLOK
6693	178	939	WIKEGELSLWERFCANIIKAGPMPKHIAFIMDGNRRYAKKCOVE
	<u> </u>		RQEGHSQGFNKLAETLRWCLNLGILEVTVYAFSIENFKRSKSEV
	i		DGLMDLARQKFSRLMEEKEKLQKHGVCIRVLGDLHLI.PLDLOFI.
1			IAQAVQATKNYNKCFLNVCFAYTSRHEISNAVREMAWGVEQGLL
	! !		DPSDISESLLDKCLYTNRSPHPDILIRTSGEVRLSDFLLWQTSH
6694	292	813	SCLVFQPVLWPEYTFWNLFEAILQFQMNHSVLQK
0031	232	913	SLLLHLAPPGAYTPSQPLSSVSTETASSVRRQAAESRQHELPVR
			EVHSLGQILPQDGLTAEAGPPEAQDPWGSPGISLPAAHIGFAAA
			LAVGPSGCHTEP\FDEVWPSLFLGDAYAARDKSKLIQLGITHVV
6695	292	813	NAAAGKFQVDTGAKFYRGMSLEYYGIEADDNPFFDLSVYFLP SLLLHLAPPGAYTPSQPLSSVSTETASSVRRQAAESRQHELPVR
		013	EVHSLGQILPQDGLTAEAGPPEAQDPWGSPGISLPAAHIGFAAA
			LAVGPSGCHTEP\FDEVWPSLFLGDAYAARDKSKLIQLGITHVV
			NAAAGKFQVDTGAKFYRGMSLEYYGIEADDNPFFDLSVYFLP
6696	1	782	PRVRGRVGERWAFLSVPAAMSSEMEPLLLAWSYFRRRKFOLCAD
		_	LCTQMLEKSPYDQAAWILKARALTEMVYIDEIDVDQEGIAEMML
	1		DENAIAQVPRPGTSLKLPGTNQTGGPSQAVRPITQAGRPITGFL
	İ		RPSTQSGRPGTMEQAIRTPRTAYTARPITSSSGRFVRLGTASML
			TSPDGPFINLSRLNLTKYSQKPKLAKALIEYIFHHENDVKTALD
1			LAALSTEHSQYKDWWWK/DQIEKCYYRVGMYREAEKOIKSS
6697	3	782	PPLFLRRLNSRALRPGSRKVMAVVPASLSGODVGSFAYLTIKDR
	ŧ		IPQILTKVIDTLHRHKSEFFEKHGEEGVEAEKKAISLLSKIRNE
l			LQTDKPFIPLVEKFVDTDIWNQYLEYQQSLLNESDGKSRWFYSP
		ĺ	WLLV\ECYMYRRIHEAI\IQSPPIDYFDVFKESKEQNFYGSOES
1	Į		IIALCTHLQQLIRTIEDLD\ENQLKDEFFKLLQISLWGEISVDL
			SL\SGGESSSQNTNVLNSLEDLKPFILLNDMEHLWSLLSNCK
6698	668	754	VGSCACAGSCKCKECKCTSCKKSECRAFP
6699	325	492	EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV
1	ĺ		LLGKRKGSVGAGSFQLPGGHLEFGETWEECAQRETWEEAALHLK
			NVHFASVVNSFIEKENYHYVTILMKGEVDVTHDSEPKNVEPEKN

SEQ	Predicted	Predicted end	Amino
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			ESKRIIYNHAFFFQESKWSGGILO
6700	1098	1392	TQCWRSSTPGMRTHFRTQP/RLECGOGFSOOENGHCMDTNECTO
	ļ		FPFVCPRDKPVCVNTYGSYRCRTNKKCSRGYEPNEDGTACVERT
			LLLGLCNLLGK
6701	2	1485	AAAGPRTRVRRAAAFEGQPSPSPGLGPTSDKAAAPRTPKRRRLW
1	}		RQRQ/HPAMLCYVTRPDAVLMEVEVEAKANGEDCLNOVCRRLGT
1			IEVDYFGLQFTGSKGESLWLNLRNRISOOMDGLAPYRIKIRVKF
1			FVEPHLILQEQTRHIFFLHIKEALLAGHLLCSPEOAVELSALLA
			QTKFGDYNQNTAKYNYEELCAKELSSATLNSIVAKHKELEGTSO
1			ASAEYQVLQIVSAMENYGIEWHSVRDSEGOKLLIGVGPEGISIC
I]		KDDFSPINRIAYPVVQMATQSGKNVYLTVTKESGNSTVI.I.FKMT
1			STRAASGLYRAITETHAFYRCDTVTSAVMMOYSRDLKGHLASLF
			LNENINLGKKYVFDIKRTSKEVYDHARRALYNAGVVDLVSRNNO
			SPSHSPLKSSESSMNCSSCEGLSCOOTRVLOEKI.RKI.KEAMI.CM
			VCCEEEINSTFCPCGHTVCCESCAAQLQVGESAAHFCLOPHLSL
6702	397	1971	LLTGSRSQVLAR
1	l 33.	13/1	PLAKFLKLDLVNVLCLPMEDVFLFYRTCFCSMGLGSSCHLSLPK
			RAEALLCSRKATVVRDLVAVRMAEEQEFTQLCKLPAQPSHPHCV
1			NNTYRSAQHSQALLRGLLALRDSGILFDVVLVVEGRHIEAHRIL
			LAASCDYFKGMFAGGLKEMEQEEVLIHGVSYNAMCQILHFIYTS
1			ELELSLSNVQETLVAACQLQIPEIIHFCCDFLMSWVDEENILDV
j ,			YRLAELFDLSRLTEQLDTYILKNFVAFSRTDKYRQLPLEKVYSL LSSNRLEVSCETEVYEGALLYHYSLEQVQADQISLHEPPKLLET
1	[VRFPLMEAEVLQRLHDKLDPSPLRDTVASALMYHRNESLQPSLQ
	ŀ		SPQTELRSDFQCVVGFGGIHSTPS\MSSATRPKYLNPLLGEWKH
			FTASLAPRMSNQGIAVLNNFVYLIGGDNNVQGFRAESRCWRYDP
1			RHNRWFQIQSLQQEHADLSVCVVGRYIYAVAGRDYHNDLNAVER
			YDPATNSWAYVAPLKREVYAHAGATLEGKMYITCGRKGRIT
6703	45	1244	GVGPRAAAMPLELELCPGRWVGGQHPCFIIAEIGQNHQGDLDVA
1 1	l		KRMIRMAKECGADCAKFQKSELEFKFNRKALERPYTSKHSWGKT
1 [YGEHKRHLEFSHDQYRELQRYAEEVGIFFTASGMDEMAVEFLUE
			LNVPFFKVGSGDTNNFPYLEKTAK/TRGWHSVI.RDVCGVOI.NDE
] }	i		TSSWDVLGRVRTSKEKVLMVLVLDYSGRPMVISSGMOSMDTMKO
			VYQIVKPLNPNFCFLQCTSAYPLOPEDVNLRVISEYOKI.FDDID
			IGYSGHETGIAISVAAVALGAKVLERHITLDKTWKGSDHSASTE
ļ l	-		PGELAELVRSVRLVERALGSPTKOLLPCEMACNEKI.GKSVVAKV
1	1		KIPEGTILTMDMLTVKVGEPKGYPPEDIFNLVGKKVLVTVEEDD
6704	82	1007	TIMEE
'		1007	TMNTRNRVVNSGLGASPASRPTRDPQDPSGRQGELSPVEDQREG
		1	LEAAPKGPSRESVVHAGQRRTSAYTLIAPNINRRNEIQRIAEQE
			LANLEKWKEQNRAKPVHLVPRRLGGSQSETEVRQKQQLQLMQSK
<u> </u>		ļ	YKQKLKREESVRIKKEAEEAELQKMKAIQREKSNKLEEKKRLQE
1		İ	NLRREAFREHQQYKTAEFL/RQTEHRIARQKCLSKCCLWPTILN
Į j		-	MGQKLGLQ\DSLKAEENRKLQKMKDEQHQKSELLELKRQQQEQE RAKIHQTEHRRVNNAFLDRLQGKSQPGGLEQSGGCWNMNSGNSW
	1	f	GI
6705	2	786	RLCRNSARVPCGWSASRSLGEGAGFIGPLRGPHPRAGGTGTSFT
			SYKRKGGIMSTIAAFYGGKSILITVATGFLGKELMEKLFRTSPD
			LKVIYILVRPKAGQTLQHRVFQILDSKLFEKVIEVRPNVHEKIR
]		1	AIYADLNQNDFAISKEDMQELLSCTNIIFHCAATVRFDDTLRHA
			VQLNVTATRQLLLMASQMPKLEAFIHISTAYSNCNLKHIDEVIY
<u> </u>			PCPVEPKKIIDSLEW\LDDAIIDEITPKLIRDWPNIYTYTK
6706	130	531	FTHSSSSHSQEMLGKLNMLRNDGHFCDITIRVQDKIFRAHKVVL
ŀ		•	AACSDFFRTKLVGQAEDENKNVLDLHHVTVTGFIPLLEYAYTAT
1			LSINTENIIDVLAAASYMQMFSVASTCSEFMKSSILWNTPNSQP
		1	EK EK

SEQ	Predicted	Predicted end	I Amino
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phonylalanine, G=Glycine,
l	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
İ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
j.	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
j	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence	<u> </u>	\=possible nucleotide insertion)
6707	2233	1343	YWSGIGYELQHFHWRKFHFEKKGPPSTCQBRLYESRSRWPCIS*
	!		GMVVVGWTAVNGSW*GGQLRCVCVCTSHSSDSTRSSQRASKCHS
1	!		FFILSQ*KT*SSWENWVFAKYSRIYSYGHSCSKGRGD*DFK*NV
	İ		SQAR*SRFCGLCNPCGHCGLDINLRGGSSPWTDKHSCVHNNI.I.C
1			NRRVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRLCEH
	<u> </u>		TD*LPK*GPGYIQHFHCDSNILCILYNISFNLFSYSF*GVARYA
			C*RCHWYFEWLLYNHCGDILVACL*RRQL*SSO
6708	115 .	1729	TVGSWSRSGRSPPVGRQLLLTGRGAQAAGSPQGGMALQVELVPT
1	1		GEIIRVVHPHRPCKLALGSDGVRVTMESALTARDRVGVODFVI.I.
			ENFTSEAAFIENLRRRFRENLIYTYIGPVLVSVNPYRDLOIYSR
1			QHMERYRGVSFYEEPPHLLAVADTVYRALRTERRDOAVMISVES
[GAGKTDATKRLLQLYAETCPAPORGGAVRDRLLOSNPVLEAEGN
1			AKTLRNDNSSRFGKYMDVQFDFKGAPVGGHILSYLLEKSRVVHQ
			NHGERNFHIFYQLLEGGEEETLRRLGLERNPQSYLYLVKGQCAK
			VSSINDKSDWKVVRKALTVIDFTEDEVEDLLSIAASVLHLGNIH
1			FAANEESNAQVTTENQLKYLTRLLSVEGSTLREALTHRKIIAKG
1	j j		EELLSPLNLEQAAYARDALAKAVYSRTFTWLVGKINRSLASKDV
			ESPSWRSTTVLGLLDIYGFEVFQHNSFEQFCINYCNEKLQQLFI
			ELTLKSEQEEYEAEGIAWEPVQYFNNKIICDLVEEKFKGII\SI LDE\ECLRPGE
6709	3	894	PPHEHLFPSGERGPFSFLVSRRGLGPGKMGKKGKKEKKGRGAEK
	_	034	TAAKMEKKVSKRSRKEEEDLEALIAHFQTLDAKRTQTVELPCPP
			PSPRLNASLSVHPEKDELILFGGEYFNGQKTFLYNELYVYNIRK
1	ĺ		DTWTKVDIPSPPPRRCAHQAVVVPQGGGQLWVFGGEFASPNGEQ
			FYHYKDLWVLHLATKTWEQVKSTGGPSGRSGHRMVAWKRQLILF
1	,		GGFHESTRDYIYYNDVYAFNLDTFTWSKLSPSGTGPTPRSGCQ\
L :			IPSLPRAASSVYGGYSKQRVKKDVDKGTRHSDMF
6710	158	980	RHKMTNYRVESSSGRAARKMRLALMGPAFIAAIGYIDPGNFATN
1 1			IQAGASFGYQLLWVVVWANLMAMLIQILSAKLGIATGKNLAEQI
1			RDHYPRPVVWFYWVQAEIIAMATDLAEFIGAAIGFKLILGVSLI.
1	i		QGAVLTGIATFLILMLQRRGQKPLEKVIGGLLLFVAAAYIVELT
1	1		FSQPNLAQLGKGMVIPSLPTSEAVFLAAGVL\GATIMPHVI/VI
1	i		WHSSLTQHLHGGSRQQRYSATKWDVAIAMTIAGFVNLAIMATAA
- 6333			SELNFYGHTGVA
6711	3	347	VTECKTMTCKMSQLERNI*TMINTLHHYSVKLGHPDTLIHGEFK
1			ELVRTDLHNILMKENKNDQAI*HIMEDLDTNAHMOIIFKELTMI.
6712	118	CHO	MAMLTWSYHDNMHDADYGPGQQHRPG
"/1"	710	578	PHGQKRTRYPQVRAPGQQPQAQLAMALCLKQVFAKDKTFRPRKR
] !]		FEPGTQRFELYKKAQASLKSGLDLRSVVRLPPGENIDDWIAVHV
!!	1		VDFFNRINLIYGTMAERCS*TSCPVMAGGPRYEYRWQDERQYRR
6713	2485	3	PAKLSAPRYMALLMDWIESLI
"		د	QARGSDSEDGEFEIQAEDDARARKLGPGRPLPTFPTSECTSDVE
			PDTREMVRAQNKKKKKSGGFQSMGLSYPVFKGIMKKGYKVPTPI
1			QRKTIPVILDGKDVVAMARTGSGKTACFLLPMFERLKTHSAQTG
ļ ļ			ARALILSPTRELALQTLKFTKELGKFTGLKTALILGGDRMEDQF AALHENPDIIIATFGRLVHVAVEMSLKLQSVEYVVFDEADRLFE
]	-	1	MGFAEQLQEIIARI,PGGHQTVLFSATLPKLLVEFARAGLTEPVL
	\	İ	IRLDVDTKLNEQLKTSFFLVREDTKAAVLLHLLHNVVRPQDQTV
	1	}	VFVATKHHAEYLTELLTTQRVSCAHIYSALDPTARKINLAKFTL
		[GKCSTLIVTDLAARGLDIPLLDNVINYSFPAKGKLFLHRVGRVA
		1	RAGRSGTAYSLVAPDEIPYLLDLHLFLGRSLTLARPLKEPSGVA
[1	!	GVDGMLGRVPQSVVDEEDSGLQSTLEASLELRGLARVADNAQQQ
[]		ļ	YVRSRPAPSPESIKRAKEMDLVGLGLHPLFSSRFEEEELQRLRL
!	į	J	VDSIKNYRSRATIFEINASSRDLCSQVMRAKRQKDRKAIARFQQ
1			GQQGRQEQQEGPVGPAPSRPALQEKQPEKEEEEEAGESVEDIFS
	1	.]	EVVGRKRQRSGPNRGAKRRREEARQRDQEFYIPYRPKDFDSERG
			THE TAXABLE TELEVISION OF THE TAXABLE DE LA CONTRACTOR DE

SEQ	Predicted	1 20-	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid E_
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	-	\=possible nucleotide insertion)
			LSISGEGGAFEQQAAGAVLDLMGDEAQNLTRGRQQLKWDRKKKR
ŀ		ĺ	FVGQSGQEDKKKIKTESGRYISSSYKRDLYQKWKQKQKID*S*L
ł	1	}	GRRGILTRRRPRTEEVGEARPLAOAGCIPGPHAPPHPLOAFSA
6714			LELKTKQQILKQRRRAQKAALSLORWWPOAALCPO
6/14	169	1416	NNCQELLPPPPAPMAHIPSGGAPAAGAAPMGPOYCYCKVELSVS
ı	i		GQNLLDRDVTSKSDPFCVLFTENNGRWIEYDRTETAINNINDAE
]			SKKFVLDYHFEEVQKLKFALFDODKSSMRLDEHDFT.GOFSCST.G
			TIVSSKKITRPLLLLNDKPAGKGLITIAAORLSDNRVITLSLAG
I			RRLDKKDLFGKSDPFLEFYKPGDDGKWMLVHRTEVIKVTLDDVW
1			KPFTVPLVSLCDGDMEKPIOVMCYDYDNDGGHDFTGFFOTGUGO
			MCEARDSVPLEFECINPKKQRKKKNYKNSGIIILRSCKINRDYS
1			FLDYILGGCQLMFTVGIDFTASNGNPLDPSSLHYINPMGTNEYL
	1		SAIWAVGQIIQDYDSDKMFPALGFGAQLPPDWKVSHEFAINFNP TNPFCSGVDGIAQAYSACLP
6715	32	493	GPAGAESCELUCI DATIONA CONVIGUISMO
	İ		GPAGAESGSLHCLPATVQALAGAAHSPHGGQPPRRGPLIGSGMP GKPKHLGVPNGRMVLAVSDGELSSTTGPQGQGEGRGSSLSIHSL
	•		PSGPSSPFPTEEQPVASWALSFERLLQDPLGLAYFTEFLKKEFS
	<u> </u>		AENVTFWKACERFQQIPASDT
6716	1	176	GAGGPAPRSFGSEEPRAALERDKMSARAAAKSTAMEETAIWEQ
			HTVTLIRVSLCCSK
6717	115	896	LFAMSGFENLNTDFYQTSYSIDDQSQQSYDYGGSGGPYSKQYAG
			YDYSQQGRFVPPDMMQPQQPYTGOIYQPTQAYTPASPQPFYCNN
			FEDEPPLLEELGINFDHIWOKTLTVI.HPI.KVADGGIMNETDIAG
			PMVFCLAFGATLLLAGKIQFGYVYGISAIGCLGMFCIJ.NI.MCMT
1	l i		GVSFGCVASVLGYCLLPMILLSSFAVIFSLOGMVGIILTAGITG
6718	290	599	WCSFSASKIFISALAMEGQQLLVAYPCALLYGVFALISVF
		593	KQSSTVPGTILPSLKWHNSGLCKFPETGGKMTTFKEGLTFKDVA
			VIFTEEELGLLDPVQRNLYQDVMLENFRNLLSVGHHPFKHDVFL
6719	1	691	LEKEKKLDIMKTATQ
}]	_	0,7,1	PTRPEEQDREDGKCHKMEMNPISGNLNCDPIAMSQCSSDHGCET
1 1			DLDSDDDKIEKPNNFMKDSASQDNGLSRKISRKRVCSSDSDSSL
			QVVKKSSKARTGLLRITRRCAATAANKIKLMSDVEDVSLENVHT RSKNGRKKPLHLACTTAKKKLSDCEGSVHCEVPSEQYACEGKPP
Į j	1		DPDSEGSTKVLSQALNGDSDSEDMLNSEHKHRHTNIHKIDAPSK
			RKSSSVTSSG
6720	3	822	HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA
1 1	į		VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY
1			QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF
			LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASPEGTEDSALUG
1			IEELKKVAAGKKRVIVIGISVGLSAPFVAGOMDCCMNNTAVFLD
1			VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYOITSLLFSM
6721			SVVTLISE
".21	3	822	HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA
]		l	VPITEKSNPLTQDLDKADAENIVRLLGOCDAEIFOEEGOALgry
1			QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGDMAF
1 1			LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG
1	i		IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP
1	1		VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM
6722	1	390	SVVTLISE
	-	350	RSWSKRTWQALPMAVLFLLLFLCGTPQAADNMQAIYVALGEAVE
[İ	LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK
6723	173	659	PGRESRLRLLGNYSLWLEGSKEEDAGRYWCAVLGQHHNYQNW
}	-		VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKLQALT GNEGRVSVENIKOLLOSAUKESSERTILLOSAUKES
	ľ	!	GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL
			AEIARILRPGGCLFLKEPVETAVDNNSKVKTASKLCSALTLSGL

SSO Predicted brighting mucleotide location corresponding brighting mucleotide location corresponding brighting processes and the second corresponding brighting state and the second corresponding amino acid amino acid amino acid amino acid sequence sequen	SEQ	1 8 21 24-3		
No: nucleotide location corresponding to first amino acid research to first amino acid residue of amino acid residue of amino acid sequence sequenc	_	Predicted	Predicted end	Amino acid segment containing signal peptide
Corresponding to first amino acid acid acid acid acid acid acid acid			· ·	Managanine, Cacysteine, Dalamartic Acid to
to first amino acid residue of residue of amino acid sequence sequence 6724 173 659 VOYCTERRAINFUL SAMPHORSEPPILES 6725 356 722 REFEPVILATIVE SAMPHORSEPPILES 6726 98 714 173 659 VOYCTERRAINFUL SAMPHORSEPPILES 6726 6727 356 722 REFEPVILATIVE SAMPHORSEPPILES 6726 98 714 1831 1833 1831 1831 1833 1831 1833 1831 1833 1831 1833 1831 1833 1833 1831 1833 1831 1833 1831 1833 1831 1833 1831 1833 1833 1831 1833 1833 1831 1833 1833 1831 1833 1833 1831 1833 1831 1833 1831 1833 1831 1833 1831 1833 1831 1833 1831 1833 1831 1833 1831 1833 1831 1833 1831 1833 1831 1833 1831 1833 1831 1831 1833 1831 1831 1833 1831 1831 1833 1831 1831 1833 1831 1831 1833 1831 1833 1831 1833 1831 1833 1831 1833 1831 1831 1833 1831 1831 1833 1831 1833 1831 1833 1831 1833 1831 1831 1833 1831 1833 1831 1831 1833 1831 1831 1831 1831 1833 1831 1	, NO:			Giutamic Acid, F=Phenylalanine G-Glyging
Defirit mainto acid mainto aci	i		corresponding	h=hlstldine, I=Tsoleucine K-tycine
maino acid residue of amino acid sequence sequence sequence from the sequence from t			i i	L=Leucine, M=Methionine, N=Asparagine
residue of amino acid sequence Sescrine, T-Threonine, V=Valine,		1		P=Proline, O=Glutamine, R=Arginine
amino acid sequence development sequence sequenc	1			S=Serine, T=Threonine, V=Valine
Sequence Coding, /-possible nuclectide disertion VSVKELOREPITFEEVOSVREHIGHESDNI VSVKELOREPITFEEVOSVREHIGHESDNI COVECTARRADEGISAGGUPAVWDRESSPYEALKGLUDKLOALT GREGNSVENIKGLLOSAIKESSPNI LISGLVEGSTTHHABEIL ABIARILARGCELLEEPVETAVDNINSVITALGSAILLISGL VSVKELOREPITFEEVOSVREHIGHESDNI CAPTURE VSVKELOREPITFEEVOSVREHIGHESDNI ASWELUDPTPDLOALFVORNOGPRINGLEAVEVKSVRMTLCAG ISSYEKGROSKILLSEPLLALDESRNILOSARREDHAGESISIVD ASWELUDPTPDLOALFVORNOGPRINGLEAVEVKSVRMTLCAG ISSYEKGROSKILLSEPLLALDESRNILOSARREDHAGESISIVD ASWELUDPTPDLOALFVORNOGPRINGLEAVEVKSVRMTLCAG ISSYEKGROSKILSEPLLALDESRNILOSARREDHYPIBROGL LERNIVINFLRNGELLLPEGFRENGLLAGAREFFOLKGLAEVKS REMERCELTERITYKSPTPTLEGITUNGKLLCFPGHYFIBROGLEAVEVKSVRMTLCAG GYLVITKOKTITYKSPTPTLEGITUNGKLLCFPGHYFIAVENGK GYLVITKOKTITYKSPTPTLEGITUNGKLLCFPGHYFIAVENGK GYLVITKOKTITYKSPTPTLEGITUNGKLLCFPGHYFIAVENGK GYLVITKOKTITYKSPTPTLEGITUNGKAGARAFFOLKSKRI LERNIVINFLRNGELLLPEGFRENGLLAGAREFFOLKGLAEVKS REMERCELTERITYKSPTYLGHTUNGKGLTGFTOKKSTATT LERNIVINFLRNGELLLPEGFRENGLAGARAFFOLKSKRI LERNIVINFLRNGELLLPEGFRENGLAGARAFFOLKSKRI LERNIVINFLRNGELLLPEGFRENGLAGARAFFOLKSKRI LERNIVINFLRNGELLLPEGFRENGLAGARAFFOLKSKRI LERNIVINFLRNGELLLPEGFRENGLAGARAFOLKER LERNIVINFLRNGELLLPEGFRENGLAGARAFOLKER ROFSTYKOFCOPFFRENGENGLAGARAFOLKER ROFSTYKOFCOPFFRENGENGLAGARAFOLKER GRAIN INGLINEAT LAINGVYANGLIAMTHPELTREMMKSTFYYLREPRTSPRGKK HVPSALKEADELBRIDT USTATAGARAFOLKENGTYTOKAGARAFOLKER GYANTIME LENNIVAR LENNIVA	•		1	W=Tryptophan, Y=Tyrosine X=Unknown + Ch-
SPONSIBLE TUDELOCIDE INSERTION		1	sequence	Codon, /=possible nucleotide deletion
TOP TOP		sequence		\=possible nucleotide insertion\
CONTRACTOR CON	6704			VEVKELQREPLTPEEVOSVREHLCHESDNI.
ABLARILRPOGCLFLKSPVETAVNINSKYNTASKLCSALTLSGL VEVKELQRSPLTFEEVGSVEELLGHESDNI. RRTFSPVILATNDDDLMALRRJGESHALQCASKLCSALTLSGL VEVKELQRSPLTFEEVGSVEELLGHESDNI. RRTFSPVILATNDDDLMALRRJGESHALQCASKLCSALTLSGL ASWELVDFTDLQALFVQENDOFFRGGLANEVKWSYMTLCAG ICSYEGKGGMCSILLSSPLLKLRPRKOLLQCASKCHATLANG GYLYTTOKOTILKVPDTILLGURVGKLUCASKURWSKYMTLCAG ICSYEGKGGMCSILLSSPLLKLRPRKOLLQCASKCHATHANG GYLYTTOKOTILKVPTELGURVGKLUCASKCHATHANG REMEUGLTSELGURVGKURTSPLEGURVGKLAGEVKS RWEUGLTSTENDENGOGGLANEVKWSYMTLCAG LFRHVINFLRNGELLJEGGFRENGLAGORNCKSTLMTLANG REMEUGLTSTENTHENGOGGLAFTYRGCGTFDAGGHYFTDRGG LFRHVINFLRNGELLJEGGFRENGLAGORNCKSTLMTLNUG REMEUGLTSTENTHENGOGGLAFTYRGCGTFDAGGHYFTDRGG LFRHVINFLRNGELLJEGGFRENGLAGORNCKSTLMTLNUG REMEUGLTSTENTHENGOGGLAFTYRGCGTGTYRGCTDICCVFLL LAIVGYVANGITATHODORKVITYDDSRGEFCGKGTKNENKP VLVSKSRLDGFPERFSISSNIIGKYPTIKCTDIICCVFLL LAIVGYVANGITATHODORKVITYDDSRGEFCGKGTKNENKP VLYFYRIVKCASPLVLLEFCOTTPOICVEKCPDRVITJHANGSS RDFSYYKOPCVPGFKNIKKAVABVLAGORAVITISKRAGGVLERA ROLAMRIFEDYTVSHAVDIISGRAVITYDDSRGEFCGKGTKNENKP ROLAMRIFEDYTVSHAVDIISGRAVITYDDSRGEVITISKRAGGGCA ROLAMRIFEDYTYSHAVDIISGRAVITYDDSRGEVITISKENGGCAA ROLAMRIFEDYTYSHAVDIISGRAVITYDSRGARTVILLERGINKKVLGI ROLAMRIFEDYTYSHAVDIISGRAVITYDSRGARTVILLERGINKKVLGI LIFNOPDRGCGGRAGGGGGGGGGGGGGGGGGGGGGGAA ROLAMRIFEDYTYCGCGGCGGGGGGGGGGGGGGGCAA VUDDVMABEHVVQDGTBARRIVUSVGTTSVLLENGINKKVLGI LIFNOPDRGCGGRAGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	6724	173	659	VCQYCTARMADFGISAGOFVAVVNDKSSDVRALKCI VDVI CALE
6725 356 722 RRETPEVILATEDDDLMLALRIQUESMINLOGARENHAQESLISUM VEVAELOREPLTPEVEVSVEREILGRESUM ASSELVENTEDLOGAL PROMOCPHROGENES ASSELVENTEDLOGAL PROMOCPHROGENES ASSELVENTEDLOGAL PROMOCPHROGENES ASSELVENTEDLOGAL PROMOCPHROGENES ASSELVENTED AND ASSELVENTED AND ASSELVENTEDLOGAL PROMOCPHROGENES ASSELVENTED AND ASSELVENTED AND ASSELVENTED AND ASSELVENT AND ASSELVENTED AND ASSELVENT AND ASSELVENT AND ASSELVENT AND ASSELVENT ASSELVENT AND ASSELVENT ASSELVENT AND ASSELVENT ASSELVENT AND ASSELVENT ASSELVENT AND ASSELVENT	ł			GNEGRVSVENIKQLLOSAHKESSFDTTI,SCI,VDCcqqqqttichert
6725 356 722 RRRTPPVILLATNDDDLMLAURLGEMENHAGESLSLVD ASWELUDPTPDLOALFVORNOOF PREGLEAVEVEWSYMTLCAG (CSYEGGGMCSILLSPLKLURVEWFV) 6726 98 714 HLQWIGEKINREEKEKSYGKINSLEDTDQGMCKSTLMTLAVG GVILTTOKQTOTTLKYPTELLGUTVGKLURVEWFV (CSYEGGGMCSILLSPLKLURVEWFV) 6727 1 HLQWIGHTHYLDDLMLAURGEMENHAGESLSLVINDLAURGEMEN (CSYEGGGMCSILLSPLKLURVEWFV) 6727 1 831 FRAMEWOLTERPTIFLEITUNGSCOLGEN (CSTLMTLAVG KURLER (CSYEGGGMCSILLSPLAUR) (CSYEGGGMCSILLSPLAUR) (CSYEGGGMCSILLSPLAUR) (CSYEGMCSILLSPLAUR) (CSYEGMCSILL		1		AEIAKILRPGGCLFLKEPVETAVDNNSKVKTASKI.COALTI.CCI
RRRTEFULLATMODDLINLARLIGEENINGEREIDHQESLSIUD ASWELUDPT TDIOLADI-VOPNODO PHOGRAVUM SURVIVIOR ASWELUDPT TDIOLADI-VOPNODO PHOGRAVIMENT LOAG ICS YEGKGGMCSIRLS EPLIKLIPER RDI LVEVEY HIGKWEERK INREKEEKE EEKENSLEIDEGKENEKET LWITLING GYLYITOKOTLIKY POTPILEG I VINGKILCP FDADGHYF I DROGL LERHVILMFLENGELLIJE PER PER OLLAGREF FOLKGLAEEVKS RREKEOLTPRETTFILE I TDINHDRSGGLAI I PER POLKGLAEEVKS RREKEOLTPRETTFILE I TDINHDRSGGLAI I PER POLKGLAEEVKS RREKEOLTRETTFILE I TDINHDRSGGLAI I PER POLKGLAEEVKS RREKEOLTRETTFILE I TDINHDRSGGLAI I PER POLKGLAEEVKS RREKEOLTRETTFILE I TDINHDRSGGLAI I PER POLKGLAEEVKS RREKEOLTRETTFILE I TDINHDRSGGLAI I PER POLKGLAEEVKS LEFKYLVIK SKAPILLIE FOLTPPGI LYGEKKEPRIVITINARSS RDFSYTKQREVERFKNINGVAEVLSPOLTEKKEPRIVITINARSS RDFSYTKQREVERFKNINGVAEVLSPOLTEKKEPRIVITINARSS RDFSYTKQREVERFKNINGVAEVLSPOLTEKKEPRIVITINARSS RDFSYTKQREVERFKNINGVAEVLSPOLTEKKERFTILIGE IN REKENTINGLES RGMININILIJULGY FOLKMENT SKAPILLIE FRANKERSTRUTTE PER POLKGLAE RQMININILIJULGY FOLKMENT SKAPILLIE FRANKERSTRUTTE PER POLKGLAE ROMANNINILIJULGY FOLKMENT SKAPILLIE FRANKERSTRUTTE PER POLKGLAE LIFWODDRROLLMAITHPEIRKEMMKETFKYFLREPTS PRGKK HVPSALKEADSLIMREDT AUGUSTROLLMAITHPEIRKEMMKETFKYFLREPTS PRGKK HVPSALKEADSLIMREDT GEGRGGERGREPTER PORGREGGEOLYPE PROTOGROUND PROT				VEVKELQREPLTPEEVOSVREHLGHESDNI.
6726 98 714 HIQMERKINREKEKETEGKRISLEDTIOGKNESTIMITIANG GYLVITOKOPITLEGI YORKILOPPDADGHYPT DROD LFRHVIMFIRNGELLIPEGRER MOLLAGEAF FPOLKGLAEEVKS RMEKGOLT PRETTFIEL TIDNHERSGELIC LOPPDADGHYPT DROD LFRHVIMFIRNGELLIPEGRER MOLLAGEAF FPOLKGLAEEVKS RMEKGOLT PRETTFIEL TIDNHERSGELI LOPKYPT KR UVSKSRLOGFPEETS ISSNI LOPKYFT KR FREMCEBERHYYGKHOTPOKYDPTEKGFINNGCTETLICOVEL LAIVOYVAVGITAMTHGDPRKVITTIDSGEF GGOGGTENENKP YLLPYFNIVKCASPLVILLEFOCPTPOLOCKCPDRVLITYLINARSS RDFFSYKGROFOKHOKGVAEVLAGGARVLITEKHERAKTEK RGLAMRI FEDYTVSSYMDI ISLGIAMASSLIFI ILLRFLAGIMG RGMI INGILIVLOY 6728 486 935 FCSSWLRSLADSSLSWKNFLVGJITGG IASCKSVJOVFQOLGCA VIDVDUMARHVVOPGYPAHRRI VEVFGTEVLLENGGINRKVLGJ LIFNOPROKLINALT HPEIRKEMKETFKYPLREPRTSPRGKK HVPSALKEADSLIMRDT 6729 259 1191 VOLTGAGSGETASMGEDGRAVAGPALREKLLGTVTVGFLAGSV LAGVKKPDVPCCGRGRCGGGCCYPEKGGRGQPFGPGGONGHP GLOSP POLGGRKGDKERGAFOVTOP KROUGARGVGSPFGADGI POHPGGGFRAR POLGORKONKOGSGEGPGGFPGFGONGHP GLOSP POLGGRKGDKERGAFOVTOP KROUGARGVGSPFGADGI POHPGGGFRAR POLGORKONKOGSGEGPGFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	6725	356	722	RRRTPPVILATMODDLMLALRLOEEWNLOEAERDHAOEGICIUD
6726 98 714 HIQMEREKINREKERKEVEKINSLEDTÖĞÜNÜKÜLÜPFENDÜLÜNÜKÜ GYLYITÜKÖTLIKYPÜTLEĞI ÜNÜĞILÜPFENDÜLÜĞÜNÜKELÜKEPI ÖNÜĞÜLÜPRIVLINÜKÜLÜPFÜNÜĞÜLÜPFENDÜLÜLÜPĞÜNÜĞÜLÜPRIVLINÜKÜLÜPFÜNÜĞÜLÜĞÜLEĞÜKÜKÜNÜ LYFRINLINERÜĞÜLÜLÜPĞÜREĞÜLÜĞÜĞEFÜKÜLÖĞÜLÜFÜLÜĞÜLÜKÜKÜNÜ 6727 1 831 FRÜMÜDERPİYYÜKÜĞITPÖKYÜDİFKĞI YÜNEĞÜTÜLÜÇÜLÜL LAIVQYYAVĞI LAMİRDÜPKÜYİTPÜĞIĞÜĞÜKÜĞITÜLÜKÜĞÜLÜLÜRÜÇÜLÜLÜRÜÇÜLÜLÜRÜÇÜLÜLÜNÜĞÜLÜRÜLÜNÜLÜRÜLÜNÜLÜRÜLÜNÜLÜRÜLÜNÜLÜRÜLÜNÜLÜRÜLÜNÜLÜRÜLÜNÜLÜRÜLÜNÜLÜRÜLÜNÜLÜRÜLÜNÜLÜRÜLÜNÜLÜRÜLÜNÜLÜRÜLÜNÜLÜRÜLÜNÜLÜRÜLÜNÜLÜRÜLÜNÜLÜRÜLÜR		1		ASWELVDPTPDLQALFVOFNDOFFWGOLRAVENKWSVDMTLCAC
HLQKMERKINSLEDTDGGNNCKSTLMTLNVG GYLYITCKQTLTKYPDTFLEGIVNSKLICFPDDAGFYPIDREGI LFRHVLNFLRNGELLLPEGIFNSKLICFPDDAGFYPIDREGI LFRHVLNFLRNGELLLPEGIFNSKLICFPDDAGFYPIDREGI LFRHVLNFLRNGELLLPEGIFNENGLLAQEAEFFOLKGLAEEVKS RMEKEGUTPRETTJELITDNINGGURI FCNAPFISKIKSRI VLVSKSKLIGFPEEFSISSINIJOFKYPIK FFRMGDAGERFHYVKGKHFTPGKYDFFFKGPTIVRGCTDIICCVFLL LAIVCYVAVGILAWTHGDRKVIYTDTSRGEFCGGKGTKNENKP YLFYFNIVKASFLULLEFCCPTFQICVECCDRYLTYLNARSS RDFFYYKQFCVPGFKNNKOVAEVLRGDCCPAVLISKPLARKCF PAHLAYKGUNWONETTYEDGHGSRKNITULVEGAKKANGVLEA RQLAMRIFEDYTVSWWDIISLGIKHRGLEFGBYLAUTLLARGSURA RGMIMGILVLGY FCSSWLESLADSSLSWKMFLVGLTGGTGASKSSVJOVPQOLGCA VIDUDWARRHVVQPGYPAHRRIVEVFGTEVLLENGDINRKVLGD RGMIMGILVLGY 6729 1191 VULTGAGGGRTASMGRDGRAVAGPALRRWLLLGTVTVGFLAGSV LAGVKKFDVPCGGRDCSGCCCYPEKGGRGQPGFVGPQCQXNGPP GLQGFPGLOGRKGDKGERGAFGVTGFKGGWGAGFYGPGPGCQ PGAGAGGGRTASMGRDGRAVAGPALRRWLLLGTVTVGFLAGSV LAGVKKFDVPCGGRDCSGCCCYPEKGGRGQPGFVGPQCQXNGPP GLOGPFGLOGRKGDKGERGAFGVTGFKGGWGAGFYGPGPGGPG PKGQKGEPYAD KEERDRYRGEPGGPGGPGGPGFGGPGFGFGPGPGPG GFWGAGGFRGPFGPGGPGGGGGGPGPGFGGPGFGFGGPGFGGP				ICSYEGKGGMCSIRLSEPLLKLRPRKDI.VEVERV
G727 1 831 FRINTUNGERIERULAGEREPKOLAGEREPKER RWEKEQLTPRETTFLEITDNIBRSGGERIFKUNDFISKIKSRI VLVSKSKLIDSFPERSJISSNIIGPEREFGGKRIEREVKER RWEKEQLTPRETTFLEITDNIBRSGGERIFKUNDFISKIKSRI VLVSKSKLIDSFPERSJISSNIIGPEREFGGKGTKNENKP VLVSKSKLIDSFPERSJISSNIIGPEREFGGKGTKNENKP VLFYENIVKCASPLVLLEFCCTFPCICVEKCDRYLTYLNARSS RDFEYYKQFVPGFKRNKVAEVLRDGDCFAVLIPSKFLARRCF PAIHAYKGVLMYUNDETTTYEDHGSRNIITDLVEGKKRNGVLER RQLAMRIFEDTYVSWYWDIISLGIAMMSLLFIILLRFLAGIMG RGMIIMGILVLGY 6728 486 935 FCSSWLRSLADSSLSWKMFLVGLTGGTASKSVIQVPQQLGCA VLTPVAKKARSVLERA RQLAMRIFEDTYVSWYWDIISLGIAMMSLLFIILLRFLAGIMG RGMIIMGILVLGY UDVDWAMRHVVOPGYPAHRRIVEYFTSVLLENGDINRKVLGD LIFNOPDRRQLIMATHPBIRKEMMKETFKYFLREPRTSPRGKK HYPSALKEADSLUMRDDT 6729 259 1191 VGLTGAGSGRTASMGRDQRAVAGPALRRWLLLGTVTVGFLAGSV LAGVKKFDVPCGGRDCSGCCCYPEKGGRQDGPVGGVNGPP GLGVKFFDVPCGGRPGCGGVPGPGGVNGPP GLGVKFFDVPCGGRPGCGCYPFEKGGRGPFGGVGGPPGGVNGP GLGVKFPDVPCGGRPFGCGGVPFPGGVNGPP GLGVKGFPGADGT GFFLAGKGVGFFGADGT GFFLAGKGVGFFADDGT GFFLAGKGVGFFAGKGVGFAGKGVGFFADDGT GFFLAGKGVGFFADDGT GFFLAGKGVGFFADDGT GFFLAGKGVGFAGKGVGFAGKGVGFFADDGT GFFLAGKGVGFAGKGCFAGKGTAKKKTSA LIKTAKVALKKHFAGTAGKTAKAKTAKKTAGKGFAGKGFAGKGTAKKTAKTAKTAKAKTAGKGFAGKGF	6726	98	714	HLQKMERKINRREKEKEYEGKHNSLEDTDOGKNOKSTI MTI NDIG
6727 1 831 PERMULAYLENGELLIPEGFEROLLAQUESFFOLKGIABEVKS NUMBERCITYPETTIFLETITNINDRSGIGLRIPCANPIFISKIKSRI VLVSKSRLDGFPEFSISSNIIGPKYPIK PERMUSDERPHYYKKHKITPOKUPPJFKGFIYNRGCFDIICCVFLL LAIVGVVAVGIIAMTHGDPRKVIYPTDSRGFPCGKGTKNENKEN VLFYPHIVKCAS PLVLLBFQCPTFQICVECCDR/LITYLNARSS RDFEYYKQPCVPGFKNNKOVAEVLISGAKRANGULFA KAIVGVVAVGIIAMTHGDPRKVIYPTDSRGFPCGKGTKNENKEN PAIHAYKGUMVANDITITEDGHGSRKNITULVGGAKKANGVIEA RQLAMRIFEDYTVSWWDIISLGIAMMSLLFIILLRFLAGIMG RGMIIMGILVJGY PAHRIVEVPGTEVLLENGDINRKVLGG RGMIIMGILVJGY LIPOPORGLLANITHPEIRKEMMKETFKYFLRFPRTSPRGKK VIDVDVMARRVVQPGYPAHRRIVEVPGTEVLLENGDINRKVLGG LIFNOPDRRGLANAITHPEIRKEMMKETFKYFLRFPRTSPRGKK HVPSALKEADSLMRRDT VGLTGGAGGGGGFPGPGGGGGGGGGGGGGGGGGGGGGGGGGGG		ļ		GYLYITQKQTLTKYPDTFLEGIVNGKILCPFDADGUVETDBDGI
6727 1 831 FRGMODERPHYGKHOTPOKYDPHSGGTDICCYPLL LAIVGYVAVGILAMHGDPRKVIPTKGCTDICCYPLL LAIVGYVAVGILAMHGDPRKVIPTKGCTDICCYPLL LAIVGYVAVGILAMHGDPRKVIPTKGCTDICCYPLL LAIVGYVAVGILAMHGDPRKVIPTKGCTDICCYPLL LAIVGYVAVGILAMHGDPRKVIPTDENGEFCGOKGTNENKY YLFYFNIVKCASPLULLEFCCTFOICVEKCPDRYLTYLMARS RDFFYYKOFCVPPFKNKGVAEVLRDGDCFAVLIPSKPLARRCF PAHLAYKGVLMVGNETTTEDGHSSRNITDLVEGKKKANGVLEA RQLAMRIFEDTYVSWYMDIISLGIAMAMSLIFILLERLAGIMG RGMIIMGILVLGY GRMIIMGILVLGY LIFNOPDRRQLIMATTHPEIRGEMSKSSVIOVFOOLGCA VIDVUVMARHVVGPGYPAHRRIVEVFGTEVLLENGDIMRKVLGD LIFNOPDRRQLIMATTHPEIRKEMMKETFKYFLREPRTSPRGKK HVPSALKRADSLMRRRDT GOLGFPGLOGRAGGAVAGPALRRWLLIGTVTVGFLAGSV LAGVKKRDVPCGGRDCSGGCCYPERGGRGGOFPGGVOGNNGPP GLOGFPGLOGRAGGNGRGGGRAPGVGRAGGVGFPGADGI PGHRGGGGPRGPGGGCOTPGKGGNGAGGGFPGCGNNGPP GLOGFPGLOGRAGGNGRGGFPGCGNGRGFPGCGNGPPGG PKGNGKGEPYADPKERERDRYRGEFGEGLUGFGGPPGPGPGGP GFWGABGGRPGPGPGGPGGPGGPGGPGGPGGPGGPGGPGGPGGPGG		i		LFRHVLNFLRNGELLI, PEGFRENOLI, AGENFEROLKGI A FRIMC
1 1 1 1 1 1 1 1 1 1	j	i		RWEKEOLTPRETTFLEITDNHDRSOGLPIECNARDETSKIKERY
FRGMCDERPHYYGKHETPOKYDFTKEGTDIICCVELL LAIVEVVAVGI LAHTHGDPKVITYEDGRGETCGOKGTKNENKP YLFYFNIVKCAS.PLVILEFQCPTFQICVEKCPDRYLTYLMARSS RDFEYYKQFCVPGFKMUNDETTYBEGGGSKRTKTDLVEGAKKANGYLER RQLAMRIFEDYTVSWWIDIISLGIAMAMSLLFIILLRFLAGIMG RGMIMGILVILGS FCSSWLESLADSSLSWKMFLVGLTGGIASGKSSVJQUFQQLGCA VIDUDVMARHVVQGYPAHRRIVEVYGTEVLLENGDIRKVLGD LIFMOPDRRQLLNAITHPBIRKEMKEFTKYFLREPRTSPRGKK HVPSALKEADSLMRRDT 6729 259 1191 VGLTGAGSGKTAMGRDQRAVAGPALRRWLLLGTVTVGFLAGSV LAGVKKPDVPCGGRDCSGGCQCYPEKGGRGQPGPVGPCGYNGPP GLQGFPGLGGRKGDKGERGAPVTRGEDVGARGVSGFPQADGI PGHEGGGBRGRPGVPCGCGTGGDSGPQDPGSEGGTGPPGPCG PKGKGEPYALPKEERDRYRGEPEGEPGLVGGCPPGPVGPCGYNGPP GIPSDTLHPIIAPTGVTFHPPQYKGEKGSEGPGPGPGPGPG GIPSDTLHPIIAPTGVTFHPPQYKGEKGSEGPGFYGPKEGE 6731 1 446 GIRKRLHGAVVPRVEVGCPWETRESEGVHLERFTSPLKNNDEGS LDIYAGLDSAVSDSASKSCVPSRNCLDLYSEILTESGTAKEATY NDLQVSYGKCQLQMKELMKKPKGTQNFSLINENQSLKKNISA LIKTARVEINRKDEEI GRRGRPPPFSPPLWCLQPGGSDPQQDTGUSLKKVISA LIKTARVEINRKDEEI GRRGRPPPFSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTFW AGROVCYTAATTOAAAPATRNCLPDHSGHRPTPPRSHRHHRQEN LGSIKPSSRTKATSTTMAGGGRRABAVERGWGVVTTPRAPIRE GRRLAPQNGGSSDAPANTTPSRGGRREWFSDEPPBVYGDFE PLVAKERSPVGKTRLLEEFRSDSAKEEVRSDEPPBVYGDFE PLVAKERSPVGKTRLLEEFRSDSAKEEVRSDEPPBVYGDFE PLVAKERSPVGKTRLLEEFRSDSAKEEVRSDEPPBVYGDFE PLVAKERSPVGKTRLLEEFRSDSAKEEVRSDEPPBVYGDFE PLVAKERSPVGKTRLLEEFRSDSAKEEVRSDESSE DEASSOTDLSQTISKKTVRSIQAEAPVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEEDDDDSSHSSTVTVKARSRDSESG DKTTRSSSQYTESW 6733 613 1311 RSCRCVGRRSRNGGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKNRREDDVMASGTVKHLLKTSGECERKYKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR LLEGKAYQARKE LLAEKCHRRTVYELLENKKHELLVSGECERKTKKSLELSSEADLI LLAEKCHRRTVYELLENKKHELLUSGECERKTKKSLELSKEDLI LLAEKCHRRTVYELLENKKHELLUSGECERKTKKSLELSKENDLI LLAEKCHRRTVYELLENKKHETTYMKSDDFTNILLEGERERLKK LLEGKAYQARKE SAMMPFVSGCFGELQEKNKSLELVSFEEVAHTEWERDOLDD		<u></u>		VLVSKSRLDGFPEEFSISSNTIOFKVETK
LAIVGYAVGIIAMTHGDPRXVITPTDSRGEFGGQKGTKNENKPY YLFYFNIVKASPIJLLEFGTPQICUEKGDRYLITYLMARSS RDFEYYKQFCVPGFKNIKKQAPQUIRGDCPAVLIPSKPLARRCF PAIHAYKGUAWKGETTYEDGHGSKNITDLVEGARKANGVLER RQLAMRI FEDYTVSWYMDIISLGIAMAMSLLFIILLGFLAGING RGMIIMGILVLGY FCSSWLRSLANSSLSWKMFLVGLTGGIASGKSEVIQVFQQLGCA VIDVDUVARRHVVQPGYPAHRRIVEVFGTEVLLENGGINRKVLGD LIFMQPDRRQLLNAITHPEITREMMKETFKYFLREPRTSPRGKK HVPSALKEADSLMRRDT G729 259 1191 VGLTGAGGSGFTASMGRDDQAVAGPALRRWLLLGTVTVGFLAQSV LAGWKKFDVPCGGRDCSGCQCYPEKGGRQPGVPGPQGYNGPP GLQGFPGLQGRKGDKGERGAPGVTGFKGDWGARGVSGFPGADGI PGHBGGGSPRGRPYDCTGCGSGCQCYPEKGGRQPGPVGPQGYNGPP GLQGFPGLQGRKGDKGERGAPGVTGFKGDWGARGVSGFPGADGI PGHBGGGSPRGRPYDCTGCGSGCQCYPEKGGRQPGPVGPQGYNGPP GLQGFPGLQGRKGDKGERGAPGVTGFKGDWGARGVSGFPGADGI FGHBGGGSPRGRPYDFGCAKGGKGGWGGGFGGGGFGTGFGPGPG PKGQKGEPYALPKEERDRYRGEPGEPLVGGOPPGRPGHVGQM GFVGAAFGRGPFGPBGPGKGGGKRGLGFFGVKGEKGDVQOPPGN GIPSDTLHPIIAPTGVTFHPDQYKGEKGSEGGTGGPGPGG FKGQKGEPYALPKEERDRYRGEPGEPLVGGOPPGRPGHVGQM GFVGAAFGRCPFPGPGPGPGGKGGKRGLGFTGVKGEKGDVQOPPGN GIPSDTLHPIIAPTGVTFHPDQYKGEKGSBGVGPPENKEEAE RKFKEVAEAFVEULSNDEKRDIYDKYTEGLNEF FINALGAVVERVEVGCFWETTESEGVELLEFTFSPLKNNDEGS LDIYAGLDSAVSDSASKSCVPSRNCLDLYEELTTEGTAKEATY NDLQVYSKCCLQMKSLMKKFKEIQTQNFSLINENQSLKKNISA LIKTARVEINRKDESI GRGRAPPGPSPPLWCLQPGGGSDPQGLTOLRHCLSHSPQDTFW AQRQVCYTAATTQAAAPATRNCLPDESGHRFTPPRSHHHHQGEN LGSIKFSSRSTKATSTTMAGGGRAEAVEGWGYVYTRAPIRE GRGRALAPQNGGSSDAPANTFTRLQQCHSCHSPGDPPBWYGDFE PLVAKERSPVGKRTRLEEFRSDSAKECWFSDPPBWYGDFE PLVAKERSPVGKRTRLEEFRSDSAKECWFSDPPBWYGDFE PLVAKERSPVGKRTRLEEFRSDSAKECWFSDPPBWYGDFE PLVAKERSPVGKRTRLEEFRSDSAKECWFSDPPBWYGDFE PLVAKERSPVGKRTRLEEFRSDAKESWGYVVTRAPIRE DEASSGTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPFRYPR YEATSVQQKVNPSBEGGETFEDDQDSSHSVTTVKARSRDSDESG DKTTRSSSQYIESFFW VEATSVQQKVNPSBEGGTFEDDQDSSHSVTTVKARSRDSDESG DKTTRSSSQYIESFFW VEATSVQQKVNPSBEGGTFEDDQDSSHSVTTVKARSRDSDESG DKTTRSSSQYIESFFW LLAGKKATADDAASGTVKRHLKTGGCERKTKKSLELSKEDLI QLLSTMEGGLQAREDVIIMLKTEKTKPEVLEAHYGSAEPEKVK LLAEKCHRTTYYELENEKKHTDYMNRSDDFTNLLEGCERFLKK LLEGKAAQAAKE LLAMPFVSGGCFGELQEENKSLELVSFEWAVHFTWERWONLDD	6727	1 .	831	FRGMGDERPHYYGKHGTPOKYDDTEYCDIYMDGCEDIYGG
### A ### A		l i		LAIVGYVAVGIIAWTHGDPPKVIVPTDGPGPFGGGVGWGWGVGV
RDFYYKOFCVPGFKNKWQAEVILDGDCRAVLIPSKPLARRCE PAILAYKGVLWQKETTYEDGHGSRKNITDLVSGAKKANGVLEA RQLAMR IFEDYTVSWYWDI ISLGIAMAMSLLFI ILLRFLAGIMG RGMI IMGILVLGY FCSSWLRSLADSSLSWKMFLVGLTGGIASGKSEVIQVFQQLGCA VIDVDUVARRHVVQPGYPAHRRIVEVFGTEVLLENGDINRKVLGD LIFMOPDROCLUANITHPEIRKMKEFFKYFLEPRTSPRGKK HVPSALKEADSLMRRDT VGLTGAQSGRTASMGRDQRAVAGPALRRWLLLGTVTVGFLAGSV LAGVKKFDVPCGGRDCSGGCQCYPEKGGRQPGPVGPQGYNGPP GLQGFFGLQGRKGDKGBRGAPGVTGPKGDKGARGVGSPPGPQG PKGQKGBPYALPKEBRRYYRGEPGSEGTTGPPGPQG PKGQKGBPYALPKEBRRYYRGEPGSEGTTGPPGPQG PKGQKGBPYALPKEBRRYYRGEPGSEGTTGPFGPQG GIPSDTLHPI IAPTGVTFHPDQYKGEKGEGEGDGTGPGRFCKGCG GPVGAPGRPGPPGPPGPGCQGNRGLGFYGVKGEKGUDQQPGPN GPVGAPGRPGPPGPPGPKGQCONRGLGFYGVKGEKGUDQQPGPN GPSDTLHPI IAPTGVTFHPDQYKGEKGEGEBGTRGISLKGEE GIM 6731 1 446 GIRKRLHGAVVPRVENGCWETTESEGVLLERFTSPLKNNDEGS LDIYAGLDSAVSDSASKCVPSRCLDLIVEE ILTBEGTAKEATY NDLQVEYGKCQLOMKSLMKKFKEIQTQNFSLINENQSLKKNI SA LIKTARVEINRKDEEI GRGRLAPDNGGSSDAPANTPPRSRCLDLIVEELTITBEGTAKEATY NDLQVEYGKCQLOMKSLMKKFKEIQTQNFSLINENQSLKKNI SA LIKTARVEINRKDEEI GRGRLAPDNGGSSDAPANTPPSRGRREVRFSDEPPEVYGDFE PLVAKRSSVGKTRATSTTMAGGRAEAVERGWYVTPRAPIRE GRGRLAPDNGGSSDAPANTPPSRGRREVRFSDEPPEVYGDFE PLVAKRSSVGKTRATSTTMAGGRAEAVERGWYVTPRAPIRE GRGRLAPDNGGSSDAPANTPPSRQGREVRFSDEPPEVYGDFE DEASSGTDLSQTISKTVTRS (QEAPAVSEDLVIRLRRPPLRYPR YBATSVQCKVNPSEGGFTEDDQDSSHSSVTTVKARSRDSGEG DEASSGYDLSGYISFW DKTTRSSSQYIESFW DKTTRSSSQYIESFW OKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSTMEGGLQAREDVHIMLKTEKKPSULFAHYGSABPEKVLR VLHRCBALDAGAREM LLEGEKANQARKE LLEGEKANQARKE 6734 189 551 SAMMFPVFSGGFQELQEENKSLEUSPEVAVHFFWERWOLDD	[YLFYFNIVKCASPLVIJEFOCPTPOTCVEVCPDDVI TVI NA DOD
### ROLLANY KOULMY GENTTY TEDGIGS RKNITOLUEGAKKANG VLEAR RQLAMRI FEDTTY SWAND LIGIAMAM SLIFI I LIRPLAGIMG RGMIIMGILVLGY #### ROLLAND RESEARCH TO THE PROPERTY OF THE PROPERTY	Ī.			RDFEYYKOFCVPGFKNNKGVAEVI, PDGDCPAVI, I DGWDL A DDGD
6728 486 935 FCSSWLRSLADSSLSWKMFLVGLTGGIASGKSSVIQVFQQLGCA VIDVDVMARHVVQPGYPAHRILVEVFGTEVLLENGDINKKVLGD LIFNOPDRRQLLNAITHPEIREMMKETFKYLREFFTSPRKK HVPSALKEADSLMRRDT 6729 259 1191 VGLTGAGSGRTASMGRDQRAVAGPALRRWLLIGTVTVGFLAGSV LAGVKKFDVPCGGRDCSGGCQCYPEKGGRGPGPVGPQGYNGPP GLQGFPGLQRKGENGFGGBGERGAFGVTDFKGDWGARGVSGFPGADGI PGHPGGGSPRGRPGYDGCNGTGGDSGPQGPPGSEGFTGPGDCDG GPWAPGRFGCPPGPPGPGPGWGRGGPGSGCQPPSEGGTGPGPGDG GPWAPGRFGCPPGPPGPGPGWGRGSGEGEGEGEGWGGPGPGPGPGPG GEVGAPGRFGPPGPPGPGGWGGCONGLGFYGVWKGEKGDWGPGPN GIPSDTLHPIIAPTGVTFHPDQYKGEKGSEGEPGIRGILKEE GIM 6730 784 1015 NMWDYYEVLGLQRYASPEDIKKAYHKVALKWHPDKNPENKEEAE RKFKEVAEAVEVLSNDEKRDIYDKYGTEGLMEF GIRRLHGAVVPRVEVGCPWETRESEGVHLEFFTSPLKNNDEGS LDIYAGLDSAVSDSASKSCVPSRNCLDLYEELILTEEGTAKEATY NDLQVEYGKCQLQMKELMKKFKEIQTQNFSLINENQSLKKNISA LIKTARVEINRKDEEI GRORRPPPSPPLWCLQPGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHRQEN LGSIKFSSRSTKATSTTMAGDGRRAEAVREMGWYVYPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQRREWFGYDPTRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQRREWFGYDPTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQRREWFTSDEPPEVYGDFE PLVAKERSPUGKRTRLEFBDQDSSHSSVTTVKARSRDSDESG DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRPPPLRYPR POETEEMKTRRTTRLQQQHSEQPPLQPSPWTTRNGLRSHSSEE DEASSCTDLSGTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR VEATSVQCKVNFSEEGGTESDQDSSHSSVTTVKARSRCDSCS DKTTRSSGYIESFW 8CKKKNNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI CLLSIMEGELQAREDVIHMLKTEKTKFEVLEAHYGGAPPEKVLR VLHRDAILAQEKSIGEDVERT SELDRLEEKQKFTYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMKKSDDFTNLLEQERERLKK LLEQEKAYQARCE 6734 189 551 SAMPFVFSGCFQELQEKNKSLELVSFEEVAVHFTWEFWONLDD				PAIHAYKGVLMVGNETTVEDGHGSPKNITTDIVEGAVKANGUE
6728 486 935 FCSSMIKASILADSSLSWKMFLVGLTGGTASGKSSVIQVFQQLGCA VIDUDVMARHVVQPGYPAHRRIVEVFGTEVLLENGDINRKVLGD LIFNOPDRRQLLNATTHPETKEMMKETFKYFLREPRTSPRGKK HVPSALKEADSLMRRDT 6729 259 1191 VGLTGAGSGRTASMGRDQRAVAGFALRRWLLIGTVTVGFLAGSV LAGVKKFDVPCGGRDCSGGCCYPEKGGRGQFGPVGPGYNGPP GLQGFPGLQGKGDKGERGAPGVTGPKGDWGARGVSGFPGADGI PGHEGQGGPRGPFGPDGCGCCYCPEKGGRGDGPVGGPGPGPG PKGGKGEPYALPKEERDRYRGEPGEPGLVGFQGPPGPGPGPGPGPGPGPGPGPGPGPGPGPGPGPGPGP				ROLAMRIFEDYTVSWYWDITSLGTAMAMSLIFITLIDBLAGTAG
FCSSWLRSLADSSLSWKMFLVGLTGGIASGKSSVIQVFQQLGCA VIDVDVMARHVVQPGYPAHRIUEVFGTEVLLENGDINKKVLGD LIFNQPDRRQLINAT HTPETRKEMMKETFKYFLEPRTSPRGKK HVPSALKEADSLMRRDT VGLTGAQSGRTASMGRDQRAVAGPALRWLLLGTVTVGFLAQSV LAGVKKFDVPCGGRDCSGGCQCYPEKGGRGQPGPPGPQGYNGPP GLQGFFGLQGRKGDKGERGAPGVTGPKGDWGARGVSGFPGADGI PGGHGGGGGPRGRPGYDGCMGTQGDSGPQGPPGSEGFTGPGPGG GFWGAPGRPGPPGPGCMGTQGDSGPQGPPGSEGFTGPGPGG GFWGAPGRPGPPGPPGPCQGRAGLGFYGVKGEKGDWGPGPN GIPSDTLHP11APTGVTFHPDQVKGEKGSEGEPGIRSLKGEE GIM 6730 784 1015 NMVDYYEVLGLQRYASPEDIKKAYHKVALKWHPDKNPENKEEAE RKKEWAEAVEVLSNDEKRDIVDKKTTGGINEF 6731 1 446 GIRRGLKGAVVPRVEVGCPWFTRESEGVHLERPTSPLKNNDEGS LDIYAGLDSAVSDSASKSCVPSRNCLDLYEELITEEGTAKEATY NDLQVEYGKCQLQMKELMKKFKEIQTQNFSLINENQSLKKNISA LIKTARVEINRKDEI 6732 102 1205 GRWGRPPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AGRQVCYTAATTQAAAPATRNCLPPHSGRRPTPPRSHRHHRQEN LGSIKPSSRSTKATSTIMAGDGRAEAVEGWGVYVTPRAPIRE GRGRLAPQNGGSSDAPAAYTPPSRQGRREVFFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEEVESAYYLRSRQRRQPP POETEEMKTRRTTTRLQQCHSEQPPLQPSPVMTRGGLRDSHSSEE DEASSGTULSGTISKKYTVSLQQAFAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEEDDQDSSHSVTTVKARSRDSDESG DKTTRSSSGYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKSMRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPPULERKOKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCGGELOEKNKSLELVSFEEVAVHFTWERENGDLDD				RGMIMGILVLGY
LIFMOPDRACHAVOPGYPAHREIVEVFGTEVLLENGDINKKULGD LIFMOPDROLINATIHPETRKEMMKETFKYFLEPRTSPRGKK HVPSALKEADSLMRRDT 1191 VGLTGAGSGRTASMGRDQRAVAGPALRWLLLGTVTVGFLAGSV LAGVKKPDVPCGGRDCSGGCOCYPEKGGRGCOPPGPGOGNGPP GLOGFPGLOGRKGDKGERGAPGVTGPKGDVGARGVSGFPGADGI PGHPGQGGPRGRPGYDGCGTGTGDSDPQGPPGFPGPGAGGI PKGQKGEPYALPKEERDRYRGEPGEPGLVFGCPPPGPGGG GPVGAPGRPGPPGPPGPGPGRGHVGOM GPVGAPGRPGPPGPPGPCOCORRGLGFYGVKGEKGDVGQPGPN GIPSDTLHP11APTGVTFHPDQYKGEKGSEGEPGIRGISLKGEE GIM 6730 784 1015 NMVDYYEVLGLQRYASPEDIKKAYHKVALKWHPDKNPENKEEAE RKPKEVARAYEVLSNDEKKDIVDKKGKGGNGF GIRRCHGAVVPRVEVGCPWETRESEGVHLERPTSPLKNNDEGS LDIYAGLDSAVSDSASKSCVPSRCLDLYEELITEEGTAKEATY NDLQVEYGKCQLQMKELMKKFKEIQTQNFSLINENQSLKKNISA LIKTARVEINRKDEEI 6732 102 1205 GRWQRRPPPPSPFWCLQFGGGSDPQOLTOLRHCLSHSPQDTPW AQRQVCYTAATTQAADATRNCLPDHSGRRPTPPRSHRHHRQEN LGSIKPSSRSTKATSTMAGDGRRAEAVREGWGVYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRGGRREVRFDEPPEVYGDFE PLVAKERSPVGKETRLEEFRSDSAKEEWSESAYYLKSROGROPR PQETEEMKTRRTTRLQQQHSSCPPLQPSPVMTRGGLRDSHSSEE DEASSGTULSGTISKKTVRSIQEAPAVSEDLVIRLRRPELRYPR YEATSVQQKVNFSEEGETEEDDQDSSHSSVTTVKARSPDSDESG DKTTRSSSGYIESFW KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI CALSIMEGELQAREDVIHMLKTEKTKPBVLEAHYGSAEPEKVLK VLHRDAILAGEKSIGEDVERPISPESPEGEREKVLK VLHRDAILAGEKSIGEDVERPISPESPEGEREKVLK VLHRDAILAGEKSIGEDVERPISPESPEKVLR VLHRDAILAGEKSIGEDVERPISPESPERPRENCHLEQL LLAEKCHRRTVYELENEKKHTDYMNKSDDFTNLLEQERERLKK LLEGEKAYQAKC LLAEKCHRRTVYELENEKKHTDYMNKSDDFTNLLEGGERERLKK LLEGEKAYQAKC LLAEKCHRRTVYELENEKKHTDYMNKSDDFTNLLEGGERERLKK LLEGEKAYGARG	6728	486	935	FCSSWLRSLADSSLSWKMFLVGLTGGTASCVCCVTOVEOOLOGA
6729 259 1191 VGLTGAQSGRTASMGRDQRAVAGPALRRWLLLGTVTVGFLAQSV LAGVKKFDVPCGGRDCSGGCCYPEKGGRQPGPVGPQGYNGPP GLQGFPGLQGKKGEKGAGPGVTDFKGDGARAVSGFPGADGI PGHPGQGGPRGPGLQGKKGEKGAGPGVTDFKGDGARAVSGFPGADGI PGHPGQGGPRGPGDGCNGTQGDSGPQGPPGSEGFTGPPGPG GFVGAPGRPGPPGPPGPGKGQCNRGLGFYGVKGEKGDVGQPGPN GFPVGAPGRPGPPGPPGPGKGQCNRGLGFYGVKGEKGDVGQPGPN GFPVGAPGRPGPPGPPGPGKGQCNRGLGFYGVKGEKGDVGQPGPN GFPSDTLHPIIAPTGVTFHPDQYKGEKGSEGPGIRGISLKGEE GIM 6730 784 1015 NMVDYYEVLGLQRYASPEDIKKAYHKVALKWHPDKNPENKEEAE RKFKEVABAYEVLSNDEKRDIYDKYGTEGLNEF GIRKRLHGAVVPRVEVGCPWETRESEGVHLERFTSPLKNNDEGS LDIYAGLDSAVSDSASKSCVPSRNCLDLYEEILTEGTAKEATY NDLQVEYGKCQLQMKELMKKFKEIQTQNFSLINENGSLKKNISA LIKTARVEINRKDEEI 6732 102 1205 GRWQRRPPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHRQEN LGSIKPSSRSTKATSTTMAGDGRAEAVREGWGVYVTPRAPIRE GRGRLAPQNGGSSDAAPAYRTPPSRGRREVFRSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQOHSGPPLOPPWTRGLRDSHSSEE DEASSQTDLSGTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVMFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTKTKTREVLEAHYGSAEPEKVUR VLHRDAILAQEKSIGEDVYEKPISEDDRLEKQKRTYLEGLL LLAEKCHRRTVYGLENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQAKE 6734 189 551 SAAMFVYFSGCFGELQEKNKSLELVSFEEVAVHFTWERMODLDD				VIDVDVMARHVVOPGYPAHPRIVEVEGTERILIENGDENDUNG
1191 VGLTGAGGGRTASMGRDQRAVAGPALRRWLLLGTVTVGFLAQSV LAGVKKFDVPCGGRDCSGGCCYPKKGGRQQFQFVGPQGYNGPP GLQGFFGLQGRKGDKGERGAFGVTTGPKGDVGARGVSGFPGADGI PGHPGQGGFRGRBYGCCNGTQGDGAPQGPPGSEGFTGPFGPQG GEVGAPGRPGPPGPGPGCQRRGDKGERGAPGVTGPKGDVGARGVSGFPGADGI PGHPGQGGFRGPBGPPGCPGCQCRRGLGFYGVKGEKGDVGQPGPN GFVGAPGRPGPPGPPGRGQQCNRGLGFYGVKGEKGDVGQPGPN GFVGAPGRPGPPGPPGPKGQQCNRGLGFYGVKGEKGDVGQPGPN GFVGAPGRPGPPGPPGPKGQQCNRGLGFYGVKGEKGDVGQPGPN GFVGAPGRPGPPGPPGPKGQQCNRGLGFYGVKGEKGDVGQPGPN GFVGAPASPEDIKKAVHKVALKWHPDKNPENKEEAE RKFKEVABAYEVLSNDEKRDIYDKYGTGEINEF GFRKRLHGAVVPRVEVGCVWETRESEGVHLERFTSPLKNNDEGS LDIYAGLDSAVSDSASKSCVPSRNCLDLYEEILTEEGTAKEATY NDLQVEYGKCQLQMKELMKFKEIQTONFSLINENQSLKKNISA LIKTARVEINRKDEEI 6732 102 1205 GRWGRPPPSSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTFW AQRQVCYTAATTQAAAPATRNCLPDHSGHRFTPPRSHRHHRQEN LGSIKKSSRSTKATSTTMAGDGRRAEAVREGWGVVTVFRRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQOHSEQPPLQPSPWMTRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETTEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQVIESFS 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKFPVLEAHYGSABPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEKGKFTYRRMLEQL LLAEKCHRRTVYELLENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFVVFSGCFGELQEKNSLELVSFEEVAVHFTWERMODLDD	1 . 1	,		LIFNOPDRROLLNAITHPEIRKEMMKETEKVELDERGDINRKVLGD
1191 VCLTGAQSGRTASMGRDQRAVAGPALRRWLLLGTVTVGFLAQSV LAGVKKFDVPCGGRDCSGGCCTYPEKGGRGQFGPVGPQGYNAPP GLQGFPGLQGRKGDKGERGAPGVTGPKGRUGARGVSGFPGADGI PGHPGQGGPRGRPGYDGCNGTVGDGSPQGPPGSEGFTGPPGPGG PKGQKGEPYALPKEERDRYRGEPGEBGLUGFQGPPGSEGFTGPPGPGG GPVGAPGRPGPPGPGKQQQGNRGLGFYGVKGEKGDVQQFPGN GIPSDTLHPIIAPTGVTFHPDQYKGEKGSEGEPGIRGISLKGEE GIM 1015 NMUDYYEVLGLQRYASPEDIKKAYHKVALKWHPDKNPENKEEAE RKFKEVAEAYBVLSNDEKRDIYDKYGTEGINEF GIRKRLHGAVVPRVEVGCPWETRESEGVHLERPTSPLKNNDEGS LDIYAGLDSAVSDASSKCVPSRNCLDLYEELITEEGTAKFATY NDLQVEVGKCQLQMKELMKKFKEIQTQNFSLINENQSLKKNISA LIKTARVEINRKDEEI GRWRRFPPPSPFLWCLQPGGGSDPQOLTQLRHCLSHSPQDTFW AQRQVCYTAATTOAAAPATRNCLPDHSGHRPTPPRSHRHHQEN LGSIKPSSRSTKATSTTMAGDGRRAEAVERGWGYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAYYLRSQGRQPR PQETEEMKTRITTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEE DEASSCTDLSGTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTGSGCCRKTKKSLELSKEDLI QLLSIMGGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPPEKVLR VLHRDAILAQEKSIGEDVVEKPISEDDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQGLQEKNKSLELVSFERVAHFTWERWOOLDD				HVPSALKEADSLMRRDT
LAGYKKFDVPCGGRDCSGCCCYPBKGGRGPGPVGPQGYNGPP GLQGFPGLQGKKDKGERGAPGVTGPKGDVGARGVSGFPGADGI PGHPGQGFPGLGGKGDKGERGAPGVTGPKGDVGARGVSGFPGADGI PGHPGQGFPGAPGRPGPGDCGDGPQGPFGSEGFTGPPGPQG FKGQKGEPYALPKEERDYRGEPGBPGLVGFQGPGRPGHVGQM GPVGAPGRPGPPGPPGPKGQQGNRGLGFYGVKGEKGDVGQPGPN GIPSDTLHPIIAPTGVTFHPDQYKGEKGSGEGPGISLKGEE GIM NMVDYYEVLGLQRYASPEDIKKAYHKVALKWHPDKNPENKEEAE RKFKEVABAPGVLSNDEKKDIYDKYGTEGLNEF GIRKRLHGAVVPRVEVGCPWETRESEGVHLERPTSPLKNNDEGS LDIYAGLDSAVSDSASKSCVPSRNCLDLYEEILTEEGTAKEATY NDLQVEYGKCQLQMKELMKKFKEIQTQNFSLINENQSLKKISA LIKTARVEINRKDEEI 6732 102 1205 GRWQRRPPPFSPPLWCLQPGGGSDPQQUTOLRHCLSHSPQDTPW ADRQVCYTAATTQAAAPATRNCLPDHSGHRPTFPRSHRHHRQEN LGSIKPSSRSTKATSTTMAGDGRRAEAVREGWGVYVTFRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGREVRFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEBVRESAYYLRSRQRRQPR PQETEEMKTRRITTRLQQQHSEQPPLQPSPVMTRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKNMFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMFGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELEMEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEFWORLDD	6729	259	1191	VGLTGAOSGRTASMGRDORAVAGRALBRULLICTUTION
GLQGFFGLQGRKGDKGERGAPGVTTDFKGDWGARGVSGFPGADGI PGHPGQGGPRGRPGYDGCNGTQGDSGPQGPPGSEGFTGPPGPQG GPWGAPGRPGPPGPPGPKGQQMRGLGFYGVKGEKGDVGQPGPN GIPSDTLHPIIAPTGVTFHPDQYKGEKGSEGPGIRGISLKGEE GIM 6730 784 1015 MMVDYYEVLGLQRYASPEDIKKAYHKVALKWHPDKNPENKEEAE RKFKEVABAYBVUSNDEKRDIYDKKGTGINEF 6731 1 446 GIRKRHGAVVPRVSGCPWETRESEGVHLERPTSPLKNNDEGS LDIYAGLDSAVSDSASKSCVPSRNCLDLYEEILTEGTAKEATY NDLQVEYGKCQLQMKELMKKFKEIQTQNFSLINENQSLKKNISA LIKTARVEINRKDEEI 6732 102 1205 GRWQRFPPPSPPLWCLQFGGGSDPQQLTQLRHCLSHSPQDTFW AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHRQEN LGSIKFSSRSTKATSTTMAGDGRRAEAVREGWGVYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQRREVEREDEPPSVYGDFE PLVAKERSPVGKRTRLEEFFSDSAKEEVRESAYYLRSRQRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVMPSEEGGTEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTTSGECERKTKKSLELSKEDLI VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLEGKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGGFQELQEKNKSLELVSFEEVAVHFTWEFEWORLDD	1 1			LAGVKKFDVPCGGRDCSGGCOCVPFKGGPCODGRUGDSGWGDS
PGHPGGGGPRGRPGYDCNGTGGDSGPGSPGSEGFTGPPGPGG PKGKGEPYALPKEERDRYRGEPGEPGLVGFQGPPGRPGHVGQG GPVGAPGRPGPPGPPGPKGQCONRGLGFYGVKGEKGDVGQPGPN GIPSDTLHPIIAPTGVTFHPDQYKGEKGBGGDFGISLKGEE GIM 6730 784 1015 NMVDYYEVLGLQRYASPEDIKKAYHKVALKWHPDKNPENKEEAE RKFKEVAEAYBVLSNDEKRDIYDKYGTEGLNEF 6731 1 446 GIRKRLHGAVVPRVEVGCPMETRESEGVHLERPTSPLKNNDEGS LDIYAGLDSAVBSASKSCVPSRNCLDLYEEILTEEGTAKEATY NDLQVEYGKCQLQMKELMKKFKEIQTQNFSLINENQSLKKNISA LIKTARVEINRKDEEI 6732 102 1205 GRWQRPPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHQEN LGSIKPSSRSTKATSTTMAGDGRRAEAVRECWGVYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYISSFW 6733 613 1311 RSCRQVGMRSNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDWASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREVIIMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEFWOOLDD	1			GLOGFPGLOGRKGDKGERGAPGVTGPKGDVGAPGVGGPDGAPGA
PREGREPYALPKEERDRYRGEPGEPGLVGFQGPPGRPGHVGQM GPPCAPGRPGPPGPPGPKGQQGNRGLGFYGVKGEKGDUGQPGPN GIPSDTLHPI IAPTGVTFHPDQYKGEKGSEGEPGIRGISLKGEE GIM 6730 784 1015 NMVDYYEVLGLQRYASPEDIKKAYHKVALKWHPDKNPENKEEAE RKFKEVAEAYEVLSNDEKRDIYDKYGTEGLNEF GIRKRLHGAVVPRVEVGCPWETTESEGVHLERPTSPLKNNDEGS LDIYAGLDSAVSDSASKSCVPSRNCLDLYEEILTEGTAKEATY NDLQVEYGKCQLQWKELMKKFKEIQTQNFSLINENQSLKKNISA LIKTARVEINRKDEBI 6732 102 1205 GRWQRRPPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHRQEN LGSIKPSSRSTKATSTTMAGDGRRAEAVREGWGVYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGRREVKFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEPRSDSAKEEVRESAYYLKSRQRRQPR PQETEEMKTRRTTRLQQOHSGPPLQPSPWTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRFPPLRYPR YEATSVQQKVMFSEEGETEEDDQDSSHSSVTTVKARSRDSESG DKTTRSSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTERTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLEGERAYQARKE 6734 189 551 SAAMFPVFSGGFQELQEKNKSLELVSFEEVAVHFTWEFWOOLDD	1	1		PGHPGQGGPRGRPGYDGCNGTOGDSGPGGPGGPGGPGGPGGPGGPGGPGGPGGPGGPGGPGGPG
GEVGAPGREGPPGPRGQQGRRGLGFYGVKGEKGDVGQPGPN GIPSDTLHPIIAPTGVTFHPDQYKGEKGBEGDVGQPGPN GIM 1015 MMVDYYEVLGLQRYASPEDIKKAYHKVALKWHPDKNPENKEEAE	1 1	i		PKGQKGEPYALPKEERDRYRGEPGRPGLVGFGGRPGRPGPGG
GISSTEHPITAPTGVTFHPDQYKGEKGSEGEPGIRGISLKGEE GIM 6730 784 1015 NMVDYYEVLGLQRYASPEDIKKAYHKVALKWHPDKNPENKEEAE RKFKEVAEAYEVLSNDEKRDIYDKYGTEGLNEF GIRKGLHGAVVPRVEVGCPWETRESEGYHLERPTSPLKNNDEGS LDIYAGLDSAVSDSASKSCVPSRNCLDLYEEILTEGTAKEATY NDLQVEYGKCQLQMKELMKKFKEIQTQNFSLINENQSLKKNISA LIKTARVEINRKDEEI 6732 102 1205 GRWQRFPPPSPPLWCLQPGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATRCLPPHSGHRPTPPRSHRHHRQEN LGSIKPSSRSTKATSTTMAGDGRRAEAVREGWGVYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGRREVRESDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRPPLYPR YEATSVQQKVNFSEEGETEEDDQDSSHSSVTTVKARSRDSESG DKTTRSSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAFPEKVLR VLHRDATLAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE	1 f	į		GPVGAPGRPGPPGPPGPKGOOGNPGLGFYGVKGFYGDVGGPGN
6730 784 1015 NMVDYYEVLGLQRYASPEDIKKAYHKVALKWHPDKNPENKEEAE RKFKEVAEAYEVLSNDEKRDIYDKYGTEGLNEF 6731 1 446 GIRKRLHGAVVPRVEVGCPWETRESEGVHLERPTSPLKNNDEGS LDIYAGLDSAVSDSASKSCVPSRNCLDLYEEILTEEGTAKEATY NDLQVEYGKCQLOMKELMKKFKEIQTQNFSLINENQSLKKNISA LIKTARVEINRKDEEI 6732 102 1205 GRWQRPPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHRQEN LGSIKPSSRSTKATSTTMAGDGRRAEAVREGWGVYVTPRAPIRE GRGRLAPQNGGSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAYYLRSQORQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLELGKERKAYQARKE	1 1	1		GIPSDTLHPIIAPTGVTFHPDOVKGEKGGEGERGIRGIGIAGIA
6731 1 446 GTRKRLHGAVYPRVEVGCPWETRESGVHLERPTSPLKNNDEGS LDIYAGLDSAVSDSASKSCVPSRNCLDLYEE ILTEEGTAKEATY NDLQVEYGKCQLQMKELMKKFKEIQTQNFSLINENQSLKKNISA LIKTARVEINRKDEEI 6732 102 1205 GRWQRRPPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHRQEN LGSIKPSRSTKATSTTMAGDGRRAEAVREGWGVYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGREVRFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAYYLKSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAGEKSIGEDVYEKPISELDRLEEKQKETYRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEGEKAYQARKE				GIM
6731 1 446 GIRKRLHGAVVPRVEVGCPWETRESEGVHLERPTSPLKNNDEGS LDIYAGLDSAVSDSASKSCVPSRNCLDLYEELITEEGTAKEATY NDLQVEYGKCQLQMKELMKKFKEIQTQNFSLINENQSLKKNISA LIKTARVEINRKDEEI 6732 102 1205 GRWQRPPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHRQEN LGSIKPSSRSTKATSTTMAGDGRAEAVREGWGVYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAGEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWOOLDD	6730	784	1015	NMVDYYEVLGLORYASPEDTKKA VUVUAT VUUDDVANGANA
GIRKRLHGAVVPRVEVGCPWETRESEGVHLERPTSPLKNNDEGS LDIYAGLDSAVSDSASKSCVPSRNCLDLYEEILTEGTAKEATY NDLQVEYGKCQLQMKELMKKFKEIQTQNFSLINENQSLKKNISA LIKTARVEINRKDEEI GRWQRPPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHRQEN LGSIKPSSRSTKATSTTMAGDGRRAEAVREGWCVYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSTIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGGLQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEFWOOLDD				RKFKEVAEAYRVI.SNDEKRDI.VDKVCTECI.NEE
6732 102 1205 GRWQRPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHRQEN LGSIKPSSRSTKATSTTMAGDGRRAEAVREGWGVYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQOHSEQPPLQPSPVMTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWODLDD	6731	1	446	GIRKRIHGAVVPRVEVCCPWETTPRCECVUL PROPERTY
6732 102 1205 GROCKELMKKFKEIQTQNFSLINENQSLKKNISA LIKTARVEINRKDEEI GROCKPPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHRQEN LGSIKPSSRSTKATSTIMAGDGRRAEAVREGWGVYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWODLDD	1	i		LDIYAGLDSAVSDSASKSCUPERNOLDI VERTI TERRETARE
6732 102 1205 GRWQRRPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHRQEN LGSIKPSSRSTKATSTTMAGDGRRAEAVREGWGVYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWODLDD	1 1	1		NDLOVEYGKCOLOMKELMKYEKETOTOMEGI TATINO OF THE PROPERTY
6732 102 1205 GRWQRRPPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHRQEN LGSIKPSSRSTKATSTTMAGDGRRAEAVREGWGVYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPWMTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEGGTEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHNLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWODLDD	L I			LIKTARVEINDEDEET
AGRQVC I TAATTQAAAPATRICLPDHSGHRPTPPRSHRHHRQEN LGSIKPSSRSTKATSTTMAGDGRRAEAVREGWGVYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWODLDD	6732	102	1205	GRWORR PDD DC DD L MCL O DCCCC D DOCK TOX DVC
GRGRLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEBVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWODLDD] [·- · · · ·	AOROVCYTAATTOAAADATDMOT DOWGOOD TOUR CLEAR TO THE TOUR ADDITION OF THE T
GRGRLAPONGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWODLDD	1	1		IGSIKPSSPSTKATSTTMACDCDARTSTTMACDCARTSTTTMACDCARTSTTTMACDCARTSTTTMACDCARTSTTTMACDCARTSTTTMACDCARTSTTTMACDCARTSTTTMACDCARTSTTTMACDCARTSTTTMACDCARTSTTTMACDCARTSTTTMACDCARTSTTTMACDCARTSTTTMACDCARTSTTTMACDCARTSTTTTTACARTSTTTTTTACARTSTTTTTTTACARTSTTTTTTTTTT
PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSQYIESFW RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWODLDD	1 1	1		GRGRIA PONCCESDA DAVERDOGRARA EAVREGWGVYVTPRAPIRE
PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEEDDQDSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWODLDD		ł	İ	PLVAKER SDVCKDTDI EDERGOG TOTAL
6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWOOLDD	1	}		POETEFMETERTERI OCCURRONS OF THE PROPERTY OF TH
6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWOOLDD	1 1	ł		DEASCOTOL COMICKIMING TO THE TOTAL
6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFERVAVHFTWEEWODLDD]]	1		VEATCUOOKIA RECERCIONALIZATION DE L'ESTATORIO DE L'
RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWODLDD	!!	ľ		DETTRESCONTEGENERAL
KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWODLDD	6733	613	7311	DECENORAM DEPROCEDES AND DESCRIPTION OF THE PROCEDES AND DESCR
QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFERVAVHFTWEEWODLDD	[]		1311	KSCKQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK
VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 551 SAAMFPVFSGCFQELQEKNKSLELVSFERVAVHFTWEEWODLDD			}	AAAASINKKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI
VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 551 SAAMFPVFSGCFQELQEKNKSLELVSFERVAVHFTWEEWODLDD			1	VILLS IMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR
6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFERVAVHFTWEEWODLDD			İ	VLHRDAILAQEKSIGEDVYEKPISELDRLEEKOKETVRPMI.ROL
6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFERVAVHFTWEEWODLDD	f f		j	LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEOERERI.KK
SAAMFPVFSGCFQELQEKNKSLELVSFERVAVHFTWEEWODLDD	6734	189		LLEQEKAYQARKE
AQRTLYRDVMLETYSSLVSLGHCITKPEMIFKLEQGAEPWIVEE		103	221	SAAMFPVFSGCFQELQEKNKSLELVSFERVAVHFTWEEWQDLDD
				AQRTLYRDVMLETYSSLVSLGHCITKPEMIFKLEQGAEPWIVEE

SEQ	Predicted	Predicter nd	Amino agid
ID	beginning	nucleotic	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
-	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
-	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
ĺ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			TLNLRLSGGSKKQVFSGICHRSLVELQEVHLV
6735	280	558	KSRRAGVTKMSNPFLKQVFNKDKTFRPKRKFEPGTQRFELHKKA
			QASLNAGLDLRLAVQLPPGEDLNDWVAVHVVDFFNRVNLIYGTI
		•	XDGCT
6736	195	808	MNYELNFKREMPNIKSLGLTNLNFLLKRLSSVLPLITDYVYFEN
1			SSSNPYLIRRIEELNKTASGNVEAKVVCFYRRRDISNTLIMLAD
	1		KHAKEIEEESETTVEADLTDKQKHQLKHRELFLSRQYESLPATH
			1 RGKCSVALLNETESVLSYLDKEDTFFYSLVYDDSI,KTI,LADKG
			EIRVGPRYQADIPEMLLEGTFFCVFAVL
6737	150	1209	PVIMPLHFSPGDIVRPSCCVSSSPKLRRNAHSRLESVPDDTDLS
}	1		REDTGCNLQHISDRENIDDLNMEFNPSDHPRASTIFISKSOTOV
	!	j	REKRKSLFINHHPPGQIARKYSSCSTIFLDDSTVSOPNLKYTIK
	1		CVALAIYYHIKNRDPDGRMLLDIFDENLHPI.SKSEVPPDVDKUN
1			PEQKQIYRFVRTLFSAAOLTAECAIVTLVYLERIJTYAFTDICD
}	!		ANWKRIVLGAILLASKVWDDQAVWNVDYCOILKDTTVEDMNELE
			RQFLELLQFNINVPSSVYAKYYFDLRSLARANNI,SEDI,EDI,EDI
6738	148	653	RAHKLEAISRLCEDKYKDLRRSARKRSASADNLTLPRWSPAIIS
	110	653	CACAEQPARAEVGAATALPVRWASGEMAPSGSLAVPLAVLVLLL
{	·		WGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL
			QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHC
6739	3	631	KDGEFRRYQGPRTKKDFINFISDKEWKSIEPVSSWF
		-	SWPDMAEEEVAKLEKHLMLLRQEYVKLQKKLAETEKRCALLAAQ
1 1	ĺ		ANKESSSESFISRLLAIVADLYEQEQYSDLKIKVGDRHISAHKF VLAARSDSWSLANLSSTKELDLSDANPEVTMTMLRWIYTDELEF
1 1			REDDVFLTELMKLANRFQLQLLRERCEKGVMSLVNVRNCIRFYQ
			TAEELNASTLMNYCAEIIASHWVSEVEGVNKAL
6740	3	631	SWPDMAEEEVAKLEKHLMLLRQEYVKLQKKLAETEKRCALLAAQ
1			ANKESSSESFISRLLAIVADLYEQEQYSDLKIKVGDRHISAHKF
]			VLAARSDSWSLANLSSTKELDLSDANPEVTMTMI.PWIVTDFI.DE
1			REDDVFLTELMKLANRFOLOLLRERCEKGVMSLVMVPNCTPEVO
6741			TAEELNASTLMNYCAEIIASHWVSEVEGVNKAI.
0/41	141	960 ·	PLTLPFSSRARAGHTMNTSPGTVGSDPVILATAGYDHTVPFWOA
1 1			HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQDVSLGVQUIDM
1	ľ		YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI
1			WDLRSRNLQCQRIFQVNAPINCVCLHPNOAELTVGDOGGATUTW
1 1	ĺ		DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL
	İ		PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP
6742	141	960	
	_		PLTLPFSSRARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA
1		}	HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM YDLNSNNPNPLISYDGVNANIASYGENTAAAVQPVSLGYQHIRM
1		i	YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW
1 !	1	!	DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL
		}	PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ
			LIPKTKIP
6743	1	412	MHSTQDKSLHLEGDPNPSAAPTSTCAPRKMPKRISISKQLASVK
1 1	1	.	ALRKCSDLEKAIATTALIFRNSSDSDGKLEKAIAKDLLQTQFRN
	j		FAEGQETKPKYREILSELDEHTENKLDFEDFMILLLSITVMSDL
<u> </u>			LQNIR .
6744	95	1343	RTPARNRCAGCEVLSRFSSPNKASSFALQSAGGGLPAVRALRRD
[ſ	RQKVSTVGYGMDEVEQDQHBARLKELFDSFDTTGTGSLCOEFLT
	ļ	}	DLCHMLSLEEVAPVLQQTLLQDNLLGRVHFDOFKEALTLILSRT
	İ	i	LSNEEHFQEPDCSLEAQPKYVRGGKRYGRRSLPEFOESVEEFPE
		1	VTVIEPLDEEARPSHIPAGDCSEHWKTORSEEYEAEGOLDEWND
<u> </u>			DDLNASQSGSSPPQDWIEEKLQEVCEDLGITRDGHLNRKKLVSI

CEO	I Denodi al-	1 8	
SEQ ID	Predicted beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
140.	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
ł	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	Doque		(=possible nucleotide insertion)
1		İ	CEQYGLQNVDGEMLEEVFHNLDPDGTMSVEDFFYGLFKNGKSLT
		1	PSASTPYRQLKRHLSMQSFDESGRRTTTSSAMTSTIGFRVFSCL DDGMGHASVERILDTWQEEGIENSQEILKALDFGLDGNINLTEL
ĺ		ĺ	TLALENELLVTKNSIHOACI
6745	1	588	TFRDQGWAQRRRWLLGCASWESWEAAIAAGPGLPSSTARQQNNP
	_		AAGTECFAAVWARGTAMGSVLSTDSGKSAPASATARALERRRDP
1		ł	ELPVTSFDCAVCLEVLHQPVRTRCGHVFCRSCIATSLKNNKWTC
1	l		PYCRAYLPSEGVPATDVAKRMKSEYKNCAECDTLVCLSEMRAHI
			RTCQKYIDKYGPLQELEETA
6746	110	492	GATGAMAESAPARHRRKRRSTPLTSSTLPSQATEKSSYFQTTEI
			SLWTVVAAIQAVEKKMESQAARLQSLEGRTGTAEKKLADCEKMA
j	j		VEFGNQLEGKWAVLGTLLQEYGLLQRRLENVENLLRNRN
6747	247	484	EAVTFKDVAVVFTEEELGLLDLAQRKLYRDVMLENFRNLLSVGH
			QPFHRDTFHFLREEKFWMMDIATQREGNSVYAGVC
6748	201	665	MTTFKEAVTFKDVAVVFTEEELGLLDPAQRKLYRDVMLENFRNL
			LSVGNQPFHQDTFHFLGKEKFWKMKTTSQREGNSGGKIQIEMET
1			VPEAGPHEEWSCQQIWEQIASDLTRSQNSIRNSSQFFKEGDVPC
1			QIEARLSISXVQQXPYRCNECKQ
6749	95	719	RREVKGGDGVCPRARGSPQSQQFPSCAGGGEGLQQSGEALDGAM
			SAGGPCPAAAGGGPGGASCSVGAPGGVSMFRWLEVLEKEFDKAF
ł			VDVDLLLGEIDPDQADITYEGRQKMTSLSSCFAOLCHKAOSVSO
1			INHKLEAQLVDLKSELTETQAEKVVLEKEVHDOLLOLHSIOLOL
			HAKTGQSADSGTIKAKLSGPSVEELERELKAN
6750	3	428	SCESRRPGAKWVWASGALPRDTTGLGSEQPSGDVAQSNRATMGT
1			TAPGPIHLLELCDQKLMEFLCNMDNKDLVWLEEIQEEAERMFTR
			EFSKEPELMPKTPSQKNRRKKRRISYVQDENRDPIRRRLSRRKS
6751	152		RSSQLSSRR
6/51	152	1417	PTKATEMAGASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIV
J i			NPKQPKETPKSFSFDYSYWSHTSPEDINYASQKQVYRDIGEEML
			QHAFEGYNVCIFAYGQTGAGKSYTMMGKQEKDQQGIIPQLCEDL
į į			FSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLRVRE
			HPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETS
1	i		SRSHAVFNIIFTQKRHDAETNITTEKVSKISLVDLAGSERADST GAKGTRLKEGANINKSLTTLGKVISALAEMDSGPNKNKKKKKTD
[[ľ		FIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLR
			YADRAKQIRCNAVINEDPNNKLIRELKDEVTRLRDLLYAQGLGD
]			ITDMTNALVGMSPSSSLSALSSRNV
6752	24	1834	RNCVPPLGCYRSRVKFHSDIKMQYSHHCEHLLERLNKQREAGFL
1 1			CDCTIVIGEFQFKAHRNVLASFSEYFGAIYRSTSENNVFLDQSQ
			VKADGFQKLLEFIYTGTLNLDSWNVKEIHQAADYLKVEEVVTKC
			KIKMEDFAFIANPSSTEISSITGNIELNQOTCLLTLRDYNNREK
ļ l			SEVSTDLIQANPKQGALAKKSSQTKKKKKAFNSPKTGQNKTVQY
, 1			PSDILENASVELFLDANKLPTPVVEQVAQINDNSELELTSVVEN
	ŀ		TFPAQDIVHTVTVKRKRGKSQPNCALKEHSMSNIASVKSPYEAE
]			NSGEELDQRYSKAKPMCNTCGKVFSEASSLRRHMRIHKGVKPYV
j l	+		CHLCGKAFTQCNQLKTHVRTHTGEKPYKCELCDKGFAOKCOLVF
]	j		HSRMHHGEEKPYKCDVCNLQFATSSNLKIHARKHSGEKPYVCDR
	1		CGQRFAQASTLTYHVRRHTGEKPYVCDTCGKAFAVSSSLITHSR
			KHTGEKPFICELCGNSYTDIKNLKKHKTKVHSGADKTLDSSAED
			HTLSEQDSIQKSPLSETMDVKPSDMTLPLALPLGTEDHHMLLPV
			TDTQSPTSDTLLRSTVNGYSEPQLIFLQQLY
6753	2	1305	VPSLPYPPQKVVAHTEFTTSSDSETANGIAKPDPVMPGGEEKAS
	l		PFGIKLRRTNYSLRFNCDQQAEQKKKKRHSSTGDSADAGPPAAG
			SARGEKEMEGVALKHGPSLPQERKQAPSTRRDSAEPSSSRSVPV
			AHPGPPPASSQTPAPEHDKAANKMPLAQKPALAPKPTSQTPPAS

SEO	Predicted	T	······································
ID	beginning	Predicted end nucleotide	
NO:	nucleotide	location	I MATALONINE LECVETPINA NAMESALIA E I I
1	location	corresponding	Gracamic Acia, Febranylelenine dedi.
1	corresponding	to first	n-nibulgine, i=isoleugine V-t
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	J	\=possible nucleotide insertion)
1			PLSKLSRPYLVELLSRRAGRPDPEPSEPSKEDORGGPPPP
İ	1		GFEEKAGUAKUEEEEATERKPASPDI.DATOOFEDCOMPER COMP
l			I REMOVORADOUGKLIEKVETAODI WITTAI OVOVOROBOGO TO
	[1	LEAR VAREAR VAEKLSKENVSVSVOPGSSSWGDACCT WWGDAT D
į	1		BEARFEIAVSKLERREOLKKANTI,DTGV/TVFTCVCCD225
6754	2		VSARESSPUDAPVSSEPAWLALAKRKAKAWGDCDI TTV
	2	413	FVRRRRRLGGPEVNTMSSLHKSRTADEODVLKERSTALEKKAR
1			DOFOGIFCEGGLRCLCWKILLNYLDI.ERAGMTGILAVOREL 150 C
ŀ	ĺ		FURENITIQUETAKANMGVSREDVTFEDHPLNPNPDSPWNTVEVD
6755	298	1343	MEADE
ł		1242	PGLQLQVALEADWFLDMPGGRRGPSRQQLSRSALPSLQTLVGGG
	1		CONGIGURINGSAIGLEVEETTAI.TTECHIRICATERS FIRMS
			LLFEFLFFIYLLVALFIQYINIYKTVWWYPYNHPASCTSLNFHL
- 1	1 1		IDYHLAAFITVMLARRLVWALISEATKAGAASMIHYMVLISARL
			VLLTLCGWVLCWTLVNLFRSHSVLNLLFLGYPFGVYVPLCCFHQ DSRAHLLLTDYNYVVQHEAVEESASTVGGLAKSKDFLSLLLESL
	l		KEQFNNATPIPTHSCPLSPDLIRNEVECLKADFNHRIKEVLFNS
			1 DESALIVAE LEDCEVKVSGYLTEMOET DICUMVENTATION
6756	180	754	TERALGSLPLSIPVSWGSLRTLKVOOOPLDDWG LGOTTLE
			1 DESTRUCTED AND THE PROPERTY OF THE PROPERTY
	[]		REAVARARRESGMALTOGPLTFPDVATPPDATPWGT Date
-	1		I WALL MOVING MIKNOVELGKONFALEVKI CODVET VET GOT OND
6757	2	450	PERILITEALLITHK
Į .	-	459	NSRVEAPEAHSRESQGSDAMRKHLSWWWLATVCMLLFSHLSAVQ
1	1		INGIANKIKWNKKALPSTAOITEAOVAENDDCAEIVOGDVC
1	; !		FGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQ AANQGEFQKPDNKLHQQVLW
6758	1	1008	ASCDEL DCDD DDDD DDDD DDDDD DDDDDDDDDDDDDD
			ASGPELPGRRFRDRAPWLPARLLRGVLAVWVSLSALGPGSFCRR
į.			RVPSLAQLGHSEAAPSPDDVRWSRVPDRCPEERDRAWPPPPPPPS LPPSFRRNMANNSPALTGNSQPQHQAAAAAAQQQQQCGGGGATK
	1		PAVSGKQGNVLPLWGNEKTMNLNPMILTNILSSPYFKVQLYELK
	!!!		TIME V V DETTER V THVEPWEKGSRKTAGOTGMCCGUPGUGGGG
1	1		VSIACUUIALETLALIRKOVMGI,TTHTDQDVTDAI GBARTTON
1 1	1	j	VEFIDENDWEESELDDEEDLDVKAGGGGCVMTTGPMI DOWN OVER D
6759	1		MEST DE BET E A DO NOTO DO LE MEST DE BET E LA COMPONITION DE LA C
	-	513	RKHNFHSLDGTSTRAFHPQTGLPLLSSPVPQRKTQSGCFDLDSS
]	İ		DUMBASESSKSPRPCLNIEDDPDTHEKDFLEGGADDIMGE GE - G
[]	-		MELECVENIKE DELGIVDGFTAEVGASGAECDTELLTI DEPENDENT
6760	239	606	SVSDDNAPSPYMGVITLESLGKRGYRVPPSGTIQVVCVL
1 1]		VLSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGIT
<u> </u>		1	AMSVKEVLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLE VLESQLSEGSQKHASLQKSIEKAKIGRCETEERT
6761	29	1733	ERTLEGIPENA DEDUNDA MODECO
!	i	į	ERTLEGLEEVAAPSDVADAAVSREGECCCCHCTQTQVAQDCPS SSSSVQRCELSLFQSLHTMTSKKLVNSVAGCADDALAGLVACNP
1	1		NLQLLQGHRVALRSDLDSLKGRVALLSGGGSGHEPAHAGFIGKG
1	j		MLTGVIAGAVFTSPAVGSILAAIRAVAQAGTVGTLLIVKNYTGD
[RLNFGLAREQARAEGIPVEMVVIGDDSAFTVLKKAGRRGLCGTV
! <u> </u>	į į		DIRKVAGALAEAGVGLEEIAKOVNVVTKAMGTI GUGL GCGLTDG
l f		1	SKELFELSADEVELGLGIHGEAGVRRIKMATADETUVIMI DIDAT
	·	1	NI INASHVPVQPGSSVVMMVNNLGGI,SFLELGI IADATUDGI EG
		1	KGVKLAKALVGTFMSALEMPGISLTIJJVDFDIJVI TDADOWAR
		1.	AWPNVAAVSITGRKRSRVAPAEPOEAPDSTAACCGAGUDMATIII
1		·	ERVCSTLLGLEEHLNALDRAAGDGDCGTTHSDAADATORUL KHO
i	ĺ	1	FFFASFAQLUSKLSVLLLEKMGGSSGAT,VGT.FT.TAAAAAT KAKT
			SLPAWSAAMDAGLEAMQKYGKAAPGDRTMLDSLWAAGQEL

Mocilectide nucleotide nu	SEQ	Prodicted	1 70 31 3	·
Mo: nuclectide location corresponding to first amino acid residue of residue of amino acid residue of amino acid sequence first amin		Predicted	Predicted end	Amino acid segment containing signal peptide
Cocation Corresponding	1	nucleotide		(A=Alanine, C=Cvsteine D-Aspartic Acid to
corresponding to first amino acid residue of amino acid residue of amino acid sequence sequen	1 .,,,		1	Glucina Gellucina
to first amino acid residue of amino acid amino acid asequence 6762 3 613 ASTIGNELVAGARERREVEVAGERAGGAMENTILANISTY OVAFITLAVAGUYYLARLIERYTVATSRI IKVMINESTAVIG LIVVERFETSRI UNGULFITNIVTY GLOVER FOR SULVERFETSRI IKVMINESTAVIG LIVVERFETSRI UNGULFITNIVTY GLOVER FOR SULVERFETSRI UNGULFITNIVTY GLOVER FOR SULVERFETSRI UNGULFITNIVTY GLOVER FOR SULVERFETSRI UNGULFITNIVTY GLOVER FOR SULVERFETSRI UNGULFITNIVTY GLOVER FOR SULVERFETSRI UNGULFITNIT				Hanistidine, Ialsoleucine, Kalysine,
amino acid residue of amino acid amino acid sequence control c	1			Paperoline, Mamethionine, Nasparagine,
maino acid sequence 6762 3 613 613 613 613 613 613 613 6				Sasarine Tarbananda, RaArginine,
amino acid sequence sequence sequence Apossible nucleotide distance	1			Watryptophan Variable V Wales
6762 613 613 ASTISHRICANGAERREPVENGAERAGGAMMENTALISMISLEFT (OVAFITAVAAGLYTLABLIEETTAATSRIIKYMIWSTAPIJO (DVAFITAVAAGLYTLABLIEETTAATSRIIKYMIWSTAPIJOE LIVVENHYTAAGLAGUTYLABLIEETTAATSRIIKYMIWSTAPIJOE LIVVENHYTAAGLAGUTYLABLIEETTAATSRIIKYMIWSTAPIJOEG LIVVENHYTAAGUTYTGAAGMELGAHDUNISAAFILVENSIA GENNLESTINGGODUVSHYTTKOKKOK GENNLESTINGGODUVSHYTKOKKOK ROEGNIJESTAAGAMELGAHDUNISAAFILVOCHSUVUGRR SCHALLSHAVKSIGASETVAGUTSUSVUGRR SSULACILLSAATNYFLFVAARVSAIFKHTLEISKA LLISHAVKSIGASETVAGUTSUSVUGRR SSULACILLSAATNYFLFVAARVSAIFKHTLEISKA SULACILLSAATNYFLFVAARVSAIFKHTLEISKA SLALSHAVELSAATATSAATUT LINGALWEPPERREAKOST LLISHAVKSIGASETVAGUTSUSVUGRR SSULACILLSAATNYFLFVAARVSAIFKHTLEISKA LLISHAVKSIGASETVAGUTSUSVUGRR SSULACILLSAATNYFLFVAARVSAIFKHTLEEDGF YLITHAFICTERIT LANGAUTHELEGGF YLITHAFICTERIT LANGAUTHELEGGF YLITHAFICTERIT LANGAUTHELEGGF YLITHAFICTERIT LANGAUTHELEGGF YLITHAFICTERIT LANGAUTHELEGGF YLITHAFICTERIT LANGAUTHELEGGF YLITHAFICTERIT LANGAUTHELEGGF YLITHAFICTERIT LANGAUTHELEGF YLILAGAUTHELEGF Y		amino acid		Codon /-possible musleshide del di
ASTISMICVAGAEARRYPYNAGERAGGAMMFMYLLSMISJEFT QUAPITIAVAGALYNIALIEETTVATSTILTMWSTADLIG LYVERFTSMIGVGLFTNLVYGGLAUTFFFLMISSNFILSCG LVVUNNIYLAFPFAERYYPFSEVLAYFFFCHUMFSTADLIG LYVERFTSMIGVGLFTNLVYGGLAUTFFFLMISSNFILSCG LVVUNNIYLAFPFAERYYPFSEVLAYFFFCHUMFSTADLIG GENVLDSTMOPGODVVSNYFTKOKRGK 80 760 SGPPPFORGREGCCCVPFPAGAMELGGIMDANSAPELVSETAE RKOEQKIGTEABADSGAVGARFFLLCHIAGFLDLEGVSMVVP LLSHAVSLGASFTVAGIVOSSTGILGLESTVICKSDEVVGRR SSLLACILLSALGYLLLGAATNYFLFVLARVPAGIFKHTLSISR ALLSDWYERKERFLVIGHFFINAGGGFTLIGHCKSDEVVGRR SSLLACILLSALGYLLLGAATNYFLFVLARVPAGIFKHTLSISR ALLSDWYERKERFLVIGHFFINAGGGFTLIGHCKSDEVVGRR SSLLACILLSALGYLLLGAATNYFLFVLARVPAGIFKHTLSISR ALLSDWYERKERFLVIGHFFINAGGGFTLIGHCKSDEVGFR SSLLACILLSALGYLLLGAATNYFLFVLARVPAGIFKHTLSISR ALLSDWYERKERFLVIGHFFINAGGGFTLIGHCKSDEVVGFR SSLLACILLSALGYLLLGAATNYFLFVLARVPAGIFKHTLSISR ALLSDWYERKERFLVIGHFFINAGGGFTLAGEVARVP LLSBWYTANGARGATELLGAATSCATTATACT ROPARAGCATACT AND ARTSENDHALGWYTHAGAGGATTACT ROPARAGCATACT ROPARAGC		sequence	-	\=possible nucleotide incombine)
UVPERFEYSHIGGGFTHUTVFELLGTPHUTSENFILISCE LTVVENHYLAFOFFABEYYPFSULAYFTCLMIIPPAFFVSLSA 6763 2 760 SEPPFERRENCCURFPABEYYPFSULAYFTCLMIIPPAFFVSLSA ROPONTOSTOPPENRENGCCVRFPABEGMELIGGMDMNSAPRLUSETAB ROPONTOSTOPPENRENGCCVRFPABEGMELIGGMDMNSAPRLUSETAB ROPONTOSTOPPENRENGCCVRFPABEGMELIGGMDMNSAPRLUSETAB SELLACILLSALGYLLLGBAANVLFVLAMPAGIFKHTLSISN ALLSDUVFERREPLVIGHTNTASCVGFTLGPVVGGVITELEDGF VLTAFICFLVFILNAGLWAFFPERRENGGFTLGPVVGGVITELEDGF 1 1287 LKKMORTDHELGKYMDLIMMFFFRERAKDGVGFTLGLAFFEDFF ROPONTOSTOPPHONE 6765 3 550 ARYSKVDHECKYMDLIMMFERGLDVGRVGLLAGFFEDFF ROPONTOSTOPPHONE RGSVLVSRALSGSAMDGIVTEVAVGVKRGSDELLGGSVLSSPNS NMSMVVTANONDSKKFKGEKWDGAPFSESRHFLAACVARAM RGSVLVSRALSGSAMDGIVTEVAVGVKRGSDELLGGSVLSSPNS NMSMVVTANONDSKKFKGEKWDGAPFSESRHFLAACVARAM RGSVLVSRALSGSAMDGIVTEVAVGVKRGSDELLGGSVLSSPNS NMSMVVTANONDSKKFKGEKKWADARFFLLGFPSGSRHFLAACVARAM RGSVLVSRALSGSAMDGIVTEVAVGVKRGSDELLGGSVLSSPNS NMSMVTANONDSKKFKGEKKWADARFFLLGFPSGSRHFLAACVARAM RGSVLVSRALSGSAMDGIVTEVAVGVKRGSDELLGGSVLSSPNS NMSMVTANONDSKKFKGEKKWADARFFLLGFLFRENGGVOVF VILLGLPFGKVTNILMLKGKNQAFLELATEBAAITNGNYTSAVT VILLGLPFGKVTNILMLKGKNQAFLELATEBAAITNGNYTSAVT VILLGLPFGKVTNILMLKGKNQAFLELATEBAAITNGNYTSAVT VILLGLPFGKVTNILMLKGKNQAFLELATEBAAITNGNYTSAVT VILLGLPFGKVTNILMLKGKNQAFLELATEBAAITNGNYTSAVT VILLGLPFGKVTNILMLKGKNQAFLELATEBAAITNGNYTSAVT VILLGLPFGKVTNILMLKGKNQAFLELATEBAAITNGNYTSAVT VARIANGUS SOPPTARFTLISTLLORGHVALTER LIGHTPGFT KFVDEGKATVELKEPPVILLSTLLORGHVALTER LIGHTPGFT KFVDEGKATVELKEPPVILLSTLLORGHVALTER LIGHTPGFT KFVDEGKATVELKEPPVILLSTLLORGHVALTER LIGHTPGFT KFVDEGKATVELKEPPVILLSTLLORGHVALTER LIGHTPGFT KFVDEGKATVELKEPPVILLSTLLORGHVALTER LIGHTPGFT KFVDEGKATVELKEPPVILLSTLLORGHVALTER LIGHTPGFT RNISLEYLLDFGTFTGFTATTMALLST QTSYCLUMMRALCLSSLEVALICHTHUKKKALDATTGOTGCT LGELKINIKLLDDNSLLTGFTCKTGAVTTMALLST PFSSRITPHLCQDLDTAKLCVCGRFCLHSFTTSTTMALLBVAL FFTSTLLHGVKKKKALL FFTSTLLGGSTTLGFTCHTALLSTLLSTATTLHRAFT PGSSTLVEWARGATTALTAKTGATGATATATATATARTKFTE LGRSTTDLFGLGSGATATATATATATATATATATATATATATATATATATA	6762	3	613	ASTISWRLCVAGAEARRPVPVAGERACCCAMMENT I CHY OF FI
LYVERPTSHIGVGETRILVTFGLIGTFFFIMLTSRPILGS LVVNNYLARPOFFABELTYPFSULAYTFGLIGTFFFIMLTSRPILGS GENVLOSTROPGODUVSNYTKGKRK SOPPFFGREFFRGCCCVEPPSCAGMELGGHDDMNSAFRLVSETAE RKGEQKTGTEAEAADGAVGARRFLLCTLIGGFLDLGYSMVUP LLSHHVSLGASPTVAGIVGSSYGILQLGGYSMVUPGR SLLACILLSALGYLLLGAATNVLFVLANVPAGIFKHTLGISK ALLSDVVERKERPLVITINAGLVWFFPREAKPGSTF KKWGTDHELGKYKDLLMKASTERSALDVMLKHARNQUDVSIKR RORBADCEKHERGOLGT BERLMEDTSGET FLOARDFEDFE KKWGTDHELGKYKDLLMKASTERSALDVMLKHARNQUDVSIKR RORBADCEKHERGOLGT BERLMEDTSGSIO 6765 3 550 ARYSKVDHEGERREGAVARAFFFLLQPFSFFSRHFLAACVARWL RORSHADCEKHERGOLGT BERLMEDTSGSIO 6766 1 1287 EGGSFKASLTWIPLGEMKLGEVEVUSRHLPALGERNYSAUT PHLRWO 6766 1 1287 EGGSFKASLTWIPLGEMKLGEVEVUSRHLPALGERNYGKGV VDTPVSTLITVYKTSFEERFKKNVITSKOMETSKYPSAUSH GTSYGCLVRVUDMMLCLKSLRKLDLSHNIKKLPATIGDLTHLQ CTSYGCLVRVUDMMLCLKSLRKLDLSHNIKKLPATIGDLTHLQ CTSYGCLVRVUDMMLCLKSLRKLDLSHNIKKLPATIGDLTHLQ CTSYGCLVRVUDMMLCLKSLRKLDLSHNIKKLRAPVOFCO LQELKNLKLDDNELJOFFCKIGGLINLFFLSSAARIKLBPLDFFS RNLSEYLDLFGSTFFGOKVLPVILAGAPTSLESSARTIHBR TPGSHIIPPHLCQDLDTAKLTCVGRFCLSSDDT RHWTVLVDNLGGGFAFIISTYCSLCVCYNSDDT RHWTVLVDNLGGGFAFIISTYCSLCVCYNSDDT RHWTVLVDNLGGGFAFIISTYCSLCVCYNSDDT RHWTVLVDNLGGGFAFIISTYCSLCVCYNSDDT RHWTVLVDNLGGGFAFIISTYCSLCVCYNSDDT RHWTVLVDNLGGGFAFIISTYCSLCCVNSDDT RHWTVLVDNLGGGFAFIISTYCSLCCVNSDDT RHWTLANDLGGGFAFIISTYCSLCCVNSDDT RHWTLANDLGGGFAFIISTYCSLCCVNSDDT RHWTVLVDNLGGGFAFIISTYCSLCCVNSDDT RHWTLANDLGGGFAFIISTYCSLCCVNSDDT RHWTLANDLGGGFAFIISTYCSLCCVNSDDT RHWTLANDLGGGFAFIISTYCSLCCVNSDDT RHWTLANDLGGFAFIISTYCSLCCVNSDDT RHWTLANDLGGGFAFIISTYCSLCCVNSDDT RHWTLANDLGGFAFIISTYCSLCCVNSDDT RHWTLANDLGGGFAFIISTYCSLCCVNSDDT RHWTLANDLGGGFAFIISTYCSLCCVNSDDT RHWTLANDLGGGFAFIISTYCSLCCVNSDDT RHWTLANDLGGGFAFIISTYCSLCCVNSDDT RHWTLANDLGGGFAFIISTYCSLCCVNSTRUFHLIPAT RPGSTKEWMRARABLANDRGGGFAFITHTWGAMGGGFAFIITHMCHAGA CTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	1			QVAFITLAVAAGLYYLAELTEEYTVATSPITKYMTWESTANT
6763 2 760 SEPPFORRENCECVRPPSEALAMPTICMITIPAFFVSLSA GENVLDSTUNGEDDVUSNYFTKGKRK SEPPFORRENCECVRPPAGAGMELGGIMDMINSAPELVSETAE RKOENKTETAEAADSGAANGARRELLGULGGFLDLFGVSWAVP LISHHVESIGASPFVAGIVGSSYGILQLFSSTLVGGCHSDVVGGR SELLACILLSALGYLLLGAANTAVELVHAPGIFWHTLSISK ALLSDVPEKERPLVJGHENTASCVGFLIGDFVVGGVIHELBOOF VLTAFICELVFILMAGLWFPFRERANDFGFFRENCHSOFDVVGGVIHELBOOF VLTAFICELVFILMAGLWFPFRERANDFGFFRENCHSOFDVGFFR SELLACILLSALGYLLLGAANTVELFULAGFFEDFFRENCHSOFDFF KROORTDHELGKYKDLMKRATERSALDVKLKHARROVDVSIKR RORAEADCEKLERQIQLITESEMEVOFIGLAKOFPEDFR KROORTDHELGKYKDLMKRATERSALDVKLKHARROVDVSIKR RORAEADCEKLERQIQLITESEMEVOFIGLAKOFPEDFR KROORTDHELGKYKDLLMKRATERSALDVKLKHARROVDVSIKR RORAEADCEKLERQIQLITESEMEVOFIGLAKOFPEDFR KROORTDHELGKYKDLLMKAATERSALDVKLKHARROVDVSIKR RORAEADCEKLERQIQLITESEMELMCDTSGGIS ROSVILVSBALGGSAMDGITVSVAVGVKRSDELLSGSVLSSPINS NMSSMVVTANGNISKEFKGEDKMIGAPSRVLHITKLEGEVIETE VIALGLPFSGVTTIMLKIKSKOPFLESSVLSSPINS NMSSMVVTANGNISKEFKGEDKMIGAPSRVLHITKLEGEVIETE VIALGLPFSGVTTIMLKIKSKOPFLESTATIGRYYSAVT PHERMO 5766 1 1287 EGGSFKASLTHUMPLGEMKLHCEVEVISRHLPALGLRNRGGVK AVISLCQGTSRSOPPVRAFILLISTLKDKRGTRVERRENIEGFFT KFYDEKASTVALKSEPPVIGLISKANDSLAHATINGGNYSAVT PHERMO VDTPVSTLTPVKTSEFENFKIKNVITSKKOYPLSKNFTSLEFULFUL GTSYCGLVAVDRMMLCLKSKKLDLSHNHLKPATIGDLIHLO ELMINDNIHLSFSVALCHSTLOKSKIDLSKNKIKALPVOFCO LQEKINLKUDNELIOFFEKIGGLINLERAFIKOPTITÄNLHSV AHTVULVDNILGGTEAPIISTLOKSKIGDLSKNKIKALPVOFCO LQEKINLKUDNELIOFFEKIGGLINLERAFIKLOPTITÄNLHSV AHTVULVDNILGGTEAPIISTLOKSCOPTITÄNLHSV AHTVULVDNILGGTEAPIISTSCOLGIVINSSDILTHKLARVOFF ROSSTISCVILLSGSSIDJOFFYKEAFILDRGGIGTVCKOPTITÄNLHSV APHICLCSSDIDFFYKEAFILDRGGIGTVCKOPTITÄNLHSV APHICLTSSDIDFFYKEAFILOKATCUCGRECHARVELAFILLEROFT POSSKVEMBARABALDANARGIGLGGAFKARGAVERADDHOGGGEV NDDATELLHVKKKKALL FOSTISCVILLSGSSIDJOFFYKEAFILDRGGGSODMGKSDERLLOAV NDDATELLHVKKKKALL FOSTISCVILLSGSSIDJOFFYKEAFILDRGGGSODMGKSDERLLOAV ENNORMANNIGVERIALBRGGGAFT TINNGVGBALDARVILLTRGGATTLAGTHYSVSVOOVFORGKFR TINNGVGBALDARVILLTRGGATTLAGTHYSVSVOOVFORGKFR TINNGVGBALDARVILLTRGGATTLAGTHYSVSVOOVFORGSRAFT AVPILGFTRGGGGATTLAGTHYSVSVOOVFORGAAFTI APHICACASCO	i			LYVFERFPTSMIGVGLFTNLVYFGLLOTEPFIMLTSPNELL
6763 2 760 SEPPFERERFRECCCVEPPEAGAGHELGGKNDMNSAPRLVSETAE RKOEQKTGTEAEAADGAVGARRFLLCTVLGGFLDLGYSMVVUP LLSHHVSLGASPTVAGIVGSSYGILQLGSSTLUGGVSDVVGRR SLLACILLSALGGYLLIGAATNVLFVLARVPAGIFRHTLGISK ALLSDVVERERFREVLTGHFVTLASCOPFLVGGVSTUVGGVIFTELEDGP YLTAFICFLVFILMAGLWFFPRERAKPGSTE KKMGTMELGKERPLDLTGHFVTLASCOPFLVGGVIFTELEDGP YLTAFICFLVFILMAGLWFFPRERAKPGSTE KKMGTDHELGKYKDLLMKASTERSALDVULKHARNQVDVEIR ROREADGLEKLERGIQLIFURFVELESGENGVOFFLGLAKOFEDFF KKMGTDHELGKYKDLLMKASTERSALDVULKHARNQVDVEIR ROREADGLEKLERGIQLIFURFWLEDSGFSRHFLAACVARWL ROREADGLEKLERGIQLIFURFWLEDSGFSGFSRHFLAACVARWL ROSSULVSEALGGSAMDGIVTEVAVGVKRGSDELLSGSVLSSPNS MASSMVVTANGNIDSKYFKGEDRHGAGAPSTHLAFLOFFSGFSRHFLAACVARWL ROSSULVSEALGGSAMDGIVTEVAVGVKRGSDELLSGELSSPNS MASSMVVTANGNIDSKYFKGEDRHGAGAPSTHLAFLGFSGFSRHFLAACVARWL PHERMO 5766 1 1287 EGGSFKASLTWLMFLGGMKIGAGAPSTHLAFLAFBAGTVYSAVT PHERMO VDTPVSTLIFVTVSTFEFERFKTRVTITSKOFTSKJENSTSVSLSSPNS NASSMVVTANGNIDSKYFKGEDRHGAGAPSTHLTRKLDGEVTETE KFVDBGKATVELKEPFVOILGSKANDSSLKGFLSANRLAHRGCV VDTPVSTLIFVTKTSFEFERFKTRVTITSKOFTSKJENSTSVSLEHL GTSYCGLVRVUMSMILGLKSERKLDISHHIKKLPATIGDLIHLQ CTSYCGLVRVUMSMILGLKSERKLDISHHIKKLPATIGDLIHLQ CTSYCGLVRVUMSMILGLKSERKLDISHHIKKLPATIGDLIHLQ CTSYCGLVRVUMSMILGLFGFCKIGGLINLEFISSAARIKLHRG GTSYCGLVRVUMSMILGLFGFCKIGGLINLEFISSAARIKLHRGVFG KFUDGKATVELKEPFVOILGFGKTGGVKFVTKIALDFUNSKYFSLEHL GTSYCGLVRVUMSMILGLFGFCKIGGLINLEFISSAARIKLHRGVFGF RNISLEYLDLGGFTFGFGVKFVTKIVTISKGVKKYKALDVFDFOSK RNISLEYLDLGGFTFGFGVKFCTKITGKTSMKTKALDVFGFG GRIGGSMSTKYKAPAKSRSGPFSTDOPGLINKFKITAGVGFG GRIGGSMSTKYKAPAKSRSGPFSTDOPGLINKFKGARGQLASDVHY ROPLOPTCDPEGLGIRRAGKAHGUGSDVKYKSDLINTRGVGHT PROSKYKVMBARRABELANRAGLIGLGGAVGRAGGABPTAFT RVGGVFTGKVKTARTAGRAGATATATATARGKYGFG KTRGGAPTLGCKVKTLAGRENGEPPERLITTARGVARTORGAT FROMTAFTAATAGATATATATATATATAGARGATATATATARGKYGFG KTRGGAPTLGCKVKTLAGRENGEPPERLITTARGVARTORGATATATATARGKYGFG KTRGGAPTLGCKVKTLAGRENGEPPERLITTARATATATAGAPTATATATATAGARGATATATATATATATAGARGA CTTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	ł			LVVVNHYLAFOFFAEEYYPFSEVLAYFTFCLWIIDFAFFUCICA
SGPPPGREFRGCCVERPEAGAMELIGGHDMISARERLUSETABLE RKOPKNIGTERBARDSGNOARNFILLIGGELLLEGYSWIVD				GENVLPSTMQPGDDVVSNYFTKGKRGK
RKGEQKTGTEABADSGAVGARFILCLYIGGFLDLFGYSMVUGR LLSIHVSSLGASPTVAGUVGSSTGILGPSTLVGCMSDVUGRR SSLLACILLSALGYILLGAATNYFLFVLARVPGSTLVGCMSDVUGRR ALLSDVVFKERPLVIGHTNAGGGFTLGPVVGGYITELBGGF XLTAFICFLVFILMAGLVMFFFFREAKRGSTE LKKMDTMMISVENITEGDUFEVGFILGAKOFDEFR KKMGRTDHBLGKYKDLIMKAPTERRALDVKLKHARNQVDVEIRR RORAEADCEKLERQIQLIREMIMCDTSGSIQ RGSVLVSBALSGSAMDGIVTEVAGVKRGSDELLSGSVLSSPNS MSSMVTVATNAGNDSK KRGEDMDGASFRVLHIRKLDGEVTETE VIALGLPFGKVTNILMLKGKNGAFIELATERAAITNGNYYSAVT PHERMO 6766 1 1297 BGGSFFASLTWWFLGEMKLHCEVEVISRILBAGLRNERGKY VIALGLPFGKVTNILMLKGKNGAFIELATERAAITNGNYYSAVT PHERMO AVISLCCOOTSSOPPVBAFILLSTIKKDKGTFYBERRIEDFFT KFVDEGKATVELKEPPVDICLSKANSSLKGFLSAMLAHRGCN VDTPVSTLTPVKTSEFFENFKTKMUTSKKGTFYBERRIEDFFT KFVDEGKATVELKEPPVDICLSKANSSLKGFLSAMLAHRGCN VDTPVSTLTPVKTSEFFENFKTKMUTSKKGTFYBERRIEDFFT KFVDEGKATVELKEPPVDICLSKANSSLKGFLSAMLAHRGCN VDTPVSTLTPVKTSEFFENFKTKMUTSKKGTFYBERRIEDFFT KFVDEGKATVELKEPPVDICLSKANSSLKGFLSAMLAHRGCN VDTPVSTLTPVKTSEFFENFKTKMUTSKKGTFYBERRIEDFFT KFVDEGKATVELKEPPVDICLSKANSSLKGFLSAMLAHRGCN VDTPVSTLTPVKTSEFFENFKTKMUTSKKGTFYBERRIEDFFT KFVDEGKATVELKEPPVDICLSKANSSLKGFLSAMLAHRGCN VDTPVSTLTPVKTSEFFENFKTKMUTSKKGTFYBERRIEDFFT KFVDEGKATVELKEPPVDICLSKANSSLKGFLSAMLAHRGCN VDTPVSTLTPVKTSEFFENFKTKMUTSKKGTFYBERRIEDFFT KFVDEGKATVELKEPPVDICLSKANSSLKGFLSAMLAHRGCN VDTPVSTLTPVKTSEFFENFKTKMUTSKKRGTPYBERPYSLEHL OTSYCLURVDMRHLGSFSVALCHSTLLSKINSLLKRAFTVORFT KFVDEGKATVELKEPPVDICLSKANSSLKGFLSAMLLHRGCH VDTPVSHIPPHLODLDTAKLUDARITIKKALPVOFCO LGLKNILKLDDNBLIQFPCKIGQLINLRFLSARRIKLEPPISFF RNISLEYLDLFGNTFKCOPKVLGKGLINLRFLARKHENFUNG GRIQSDNSYKKDFAKSRSOFFISSTDOPGLIGAKRSQLASDVHY GRIQSDNSYKKDFAKSRSOFFISSTDOPGLIGAKRSQLASDVHY ROPATELLHVKKKALLL 6767 336 919 AFPICCESDLOFTKYRGFALBRENGCIGGCSVSDDDFFMKHFLNV GRIQSDNSYKKDFAKSBODDWKSSDERLHONGSGEV NDAMTELHVKKKALLL FORDATOR RNYGVINSSTRAKLENDTYRDEVKKHRINGVKSDLOMTORODWKSCHEK KTANGVYFICCESCHAFTENDTHAGATHAGATALLEBENKECHER 6768 2 363 955 AFRITSGVLVGCKNANDFERNSTRONDWKSCHEKTHAGATHAGATALLEBENKECHER 6769 284 396 MSTPDFSTRAKLDTYRDFORRODWKSCHERDSKAND 6770 1 397 ORNYGVINSSTRAKLENDTYRDFORRODWKSCHERDSKAND 6771 3 378	6763	2	760	SGPDFPGRRFRGCCCVRPPAGAGMELGGHWDMNSAPRLVSETAE
LLSHWKSIGASPTVAGIVGSSYGILQUFSSTILTGCGNDUVGGG SILLAGUTLLSAGTVILLGAATNIFT/LARVPAGIFKHTLSISK ALLSDVVPEKERPLVIGHENTASGVGFILGPVOGGVITELEDGGF VLTAFICELVFILMAGLWFFERREAKRGSTE LKKMDTMMLSVKNLFEGUVERVETLSEGNEVQFIQLAKDFEDER KKMQTTMHLSVKNLFEGUVERVETLSEGNEVQFIQLAKDFEDER KKMQTTMHLSVKNLFEGUVERVETLSEGNEVQFIQLAKDFEDER KKMQTTMHLSVKNLFEGUVERVETLSEGNEVQFIQLAKDFEDER RQRAEADCEKLERGIQLIESMLMCDTSGSIQ RQSACHOEKLERGIQLIESMLMCDTSGSIQ RQSACHOEKLERGIQLIESMLMCDTSGSIQ RQSACHOEKLERGIQLIESMLMCDTSGSIQ RQSACHOEKLERGIQLIESMLMCDTSGSIQ RQSACHOEKLERGIQLIESMLMCDTSGSIQ RQSACHOEKLERGIQLIESMLMCDTSGSIQLISGSVLSSPNS RQSACHOEKLERGIQLIESMLMCDTSGSIQLISGSVLSSPNS RQSACHOEKLERGIQLIESMLMCDTSGSIQLISGSVLSSPNS RQSACHOEKLERGIQLIESMLMCTSGSICLISGNSVLSSPNS RQSACHOEKLERGIQLIESMLMCTSGACHLERGIQLISGNSKSPNSCHLSKNSKNSHVSACHLERGIQLISGNSKSPNSCHLSKNSKSSPNSSPNS RQSACHOEKLERGIQLIESMLMCTSGACHLERGIGLISGNSKSPNSSPNS RQSACHOEKLERGIQLIESMLMCSGLSAGNLSHARGICN RQSACHOEKLERGIQLIESMLMCSGLSAGNLSHARGICN RQSACHOEKLERGIQLIESMLMCSGLSAGNLSHARGICN RQSACHOEKLERGIGLIESMLMCSGLSAGNLSHARGICN RQSACHOEKLERGIGLIESMLMCSGLSAGNLSHARGICN RQSACHOEKLERGIGLIESMLMCSGLSAGNLSHARGICN RQSACHOEKLERGIGLIESMLMCSGLSAGNLSHARGICN RATEGORY RUCKUSTAGENSTAGNLSHARGICN RQSACHOEKLERGIGLIESMLSAGNLSHARGICN RQSACHOEKLERGIGLIESMLSAGNLSHARGICN RQSACHOEKLERGIGLIESMLSAGNLSHARGICN RQSACHOEKLERGICN RQ				RKQEQKTGTEAEAADSGAVGARRFLLCLYLGGFLDLFGVSMAND
SSLIACTLISAIGYILLGAATIVFI, FVLARVPAGFIRIFILE ISB ALISDVYEKREPLUVIGHNTAGGGEFILGPVYGGYITLE BOGG YLTAFICETUT ILNAGLIVEFFPREAKRGSTE 6764 80 438 LKKMDTMILSVRINGEGDURFVET ILSGENEVOPIQLAKDFEDFR KKMORTDHELGKYKDLIMKABETERSALDVILKUARNOVDVETKR RQRAEADGEKKERGOLDLIREMIMCHTSEGNEVOPIQLAKDFEDFR KKMORTDHELGKYKDLIMKABETERSALDVILKUARNOVDVETKR RQRAEADGEKKERGOLDLIREMIMCHTSEGNEVOPIQLAKDFEDFR KKMORTDHELGKYKDLIMKABETERSALDVILKUARNOVDVETKR RQRAEADGEKKERGOLDLIREMIMCHTSEGSVILSSPNS NMSSMVTANGNDSKKFKGEDKMGABERVILHIRKLGEGVETETE VIALGLIPGKVTNILMIKGKNOAFLELATERAATINGNYYSAUT HURRNO 6766 1 1287 EGGSFKASLTWINGLGEKKHCEVEVISRHLBALGKINGKKGK VANDSKOATIVELKARDSKKFKTRYELRENIEGFFT KFVDEGKATVELKEPPUDICLSKANSSSLKGFLSAMKLAHRGCN AVISLCGOTSSROPPVARFILLSTILKDKGTRYELRENIEGFFT KFVDEGKATVELKEPPUDICLSKANSSSLKGFLSAMKLAHRGCN VDTPVSTITPVKTSEFERPKFKTMVITSKKGTRYELRENIEGFFT KFVDEGKATVELKEPPUDICLSKANSSSLKGFLSAMKLAHRGCN VDTPVSTITPVKTSEFERPKFKTMVITSKKGTRYELRENIEGFFT KFVDEGKATVELKEPPUDICLSKANSSLKGFLSAMKLAHRGCN VDTPVSTITPVKTSEFERPKFKTMVITSKKGTRYELRENIEGFFT KFVDEGKATVELKEPPUDICLSKANSSLKGFLSAMKLAHRGCN VDTPVSTITPVKTSEFERPKFKTMVITSKKGTRYELRENIEGFFT KFVDEGKATVELKEPPUDICLSKANSSLKGFLSAMKLAHRGCN VDTPVSTITPVKTSEFERPKFTMVITSKKRGTRYELRENIEGFFT KFVDEGKATVELKERPPUDICLSKANSSLKGFLSAMKLAHRGCN VDTPVSTITPVKTSEFERPKFTMVITSKANFLENIEGFFT KFVDEGKATVELKERPPUDICLSKANSSLKGFLSAMKLAHPGCOLLENNE LENSTDIEGFTYKRAFLENIEGHT KKLPPVTLOCH LENSTDIEGFTYNGATHALBESARTILHRR OTSYCLURUMRHLESFSVALCHSTILLSKANSLAGFGATSKANSLAGGATSKANS	Ì			LLSLHVKSLGASPTVAGIVGSSYGILOLFSSTLVGCWSDVVGRR
ALLSDVYPEKRPLVIGHTNIAGCVGFILGPVYGGYITELEDGF YLTAFLEFLYFILINGLWFFPFREKPGSTE LKKMDTMILGVKFPFREKPGSTE LKKMDTMILGVKFPFREKPGSTE KKMDTMILGVKFNIEGLURRVEI LEEGNEVOFIQLAKD FEDFR KKMDTMILGVKRIEGLURRVEI LEEGNEVOFIQLAKD FEDFR ROGRAEADCEKLEROJOLIERHLMCDTSGSIQ ARYSEVDHFCRRRCRAVARAPRFILLOFFSGFSRHFLAACVARML ROGREADCEKLEROJOLIERHLMCDTSGSIQ RGSVLVSEALSGSANDGIVTEVAVRGSDELLSGSVLSSPNS NMSMVVTANGBDSKKFKGBUKNGAPSRVLHIRKLDGEVTETE VIALGLDFGKVRTILIMLKGKNORFLELATERAATINDKYSAVT PHLRNQ EGGSFKASLTMLMPLGEMKLHCEVEVISHLPALGLRRRGKGVR AVLSLCQOTSRSOPPVRAFILISTILKDKRGTRYSLRRNIEOFFT KFUDEGKATVRLKERPPVDICLSKANSSLKGFLSAMKLAHRGCN VDTPVSTLIPVKTSEFENFXTRAVITSKODTPLSKMPFYSLEHI QTSYGLAVDNMRMLCKKSLRKLDLSHNINKLDATIGDLIHLQ ELNANDNHLESFSVALCHSTLOKSUNSLDLSKNIK KALPVQFCQ LQBLKNLKLIDDNELIQFPCKLGGLINLERLSANKLDPUFDSFF RNILSEYLDLFGNTFEOFKVLPVILOPAITLLESSARTILHNR IPYGSHIIPPHLCQDLDTAAICVCGRFCLNSFIGGTTTMNLHSV AHTVULVNLNGGTEAPIISYFSCLGVVNSSDI APHVLCCSSDLOFFYKRAFIRDRGLOIGYCSVDDDPRMKHFJLNV GRQLSDNSYKKDFAKSRSOPHSSTOGLLQAKRSQOLASDVHY RQPLPQPTCDPEOLGLRHAQKAHQLQSDVKYKSDLASTROVWY RQPLPQPTCDPEOLGLRHAQKAHQLQSDVKYKSDLASTROVWY RQPLPQPTCDPEOLGLRHAQKAHQLQSDVKYKSDLASTROVWY RQPLPGTPTCDPEOLGLRHAGKAHQLQSDVKYKSDLASTROVWY RQPLPGTPTCDPEOLGLRHAGKAHQLQSDVKKSDLASTROVWY RQPLPGTPTCPEOLGLRHAGKAHQLQSDVKKSDLASTROVWY RQPLPGTPTCPEOLGLRHAGKAHQLQSDVKKSDLALTRGVGWT RDSTYLLSFESTLENGERAMERGSQDMGKSGDERLLQAV 6768 2 363 PGSTISCYLLSEGSLPLCMOVACGEEKHRAFTMKTLRAKFKKTE LELSFTDLGSCPPCGPCPTPKPAARGRRQSQDMGKSGDERLLQAV NPDATEILHVKKKKLLL 6769 284 396 MSTEPJSTAENCELARBVSCLKARHLTHLMQAMGQAD 6770 1 397 QNNYQVINSTMAKLHDYYKDEVVKLMTENNISWOOPEVGE KTRQGYPIGCKVTLRGERMHEFFERLITIAVPRIRDFRGLSAKS 6771 3 378 APAGTLANTGSVVKDVDRYQGVILANSLEG RNSMNIGVFICIRCAGIHRNIGVITSGLSRYQLUVRLOFGLIQCH RNSMNIGVFICIRCAGIHRNIGVTISGLSRYQLUVRLOFGLIQCH HVGGKLAULTYBENGRTELTTESPLKVSLUNDAVFLIGGGAAFFT APPLAGRAVALDAVYTLANGLGSGTLASSYDIAA CLCLTFVSYFGGSG\HKPRMLGWGR\VLMGTGSLAPSYDIAA CLCLTFVSYFGGSG\HKPRMLGWGR\VLMGTGSLAPSYDIAA CLCLTFVSYFGGSG\HKPRMLGWGR\VLMGTGSLAPSYDIAA CLCLTFVSYFGGSG\HKPRMLGWGRSVANDSTGSGAAFFT APPLAGASCOPPHTSPUCGSGGTWSCHGSGLAPSTWTDMC FCLCCTVVSLLG				SSLLACILLSALGYLLLGAATNVFLFVLARVPAGTERHTIGTGD
6764 80 438 LKKMDTMLSVENLEGOURNEVELEGOENDOF IOLAKDFEDER KKWORTDHELGKYKDLLMKASTERSALDVIKLHARNOVDVEIR RORABADCEKLEROJOLIEMLMCTOSGIQ 6765 3 550 ARYSEVDHFCRRCRAVARAPRILLÖFFSGFSRHFLÄACVARML RGSVLVSALSGSANDGIVTEVAVGVKRGSDELLGGSVLSSPNS NMSSMVVATNAGDISKKFKGEDKHÖRSPSKHLHRKLOEVTETE VIALGLDFGKVYNTLIMLKGKNOAFLELATERAALTNGNYYSAVT PHLRNO 6766 1 1287 EGGSFKASLTWLWPLGEMKLHCEVEVISRHJPALGLENNEGGVR AVLSLCOOTSRSOPVARPLLISTLKKKRGTYPELRALGLENNEGGVR VUDTPVSTLTPVKTSEFENFTKRVITSKOVPLSKNYFYSLEHL GTSYCGLVRVDMRHLCKSLRKLDISHNIKLPATIGDLIHLO ELMINDNHLBSFSVALCHSTLOKSLWSLDLSKNIKALPVOFCO LOELKINLDDNELIGPPCKIGGLINRFLGARMKLAPLOFFO RNLSLEYLDLEGNTFEOPKVLPVIKLOADITLBSSARTILHEN 1PYGSILIPPHILGPPCKIGGLINRFLGARMKLAPLOFFO RNLSLEYLDLEGNTFEOPKVLPVIKLOADITLBSSARTILHEN 1PYGSILIPPHILGDLTARICVCGREINSFLGGTTTMNLHSV AHTVULVIDNLGGTEAPIISYFCSLGGYVANSSDI 6767 336 919 APHICLSSDLOFRYKEDFAKSRSOFHSSTDOPGLLQAKRSQOLASDHY ROPLEPPTCDPEOLGIRHAQKAHOLQSDVKYKSDLALTRGVGWT PGSTKVEMBARAALALBARGGILGGVARGABEVAERDIGGGEV NPDATEILHVKKKALLL 6769 284 396 MSTPDFSTAENNGELANRGUSGAVRGABVAERDIGGSGEV ENNDAPVAALIARKSLVPTKLDPEKKSARHL 6770 1 397 QRNYQVINSSTWAKLIDNAADLASGGKPLTKARSVAGF KIRQGYPIGCKVULRGERNWEFFERLITIADPRIRDFRGLSAKS APAGTILAHTGKSVENDERVORTORGENWEFFERLITIADPRIRDFRGLSAKS APAGTILAHTGKSVENDERVORTORGENWEFFERLITIADPRIRDFRGLSAKS APAGTILAHTGKSVENDERVORTORGENWEFFERLITIADPRIRDFRGLSAKS APAGTILAHTGKSVENDERVORTORGENWEFFERLITIADPRIRDFRGLSAKS APAGTILAHTGKSVENDERVORTORGIANGLVERVENDLEG 6771 3 378 APAGTICHLEENDERVENDERVENSVENLOUGTUPLEVENLOG CEMCGKANRLYEAVLDPETFRRPQIDPYLWENLEG GRMGKANRLYEAVLDPETFRRPQIDPYLWENLEG APAGTICHTUPLISTLETENSVENSVENLOUGTUPLAGGAAFPT APPLAGGRGVANRELYEAVLDPETFRRPQIDPYLWENLEG CLCLIFVSYFGGSG\KRPWLLWGR\VINTSLERSVENDLAGGFT APPLIGANTYTISTLETENTENTENTSVENDEROPGKT APAGTICHTUPLISTLETENTENTENTSVENDEROPGKT APAGTICHTUPLISTLETENTENTENTSVENDEROPGKT APAGTICHTUPLISTLETENTENTSVENDERSVENLAGERPT APPLIGATENTYTISTLETENTENTSVENDEROPGKT APPLIGABLUTINTENTENTENTENTENTSVENDEROPGKT APAGTICHTUPLISTLETENTSVENDERVENTSVGSGLAFENTDRG CLCLIFVSYFGGSG\KRPWLLGLAGGAAFPT APPLIGATENT	1			ALLSDVVPEKERPLVIGHFNTASGVGFTLGPVVGGVLTFLEDGE
6765 3 550 ARYSEN/DEGINVENCET-LEGGNEVOFTGLAKDFEDFER RORAEADCEKLEROJQLIREMIMCDTSGSIQ ARYSEN/DHFCRRCARCAVARAPET-LOPESFEPSHFLAACVARML RGSVLVSEALSGANDGIVTEVAVGVKRGSDELLSGSVLSSPNS NMSSMVVATANGDISKFKEGENNDGAFRVLHIRKLDGEVTETE VIALGLPFGKVTNILMLKGKNQAFLELATERAATINGNYSAVT PHLKUN 6766 1 1287 EGGSFKASLTWLWPLGEMKLHCEVEVISRHLPALGLERNRGKGVR AVLSLCQOTSRSQPPVRAFLLISTLKDKKGTRYSLRENIEQFFT KFVDEGKATVELKEPPVDICLSKASSLKGFLSAMFLAHRGCN VDTPVSTLIPVKTSEFENFKTKWITSKDVPLSKNPYSLEHL GTSYCGLVEVDMFMLCKSLRKLDLSHNHIKLDATIGDLIHLO ELMINDNHLBSFSVALCHSTLOKSLBSLDLSKNKIKALPVOPFCQ LOEKKAKLDDNELLGPPCKIGGLHAFLSAARNKLPFLPFSEF RNISLEYLDLFGNTFEQPKVLPVIKLQAPHILLESSARTILHNR IPVGSHIPPHLCQDLDTAKICVCGRFCLHSFIGGTTTMNLHSV AHTVVLVDNLGGTEAPIISFTSCLGCYVNSSDI 6767 336 919 APMICLCSSDLOFFYKBAFLRDRGLOIGYGSVDDDPRMKHFLNV RQPLPQPTCDPEQLGLRHAQKAHOLQSDVKKSDLALKTGVGWT PGSTXSVMARRAALBLANARGLOLGSDVKKSDLALKTGVGWT RQPLPQPTCDPEQLGLRHAQKAHOLQSDVKKSDLALKTGVGWT PGSTXSVMARRAALBLANARGLOLGSDVKKSDLALKTGVGWT PGSTXVEMBARRAALBLANARGLOLGSDVKKSDLALKTGVGWT PGSTXSVMARRAALBLANARGLOLGSDVKKSDLALKTGVGWT PGSTXSVMARRABLANARGLOLGSDVKKKSDLALKTGVGWT PGSTXSVMARRABLANARGLOLGSDVKKKSDLALKTGVGWT PGSTSTZVLLSGEGBLPCMQVACGEEKHRAPTMKTLRAFFKKTE LRISPTDLGSCPPCGPCPIPKPAARGRRQSCOMGKSDERLLOAV ENDLAPRIVALLARLANGVETKLDPBGKSBEFLL 6769 284 396 MSTPDFSTRENDCLARBVSCLKAMLITLMLQAMGQAD 6770 1 397 QRNYQVINSSTMAKLHDYKDEVVKKLMTEFNYNSWOOPRVEK ITINNGVGBATADKLLDNAALDLALEGOKPLITKARSVAGF KIRQGYPIGCKVTLRGERMWEPFELITTLAPPIRPFRGLSAKS APGTLAHTGSSVEVDERVYQAGGEKVLTMCGGREVNLGGGSLASSFPR WASMNIGVFICIRCAGIHRNLGVHLSVNSLOGDELJARS P+*GKLADAGNTCPANRF\PVCGAGGK\NFRWLLGGRKPLITKAPGLARS LCLLTFVSYFGGGG\KPRWLLGGRK\UMGTGSLVFALPHTAG CLCLTFVSYFGGGG\KPRWLLGGRK\UMGTGSLVFALPHTAG LCLLTFVSYFGGGG\KPRWLLGGRK\UMGTGSLVFALPHTAG LCLLTFVSYFGGGG\KPRWLLGGRK\UMGTGSLVFALPHTAG LCLLTFVSYFGGGG\KPRWLLGGRK\UMGTGSLVFALPHTTAG LCLLTFVSYFGGGG\KPRWLLGGRK\UMGTGSLVFALPHTTAG P+*GKLADAGNTCPANRF\PVTGGSGK\HTGMLTGGSLFYQUVMLQGFL HUGGATPLYTLGTTYLTDLENVKSSCSPIYANDFLGGFT APPLIAACSCOPPHIYSPUCGSGLMFTGGFFVNKLRIRGGAVIK FCLLCTVVSLLGILVPSHCPSVPMAGVTASYGGSLLPEGHLINL TAPCNAACSCOPPHI	5764	90	4.2.0	YLTAFICFLVFILNAGLVWFFPRREAKPGSTE
6765 3 550 ARYSRVDHFCRRCRAVARAPRELLOPPSGPSRIFLACVARRIL RGSVIUVSEALSGSAMDGIVTEVAVGVKRGSDELLSGSVLSSPNS NMSSMVTANGNDSKKFKGEDKMDGAFVHIRIKLDGEVTETE VIALGLPFGKVINILMLKGKANGAFLELATERAAITMGNYYSAVT PHIRNQ 6766 1 1287 EGGSFKASLTWLWPLGEMKLHCEVEVISRHLPALGLRINRGKGVR AVLSLCQOTSRSOPPVRAFILLISTLKDKRGTRYELRENIEOFFT KFVDEGKATVTLKEEPPVILCLSKANSSLKGFLSAMRLAHRGCIN VDTPVSTLTPVKTSEFENFKTKMVITSKKPYPLSKNFPYSLEHL QTSYCGLVRVOMRMLCLKSLKRLDLSINHHKKLPATIGDLIHLQ ELMINDNHLBSFSVALCHSTLOKSLMSSLLKSFLSAMRLAHRGCIN LGELKNLKLIDDMELIQFFCKIGGLINLAFISAARNKLPFLPESF RNLSLEYLDLFGNTFEQPKVLDYLKLOAPITLLESSARTLIHNR IPYGSHIPPHLCODLDTAKICVCGRFCLASFIGGTTTMNLHSV AHTVULVDNLGGTEAPIISYRCGVWNSDII 6767 336 919 APMICLCSSDLQFRYKEAFLRDRGLGTGYCSVDDDPRMKHFLNV GRIQSDNSEKKDFAKSRSOFHSSTDOPGLIQKRSQOLASDVHY RQPLEQPTCDPSGLGLRHAQXAHQLQSDVKYKSDLNLTRGVGWT PROSYKVEMARRAABLANARGLGLGGAYRGAEAVEAGDHQSGEV NDATTSLHLVKKKALLL NDATTSLHLVKKKALLL 6769 2 363 PGSTISCYLLSEGSLPLCMQVACGEEKHRAPTMKTLRARFKKTE LRLSPTDLGSCPPCGPC1PKPAARGRRSQDWGKSDERLLOAV ENNDAPRVAALIARKGLUPYLDDFEKSAFHL 6769 284 396 MSTPDFSTAENNQELANEVSCLKAMITLMIQAMGQAD 6770 1 397 QRNYQVINSSTMAKHDYYKDEVKIMTEFNYNSTWOVPRVEK ITLINMSVGBAIAHGLSVKVLDNRYQAVKIMTEFNYNSTWOVPRVEK KRQGYPIGCKVTLRGGRMEFFERLITTLAPRIRDFRGLSAKS KRQGYPIGCKVTLRGGRMEFFERLITTLAPRIRDFRGLSAKS 6771 3 378 APAGTLANTGKSVKDVDRYQAVKIMTEFNYNSTWOVPRVEK CTLANTGKSVKDVDRYQAVKIMTEFNYNSTWOVPRVEK GRINGKANRILYEAYLDETTERRCIDPYLFMSNLEG 0PMGRKANRILYEAYLDETTERRCIDPYLFMSNLEG 0PMGRKANRILYEAYLDETTERRCIDPYLFMSNLEG 0PMGRKANRILYEAYLDETTERRCIDPYLFMSNLEG 1LGGALLNITYEMGRRTELLTESPLWOARMUSTIGSGAAAFPT AVPLIGYPRGLEGNITIGVTSLCAGGHTHAGLHTSGRSVLIVPALPHTTAG PN-GKKLDAGWTCPAHPRIPUCAGGGTTLLGGFVNKLERGSAVIK PCLCTTVSLIGLINITYTLGVSGGGTTLGGFVNKLERGSAVIK PCLCTTVSLIGLINTFSLKCPSVPMAGVTSSCSLLPEGGHLIL TAPCNAACSCQPBTILGGFVNKSCGGTFLEGGFVNKLRRGSSAVIK PCLCCTVVSLIGLINTSLICCPSVPMAGVTSCCSLLPEGGHLIL TAPCNAACSCQPBTLSGGCTFLEGGFVNKLRRGSGANIK FCLCCTVVSLIGLINTSLICCPSVPMAGVTSCCSLLPEGGLILL TAPCNAACSCQPBTLSGFVSCLGAATETNVIC	8764	80	438	LKKMDTMMLSVRNLFEQLVRRVEILSEGNEVQFIQLAKDFEDFR
ARYSNOHFCRRCRAVARAPRFILOFPSGPSRIFILAGVARRIL RGSVLVSEALSGSAMDGITUFUVERGSDELLSGSVLSSPNS NMSSMVVTANGNDSKKFKGEDKMDGAPSRVLHIRKLDGEVTETE VIALGLPGKVINILMLKGKNQAFLELATERAAITNGNYYSAVT PHERNQ 6766 1 1287 EGGSFKASLTWLWPLGEMKLHCEVEVISRHLPALGLENRGKGVR AVASLCQOTSRSOPPVRAFLLISTILKDKRGTRYELRENIEQFFT KFVDEGKATVRLKEPPVDICLSKANSSSLKGFLSARRLAHRGCN VDTPVSTLTPVKTSEFENFKTKMVITSKKDYPLSKAFPYSLEHL GTSYCGLVRVDMRMLCLKSLEKDLISNHHKKLPAFIGDLIHNG ELNINNHHESFSVALCHSTLQKSLMSLDLSKNKIKALPVGFCO LQELKNIKLDDBELGOFPCKLGDLINEFISARRKLPFLPGSEF RNISLEYLDLFONTFEQEKVLPVIKLQAPITLLESSARTILHNR IPVGSHLIPPHLCQDLDTAKLCVCGRFCLMSFIQGTTINNLHSV AHTVULVDNLGGTEAPIISYTCSLGCYVNSDI 6767 336 919 APMICLCSSBLQFRYKEAFLEDRGLGIGYCSVDDDFRMKHFLNV GRIQSINEYKKDFAKSSOFFISAGGLASGOLASDWHY RQPLPQPTCDPBOLGLRRAQXAHQLQSDVKYKSDLNLTRGVGWT PPOSSYXVEMARRAAELANARGLGLQGAYRGEAVEAGHQSGEV NPDATEILHVKKKKALL 6758 2 363 PGSTISCYLLSEGGIPLCMQVACGEEKHRAPTMKTLRAFFKKTE LRLSFTDLGSCPPCPPCPPKAARGRRQSQDWSGDERLLOAV ENNDAPRVAALIARKGLUPTKLDPEGKSAFHL 6769 284 396 MSTPDFSTAENNQELANEVSCLKAMITLMLQAMGQAD 6769 284 396 MSTPDFSTAENNQELANEVSCLKAMITLMLQAMGQAD 6770 1 397 QRNYQVINSSTMAKLHDYYKBURGHFRYNSVMQVPRVEK ITINMGVGBAIADKKLLDNAADLAAISGOKLITYKARKSVAGF KRQGYPIGCKVTURGERMMEPFERLITLAVBRIBDFRGLSAK 6771 3 378 APAGTIAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR WASNNIGHYICIRCAGHRRILGHTISVSVNLDQWTQEQIQCM OBMGNGKANRIYEAYLDETTERRQIUPYLFBYRGUGGGTLASSYDIAA CLCLLTVSYFGGSG HKPRRILGSVLVMGTGSLVALPHPTAG P**GWKLDAGVRTCPANPR\PVCAG\HTSGLTSVQLVFMLOGFL HCVGATFLYTLGYTYLGYTYLDETAGLISGGSGAAAFPT AVPILGYPRQLPGGGRYAVWRAAEMHQLKDSSRGEASNPDFGKT RDLPLSWLLGGSGRYAWRAAEMHQLKDSSRGEASNPDFGKT RDLPLSWLLGWNFFILLCLAGAFFATLITYMATIGSGAAAFFT AVPILGYPRQLPGSGRYAWWRAAEMHQLKDSSRGEASNPDFGKT RDLPLSWLLKHMPTFILLCLLGAGTFAGTLITTGMSTFSPKREE QFSLASASAATLFGYLVVRAGGGGTFLGGFFVNKLRIRGSGAVIK PCLECTVVSLLGILVFSLUCPSVPMAGVFSGCSLLPEGHLINL TAPCNAACSCOPPHYSPSUCCSCOPAATETNVIG				KKWQRTDHELGKYKDLLMKAETERSALDVKLKHARNQVDVEIKR
RGSSVUSEALSGSAMDGIVEVANGVKRGBELLGGSVLSS PNS NMSSMVVTANGNDSKKFKGEDKMDGAPSRVLHIRKLDGEVTETE VIALGLEFGEVTNILMLKGKNOGAFLELATERAAITNGNYYSAVT PHURNO 6766 1 1287 EGGFYKASLTWLWPLGEMKLHCEVEVISRHLPALGLRNRGKGVR AVLSLCQOTSRSQP PVRAFILLISTLKDKKGTRYELRENI EQFFT KFVDEGKATVRLEPEVDICLSKAMSSSLKGFLSAMRLAHRGCN VDTPVSTLTEVKTSEFENFSTKRWITSKKDYPLSKNFFYSLEHL QTSYCGLVRVDMEMLCLKSLRKLDLSHNHIKKLPATIGDLIHLO LELNINNHLBSFSVALCHSTKKAULSPHILSKNFKYSLEHL QTSYCGLVRVDMEMLCLKSLRKLDLSHNHIKKLPATIGDLIHLO LELNINNHLBSFSVALCHSTKKAULDSHNHIKKLPATIGDLIHLO LELNINNHLBSFSVALCHSTCKSLBSLDLSKNKIKALDAVPCO LQELKNIKLDDNELIOFPCKLGCLINLFPLSAARNKLPFLPSEF RNLSLEYLDLFGNTFFEOPKVLPVILOPBLIKTKTALDAVPCO LQELKNIKLDDNELIOFPCKLGCLINLRPLSAARNKLPFLPSEF RNLSLEYLDLFGNTFFEOPKVLPVILOPBLICGSTUTMLHSV AHTVULVDRLGGTEAPIISYFCSLGCYVMSSDI APPHCLCSSBLOFFTKEAPIRGLGIGKSVDDDPRMKHFLNV GRLQSNDEYKKDFAKSRSOFHSSTDOPGLLOAKRSQOLASDVHY RQPLPOPTCDPBCLGLRHARAGHQLOSDVKYKSDLNLTRGVGWT PPGSYKVEMARRABELANARGIGLQGAYGABAVCAGEHOGSEV NPDATEILHVKKKKALLL 6769 284 396 MSTPDFSTAENGGLIANGVGGEEKHRAPTMKTLRARFKKTE LRLSPTDLGSCPPCOPCIPKPAARGRQSODWGKSDERLLQAV ENNDAPKVAALIJARKGLVPTKLDPBGKSAFHL 6770 1 397 ORNYOVIMSTAMLHDVYKLDEVKKLMTEFNYNSVMOVPRVEK ITLNMGVGBAIADKKLLDNAADADAAISGCKPLITKARKSVAGF KURQGYPIGCKVTLKGGERMBEFFERLITAVPRINSVMOVPRVEK ITLNMGVGBAIADKKLLDNAADADAAISGCKPLITKARKSVAGF KURQGYPIGCKVTLKGGERMBEFFERLITAVPRINSVMOVPRVEK MASMNIGFICIRCAGIHRNLGVHISRVKSVNLDOWTOEQIQCM DEMGRKANRIVAVALVPATHUGHDPLIPSVNLEG 6772 1 1400 AAAFLQGMTVNGFINTVITSL\ERRYDLHSYQSGLTASSYDIAA CLCLTFVSYFGGSG\HKPRMLGWGR\VLMGTGSLVFALPHFTAG HGVGATPLYTLGVYTLDENVKSCSPIYIAIFTYAALIGPAAGY LIGGALINIYTEMGRRTELLTERSPLUVGAMWGRGGSAAAFFT AVPILGYSPGGSGRYAVMRAABMHOLKDSSRGEASNPDFGKT IRDLPLSIMLILKNPTFILLCLAGGGTFLGGFFVMKLELRGSAVIK FCLECTVVSLIGILVFSLHCPSVEMAGGGSTFLAGFFVMKLELRGSAVIK FCLECTVVSLIGILVFSLHCPSVEMAGGGSTFLAGFFVMKLELRGSAVIK FCLECTVVSLIGILVFSLHCPSVEMAGGSTFLEGHAIL	6765		EFO.	RQRAEADCEKLERQIQLIREMLMCDTSGSIQ
NMSSMVTAKGNDSKKFKGEDKNDGAPSRVLHIRKLØGEVTETE VIALGLÞFGKVTNILMLKGKNQAFLELATERAAITNGNYYSAVT PHLRNQ GGSFKASLTWLWPLGEMKLHCEVEVISRHLPALGLRNRGKGVR AVLSLCQOTSRSQPPVRAFLLISTLKDKRGTRYELRENIEGOFFT KFVDEGKATVRLEPPUDICLSKANSSSLKGFLSAMRLAHRGCN VDTPVSTLTPVKTSEFENPKHVNITSKKDPYSLEHL QTSYCGLVRVDMRMLCLKSLRKLDLSHNHIKKLPATIGDLIHLQ ELNLNDNHLESFSVALCHSTLCKSLDLSKNKIKALPVQPCQ LQELKNLKLDDBELIGFPCKIGGLINLRFLSAARNLLPFLPESF RNLSLEYLDLFGNTFEPPKVLPVIKLQAPITLLESSARTILHNR 1PYGSHITPPHLQODLDTAKICVCGRFCLNSFIGGTTTMNLHSV AHTVVLVDNLGGTEAPIISYFCSLGCYVNSSDI APMICLCSSDLQFRYKEAFLRDRGLQIGKCSVDDDPFMKHFLNV GRLQSDNEYKKPFAKSRSQFHSSTDOPGLLQAKRSQOLASDVHY RQPLPQPTCDPEDLGLRHAQKAHQLQSDVKYKSDLNITRGVGWT PPGSYKVEMARRABLANARGLGLAGAYRGAEAVEAGDHQSGEV NPDATBILHVKKKKALLL 6769 2363 FGSTISCYLLSEGSIPLCMQVACGEEKHRAPTMKTLRARFKKTE LRLSFTDLGSCPPCGPCPIPKPAARGRRQSQDWGKSDERLLQAV ENNDAPRVALITARKGLVPTKLDPBKGASFHL 6769 284 396 MSTPDFSTAENGELANBVSCLKAMLTLHLQAMGQAD 6770 1 397 QRNYQVIWSSTNAKLHDYYKDEVVKKLMTETNYNSVMQVPRVEK ITLNNGVGEAIADKHLDNAAADLAAISGQKPLITKARKSVAGF KKRQYPICKVTLRGERNWEFRELTITIAVPRIRDFRGLSAKS APAGTLAMTGKSVKDVBRYQAVLANLLLEENNKFCADCQSKGPR WASMIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQCQIQCM QEMGRGKANRLYEAVLFBETRRPQIDPYLFWSNLEG 6772 1 1400 AAAFLQGMTVNSFINTVITSL\ERRYPLBSQSGLXASSVDIAA CLCLTTVSYFGGSG\HKPRWGRVLVLMTSGLXPALPHTTAG P**GMKLDAGVTLFGRSGNYRGRVLVLMTSGLXPALPHTTAG P**GMKLDAGVTLFGRSGNYRKSCSPIYIAIFTTAALGPAAGY LIGGALLNIYTEMGRRTELLTEABLVADAWGPLGSGLAAFFT AVPILGYPROLFGSG\HKPRWGRSCLVFALPHTTAGFLFFACT LIGGALLNIYTEMGRRTELLTGAGTEATLITCMSTFSPKFLES QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLELRGSAVIK PCLECTVVSLIGILVFSLHCPSVEMAGVTASYGGSLLPEGHLINL TAPCNAACSCQPEHYSPVCGSDIAMYSSCGSLAPEGLINUNG FCLECTVVSLIGILVFSLHCPSVEMAGVTASYGGSLLPEGHLINL TAPCNAACSCQPEHYSPVCGSDIAMYSSCGHANDTSCGSLLPEHLINLI TAPCNAACSCQPEHYSPVCGSDIAMYSSCGHANDTSCGSLLPEHLINLI TAPCNAACSCQPEHYSPVCGSDIAMYSSCHARDLERGSAVIK PCLECTVVSLIGILVFSLHCPSVEMAGVTASYGGSLLPEGHLINL TAPCNAACSCQPEHYSPVCGSDIAMYSSCHARDLERGSAVIK PCLECTVVSLIGILVFSLHCPSVEMAGVTASYGGSLLPEGHLINL TAPCNAACSCQPEHYSPVCGSDIAMYSSCCHARCPAACTENTUNG	1 0.05		550	ARYSRVDHFCRRCRAVARAPRFLLQFPSGPSRHFLAACVARWL
6766 1 1287 EGGSFKASLTWLWPIGEMKLHCEVEVISRHLPALGLRNRGKGVR AVLSLCQQTSRSQPPVRAFLLISTLKDKRGTRYELRENIEQFFT KFYDEGKATVRLKEPFVDICLSKANSSLKGFLSAMKLAHRGCN VDTPVSTLTPVKTSEFENFKXKWITSKKDYPLSKNFYSLEHL QTSYCGLVRVDMRMLCLKSLRKDLSHNHIKKLPATIGDLIHLQ ELNLNDNHLBSFSVALCHSTLQKSLWSLDLSKNKIKALPVOPCQ LQELKALKLDDNELIGFPTFGKYLFVIKLORPITLESSARNKLPFLPSEF RNISLEYLDLFGNTFEQFKVLPVIKLORPITLESSARNKLPFLPSEF RNISLEYLDLFGNTFEQFKVLPVIKLORPITLESSARTILHNR IPYGSHIPPHLCQDLDTAKICVCGRFCLNSFIQGTTTMNLHSV AHTVVLVDNLGGTEAPPISYTCGCYVNSDI GRIQSDNEYKKDFAKSRSQFRSTDQPGLLQAKRSQOLASDVHY RQPLPOPTCDPEOLGLRANGAHQLGSDKYKSDLNLTRGVGWT PPGSYXVEMARRAAELANARGLGLQGAYRGAEAVEAGDHQSGEV NPDATEILHVKKKAALL 6769 284 396 PGSTISCYLLSEGSLPLCMQVACGEEKHRAPTMKTLRARFKKTE LRISPTDLGSCPPCGPCPIPKPARAGRRQSQDWGKSDERLLQAV ENNDAPRVAALIARKGLVPTKLDGKKSAPHL 6770 1 397 QRNYQVIWSSTMAKLHDYYKDEVKKIMTEFNNSVWQVPRVEK ITINMSVGEALDAKKLLDNAADLAAISGQKPLITKARKSVAGF KIRQGYPIGCKVTLRGERNWEFFERLITIAVPRIRDFRGLSAKS 6771 3 378 APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR MASMNIGVFICTRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCM QEMGKGKARRLVEAYLPETFRRPQIDPYLFWSNLEG 6772 1 1400 AAAFLQGWTVNTFINVTSLLEEDNKFCADCQSKGPR MASMNIGVFICTRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCM QEMGKGKARRLVEAYLPETFRRPQIDPYLFWSNLEG CLCLITFVSYFGGSG\HKFRLWGRSVLSYDLAGFSLASSTDIAA CLCLITFVSYFGGSG\HKFRLWGRSVLSYDLAGFSLASSTDIAA CLCLITFVSYFGGSG\HKFRLGWTSSLVSSCLASSTDLAG IRDLPLSTWLLLKNPTFILLLCLAGATEATLITGMSTFSPKFLES QFSLSASAATLFGYLVVPAGGGGTFLGGFFVNKRLRGSAVIK FCLFCTVVSLLGILVFSLHCRSGFRWAGVFSSPLFSFFKELS QFSLSASAATLFGYLVVPAGGGGTFLGGFFVNKRLRGSAVIK FCLFCTVVSLLGILVFSLHCRSSDFMFSDKFLES	ļ			RGSVLVSKALSGSAMDGIVTEVAVGVKRGSDELLSGSVLSSPNS
6766 1 1287 EGGSFKASLTWLWPLGEMKLHCEVEVISRHLPALGLRNRGKVR AVISLCQOTSRSQDPVRAFLLISTLKDKRGTRYELRENIEGFFT KFVDEGKATVRLKEPPUDICLSKANSSLKGFLSAMRLAHRGCN VDTPVSTLTEVKTSEFERITGVFTSKEWTITSKKDPTSLEHL QTSYCGLVRVDMRMLCLKSLRKUDLSKNKLKDPLSKNPFYSLEHL QTSYCGLVRVDMRMLCLKSLRKUDLSHNHIKKLPATIGDLIHLQ ELMINDHLIBSFSVALCHSLOKSLNSLODLSKNKIKALPVQFCQ LQELKNIKLDDNELIQFPCKIGQLINLRFLSAARNKLPFLBSEF RNLSLEYLDLFGNTFTFOPKVLPVIKLQAPLTLLESSARTILHNR IPYGSHIIPHLCQDLDTAKCUCGRFCLNSFIQGTTTMLHSV AHTVULVDNLGGTEAPIISTFCSLGCYWSSDI AHTVULVDNLGGTEAPIISTFCSLGCYWSSDI AHTVULVDNLGGTEAPIISTFCSLGCYWSSDI PPKSENDGPKYKEPLBRGLQIGYCSVDDDPRMKHFLNV GRUOGNDWYKKDFAKSRSOFHSSTDQPGLLQAKRSQQLASDVHY RQPLPQFTCDPBCLGLRHAQKAHQLQSDVXYKSDLNITRGVGWT PPGSYLVEMARRABELIANGGLAGAYRGAEAVEAGDHQSGEV NPDATSILHVKKKKALLL LRLSPTDLGSCPPCGPCPIPKPAARGRCGSQDWGKSDERLLQAV ENNDAPRVABLIARKGLVPTKLDPEGKSAFHL LRLSPTDLGSCPPCGPCPIPKPAARGRCGSQDWGKSDERLLQAV ENNDAPRVABLIARKGLVPTKLDPEGKSAFHL STENDAPRVABLIARKGLVPTKLDPEGKSAFHL STENDAPRVABLIARKGLVPTKLDPEGKSAFHL ITLNMGVGEAIANKLLDNAAAALAAISGCKPLITKARKSVAGF KIRQGYPIGKVTLRGGERMWFFERLITLAPMINDFRIDSAKS KIRQGYPIGKVTLRGGERMWFFERLITLAPMINDFRIDSAKS KIRQGYPIGKVTLRGGERMWFFERLITAVPRINDFRISJAKS KIRQGYPIGKVTLRGGERMWFFERLITAVPRINDFRISJAKS VASWMIGVFUCTRCAGIHRNLGVHISRVKSVNLDQWTQEGIQCM QEMGNGKANRLYEAYLPFTRRPQIDPYLFWSNLEG CLCLTFVSYFGGSG HKRPMLGWGR VLMGTSLVFALPHFTAG CLCLTFVSYFGGSG HKRPMLGWGR VLMGTSLVFALPHFTAG CLCLTFVSYFGGSG HKRPMLGWGR VLMGTSLVFALPHFTAG CLCLTFVSYFGGSG HKRPMLGWGR VLMGTSLVFALPHFTAG PY*GMKLDAGWTCPANPR VPCAGNATSLVFALPHFTAG PY*GMKLDAGWTCPANPR VPCAGNATSLVFALPHFTAG CLCLTFVSYFGGSG HKRPMLGWGR VLMGTSLVFALPHFTAG FY*GMKLDAGWTCPANPR VPCAGNAFFT AVPILGFROGSG HKRPMLGWGR VLMGTSLVFALPHFTAG FY*GMKLDAGWTCPANPR VPCAGNAFFT AVPILGFROGSG HKRPMLGWGR VLMGTSLVFALPHFTAG FY*GMKLDAGWTCPANPR VPCAGNAFFT AVPILGFROGSG HKPSLCHAGGPATFTSP KFLES OFSLASEABAFFT AVPILGFROM MUSPLEGGFFONKERLRGSAVIK FCLECTVVSLLG ILVFSLHCGSGFFONKERLRGSAVIK FCLECTVVSLLG ILVFSLHCGSGFLHGCPANTFSP KFLES OFSLASEAGLHGGCAGAFFT AVPILAGRAFFALHUNGGSGGFFLEGFFONKLRLRGSAVIK FCLECTVVSLLG ILVFSLHCGSGFFONKERLRGSAVIK FCLECTVVSLLG ILVFSLHGGSGFLHGGCS				VIALCE DECLURATION MORE TO THE TENER OF THE PROPERTY OF THE PR
6766 1 1287 EGGSFKASLTWLWPLGEMKLHCEVVISRHLPALGLRNRGKGVR AVLSLCQCTSRSQPPVRAFLLISTKDKRGTRYELRENIEQFFT KPVDGGKATVRLKEPPVILCISKANSSLKGPLSAMKLAHRGCN VDTPVSTLTPVKTSEFENFKTKMVITSKKDYPLSKNFPYSLEHL QTSYCGLVRVDMRMLCLKSLRKULDSKNIKKALPVGFCQ LQELKNLKLDDNELIQFPCKIGQLINLFFLSAARNKLPPLPSEF RNISLEVLDLFGNFTFGGVLDVATKLQAPHTLLESSARTILHNR IPYGSHIIPPHLCQDLDTAKICVCGRFCLNSFIGGTTTMNLHSV AHTVVLVDNLGGTEAPIISYFCSLGGVUNSDI 6767 336 919 APMICLCSSDLGFRYKEAFLEDRGLQTGVSDDDPRMKHFLNV GRLQSDNEYKKDFAKSRSQFRSTDOPGLLQAKRSQOLASDVHY RQPLPOPTCDPEDLGLRHAQXARQLGSDKYKSDLNITRGYGWT PPGSYKVEMARRABELANARGLGLQGAYRGAEAVEAGDHQSGEV NPDATEILHVKKKKALLL 6768 2 363 FGSTISCYLISEGSLPLCMQVACGEEKHRAPTMKTLRARFKKTE LRISPTDLGSCPPCGPCPIPKPAARGRQSQDWGKSDERLLQAV ENNDAFRVAALIARKGLVPTKLDPEKSARHL 6769 284 396 MSTPDFSTAENNQELANEVSCLKAMTTLNLQAMGQAD 6769 284 397 QRNYQVIWSSTMAKLHDYYKDEVKKLMTEFNYNSVMQVPRVEK ITINMSVGGALDAKKLDNAADLAAISQKPLITKARKSVAGF KIRQGYPIGCKVTLRGERMWEFFERLITLAVPRIRPFGLSAKS KIRQGYPIGCKVTLRGERMWEFFERLITLAVPRIRPFGLSAKS KIRQGYPIGCKVTLRGERMWEFFERLITLAVPRIRPFGLSAKS MASMYLGVFICTRCAGIHNLGWHISRVKSVNLDQWTQEQIQCM QRMGKGKANRLVEAYLPETFRPQIDPYLFWSNLEG CLCLITFVSYFGGSGHKPRULGWGRVLMGTSLVKSVNLDQWTQEQIQCM QRMGKGKANRLVEAYLPETFRPQIDPYLFWSNLEG P1*GKKLDAGVTTSLLERRYDLHSYQSGLLASSVDIAA CLCLITFVSYFGGSGHKPRULGWGRVLMFGSLVRALPHPTAG P1*GKKLDAGVTTVTSLLERRYDLHSYQSGLLASSVDIAA CLCLITFVSYFGGSGHKPRULGWGRVLMFGSLVRALPHPTAG P1*GKKLDAGVTTVTSLLERRYDLHSYGSGLASSVDIAA CLCLITFVSYFGGSGHKPRULGWGRVLMFGSLVRALPHPTAG P1*GKKLDAGVTTVTSLLERRYDLHSYGSGLASSFDIAA CLCLITFVSYFGGSGHKPRULGWGRVLMFGSLVRALPHPTAG P1*GKKLDAGVTTVTSLLERRYDLHSYGSGLASSFDFGKT IRDLIPLSIWLLLKNPFTILLCLAGATEATLITGMSTFSPKFLES OFSLASEAATLFGYLVVPAGGGGTFLGGFFVNKRLRGSAVIK FCLFCTVVSLLGILVFSLHCGSGGLFFSCHLNIL TAPCNAACSCOPEHYSPVCGSGGLMYFSLCHAGGPAATFTNVDG				PHIRMO
AVLSLCQQTSRSQPPVRAFILISTLKDKRGTRYELRENIEQFFT KFYDEGKATVELKEEPDICLSKAMSSSLKGFLSAMRLAHRGCN VDTPVSTLTPVKTSEFENFKTKMVITSKKDYPLSKNFPYSLEHL QTSYCGLVRUDMRMLCLKSLRKLDLSHNHIKKLPATIGDLIHLO ELBLINDNHLBSFSVALCHSTLCKSLWSLDLSKNKIKKLPVOPCO LQELKNLKLDDNELIQFPCKIGQLINLRFLSAARNKLPFLPSEF RNILSLEYLDLFGNTFEQPKVLEVIKLQAPLITLESSARTILHNR IPYGSHIIPPHLCQDLDTAKICVCGRFCLNSFIQGTTMNLHSV AHTVVLVDNLGGTEAPIISYFCSLGCYVNSSDI 6767 336 919 APMICLCSSDLQFRYKEAFLRDGGLQIGYCSVDDDPRMKHFLNV GRLQSDNEYKKDFAKSRSQFHSSTDOPGLLQAKRSQQLASDVHY RQPLPQPTCDPEOLGLRHAQKAHQLQSDVKYKSDLNLTRGVGWT PPGSYKVEMARRAAELANARGLGLQGAYRGAEAVEAGDHOSGEV NPDATEILHVKKKKALLL 6768 2 363 PGSTISCYLLSEGSLPLCMQVACGEEKHRAPTMKTLRARFKKTE LRLSPTDLGSCPPCGPCPIPKPAARGRQSQDWGKSDERLLQAV ENNDAPRVAALIARKGLVPTKLDEGKSAFHL 6769 284 396 MSTPDFSTAENNOELANEVSCLKAMILTUKLQAMQAD 6770 1 397 QRNYOVIWSTMAKLHDYKDEVVKKLMTEFNYNSVMQVPRVEK ITLNMGVGBAIADKKLLDNAADLAAISGQKPLITKARKSVAGF KIRQGYPIGCKVTLRGERMWEFFERLITTIAVPRIRPFRGLSAKS 6771 3 378 APAGTLAMTKSKYUDDVAVALANLLLEEDNKFCADCQSKGPR WASWNIGVFICIRCAGIHRNLGVHISRVKSVNLDDWTCBCQICKM WASWNIGVFICIRCAGIHRNLGVHISRVKSVNLDDWTCBCQICKM PP-*GMKLDAGVRTVGFINTVITSIL*PRYPLIEYQSGLLASSYDIAA CLCLTFVSYFGGSG\HKPRWLGWGR\VLMGTGSLVFALDPHFTAG P**GMKLDAGVRTVGFINTVITSIL*PRYPLBTYGAGYL LIGGALHNIYTEMGRRTELTTESPLWVGAWWVGFLGGGAAAFFT AVPILGYPRQLPGSGRYAVWRAARMHQLKDSSRGFASNPDFGKT IRDLPLSIMLLLKNPPTILLCLAGATEATLITGMSTFSPKFLES GFSLSASRAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVFSLLCPSVWGGSLLTASGLSPLDEGHUNL TAPCNAACSCQPEHYSPVCGSDGLMYSTSCHAGGPAAATETNUDG	6766	1	1287	
RFVDEGKATVELKEPPVICLSKANSSSLKGFLSAMKLAHRGON VDTPVSTITPVKTSSFEPRKTKMVITSKKDYPLSKNFPYSLEHL OTSYCGLVRVDMRMLCLKSLRKLDLSHNHIKKLPATIGDLTHLQ ELNLNDMHLBSFSVALCHSTLOKSLMSLDLSKMKIKALPVOFCQ LQELKNIKLDDNELJQFPCKIGQLINLRFISAARNKLPFLBSEF RNISLEVLDLEGNTFEQPKVLDVIKLQAPLTLLESSARTILHNR IPVGSHIIPPHLCQDLDTAKICVCGRFCLNSFIQGTTTMNLHSV AHTVVLVDNLGGTEAPIISYFCSLGCYVNSSDI APMICLCSSDLOFFYKEAFLRDRGLQIGYCSVDDDPRMKHFLNV GRLQSDNGYKKDFAKSRSOFHSSTDOPGLLQAKRSQQLASDVHY RQPLPQPTCDPEQLGIRHAQKAHQLQSDVKYKSDLALTRGVGWT PPGSYKVEMARRAAELANARGLGLQGAYRGAEAVEAGDHQSGEV NPDATEILHVKKKKALLH NPDATEILHVKKKALHL LRLSPTDLGSCPPCGPCPIPKPAARGRRGSQDWGKSDERLLQAV ENNDAPRVAALIARKGLUPTKLDPEGKSAFHL ARLSPTDLGSCPPCGPCPIPKPAARGRAGSQDWGKSDERLLQAV ENNDAPRVAALIARKGLUPTKLDPEGKSAFHL STILNMGVGEALAKKLLDNAAADLAAISGQKPLITKARKSVAGF KIRQGYPIGCKVTLRGERMWEFFERLITTAVBRIRDFRGLSAKS APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGFR WASMNIGVFLCIRCAGIHRNIGVHISRVKSVNLDDWTQEQIQCM QEMGRKAANRLYEAYLPETFRPQIDPYLFMSNLEG CLCLTFVSYFGGSG\HKPRHLGWGR\VLMGTGSLVFALDPHFTAG P**GMKLDAGVRTCPANPR\PVCAG\HTSGLSRYQLVFMLGQFL HGVGATPLLYTLGYTYLLGWTYLGWKSCSPIYIAIFYTAAILGPAAGY LICGALLNIYTEMGRRTELTTESPLWVGAWWVGFLGSGAAAFFT AVPILGYPRQLPGSGRYAVWRAARMHQLKDSSGRGASNBDFGKT IRDLPLSIKHLLKNPTFILLCLAGATEATLITGMSTFSPKFLES QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVFSLLCPSVPMAGVTASYGGSLLPEGHINIL TAPCNAACSCQPEHYSPVCGSDGLMYSTSLCHAGGPAAFTETNUGG				AVISI-COOTSRSOPPUBARILITETT KOMOTOWN PROTECTION
VDTPVSTLTPVKTSERENFTKMVITSKKDYPLSKSPPYSLEHL QTSYCGLVRUMMRLCLKSLRKLDLSHNHIKKLPATIGDLIHLQ ELNLNDNHLBSFSVALCHSTLQKSLMSLDLSKNKIKALPVQFCQ LQELKNLKLDDNELIQFPCKIGQLINLRFLSAARNKLPFLPSEF RNISLEVLDLEGNTFEQPKVLPVIKLQAPLTLLESSARTILHNR IPVGSHIIPPHLCQDLDTAKICVCGRFCLNSFJQGTTTMKLHSV AHTVVLVDNLGGTEAPIISYFCSLGCYVNSSDI APMICLCSSDLQFFXKEFILDREGNIGVGVSVDDDPRMKHFLNV GRLOSDNEYKKDFAKSRSQFHSSTDQPGLLQAKRSQOLASDVHY RQPLPQPTCDPEQLGLRHAQKAHQLQSDVKYKSDLNLTRGVGWT PPGSYKVEMARRABLALARGLGLQGAYRGAEAVEAGDHQSGEV NPDATEILHVKKKKALLL 6768 2 363 PGSTISCYLLSEGSLPLCMQVACGEEKHRAPTMKTLRARFKKTE LGLSPTDLGSCPPCGBPCPIPKPAARGRRQSQDWGKSDERLLQAV ENNDAPRVAALIARRGLVPTKLDPEGKSAFHL 6769 284 396 MSTPDFSTAENNQELANEVSCLKAMLTLMLQAMGQAD 6769 284 396 MSTPDFSTAENNQELANEVSCLKAMLTLMLQAMGQAD 6770 1 397 QRNYQVIWSSTMAKLHDYYKDEVVKKMTEFNYNSVMQVPRVEK ITLNMGVGEALADKKLLDNAAADLAAISGQKPLITKARKSVAGF KIRQGYPIGCKVTLRGERNWEFFERLITIAVPRIRDFRGLSAKS 6771 3 378 APAGTLAMTCKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR WASWNIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCM QEMGNGKANRLYEAYLPETFRPQIDPYLFWSNLEG 6772 1 1400 AAAFLQGMTVNGFINTVTTSL\ERRYDLHSYQSGLASSYDIAA CLCLTFVSYFGGSG\HKPRWLGWGR\VLMGTGSLVFALPHFTAG P**GWKLDAGVRTCPANPR\PVCAG\HTSGLISRYQLVFMLGGFL HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFTYAALLGPAAGY LIGGALINIYTEMGRRTELTTESPLWVGAWWVGFLGSGAAAFFT AVPILGYPRQLPGSQRYAVMRAAEHHQLKDSSRCEASNPDFGKT IRDLPLSIMLLLKNPTFILLCLAGATEATLITEMSTFSPKFLES QFSLSASEAATLEGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLIGLIVFSLYCGSDGLMYFSLCHAGGSCLAPEGHLNL TAPCNAACSCQFEHYSPVCGSDGLMYFSLCHAGCPAATETHVDG				KFVDEGKATVRLKEPPVDICI SKANGSGI KCEL SAMEL BURGOL
GTSYGGLVRVDMRMLCLKSLRKLDLSHNHIKKLPATIGDLIHLO ELNLINDNHLBSFSVALCHSTLOKSLWSLDLSKNKIKALPVQFCQ LQELKNLKLDDNELIQFFCKIGQLINLRFLSAARNKLPFLPSEF RNISSLEYLDLFGNTFEQPKVLPVIKLQAPLTILESSARTILHNR IPYGSHIPPHLQQDLDTAKICVCGFFCLNSFIQGTTTMNLHSV AHTVVLVDNLGGTEAPIISYFCSLGCYVNSSDI 6767 336 919 APMICLGSSDLQFRYKEAFILDRGCIQTGYGVDDDPRKHFLNV GRLOSDNEYKKDFAKSRSQFHSSTDQPGLLQAKRSQQLASDUHY RQPLPQPTCDPEQLGLRHAQKAHQLQSDVKYKSDLNLTRGVGWT PPGSYKVEMARRAABLANARGLGLQGAYRGAEAVEAGDHQSGEV NPDATEILHVKKKKALLL LRLSPTDLGSCPPCGPCPIPKPARGRRQSQDWGKSDERLLQAV ENNDAPRVALILARKGLVPTKLDPEKSAFHL 6769 284 396 MSTPDFSTAENNQELANEVSCLKAMLTIMLQAMGQAD ENNDAPRVAALIARKGLVPTKLDPEKSAFHL 6770 1 397 QRNYQVIWSSTMAKLHDYYKDEVVKKLMTEFNYNSVMQVPRVEK ITLNMCVGBALDKKLLDNAADLAAISGCKPLITKARKSVAGF KIRQGYPIGCKVTLRGERNWEFFERLITLAVPRIRDFRGLSAKS 6771 3 378 APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGFR WASWNIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCM QEMGNGKANRLYEALYHPETFRRPGIDPYLFWSNLEG 6772 1 1400 AAAFLQGMTVNGFINTVITSL\ERRYDLHSYQSGLIASSYDIAA CLCLITFVSYFGGSG\HKPRWLGWGR\VLMGTGSLVFALPHFTAG P**GWKLDAGVRTCPANPR\PVCAG\HTSGLSRYQLVFMLGQFL HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFTTAALIGPAAGY LIGGALINIYTEMGRRTELTTESPLWGAMWVGFLGSGAAAFFT AVPILGYPRQLPGGQRTVAWRAAEMHQLKDSRGEASNDPGGKT IRDLPLSIMLLLKNPTFILLCLAGATEATLITGMSTFSPKFLES QFSLSASEAATLEGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPGGHINL TAPCNAACSCQPEHYSPVCGSDGLWYFSLCHAGGPAATETNVDG	1 1			VDTPVSTLTPVKTSEFENFKTKMVLTSKKDVDLSKNEDVGLEU
ELMINDNHLBSFSVALCHSTLQKSLMSLDLSKNKI KALPPUFCQ LQELKINKLDIDMELQPFCKIGQLINLRFLSAARNKLPFLPSEF RNLSLEYLDLFGNTFEQPKVLPVIKLQAPLTILLBSSARTILHNR IPYGSHIIPPHLQDLDTAKICVCGRFCIMSFIQGTTTMNLHSV AHTVVLVDNLGGTEAPIISYFGSLGCYVNSSDI 6767 336 919 APMICLCSSDLQFRYKEAFLRDRGLQIGYCSVDDDPRMKHFLNV GRLQSDMEYKKDFAKSRSQFHSSTDQPGLLQAKRSQOLASDVHY RQPLPQPTCDPBOLGGRHAQKAHQLQSDVKYKSDLNLTRGVGWT PPGSYKVEMARRAAELANARGLGGAYRGAEAVEAGDHQSGEV NPDATEILHVKKKALLL 6768 2 363 PGSTISCYLLSEGSLPLCMQVACGEEKHRAPTMKTLRAFFKKTE LRLSPTDLGSCPPCGPCPIPKPAARGRRQSQDWGKSDERLLQAV ENNDAPRVAALIARKGLVPTKLDPBGKSAPHL 6769 284 396 MSTPDFSTAENNQELANEVSCLKAMLTLMLQAMGQAD ENNDAPRVAALIARKGLVPTKLDPBGKSAPHL 6770 1 397 QRNYQVIWSSTMAKLHDYYKDEVVKKLMTEFNYNSVMQVPRVEK ITLNMGVGBATADKKLLDNAAADLAAISGQKPLITKARKSVAGF KIRQGYPIGCKVTLRGERMWEFFERLITIAVPRIRDFRGLSAKS 6771 3 378 APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGFR WASWNIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCM QEMGNKANRLYEAVLPETFRRPQIDPYLFWSNLEG 6772 1 1400 AAAFLQGMTVNGFITNVITSL\ERRYDLHSYQSGLTASSYDIAA CLCLTFVSYSGSG\HKPRNLGWGR\VLMGTGSLVFALPHFTAG P**GWKLDAGVRTCPANPR\PVCAG\HTSGLSRVJUFMLGGFL HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRRTELTTESPLWVGAWWGFLGSGAAAFFT AVPILGYPRQLPGSQRYAVMRAAEMHQLKDSSRGEASNPDGKKT IRDLPLSIMLLKNPTFILLCLAGATEATLITGMSTFSPKFLES QFSLSASEAATLFGYLVVBAGGGGTFLGGFPVNKLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGSSLPEGGHINL TAPCNAACSCQPEHYSPVCGSDGLMYFSLCHAGCPAATETNYDG				QTSYCGLVRVDMRMLCLKSLRKLDLSHNHTKKLDATICDLTUIO
COMMINGED COMM				ELNLNDNHLESFSVALCHSTLOKSLWSLDLSKNKIKALDVORCO
RNISLEYLDLFGNTFEQPKVLPVIKLQAPLITLESSARTILHNR IPYGSHIIPPHLCODLDTAKICVCGRFCLNSFIQGTTTMNIHSV AHTVVLVDNLGGTEAPIISYFCSLGCYVMSSDI APMICLGSSDLQFRYKEAFLRDRGLQIGYCSVDDDPRMKHFLNV GRLQSDNEYKKDFAKSRSQFHSSTDQPGLLQARRSQOLASDVHY RQPLPQPTCDPEGLGRHAQKAHQLQSDVKYKSDLNLTRGVGWT PPGSYKVEMARRAAELANARGLGLQGAYRGAEAVEAGDHQSGEV NPDATEILHVKKKKALLL 6768 2 363 PGSTISCYLLSEGSLPLCMQVACGEEKHRAPTMKTLRARFKKTE LRLSPTDLGSCPPCGPCPIPKPAARGRRQSQDWGKSDERLLQAV ENNDAPRVAALIARKGLVPTKLDPEGKSAFHL 6769 284 396 MSTPDFSTAENNQELANEVSCLKAMLTIMLQAMGQAD 6770 1 397 QRNYQVIWSSTMAKLHDYYKDEVVKKIMTEFNYNSVMQVPRVEK ITLNMGVGEAIADKKLLDNAAADLAAISGQKPLITKARKSVAGF KIRQGYPIGCKVTLRGERMWEFFERLITIAVPRIRDFRGLSAKS 6771 3 378 APAGTLAMTGKSVKDVDRYQAVLANLLLEEDKKFCADCQSKGFR WASWNIGVFICIRCAGIHRNLGVHISRVKSUNLDQWTQQQIQCM QEMGNGKANRLYEAYLPETFRRPQIDPYLFWSNLEG 6772 1 1400 AAAFLQCMTUNGFINTVITSL\CRRYDLHSYQSGLASSYDIAA CLCLLTFVSYFGGSG\KKPRWLGWGR\VLMGTGSLVPALPHFIAG P**GWKLDAGVRTCPANPR\PVCAG\HTSGLSRYQLVFMLGGFL HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRITELTTESPLWVGAWWVGFLGSGAAAFFT AVPILGYPROLPGSGRYAVMRAAEMHQLKDSSRGEASNPDFGKT IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKFLES QFSLSASEAATLFGYLVVPAGGGGFFLGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEEHHINL TAPCNAACSCQPEHYSPVCCSDGLMYFSLCHAGCPAATETNVDG	1 1			LQELKNLKLDDNELIOFPCKIGOLINLRFI.SAARNKI.DET.BCDD
APHTVLVDILGETAPH ISTSCLGCYVNSSDI APHICLCSSDLQFRYKEAFLRDRGLQIGYCSVDDDPRMKHFLNV GRLQSDNEYKKDFAKSRSQFHSSTDQPGLLQAKRSQQLASDVHY RQPLPQPTCDPEQLGLRHAQKAHQLQSDVKYKSDLALITRGVGMT PPGSYKVEMARRAAELANARGIGLQGAYRGAEAVEAGDHQSGEV NPDATEILHVKKKKALLL 6768 2 363 PGSTISCYLLSEGSLPLCMQVACGEEKHRAPTMKTLRARFKKTE LRLSPTDLGSCPPCGPCP1PKPAARGRRQSQDWGKSDERLLQAV ENNDAPRVAALIARKGLVPTKLDPEGKSAFHL 6769 284 396 MSTPDFSTAENNQELANEVSCLKAMITIMLQAMGQAD ENNDAPRVAALIARKGLVPTKLDPEGKSAFHL 6770 1 397 QRNYQVIWSSTMAKLHDYYKDEVVKKLMTERPYNSYMQVPRVEK LTLINMGVGEALADKKLLDNAAADLAAISGQKPLITKARKSVAGF KIRQGYPIGCKVTLRGERMWEFFERLITIAVPRIRDFRGLSAKS 6771 3 378 APAGTLAMTGKSVKDVDRYQAVLANILLEEDNKFCADCQSKGFR WASWNIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCM QEMGNGKANRLYEAYLPETFRRPQIDPYLFWSNLEG 6772 1 1400 AAAFLQGMTVNGFINTVITSL\ERRYDLHSYQSGLIASSYDIAA CLCLTFVSYFGGSG\HKPRWLGWGR\VLMGTGSLVFALPHFTAG P+*GWKLDAGWTCPANPR\PVCAG\HTSGLSRYQLVFMLGQFL HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRREITTESPLWVGAWWVGFLGSGAAAFFT AVPFILGYPROLPFGSQRYAVMRAAEMHQLKDSSRGEASNPDFGKT IRDLPLSIWLLLKNPTFILLCLAGATEATLITCMSTFSSKFLES QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVWKLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPEHYSPVCGSDGLMYFSLCHAGCPAATETNVDG	1			RNLSLEYLDLFGNTFEOPKVLPVIKLOAPLTLLESSAPTTLUMB
APHTVLUONLGGTEAP1ISYFCSLGCYVNSSDI APMICLCSSDLQFRYKEAFLRDRGLQIGYCSVDDDPRMKHFLNV GRLQSDNSYKKDFAKSRSQFHSSTDQPGLLQAKRSQQLASDVHY RQPLPQPTCDPEQLGLRHAQXAHQLQSDVKYKSDLNLTRGVGMT PPGSYKVEMARRAAELANARGLGLQGAYRGAEAVEAGDHQSGEV NPDATEILHVKKKKALLL LRLSPTDLGSCPPCGPCPIPKPAARGRRQSQDWGKSDERLLQAV ENNDAPRVAALIARKGLVPTKLDPEGKSAFHL 396 MSTPDFSTAENNOGLANEWSCLKAMLTLMLQAMQQAD ENNDAPRVAALIARKGLVPTKLDPEGKSAFHL 397 QRNYQVIWSSTMAKLHDYYKDEVVKKMTEFNYNSYMQVPRVEK KIRQGYPIGCKVTLRGERNWEFFERLITIAVPRIRDFRGLSAKS KIRQGYPIGCKVTLRGERNWEFFERLITIAVPRIRDFRGLSAKS KIRQGYPIGCKVTLRGERNWEFFERLITIAVPRIRDFRGLSAKS WASWNIGVFICIRCAGIHRNLGHLISRVKSVNLDQWTQEQIQCM QEMGNGKANRLYEAYLPETFRRPQIDPYLFWSNLEG 6772 1 1400 AAAFLQGMTVNGFINTVITSL\ERRYDLHSYQSGLIASSYDIAA CLCLTTVSYFGGSG\HRPRWLGMGR\VUMGTGSLVFALPHFTAG P**GWKLDAGVRTCPANPR\PVCAG\HTSGLSRYQLVFMLGGFL HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRRTELTTESPLWVGAWWUGFLGSGAAAFFTT AVPILGYPRQLBFGSGRYAVMRAAEMHQLKDSSRGEASNPDFGKT IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKFLES QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPEHYSPVCGSDGLMYFSLCHAGCPAATETNVDG	1 1	i		1 PYGSHIIPFHLCODLDTAKICVCGRECINSFIOGTTTMNI MON
GRICSDILGFRYKEAFLROGLGIGYCSVDDDPRMKHFLNV GRLQSDDRYKKDFAKSRSQFHSSTDQPGLLQAKRSQQLASDVHY RQPLPQPTCDPEQLGLRHAQKAHQLQSDVKYKSDLNLTRGVGWT PPGSYKVEMARRAAELANARGLGLQGAYRGAEAVEAGDHQSGEV NPDATEILHVKKKRALLL 6768 284 396 PGSTISCYLLSEGSLPLCMQVACGEEKHRAPTMKTLRARFKKTE LRLSPTDLGSCPPCGPCPIPKPAARGRRQSQDWGKSDERLLQAV ENNDAPRVAALIARKGLVPTKLDPEGKSAFHL 6770 1 397 QRNYQVIWSSTMAKLHDYYKDEVVKKLMTEFNYNSVMQVPRVEK ITLNMGVGEAIADKKLLDNAAADLAAISGQKPLITKARKSVAGF KIRQGYPIGCKVTLRGERMWEFFERLTTIAVPRIRDFRGLSAKS KIRQGYPIGCKVTLRGERMWEFFERLTTIAVPRIRDFRGLSAKS APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR WASWNIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCM QEMGNGKANRLYEAYLPETFRPQIDPYLFWSNLEG 6772 1 1400 AAAFLQGMTVNGFINTVITSL\ERRYDLHSYQSGLIASSYDIAA CLCLTFVSYFGGSG\HKPRWLGWGR\VLMGTGSLVFALPHFTAG P**GWKLDAGVRTCPANPR\PVCAG\HTSGLSRYQLVFMLGQFL HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY LIGGALINIYTEMGRRTELTTESPLWVGAWWVGFLGSGAAAFFT AVPILGYPRQLPGSQRYAWMRAEMHQLKDSSRGEASNPDFGKT IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKFLES QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPEHYSPVCGSDGLWYFSLCHAGCPAATETNVDG	6767	- 336		AHTVVLVDNLGGTEAPIISYFCSLGCYVNSSDI
GRLÖSDNEYKKDFAKSRSOFHSSTDOPGLLQAKRSQQLASDVHY ROPLPOPTCDPEQLGLRHAQKAHQLQSDVKYKSDLINLTRGVGWT PPGSYKVEMARRAAELANARGLGLQGAYRGAEAVEAGDHQSGEV NPDATEILHVKKKKALLL 6768 2 363 PGSTISCYLLSEGSLPLCMQVACGEEKHRAPTMKTLRARFKKTE LRLSPTDLGSCPPCGPCPIPKPAARGRRQSQDWGKSDERLLQAV ENNDAPRVAALIARKGLVPTKLDPEGKSAFHL 6769 284 396 MSTPDFSTAENNQELANEVSCLKAMLTLMLQAMGQAD 6770 1 397 QRNYQVIWSSTMAKLHDYYKDEVVKKLMTEFNYNSVMQVPRVEK ITLNMGVGEAIADKKLLDDYAAADLAAISGQKPLITKARKSVAGF KIRQGYPIGCKVTLRGERMWEFFERLITIAVPRIRDFRGLSAKS 6771 3 378 APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR WASWNIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCM QEMGNGKANRLYEAYLPETFRRPQIDPYLFWSNLEG 6772 1 1400 AAAFLQGWTVNGFINTVITSL\ERRYDLHSYQSGLIASSYDIAA CLCLTFVSYFGGSG\HKPRWLGWGR\VLMGTGSLVFALPHFTAG P**GWKLDAGVRTCPANPR\PVCAG\HTSGLSRYQLVFMLGQFL HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRRTELTTESPLWVGAWWGFLGSGAAAFFT AVPILGYPRQLPGSQRYAVMRAAEMHQLKDSSRGEASNPDFGKT IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKFLES QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPEHYSPVCGSDGLMYFSLCHAGCPAATETNVDG	1 0,0,	336	919	APMICLCSSDLQFRYKEAFLRDRGLQIGYCSVDDDPRMKHFLNV
PPGSYKVEMARRAELANARGLGLQGAYRGAEAVEAGDHQSGEV NPDATEILHVKKKKALLL PGSTISCYLLSEGSLPLCMQVACGEEKHRAPTMKTLRARFKKTE LRLSPTDLGSCPPCGPCPPP PKPAARGRRQSQDWGKSDERLLQAV ENNDAPRVAALIARKGLVPTKLDPEGKSAFHL 6769 284 396 MSTPDFSTAENNQELANEVSCLKAMLTLMLQAMGQAD 6770 1 397 QRNYQVIWSSTMAKLHDYVKDEVVKKLMTEFNYNSVMQVPRVEK ITLNMGVGEAIADKKLLDNAAADLAAISGQKPLITKARKSVAGF KIRQGYPIGCKVTLRGERMWEFFERLITIAVPRIRDFRGLSAKS 6771 3 378 APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR WASWNIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCM QEMGNGKANRLYEAYLPETFRRPQIDPYLFWSNLEG 6772 1 1400 AAAFLQGMTVNGFINTVITSL\ERRYDLHSYQSGLTASSYDIAA CLCLTFVSYFGGSG\KRMLGWGR\VLMGTGSLVFALPHFTAG P**GWKLDAGVRTCPANPR\PVCAG\HTSGLSRYQLVFMLGQFL HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRRTELTTESPLWVGAWWVGFLGSGAAAFFT AVPILGYPRQLPGSQRYAVMRAAEMHQLKDSSRGEASNPDFGKT IRDLPLSIWLLKNPFFILLCLAGATEATLITGMSTFSPKFLES QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPEHYSPVCGSDGLMYFSLCHAGGPAATETNVDG	1 1			GRLQSDNEYKKDFAKSRSQFHSSTDOPGLLOAKRSOOLASDVHV
6768 2 363 PGSTISCYLLSEGSLPLCMQVACGEEKHRAPTMKTLRARFKKTE LRLSPTDLGSCPPCGPCPIPKPAARGRQSQDWGKSDERLLQAV ENNDAPRVAALIARKGLVPTKLDPEGKSAFHL 6769 284 396 MSTPDFSTAENNQELANEVSCLKAMLTLMLQAMGQAD 6770 1 397 QRNYQVIWSSTMAKLHDYYKDEVVKKLMTEFNYNSVMQVPRVEK ITLNMGVGEALADKKLLDNAAADLAAISGQKPLITKARKSVAGF KIRQGYPIGCKVTLRGERMWEPFERLITIAVPRIRDFRGLSAKS 6771 3 378 APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR WASWNIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCM QEMGNGKANRLYEAYLPETFRRPQIDPYLFWSNLEG 6772 1 1400 AAAFLQGMTVNGFINTVITSL\ERRYDLHSYQSGLIASSYDIAA CLCLTFVSYGGSG\HKPRHLGWGR\VLMGTGSLVFALPHFTAG P***GWKLDAGVRTCPANPR\PVCAG\HTSGLSRYQLVFMLGQFL HGVGATFLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRRTELTTESPLWVGAWWVGFLGSGAAAFFT AVPILGYPRQLPGSQRYAVMRAAEMHQLKDSSRGEASNPDFGKT IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKFLES QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKKLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPBHYSPVCGSDGLMYFSLCHAGCPAATETNVDG]			ROPLPOPTCDPEQLGLRHAQKAHQLQSDVKYKSDLNLTRGVGWT
6768 2 363 PGSTISCYLLSEGSLPLCMQVACGEEKHRAPTMKTLRARFKKTE LRLSPTDLGSCPPCGPCPIPKPAARGRRQSQDWGKSDERLLQAV ENNDAPRVAALIARKGLVPTKLDPEGKSAFHL 6769 284 396 MSTPDFSTAENNQELANEVSCLKAMLTLMLQAMGQAD 6770 1 397 QRNYQVIWSSTMAKLHDYYKDEVVKKLMTEFNYNSVMQVPRVEK LTLNMGVGEAIADKKLLDNAAADLAAISGQKPLITKARKSVAGF KIRQGYPIGCKVTLRGERMWEFFERLITIAVPRIRDFRGLSAKS 6771 3 378 APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR WASWNIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCM QEMGNGKANRLYEAYLPETFRRQIDPYLFWSNLEG 6772 1 1400 AAAFLQGMTVNGFINTVITSL\ERRYDLHSYQSGLIASSYDIAA CLCLTFVSYFGGSG\HKPRWLGWGR\VLMGTGSLVFALPHFTAG P**GWKLDAGVRTCPANPR\PVCAG\HTSGLSRYQLVFMLGQFL HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRRTELTTESPLWVGAWWVGFLGSGAAAFFT AVPILGYPRQLPGSQRYAVMRAAEMHQLKDSSRGEASNPDFGKT IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKFLES QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPEHYSPVCGSDGLMYFSLCHAGCPAATETNVDG	[ĺ		PPGSYKVEMARRAAELANARGLGLQGAYRGAEAVEAGDHQSGEV
ERLSPTDLGSCPPCGPCPIPKPAARGRRQSQDWGKSDERLLQAV ENNDAPRVAALIAR KGLVPTKLDPEGKSAFHL 6770 1 397 QRNYQVIWSSTMAKLHDYYKDEVVKKLMTEFNYNSVMQVPRVEK ITLNMGVGEA IADKKLLDNAAADLAA ISGQKPLITKARKSVAGF KIRQGYPIGCKVTLRGERMWEFFERLITIAVPRIRDFRGLSAKS 6771 3 378 APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR WASWNIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCM QEMGNGKANRLYEAYLPETFRRPQIDPYLFWSNLEG CLCLTFVSYFGGSG\HKPRWLGWGR\VLMGTGSLVFALPHFTAG P**GWKLDAGVRTCPANPR\PVCAG\HTSGLSRYQLVFMLGQFL HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRRTELTTESPLWVGAWWVGFLGSGAAAFFT AVPILGYPRQLPGSQRYAVMRAAEMHQLKDSSRGEASNPDFGKT IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKFLES QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKKRRLSRAVIK FCLFCTVVSLIGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPEHYSPVCGSDGLMYFSLCHAGCPAATETNVDG	6768	2	363	
ENNDAPRVALIARKGLVPTKLDPEGKSAFHL 6770 1 396 MSTPDFSTAENNQELANEVSCLKAMLTIMLQAMGQAD QRNYQVIWSSTMAKLHDYYKDEVVKKLMTEFNYNSVMQVPRVEK ITLNMGVGEAIADKKLLDNAAADLAAISGQKPLITKARKSVAGF KIRQGYPIGCKVTLRGERMWEFFERLITIAVPRIRDFRGLSAKS APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR WASWNIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCM QEMGNGKANRLYEAYLPETFRRPQIDPYLFWSNLEG 1 1400 AAAFLQGMTVNGFINTVITSL\ERRYDLHSYQSGLIASSYDIAA CLCLTFVSYFGGSG\HKPRWLGWGR\VLMGTGSLVFALPHFTAG P**GWKLDAGVRTCPANPR\PVCAG\HTSGLSRYQLVFMLGQFL HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRRTELTTESPLWVGAWWVGFLGSGAAAFFT AVPILGYPRQLPGSQRYAVMRAAEMHQLKDSSRGEASNPDFGKT IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKFLES QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPEHYSPVCGSDGLMYFSLCHAGCPAATETNVDG	1	_	503	LPLSPTDI CCCDDCCDCDCDCDCDCDCDCDCDCDCDCDCDCDCDC
6770 1 397 QRNYQVIWSTMAKLHDYYKDEVVKKLMTEFNYNSVMQVPRVEK ITLNMGVGGAIADKKLLDNAAADLAAISGQKPLITKARKSVAGF KIRQGYPIGCKVTLRGERMWEFFERLITIAVPRIRDFRGLSAKS APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR WASWNIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCM QEMGNGKANRLYEAYLDETFRRPQIDPYLFWSNLEG 6772 1 1400 AAAFLQGMTVNGFINTVITSL\ERRYDLHSYQSGLIASSYDIAA CLCLTFVSYFGGSG\HKPRWLGWGR\VLMGTGSLVFALPHFTAG P**GWKLDAGVRTCPANPR\PVCAG\HTSGLSRYQLVFMLGQFL HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRRTELTTESPLWVGAWWVGFLGSGAAAFFT AVPILGYPRQLPGSGQRYAVMRAAEMHQLKDSSRGEASNPDFGKT IRDLPLSIWLLKNPTFILLCLAGATEATLITGMSTFSPKFLES QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPEHYSPVCGSDGLMYFSLCHAGGPAATETNVDG	!			ENNIDA DEMANI JARKOI MERKI DERGKER SODWGKSDERLLOAV
QRNYQVIWSSTMAKLHDYYKDEVVKKLMTEFNYNSVMQVPRVEK ITLNMGVGEAIADKKLLDNAAADLAAISGQKPLITKARKSVAGF KIRQGYPIGCKVTLRGERMWEFFERLITIAVPRIRDFRGLSAKS APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR WASWNIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCM QEMGNGKANRLYEAYLDETFRRPQIDPYLFWSNLEG AAAFLQGMTVNGFINTVITSL\ERRYDLHSYQSGLIASSYDIAA CLCLTFVSYFGGSG\HKPRWLGWGR\VLMGTGSLVFALPHFTAG P**GWKLDAGVRTCPANPR\PVCAG\HTSGLSRYQLVFMLGGFL HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRRTELTTESPLWVGAWWVGFLGSGAAAFFT AVPILGYPRQLPGSQRYAVMRAAEMHQLKDSSRGEASNPDFGKT IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKFLES QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPEHYSPVCGSDGLMYFSLCHAGGPAATETNVDG	6769	284	396	MSTPDESTARNNOF! ANDVOCE KAND THE WOODS
ITLNMGVGEAIADKKLLDNAAADLAAISGQKPLITKARKSVAGF KIRQGYPIGCKVTLRGERMWEFFERLITIAVPRIRDFRGLSAKS APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR WASWNIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCM QEMGNGKANRLYEAYLPETFRRPQIDPYLFWSNLEG CLCLTFVSYFGGSG\HKPRWLGWGR\VLMGTGSLVFALPHFTAG P**GWKLDAGVRTCPANPR\PVCAG\HTSGLSRYQLVFMLGQFL HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRRTELTTESPLWVGAWWVGFLGSGAAAFFT AVPILGYPRQLPGSQRYAVMRAAEMHQLKDSSRGEASNPDFGKT IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKFLES QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPEHYSPVCGSDGLMYFSLCHAGGPAATETNVDG	6770	1		ORNYOVI WCCTMAKI HDVVVDEHRVVI MTDTANICAMGQAD
KIRQGYPIGCKVTLRGERMWEFFERLITIAVPRIRDFRGLSAKS APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR WASWNIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCM QEMGNGKANRLYEAYLPETFRRPQIDPYLFWSNLEG CLCLTFVSYFGGSG, HKPRWLGWGR, VLMGTGSLVFALPHFTAG P**GWKLDAGVRTCPANPR, PVCAG, HTSGLSRYQLVFMLGQFL HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRRTELTTESPLWVGAWWVGFLGSGAAAFFT AVPILGYPRQLPGSQRYAVMRAAEMHQLKDSSRGEASNPDFGKT IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKFLES QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPEHYSPVCGSDGLMYFSLCHAGGPAATETNVDG	1		•	ITLNMGVGEAIADKKT.I.DNAAADT AA TGGOVDY TOVARDE
APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR WASWNIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCM QEMGNGKANRLYEAYLPETFRRPQIDPYLFWSNLEG AAAFLQGMTVNGFINTVITSL\ERRYDLHSYQSGLIASSYDIAA CLCLTFVSYFGGSG\HKPRWLGWGR\VLMGTGSLVFALPHFTAG P**GWKLDAGVRTCPANPR\PVCAG\HTSGLSRYQLVFMLGQFL HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRRTELTTESPLWVGAWWVGFLGSGAAAFFT AVPILGYPRQLPGSQRYAVMRAAEMHQLKDSSRGEASNPDFGKT IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKFLES QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPEHYSPVCGSDGLMYFSLCHAGGPAATETNVDG				KIRQGYPIGCKVTLRGERMWEFFFPI.TTTAUDDTDDDCT
WASWNIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCM QEMGNGKANRLYEAYLPETFRRPQIDPYLFWSNLEG AAAFLQGMTVNGFINTVITSL\ERRYDLHSYQSGLIASSYDIAA CLCLTFVSYFGGSG\HKPRWLGWGR\VLMGTGSLVFALPHFTAG P**GWKLDAGVRTCPANPR\PVCAG\HTSGLSRYQLVFMLGQFL HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRRTELTTESPLWVGAWWVGFLGSGAAAFFT AVPILGYPRQLPGSQRYAVMRAAEMHQLKDSSRGEASNPDFGKT IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKFLES QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPEHYSPVCGSDGLMYFSLCHAGCPAATETNVDG	6771	3	378	APAGTLAMTGKSVKDVDRYOAVIANI.I.TEEDNEECADGGGGGGGG
QEMGNGKANRLYEAYLPETFRRPQIDPYLFWSNLEG 1 1400 AAAFLQGMTVNGFINTVITSL\ERRYDLHSYQSGLIASSYDIAA CLCLTFVSYFGGSG\HKPRWLGWGR\VLMGTGSLVFALPHFTAG P+*GWKLDAGVRTCPANPR\PVCAG\HTSGLSRYQLVFMLGQFL HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRRTELTTESPLWVGAWWVGFLGSGAAAFFT AVPILGYPRQLPGSQRYAVMRAAEMHQLKDSSRGEASNPDFGKT IRDLPLSIWLLLKNPFFILLCLAGATEATLITGMSTFSPKFLES QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVMKLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPEHYSPVCGSDGLMYFSLCHAGCPAATETNVDG				WASWNIGVFICIRCAGIHRNIGVHTSPVKSIMI DOWTOPOTORS
AAAFLQGMTVNGFINTVITSL\ERRYDLHSYQSGLIASSYDIAA CLCLTFVSYFGGSG\HKPRWLGWGR\VLMGTGSLVFALPHFTAG P**GWKLDAGVRTCPANPR\PVCAG\HTSGLSRYQLVFMLGQFL HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRRTELTTESPLWVGAWWVGFLGSGAAAFFT AVPILGYPRQLPGSQRYAVMRAAEMHQLKDSSRGEASNPDFGKT IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKFLES QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPEHYSPVCGSDGLMYFSLCHAGGPAATETNVDG				QEMGNGKANRLYEAYLPETERRPOTDDVI.FWGMI.PG
CLCLTFVSYFGGSG\HKPRWLGWGR\VLMGTGSLVFALPHFTAG P**GWKLDAGVRTCPANPR\PVCAG\HTSGLSRYQLVFMLGQFL HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRRTELTTESPLWVGAWWVGFLGSGAAAFFT AVPILGYPRQLPGSQRYAVMRAAEMHQLKDSSRGEASNPDFGKT IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKFLES QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPEHYSPVCGSDGLMYFSLCHAGCPAATETNVDG	6772	1	1400	AAAFLQGMTVNGFINTVITSL\ERRYDLHQVOQGT.TAGGUDT
P**GWKLDAGVRTCPANPR\PVCAG\HTSGLSRYQLVFMLGQFL HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRRTELTTESPLWVGAWWVGFLGSGAAAFFT AVPILGYPRQLPGSQRYAVMRAAEMHQLKDSSRGEASNPDFGKT IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKFLES QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPEHYSPVCGSDGLMYFSLCHAGGPAATETNVDG				CLCLTFVSYFGGSG\HKPRWLGWGR\VI.MGTGSI.VFAI.DUBTAG
HGVGATPLYTLGYTYLDENVKSSCSPIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRRTELITTESPLWVGAWWVGFLGSGAAAFFT AVPILGYPRQLPGSQRYAVMRAAEMHQLKDSSRGEASNPDFGKT IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKFLES QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPEHYSPVCGSDGLMYFSLCHAGCPAATETNVDG		1		P**GWKLDAGVRTCPANPR\PVCAG\HTSGLSRYOLVEMT CORT
LIGGALLNI YTEMGRRTELTTESPLWVGAWWVGFLGSGAAAFFT AVPILGYPROLPGSQRYAVMRAAEMHOLKDSSRGEASNPDFGKT IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKFLES QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPEHYSPVCGSDGLMYFSLCHAGCPAATETNVDG		İ	ŀ	HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAGV
AVPILGYPRQLPGSQRYAVMRAAEMHQLKDSSRGEASNPDFGKT IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKFLES QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPEHYSPVCGSDGLMYFSLCHAGCPAATETNVDG	1	1	ļ	LIGGALLNIYTEMGRRTELTTESPLWVGAWWVGFLGSGAAAFFT
IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKFLES QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPEHYSPVCGSDGLMYFSLCHAGCPAATETNVDG		ł		AVPILGYPRQLPGSQRYAVMRAAEMHOLKDSSRGEASNDDFGKT
QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPEHYSPVCGSDGLMYFSLCHAGCPAATETNVDG				IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKFLES
FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPEHYSPVCGSDGLMYFSLCHAGCPAATETNVDG	l l			QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK
TAPCNAACSCQPEHYSPVCGSDGLMYFSLCHAGCPAATETNVDG	1		j	FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNI.
QKVYRDCSCIPQNLSSGFGHATAGKCTST				TAPCNAACSCQPEHYSPVCGSDGLMYFSLCHAGCPAATETNVDG
				QKVYRDCSCIPQNLSSGFGHATAGKCTST

SEO	Predicted		
ID	beginning	Predicted end	
NO:		nucleotide	I INTIMITATION CECVSERING Debenorate and a
NO:	nucleotide	location	Glucamic Acid. F=Phenvlalanine C_Closet==
	location	corresponding	n=nistidine, i=isoleucine K-Iveino
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid) P=Proline. O=Glutamine D-Arginia
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
- 1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u></u>	aequence		\=possible nucleotide insertion)
6773	1	630	PWEAPKEHKYKAEEHTVVLTVTGEPCHFPFQYHRQLYHKCTHKG
1	j	1	RPGPQPWCATTPNFDQDQRWGYCLEPKKVKDHCSKHSPCQKGGT
1	•		CVNMPSGPHCLCPOHLTCHHOOKTKGPPRANT
	1	1	CVNMPSGPHCLCPQHLTGNHCQKEKCFEPQLLRFFHKNEIWYRT
L_	1		EQAAVARCQCKGPDAHCQRLASQACRTNPCLHGGRCLEVEGHRL CHCPVGYTG?FCDVGE*GSGASRRPAPRWDGLAR
6774	146	389	LTELEDOON TO BETTE OF CONTROL OF
Í	1	1	LTELSDQQYFLFFILSS/WVPTFLSMDVDGRVIKADSFSKIISS
6775	104	614	GLRIGFLTGPKPLIERVILHIQVSTLHPSTFNQLMISQ
		014	TCPSQLRVLTARGGRRAPSPQLWTLVLALIEEKWRSHRILRMNS
İ	j		GRPEIMENLPALYTIFOGEVAMVTDVCAFTYTDGCDVCGLANDW
ŀ			AMSSCRVDKPSEIVDVGDKVWVKI,TGREMKNDDTKVGI CMVIIIO
6776	3	1108	QGTGKDLDPNNV\SLSKKRGGGDPSRTTT.GPPSpt.pt.c
	1	1108	HERHERHEGALSODALLRISTPLDSNMPDEKCPREVUDOWOX TIL
			INGIPPRISDADMEPCVDGWVYDRISFSSTIVTEWDIVCDCOCI
1			: 13 VARE VEMAGMMVGGILGGHLSDD EGDDEVI DWGVI GVA TVOM
1	<u> </u>		CAALAPIFLIYCSLRFLSGIAAMSI,TTNTIMI,TAEWATUDEONA
1	,		GITLGMCPSGIAFMTLAGLAFAIRDWHILOLAGUDVEVIER mo
	l		SWILLESARWLIINNKPEEGLKELRKAAHRSGMKNARDUULULETT
	i		ASIMAKE DEAAOKKKPFLGERI.HMDNTCKDTCT I DEMKRATER I
1			I TOUNDAG LIKHLIGNNVFLLOTI, FOAU /TDDCOLVT UL CIUSOS
6777	588		I KARRANCTGTEATOAM
1. ""	779	63	CFFHGPAWRDCEVRATFAKKOGOSGIISCIAFGDAODI VAGGOV
			GRSLGLYAWDDGSPLALLGGHOGGITHLCFUDDGNDFFCCARVA
1 1			ALLICWOLROSGYPLWSLGREVTTNODIVEDIDDTCODIVEGET
			SGAVSVWDTDGPGNDGKPEPVLSFT,POKDCTMGVGT.UDGI DT. G
1		-	ACEPVSVCFLSPTESGGRRGAGPSLGSPPPHVHLECPLOLING
6778			CGGARLQHP**SPRARKGR
1 0,70	311	805	IQSITDESRGSIRRKNPANTRLRLNVP\EBTAGDSE/ERSPEEE
1 1	1		VQADPKIKSASPKCPTSSPFPKGRSPFGRGPT\ DDFWATEURGR
]]	ŀ		ADAS VAEKN (KGP (SPVSSEGT KDFF SMKDENENT MOCNTADDAY)
6779	2		1 AVRUNEVIVEKSRDAKLVLLNMPGDDDNDNGDDDNT
"'''	2	535	RALRROPRLLAANGIEPESMAISEPIKGGEKBOUNDER DI VUE
1 1		1	PARCAMAGEREPPODARAEAESPGGASESDADGGUPGDDVvva.
1 1	1		AN VOARNEAPMRKKKKVSLGPVSYVI VIDSEDCDKKDIMDKKGDG
			SKREASDQKAPRGQQPAEATASTSRGPKAKPEGSPRPATNEGDV
6780			V
","	3	403	HEVNDNKPEININLMSPGKEEISYIFEGDFIDTFVALVRVQDKD
1 !	1		SOUNGET VCKUHGHGHFKI OKTVENMVI. TI THIATT DDEVD OFFICE
1 1	1		LIVIAEDRGTPSLSTVKHFTVQINDINDNPPHFORSRVEEVISE
6781			K
0,01	1	1269	APTRPVFPTLQDLSSSKEPSNSLNLPHSNELCSSLVHPELSEVS
1		1	SNVAPSIPPVMSRPVSSSSISTPI.DDNOTTVEVTCNDTOWGRAD
1 [ŀ	İ	SAALP I RIUSALMS TVVTMPNAGSKUMUSEGOS A AGNA DE DOUT
1			IFVE INSSSIIQVMKGSOPSTIPAAPI,TINGGI,MDDGIJAJITGDE
1 1		ſ	ALFUNIALSSAPVPPNALSSSPAPNIOTGPDIATIGEDAMDITOR D
1			SPECISSEVVESHEEVOOVKELNPDEASPOUNTSADONT DOGG
1 1			STTMVSPLLTNSPGSSGNRRSPVSSSKGKGKVDKIGQILLTKAC
[!		KKVTGSLEKGEEQYGADGETEGQGLDTTAPGLMGTEQLSTELDS
1			KTPTPPAPTLLKMTSSPVGPGTASAGPSLPGGALPTSVRSIVTT
		i	LVPSELISAVPTTKSNHGGIASESLAG
6782	3	1327	RKPTVIRIPAKPGKCLHEDPQSPPPLPAEKPIGNTFSTVSGKLS
			NVERTRNLESNHPGQTGGFVRVPPRLPPRPVNGKTIPTQQPPTK
		1	VPPERPPPPKISATEPCNYKI PENAGASIAN SANTANIAN SAN
[1	1	VPPERPPPPKLSATRRSNKKLPFNRSSSDMDLQKKQSNLATGLS
1	ł]	KAKSQVFKNQDPVLPPRPKPGHPLYSKYMLSVPHGIANEDIVSQ
			NPGELSCKRGDVLVMLKQTENNYLECQKGEDTGRVHLSQMKLIT
			PLDEHLRSRPNPFSPPKAPSHAQKPVDSGAPHAVVLHDFPAEQV

SEO	Predicted	Predicted end	Amino acid
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
į	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
<u> </u>			DDLNLTSGEIVYLLEKIDTDWYRGNCRNQIGIFPANYVKVIIDI
		1	PEGGNGKRECVSSHCVKGSRCVARFEYIGEQKDELSFSEGEIII
	•		LKEYVNEEWARGEVRGRTGIFPLNFVEPVEDYPTSGANVLSTKV
	1	Ì	PLKTKKEDSGSNSQVNSLPAEWCEALHSFTAETSDDLSFKRGDR
			I
6783	3	1750	SYHHHHAQQSAAASPNLTASQKTVTTTSMITTKTLPLVLKAATA
1 1			TMPASVVGQRPTIAMVTAINSQKAVLSTDVQNTPVNLQTSSKVT
			GPGAEAVQIVAKNTVTLQVQATPPQPIKVPQFIPPPRLTPRPNF
]]			L DOUBERPRACEUR OF THE PROPERTY OF THE PROPERT
1 1	· ·		LPQVRPKPVAQNNIPIAPAPPPMLAAPQLIQRPVMLTKFTPTTL
			PTSQNSIHPVRVVNGQTATIAKTFPMAQLTSIVIATPGTRLAGP
			QTVQLSKPSLEKQTVKSHTETDEKQTESRTITPPAAPKPKREEN
j			POKLAFMYSLGLVTHDHLEEIQSKRQERKRRTTANPYYSGAVFE
1 1			PERKKSAVTYLNSTMHPGTRKRGRPPKYNAVLGFGALTPTSPQS
			SHPDSPENEKTETTFTFPAPVQPVSLPSPTSTDGDIHEDFCSVC RKSGQLLMCDTCSRVYHLDCLDPPLKTIPKGMWICPRCQDQMLK
			KEEAIPWPGTLAIVHSYIAYKAAKEEEKQKLLKWSSDLKQEREQ
l			LECKTIVICI CHCTCVCMEMOTEL A POSTERIOR DE LECKTORIO CONTRACTORIO DE LECKTORIO CONTRACTORIO DE LA POSTERIO DE LA POSTERIO DE LA POSTERIO DE LA POSTERIO DE LA POSTERIO DE LA POSTERIO DE LA POSTERIO DE LA POSTERIO DE LA POSTERIO DE LA POSTERIO DE LA POSTERIO DEL POSTERIO DEL POSTERIO DE LA POSTERIO DE LA POSTERIO DE LA POSTERIO DEL POSTERIO DEL POSTERIO DE LA TERIO DEL POSTERIO DEL POSTERIO DEL POSTERIO DEL POSTERIO DEL POSTERIO DEL POSTERIO DEL POSTERIO DEL POSTERIO DEL POSTERIO DEL POSTERIO DEL POS
1 1			LEQKVKQLSNSISKCMEMKNTILARQKEMHSSLEKVKQLIRLIH
			GIDLSKPVDSEATVGAISNGPDCTPPANAATSTPAPSPSSQSCT ANCNOGEETK
6784	3	1750	SYHHHHAQQSAAASPNLTASQKTVTTTSMITTKTLPLVLKAATA
1		2.30	TMPASVVGQRPTIAMVTAINSQKAVLSTDVQNTPVNLOTSSKVT
			GPGAEAVQIVAKNTVTLQVQATPPQPIKVPQFIPPPRLTPRPNF
			LPQVRPKPVAQNNIPIAPAPPPMLAAPQLIQRPVMLTKFTPTTL
1			PTSQNS1HPVRVVNGQTATIAKTFPMAQLTSIVIATPGTRLAGP
1			QTVQLSKPSLEKQTVKSHTETDEKQTESRTITPPAAPKPKREEN
	·		PQKLAFMVSLGLVTHDHLBEIQSKRQERKRRTTANPVYSGAVFE
			PERKKSAVTYLNSTMHPGTRKRGRPPKYNAVLGFGALTPTSPQS
' i	1		SHPDSPENEKTETTFTFPAPVQPVSLPSPTSTDGDIHEDFCSVC
			RKSGQLLMCDTCSRVYHLDCLDPPLKTIPKGMWICPRCQDQMLK
ŀ			KEEAI PWPGTLAIVHSYIAYKAAKEEEKQKLLKWSSDLKQEREQ
			LEQKVKQLSNSISKCMEMKNTILARQKEMHSSLEKVKQLIRLIH
			GIDLSKPVDSEATVGAISNGPDCTPPANAATSTPAPSPSSQSCT
i			ANCNOGEETK
6785	1	528	LGNTVLHYCSMYSKPECLKLLLRSKPTVDIVNQAGETALDIAKR
	_	220	LKATQCEDLLSQAKSGKFNPHVHVEYEWNLRQEEIDESDDDLDD
į			KDSDAKKEDSDBDCEEGROSSIGBSDBT 21 2222222222222222222222222222222222
	}		KPSPVKKERSPRPQSFCHSSSISPQDKLALPGFSTPRDKQRLSY
6786	1820	1397	GAFTNQIFVSTSTDSPTSPTTEAPPLPPRNAGKGPTGPPITPHR
1		4.JJ1	RSPKVLVLAPTRELANHVSRDFKDI\TRKLTVARFYGGTSYQSQ
į.			INHIRNGIDILVGTPGRIKDHLQSGRLDLSKLRHVVLDEVDQML
ŀ	į		DLGFAEQVEDIIHESYKTDSEDNPQTLLFSATCPQWVYTVA\KK
ŀ	1		YMKSRYEQVDLDGKMTQKAATTVEHLAIQCHWSQRPAVIGDVLQ
1			VYSGSEGRAIIFCETKKNVTEMAMNPHIKQNAQCLHGDIAQSQR
1	ĺ		EITLKGFREGSFKVLVATNVAARGLDIPEVDLVIQSSPPQDVES
İ			YIHRSGRTGRAGRTGICICFYQPRERGQLRYVEQKAGITFKRVG
1			VPSTMDLVKSKSMDAIRSLASVSYAAVDFFRPSAQRLIEEKGAV
	!		DALAAALAHISGASSFEPRSLITSDKGFVTMTLESLEEIQDVSC
1	[AWKELNRKLSSNAVSQITRMCLLKGNMGVCFDVPTTESERLQAE
			WHDSDWILSVPAKLPEIEEYYDGNTSSNSRQRSGWSSGRSGRSG
	ŀ		RSGGRSGGRSGRQSRQGSRSGSRQDGRRRSGNRNRSRSGGHKRS
			FD*VFYHLVDFLSDFLVDSVYLTGRQIDHLTGLTGLIDHLTSHS
6703			SVWN
6787	2646	2270	PSSFPKNVPLEELEEPPK*KRSGLGSLTPKSQIONGP*POTFFF
6787	2646	2270	PSSFPKNVPLEELEEPPK*KRSGLGSLTPKSQIQNGP*PQTFFF FELGSPSGVISAHCNLRLLGSSDSPAPASRVAGIIGTCHHAWLI
		2270	PSSFPKNVPLEELEEPPK*KRSGLGSLTPKSQIQNGP*PQTFFF FELGSPSGVISAHCNLRLLGSSDSPAPASRVAGIIGTCHHAWLI LVFLVBMGFHHVGQAGLKLLTL\VIHPPWPPKVLGLOT
6787	2646	2270 936	PSSFPKNVPLEELEEPPK*KRSGLGSLTPKSQIQNGP*PQTFFF FELGSPSGVISAHCNLRLLGSSDSPAPASRVAGIIGTCHHAWLI

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	\A=AtdHine, C=CVSteine D-Aspartia Asia b
j	location	corresponding	Glucamic Acid, F=Phenylalaning Cocio-in-
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Troptophan V many
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
			EVILWGS*DS*GYPKGK*LLPKEVPSR/RVLLSGLTPLDATQE\
			FTEDLSK\YVTTMVCVAVNGKPMLGVIHKPFSEYTAWAMVDGGS
	İ		NVKARSSYNEKTPRIVVSRSHSGMVKQVALQTFGNQTTIIPAGG
-	1	· .	AGINVIALLDVPDKSOEKADI,YTHVTVTVKKIDYONONA TE 152 Y C
	ŀ		GHMTTLSGEEISYTGSDGIEGGLLASIRMNHQALVRKLPDLEKT
6789			GHK
0789	2	678	GNGINVLKIAPESAIKFMAYEQIKRLVW**PGDS*GF/YERLVA
			GSDAGATAQSSIYPMEVLKTRMALRKTGOVGCMI.DCARDIT ARR
			GVAAF YKGYVPNMLGIIPYAGIDLAVVETI, KNAWI OUVALAIGAD
]			PGVFVDLACGIMSSTCGOLASYPLALAPTPMOAOAGIECA DELE
1 1			MSSLFKHILRTEGAFGLYRGLAPNFMKVIPAVSISYVVYENI.KT
6790	2	4060	LIGVQSR
	~	4068	APPAGRRRMQAAPRAGCGAALLLWIVSSCLCRAWTAPSTSQKCD
j			EPDVSGDPHVAFSSSSSISGSYSPGVAKINKPGGAGGWCBCDGD
1			HYQWLQVDFGNRKQISAIATQGRYSSSDWVTQYRMLYSDTGRNW
			KPYHQDGNIWAFPGNINSDGVVRHELQHPIIARYVRIVPLDWNG
	ĺ		EGRIGLRIEVYGCSYWADVINFDGHVVLPYRFRNKKMKTLKDVI
1 1			ALNFKTSESEGVILHGEGQQGDYITLBLKKAKLVLSLNLGSNQL GPIYGHTSVMTGSLLDDHHMMANA
			GPIYGHTSVMTGSLLDDHHWHSVVIERQGRSINLTLDRSMQHFR TNGEFDYLDLDYEITFGGIPFSGKPSSSSRKNFKGCMESINYNG
1 1	ı		VNITDLARRKKLEPSNVGNLSFSCVEPYTVPVFFNATSYLEVPG
1 1			RLNQDLFSVSFQFRTWNPNGLLVFSHFADNLGNVEIDLTESKVG
1 1	1		VILLIA TOTAL
1 1	1		DEASAVRINSPLQVKTGEKYFFGGFI.NOMNNGGUGUI ODGGOGG
			MODIQUINDLYNLYEVAORKPGSFANVSTDMCATTDDCGDDAGG
}	j		HGGACSQIWDSFKCTCDETGYSGATCHNGIVEDCCEAVKILL COM
		ľ	SKI I WIDPDGSGPLGPLKVYCNMTEDKVWTI VEUDI OMORDINA
1			INFERISVIQUVYSASMDOISAITDSAFVCEOVVCVEOVAGET
1 1			NIFDGSFITWWVGKANEKHYYWGGSGPGTOKCACGTERMOTERN
1 1	1		I I CNCDAD I KOWKKDAGFLSYKDHI PVSOVVVGDTDBOCGBA ***
1			SVGPLRCQGDRNYWNAASFPNPSSYLHFSTFQGETSADISFYFK
j į		1	TLTPWGVFLENMGKEDFIKLELKSATEVSFSFDVGNGPVEIVVR SPTPLNDDOWHDYTA EDNIKOA SI OVERSKEDEN
}	1	1	SPTPLNDDQWHRVTAERNVKQASLQVDRLPQQIRKAPTEGHTRL ELYSQLFVGGAGGQQGFLGCIRSLRMNGVTLDLEERAKVTSGFI
1 1	ļ		SGCSGHCTSYGTNCENGGKCLERYHGYSCDCSNTAYDGTFCNKD
[]	1		VGAFFEEGMWLRYNFQAPATNARDSSRVDNAPDQQNSHPDLAQ
1.	İ		ELIKESESTIKAPCILLYISSETTDELAVI.VKDTCCI OTDANIC I
	İ		GIREFINIDVDHRNMANGOPHSVNITRHEKTIFI.KI.DUVDGUGU
[ALPSSSUTLENSPKSLFLGKVIETGKIDORIHKVNTDGETGGV 6
]		i i	R VYFNULAPLKAALROINASAHVHIOGELVECKOOR ODI DI GOLL
}	İ		SSATUPWHILDHUDSASADFPYNPGOGOATPMCIMIDMCATTOCKET
]		i	~ ************************************
6791	1801		REGREESMANDEETSORPIDESKKEWPHI.DCCVI.AMC
		1193	TGHEGAKGEKGDKGDLGPRGERGOHGPKGEKGVPGIDDEL /PGB
		1	SAVV SWLIAASTKVQAILLPOPLE*[GIOTAFMAGIATUFONO
	l	·	MOGILE SOVETNIGHTED VMTGREGA DVSGVVE ETECHNIZEDI.
		! :	EEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVW
6792	33	1073	LRMGNGALHGDHQRFSTFAGFLLFETK
)	į	i i	VRHTNWGVDMYLFSLGSESPKGAIGHIVSTEKTILAVERNKVLL
-		17	PPLWNRTFSWGFDDFSCCLGSYGSDKVLMTFENLAAWGRCLCAV
		;	CPSPTTIVTSGTSTVVCVWELSMTKGRPRGLRLRQALYGHTQAV
	İ	1:	ICLAASVTFSLLVSGSQDCTCILWDLDHLTHVTRLPAHREGISA ITISDVSGTIVSCAGAHLSLWNVNGQPLASITTAWGPEGAITCC
ļ		1 6	CLMEGPAWDTSQIIITGSQDGMVRVWKT/VGCEDVCSWTASRRG
Ī			APGSASKPKRPQVGEEPGLESRAGR*HCFDREAQQNQP\PVTAL
			AVSRNHTKLLVGDERGRIFCWSADG*EERGSRGSGTTVPG
			CHOLDO "EERGSRGSGTTVPG

Predicted

Predicted end

SEO

1.

SEO	Predicted	Predicted end	Amino poid
αī	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
}	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of		S=Serine, T=Threonine, V=Valine,
1	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\=possible nucleotide insertion)
}	1		PLSFQSQGSPPKGPELSLASIHVPLESIKPSSALPVTAYDKNGF
İ			RILFHFAKECPPGRPDVLVVVVSMLNTAPLPVKSIVLOAAVPKS
1			MKVKLQPPSGTELSPFSPIQPPAAITOVMLLANPLKEKURLRYK
			LTFALGEQLSTEVGEVDQFPPVEQWGNL
6799	3894	1696	STISWESLESWLNKATNPSNRQEDWEYIIGFCDQINKELEG*VS
ľ			ALWGQLRGSGLGRGTTMAKEGQPGSPRLSALECVLLVPQ\PQIA
}	}		VRLLAHKIQSPQEWEALQALTYLGDRVSEKVKTKVIELLYSWTM
1			ALPEEAKIKDAYHMLKRQGIVQSDPPIPVDRTLIPSPPPRPKNP
	İ		VFDDEEKSKLLAKLLKSKNPDDLQEANKLIKSMVREDEARIQKV
			TKRLHTLEEVNNNVRLLSEMLLHYSQEDSSDGDRELMKELFDQC
i]		ENKRRTLFKLASETEDNDNSLGDILQASDNLSRVINSYKTIIEG
1	ł		QVINGEVATLTLPDSEGNSQCSNQGTLIDLAELDTTNSLSSVLA
			PAPTPPSSGIPILPPPPQASGPPRSRSSSQAEATLGPSSTSNAL
	İ		SWLDEELLCLGLADPAPNVPPKESAGNSQWHLLQREQSDLDFFS
1			PRPGTAACGASDAPLLQPSAPSSSSSQAPLPPPFPAPVVPASVP
1			APSAGSSLFSTGVAPALAPKVEPAVPGHHGLALGNSALHHLDAL
i i	'		DQLLEEAKVTSGLVKPTTSPLIPTTTPARPLLPFSTGPGSPLFQ
			PLSEOSOGS DEVENE STATE DESCRIPTION DESCRIPTION DE L'ACTUAL DE L'AC
			PLSFQSQGSPPKGPELSLASIHVPLESIKPSSALPVTAYDKNGF
	Į į		RILFHFAKECPPGRPDVLVVVVSMLNTAPLPVKSIVLQAAVPKS
	j l		MKVKLQPPSGTELSPFSPIQPPAAITQVMLLANPLKEKVRLRYK
6800	404	1646	LTFALGEQLSTEVGEVDQFPPVEQWGNL
1		1040	RRSPSTGLSPVPQPSSPSLSDYSIPWSLLLSGTIAWATPGK*AG
			*PQAW*LGLAPAIAFI/GLTRGRKQNKEKMAEGGSGDVDDAGDC
			SGARYNDWSDDDDDSNESKSIVWYPPWARIGTEAGTRARARARA
1 1	1		RATRARRAVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILE
1	1		AALIALGNNAAYAFNRDIIRDLGGLPIVAKILNTRDPIVKEKAL
			IVLNNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLAGLRLL
i i			TNMTVTNEYQHMLANSISDFFRLFSAGNEETKLQVLKLLLNLAE
1 1			NPAMTRELLRAQVPSSLG\SLFNKKENKEVILKLLVIFENINDN
1 1		•	FKWEENEPTQNQFGEGSLFFFLKEFQVCADKVLGIESHHDFLVK
6801	2		VKVGKFMAKLAEHMFPKSQE
8801	2	1755	SAEEFESQQASVTMHDVDAESFEVLVDYCYTGRVSLSEANVERL
			YAASDMLQLEYVREACASFLARRLDLTNCTAILKFADAFGHRKL
1 1	J		RSQAQSYIAQNFKQLSHMGSIREETLADLTLAQLLAVLRLDSLD
	i		VESEQTVCHVAVQWLEAAPKERGPSAAEVFKCVRWMHFTEEDQD
] [YLEGLLTKPIVKKYCLDVIEGALOMRYGDLLYKSLVPVPNSSSS
1			/R*QQQLSCICSRKSTPETGYVCQGDGDLLWTPORSLS\RYDPY
] [l		SGDIYTMPSPLTSFAHTKTVTSSAVCVSPDHDIYLAAOPRKDI.W
1	ŀ	ĺ	VYKPAQNSWQQLADRLLCREGMDVAYLNGYIYILGGRDPTTGVK
1	Ì		LKEVECYSVQRNQWALVAPVPHSFYSFELIVVQNYLYAVNSKRM
1	•		LCYDPSHNMWLNCASLKRSDFQEACVFNDEIYCICDIDVMKUVN
1	1		PARGEWRRISNIPLDSETHNYQIVNHDOKLLLITSTTPOWKKND
1 1	}		VTVYEYDTREDQWINIGTMLGLLQFDSGFICLCARVYPSCLEDG
			QSFITEEDDARSESSTEWDLDGFSELDSESGSSSSFSDDEVWVO
6000			VAPQRNAQDQQGSL
6802	157	1341	ETFPLFFFLLSKTPGKTASMAHFVQGTSRMIAAESSTEHKECAE
1			PSTRKNLMNSLEQKIRCLEKORKELLEVNOOWDOOFRSMKELVE
[1	RKVAELKTKLDAAERFLSTREKDPHQRQRKDDROREDDRORDLT
			RDRLQREEKEKERLNEELHELKEENKLLKGKNTLANKEKEHYEC
1		j	EIKRLNKALQDALNIKCSFSEDCLRKSRVEFCHEEMRTEMEVLK
]]]	QQVQIYEEDFKKERSDRERLNQEKEELQQINETSQSQLNRLNSQ
1		1	IKACQMEKEKLEKQLKQMYCPPCNCGLVFHLQDPWVPTGPGAVQ
	ł	ſ	KQREHPPDYQWYALDQLPPDVQHKAN/DWCLAPPPVCCQAG/PR
] [TPGLK*SSCLWLPKC*NFRFILSKESPSVEVHTNRERQQATRER
	ļ	[G G G G G G G G G G G G G G G G G G G
6803	1	2203	KLSGRPYRHMGVLGTSKLYDIRKTIFTFTPQFIDQQQFYLALDN
			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
		· .	KMIVEMLRTDLSYLCSRWRMTGQPTITFPISHSMLDEDGTSLNS
	l		SILAALRKMQDGYFGGARVQTGKLSEFLTTSCCTHLSFMDPGPE
1	1	1	GKLYSEDYDDNYDYLESGNWMNDYDSTSHARCGDEVARYLDHLL
	1		AHTAPHPKLAPTSQKGGLDRFQAAVQTTCDLMSLVTKAKELHVQ
i			NVHMYLPTKLFQASRPSFNLLDSPHPRQENQVPSVRVEIHLPRD
1	1		QSGEVDFKALVLQLKETSSLQEQADILYMLYTMKGPDWNTELYN
		1	ERSATVRELLTELYGKVGEIRHWGLIRYISGILRKKVEALDEAC
1	}	l	TDLLSHQKHLTVGLPPEPREKTISAPLPYEALTQLIDEASEGDM
	ļ		SISILTQEIMVYLAMYMRTQPGLFAEMFRLRIGLIIQVMATELA
[1		HSLRCSAEEATEGLMNLSPSAMKNLLHHILSGKEFGVERK/SVR
	1		PTDSNVSPAISIHEIGAVGATKTERTGIMQLKSEIKQVEFRRLS
	1		ISAESQSPGTSMTPSSGSFPSAYDQQSSKDSRQGQWQRRRRLDG
j	1		ALNRVPVGFYQKVWKVLQKCHGLSVEGFVLPSSTTREMTPGEIK
1	1		FSVHVES\VLNVLLRPEYRQLLVEAILVLTMLADIEIHSIGSII
ŀ		i	AVEKIVHIANDLFLQEQKTLGP\DDTMLAKDPASG\ICTLR\YD
ľ	İ		SAPSGRFGTMTYLS\RAA\ATYVQEFLP\HSICAMQ
6804	1	951	GSPGKKEEKAKNKESLCMENSSNSSSDEDEEETKAKMTPTKKYN
			GLEEKRKSLRTTGFYSGFSEVAEKRIKLLNNSDERLONSRAKDR
ł			KDVWSSIQGQWPKKTLKELFSDSDTEAAASPPHPAPEEGVAEES
			LQTVAEEESCSPSVELEKPPPVNVDSKPIEEKTVEVNDRKAEFP
	1		SSGSNFSA*IPLPYLHLNRLHQSL*QKGSRQQSSVTVSEPLAPN
1	1		QEEVRSIKSETDSTIEVDSVAGELQDLQSERE*LASRF*CQCEL
j	j		KQ**SARTRTS*KSLYRSEKSERCSGRRKFIKKAEKKP*SNSGK
			QQKEGKRHK
6805	1539	206	RQPDLKYFGKSFDVSVSESSSLLSNDLPKFADGIKARNRNQNYL
			VPSPVLRILDHTAFSTEKSADIVICDEECDSPESVNQQTQEESP
			IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLQDQTDEEPPA
			KLCKILDKSQALNVTAQQKWPLLRANSSGLYKCELCEFNSKYFS
1]		DLKQHMILKHKRTDSNVCRVCKESFSTNMLLIEHAKLHEEDPYI
1			CKYCDYKTVIFENLSQHIADTHFSDHLYWCEQCDVQFSSSSELY
i	1		LHFQEHSCDEQYLCQFCEHETNDPEDLHSHVVNEHACKLIELSD
	Ì		KYNNGEHGQYSLLSKITFDKCKNFFVCQVCGFRSRLHTNVNRHV
			AIEHTKIFPHVCDDCGKGFSSMLE\IAKHLNSHLSEGIYLCQYW
			EYSTGQIEDLKIHLDFKHSADLPHKCSDCLMRFGNERELISHLP
<u></u>			VHETT
6806	272	3794	VALCFPNSDPVMFMDAFYGCLLAELGPVPIEVPLTRKDAGSQQV
ł		1	GFLLGSCGVFLALTTDACQKGLPKAQTGEVAAFKGWPPLSWLVI
			DGKHLAKPPKDWHPLAQDTGTGTAYIEYKTSKEGSTVGVTVSHA
l	Į į		SLLAQCRALTQACGYSEAETLTNVLDFKRDAGLWHGVLTSVMNR
4			MHVVSVPYALMKANPLSWIQKVCFYKARAALVKSRDMHWSLLAO
I			RGQRDVSLSSLRMLIVADGANPWSISSCDAFLNVFQSRGLRPEV
			ICPCASSPEALTVAIRRPPDLGGPPPRKAVLSMNGLSYGVIRVD
1			TREKLSVLTVQDVGQVMPGANVCVVKLEGTPYLCKTDEVGEICV
I			SSSATGTAYYGLLGITKNVFEAVPVTTGGAPIFDRPFTRTGLLG
			FIGPDHLVFIVGKLDGLMVTGVRRHNADDVVATALAVEPMKFVY
			RGRIAVFSVTVLHDDRIVLVAEQRPDASEEDSFQWMSRVLOAID
			SIHQVGVYCLALVPANTLPKAPLGGIHISETKQRFLEGTLHPCN
I			VLMCPHTCVTNLPKPRQKQPEVGPASMIVGNLVAGKRIAOASGR
			ELAHLEDSDQARKFLFLADVLQWRAHTTPDHPLFLLLNAKGTVT
1			STATCVQLHKRAERVAAALMEKGRLSVGDHVALVYPPGVDLIAA
1			FYGCLYCGCVPVTVRPPHPQNLGTTLPTVKMIVEVSKSACVLTT
]			QAVTRLLRSKEAAAAVDIRTWPTILDTDDIPKKKIASVFRPPSP
1 .			DVLAYLDFSVSTTGILAGVKMSHAATSALCRSIKLQCELYPSRO
l I			IAICLDPYCGLGFALWCLCSVYSGHQSVLVPPLELESNVSLWLS
1			AVSQYKARVTFCCYSVMEMCTKGLGAQTGVLRMKGVNLSCVRTC
			MVVAEERP\RIALTQSFSKLFKDLGLPARAVSTTFGCRVNVAIC
	i		· · · · · · · · · · · · / · · · · · · ·

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	/ A=Alanine, C=Cvsteine, D=Aspartic heid R
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence		Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LOGTAGEDETTUMENTAL PROPERTY.
	1		LQGTAGPDPTTVYVDMRALRHDRVRLVERGSPHSLPLMESGKIL PGVKVIIAHTETKGPLGDSHLGEIWVSSPHNATGYYTVYGEEAL
			HADHFSARLSFGDTQTIWARTGYLGFLRRTELTDASGGRHDALY
ŀ	İ	-	VVGSLDETLELRGMRYHPIDIETSVIRAHRSIAECAVFTWTNLL
}			VVVVELDGLEQDALDLVALVTNVVLEEHYLVVGVVVIVDPGVIP
			INSRGEKQRMHLRDGFLADQLDPIYVAYNM
6807	1444	606	VGHDTVHAMFTCFPKCLGFSPPVNVTVSPRSEESHTTTVSGGNG
			SVFQAGPQLQALANLEARRGSIGAALSSRDVSGLPVYAQSGEPR
			RLTQAQVAAFPGENALEHSSDQDTWDSLRSPGFCSPLSSGGGAE
1			SDPPGGPGHAEAGHLGKVCDFHLNHOODSDTGVI,DTDVA A DDI E
1			KILSVDSVAVDCAYRTVPKPGPOPGPHGSLLTEGCLPGLGGDLN
1	1		REPCGMEVHSGQRELESVVAVGEAMA\LKFPMGAMSVCLDDGD
6808	2062		FERKEPMGLSCPLQVQ
1 5555	2063	737	GVGSGAASALARSRPLASRLSSRRRTRAPRSGAMQRLAMDLRML
Ī			SKELSLYLEHQVRVGFFGSGVGLSLILGFSVAVAFVVLCCTAVV
	i I		PQLVTGGESFSRFLQDHCPVVTETYYPTVWCWEGRGOTI.LPDP\
į.	ļ .		ITSKPPVQYRNELIKTADGGOISIDWFDNDNSTCVMDACTDDTT
]]		LLLPGLTGTSKESYILHMIHLSEELGYRCVVFNNRGVAGENLLT
1			PRTYCCANTEDLETVIHHVHSLYPSAPFLAAGVSMGGMLLLNYL
			GKIGSKTPLMAAATFSVGWNTFACSESLEKPLNWLLFNYYLTTC
1.			LQSSVNKHRHMFVKQVDMDHVMKAKSIREFDKRFTSVMFGYQTI
			DDYYTDASPSPRLKSVGIPVLCLNSVDDVFSPSHAIPIETAKON PNVALVLTSVGGHIGELEGIMEDOGUMEN
			PNVALVLTSYGGHIGFLEGIWPRQSTYMDRVFKQFVQAMVEHGH
6809	939	65	DYSGQTPVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTQTVPQ
1 1	,		TDEANQTDSQPLHPSDPTEKQQPKRLHVSNIPFRFRDPDLRQMF
1 1			GOFGRILDVEIIFNERGSKGFGFVTFETSSDADDADEVINCTIV
1 1	1		EGRKIEVNNATARVMTNKKTGNPYTNGWKINPWGALVCDERVA
	1		VIGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPDDDDTDTVC
1			AVVIQUETYGAEI\LEATQPTDTLSPLORROPTATVTAFETOLD
6810	939		TRITIPSGPRRPTALEPCETFHRFLLGP
	239	65	DYSGQTPVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTQTVPQ
		i	TUEAAQTUSQPLHPSDPTEKOOPKRIHVSNTDFPFFDDDT DOME
1 1			GOFGRILDVEIIFNERGSKGFGFVTFETSSDADRAREKINGTIV
i i	j		EGRKIEVNNATARVMTNKKTGNPYTNGWKLNPVVGAVYGPEFYA
1 1	1		VTGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPPPPIPTYG
			AVVYQDGFYGAEI\LEATQPTDTLSPLQRRQPTATVTAESTQLP TRTITPSGPRRPTALEPCETFHRFLLGP
6811	1522	658	DLVTVWSFVDCRVIASTHGH\KSWVSVVAFDPYTTSVEEGDPME
	1	-	FSGSDEDFQDLLHFGRDRADSTQCRLSRRNSTDSRPVSVTYRFG
1	i	1	SVGQDTQLCLWDLTEDILFPHQPLSRARTHTNVMNATSPPAGSN
	į	i.	GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV
]	ĺ		SKFATLSLHDRKERHHEKDHKRNHSMGHISSKSSDKLNLVTKTK
[]	ŀ	į	TDPAKTLGTPLCPRMEDVPLLEPLICKKIAHERLTVI.TRLEDCT
6812	400-		VIACQEGFICTWGRPGKVVSFNP
"""	4001	1682	EDAVFSLDLSTI IQGTWFLNGEELKSNEPEGOVEPGALDVBIED
			KGLQHRLILHAVKHQDSGALVGFSCPGVODSAALTTOFSDURTT
		1	SPODKVSLTFTTSERVVLTCELSRVDFPATWYKDGOKVEPSELI
	[1	VVKMDGRKHRLILPEAKVODSGEFECRTEGVSAFFGVTVODBBV
	1	i	HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGORVE
1 1	i	l	ESDFVVLENEGPHRRLVLPATOPSDGGEFOCVAGDECAVETUTI
}	1		TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVPWTKDGP
[]	İ	•	EVVESPALLLQKEDTVRRLVLPAVOLEDSGEYLCEIDDESASET (
		1	VIVIEPPVRIIYPRDEVTLIAVTLECVVLMCELSREDAPVRWYK
	!	1 -	DGLEVEESEALVLERDGPRCRLVLPAAOPEDGGEFVCDAGDDSA
			FFTVTVTEPPVQFLALETTPSPLCVAPGEPVVLSCELSRAGAPV

Deginning nucleotide location corresponding to first amino acid residue of amino acid amino aci	SEO	Predicted	Predicted end	I Amino and Japanese and Amino and Amino and Amino and Amino and Amino and Amino and Amino and Amino and Amino
No: nucleotide location corresponding to first to first to first amin acid to first amin acid residue of amin acid residue of amin acid sequence sequence sequence sequence sequence sequence sequence damin acid defence d			i e	Amino acid segment containing signal peptide
location corresponding to first damino acid mino acid residue of amino acid codon, /=possible nucleotide insertion codon, /	-			Glutamia Acid Walbarra C. Clari
corresponding to first mino acid amino acid residue of amino acid sequence	""			U-Victiding T-Tagley-in- V Lucia
to first amino acid residue of amino acid residue of amino acid sequence 8-Septine, T=Thrennine, V=Valine, 8-Septine, T=Thrennine, V=Valine, 8-Septine, T=Thrennine, V=Valine, 8-Septine, T=Thrennine, V=Valine, 8-Septine, T=Thrennine, V=Valine, 8-Septine, T=Thrennine, V=Valine, 8-Septine, T=Thrennine, V=Valine, 8-Septine, T=Thrennine, V=Valine, 8-Septine, T=Thrennine, V=Valine, 8-Septine, T=Thrennine, V=Valine, V=Valine, 8-Septine, T=Thrennine, V=Valine, V=Valine, 8-Septine, T=Thrennine, V=Valine, V=Valine, V=Valine, 8-Septine, T=Thrennine, V=Valine, V=Va	1			Laleucine Mamorbionine N Assessme,
amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknom, *=Stop Codon, (=possible nucleotide deletion) \[\begin{array}{c} \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \				P-Proline O-Glutamine D-American
residue of aequence Codon, p-possible nucleotide deletion,		l '	–	S-Carine T-Thronging W.W.line,
amino acid sequence Codon, /=possible nucleotide deletion, _\possible nucleotide disection) DGGE/LES/ATTEREN/VQATPVELT/LISTMQAKLPQI G19 1 961 GIFCTEMGNFDNAN/TGEIEFAIHYCEKTHSLEGIKACKNLLAY, G2EKKKKCNPYLKTYLLPDRSSQGKRKTGVQRNTVDHFYGETLK YQVAPAQLVTRQLQVSVWHLGTLARRVPLGEVIJLATWDFEDS TTOSFRWHPLRAKALDKYEDSVPQSGRUTRAKLVLPSPRFKLO EAQEGTDQPSLHGOLCLVVLGAKNLPVRPDGTINSFVKGCLTLP DQALKLKSPVLRKQACPQWKHSFVFSGVTFAGLKQSSLELITW DQALFGMNDRLLGGT RLGSKGDTAVGGDACSGKLCWQNUSS PHLWTDWTLVLH GGMYVIVGHVPPGFFEKTONKAWFREGFNEKYLKVVURKHHRVIA GGFGHHHTDSFFMLYDDAGVVISAMFITGFVTPKTTLDGVVN GANNPAIRVFEYDRATLSLKDMVYTYPNLSQANAQGTPRELEY QUTBAYGYPDASAHSMHTVLDRIAGDGSTLGRYYVYNSVSYSAG VCDBACGRGWHCAMRQVDIDAYTTCLYAGSTTPVPQLFLLMAL LGLCT 6821 1088 518 EFDIYK/BVGGEFVPVTRDDSSNGFPTTOHGPSFPVWFDLFLLMAL LGLCT GPOPLSFFECIVAQITAGLAADISAYTSTRFPHALVPEDGI GSVIEVLQRRQEGLAS FFAFSLIEGYI\SIVMDAETQKKPSBLLITSSGGLWRWVRIG GQPLGFDECGIVAQITAGLAADISAYYISTRFPHALVPEDGI GSVIEVLQRRQEGLAS FFAFSLIEGYI\SIVMDAETQKKPSBLLITSSSGELWRWVRIG GQPLGFDECGIVAQITAGLAADISAYYISTRFPHALVPEDGI GSVIEVLQRRQEGLAS FFAFSLIEGYI\SIVMDAETQKKPSBLLITSSGELWRWVRIG GGPLGFPDECGIVAQITAGLAADISAYYISTRFPHALVPEDGI GSVIEVLQRRQEGLAS FFAFSLIEGYI\SIVMDAETQKKPUSDSNGFPTQHGFSFTVHFQFYVT YSSILRRAGCVRALAKIERFFFYERAKKAFAVVATGETALYONL LIRKGVLALNPLL LIRKGVLALNPLL LLRAGGVTALAKIERFFFYERAKKAFAVVATGETALYONL NRFLPBEAFLHRAFHLALLTHALLTLLLFLGLGRWFTGTSGS ALHICGRAVILLDLAGIGESSMFTYSTSCS ALHICGRAVILLDLAGIGESSMFTYSTSCS ALHICGRAVILLDLAGIGESSMFTYSTSCS ALHICGRAVILLDLAGIGESSMFTYSTSCS ALHICGRAVILLDLAGIGESSMFTYSTSCS ALHICGRAVILLDLAGIGESSMFTYSTSCS ALHICGRAVILLDLAGIGESSMFTYSTSCS ALHICGRAVILLDLAGIGESSMFTYSTSCS ALHICGRAVILLDLAGIGESSMFTYSTSCS ALHICGRAVILLDLAGIGESSMFTYSTSCS ALHICGRAVILLDLAGIGESSMFTYSTSCS ALHICGRAVILLDLAGIGESSMFTYSTSCS ALHICGRAVILLDLAGIGESSMFTYSTSCS ALHICGRAVILLDLAGIGESSMFTYSTSCS ALHICGRAVILLDLAGIGESSMFTYSTSCS ALHICGRAVILLDLAGIGESSMFTYSTSCS ALHICGRAVILLDLAGIGESSMFTANGTSTSCS ALHICGRAVILLDLAGIGESSMFTANGTSTSCS ALHICGRAVILLDLAGIGESSMFTANGTSTSCS ALHICGRAVILLDLAGIGESSMFTANGTSTSCS ALHICGRAVILLDLAGIGESSMFTANGTSTSCS ALHICGRAVILLDLAGIGESSMFTANGTSTSCS ALH		_	1	W-Trophon V. Trophon V. Trophon
Sequence Sequence	1		i e	Codon (-nossible muslestide deleti
DGGE/LHS/ATTERKE/VOATPVNIT/TILITSTWOARLPOI GIPCTEMGNFDNANVTGEIEPAHYCFKYHSLEICIKACKNLAY GEKKKKCNPYVKTYLLPDRSSQGKRKTGVGNNTVDPTGTGTIK YQVAPAQLVTRQLQVSWHLGTLARRVFIGSVIIPLATWDFEDS TTQSFRWHPLEAKKACKYEDSVPOSMGEITVARKLVJESRFKKQ EAQEGTDQPSHGQLCLVJUGARNLPVRPDGINSFVKGCLTLP DQOKLEKSPYLRKOACPOWKHSFYFSGVTPAQLRQSSLELTW DQOKLEKSPYLRKOACPOWKHSFYFSGVTPAQLRQSSLELTW DQOKLEKSPYLRKOACPOWKHSFYFSGVTPAQLRQSSLELTW DQOKLEKSPYLRKOACPOWKHSFYFSGVTPAQLRQSSLELTW DQOKLEKSPYLRKOACPOWKHSFYFSGVTPAQLRQSSLELTW DQOKLEGMNDRLLGGT\RLGSKGDTAVGGDACSQSKLQWQKVLSS PNLWTDMTLVLH GGFFGHHHTDSFRNLYDDAGVFISAMFITPGVTFWKTTLGGVN GANNPAIRVFFSYDRATILSLAWMYTFMNLSQANAQCFPRRELEFY QLTEAYGVPDASAHSMITVLDRIAGGDSTLGRYVVTNSV3YSAG COELSCSMQHVCAMRQVDIDAYTTCLYASGTTPVPQLFPLLMAL LGLCT	1		bequence	\-nossible nucleotide deletion,
6819 1 961 GIPCTEMGFDNANTGEIEFATHYCKFKISLEICIKACKNING GEKKKKCNPYKTYLLPDRSQGKRKTGVQNTVDPTFGETLK YQVAPAQLVTRQLQVSVWHLGTLARRVFLGEVIIPLATWDFEDS TTQSFRWHPLRAKADKYEDSVPQSNGEITVRAKULTSPRRKLQ BAQEGTDQPSLHGQLCLVVLGAKNLPVPRPGTLNSFVKGCLTLP DQQKURLKSPVLRKQACPQWKHSFVFSGVTPAQLRQSSIELTVW DQALFGMNDRILGGT\RIGSGTAVGSQDXSQSKLQWQKVLSS PNLWTDMTLVLH GGPVSTJWRKQACPQWKHSFVFSGVTPAQLRQSSIELTVW GQPFGHHHTDSFRMLYDDAGVFISAMFITPGVTPWKTTLPGVVN GANNPAIRVFBYDRATLSLKDMVTYFPHNLQANAQGTPRWELEY QUTEAYGVPDASAHSMHTVLDRIAGDGSTLQRYXVNSVSYSSAG VCDEACSWGHVCAMRQVDIDAYTTCLYASGTTFVPQLPLLLMAL LGLCT 6821 1088 518 EFDIYR/RVGGEFVPVTRDDSSNGFPRTOHGPSPTVNPLQSPDA RCVUTLDPETLPAIATTLIDVLPYSHSTFKKEAASSPPPSSIT FFAFSLIEGYI\SIVMDAETOKKFPSDLLITSSGELWRMVRIG GQPLGFDECGIVAQIAGPLAAADISAYYISTRNFDHALVPEDGI SVIEVLQRRGEGLAS 6822 1088 518 EFDIYR/RVGGEFVPVTRDDSSNGFPRTOHGPSPTVHPLQSPDA RCVUTLDPETLPAIATTLIDVLFYSHSTFKEAASSSPPPSSIT FFAFSLIEGYI\SIVMDAETOKKFPSDLLITSSGELWRMVRIG GQPLGFDECGIVAQIAGPLAAADISAYYISTRNFDHALVPEDGI GGPLGFDECGIVAQIAGPLAAADISAYYISTRNFDHALVPEDGI GGPLGFDECGIVAQIAGPLAAADISAYYISTRNFDHALVPEDGI GSVIEVLQRRGEGLAS 6823 654 221 PPKLLSRWARMGHGEIV\LSDLMFPGLLHLFVVGFWRSVQTAC GIPQLLEAVIKLLFLDTYVSSFAKKAFAVVATGETALYGNL ILRKGVJAMNPLL LLADGRGWGG\CCFFSLAVSVKMNVLLFAGGLLFLLTGFGFG GFLGASDIWGGVUNGLFFLEENFSGTERGELFFHVTV NWRFLPFALFHRAFHLALITAHLTLLLLFALCRWHRTGESLLS LLADGRSKURGVCOVIGLFFILLEPSGYLSKKAH VYHTLPYLLWAMPARWITHLIRLLVLIGHELSWNTYPSTSCSS AALHICIANVLLQUVLGLFFLEENFSKKAH VWYHTLPYLLWAMPARWITHLIRLLLVLGHELSWNTYPSTSCSS AALHICIANVLLQUVLGLFFLEENFAGLIDEFTYGCTETGLTCMVSKTM KIKPGYMMTAASCYDVQIIDDKKNVLPPGTEGLITCMVSKTM KIKPGYMTAASCYDVQIIDDKKNVLPPGTEGLITCMVSKTM KIKPGYMTAASCYDVQIIDDKKNVLPPGTEGLITCMVSKTM KIKPGYMTAASCYDVQIIDDKKNVLPPGTEGLITCMVSKTM KIKPGYMTAASCYDVQIIDDKKNVLPPGTEGDIGIRVRPIRPI GIFSGYVDNDPIKTAANIRGGPUTGPFGGTGLTTCMVSKTM KIKPGYMTAASCYDVQIIDDKKNVLPPGTEGDIGIRVRPIRPI GIFSGYVDNDPIKTAANIRGGPUTGAAPKYPRRIBETVIMLPK KIKPGYMTAANIRGPGLYRCHROUNGSTAANIRGDFTGLORGRADD GIFSGYVDNDRIKAANIRGDGEICHDGDSTLORGRADD GIFSGYVDNDRIKAANIRGDGRIKAPCAVRHERIHDDSFLLSLSLSL				DCCE (Luc /APTEUVD (VOAPDANIE) THE TOTAL OF THE
GEEKKKKCNPYWRTYLLPDRSSQGKRRTVQRTVDPTFQETIK YQVAPQLUTRQLQVSVMHLGTHARRVPLGEVTIPLATMDFEDS TTOSFRWHDLRAKADKYEDSVPQSNGELTVRAKLVLPSRPRRKLQ EAQEGTDQPSLHGQLCLVVLGARHLPVRPPGTINSFVKGCLTLP, DQQKERLKSPVERKQACPQWKNSFVFSGVTPAQDRQSSLELTVW DQALFGMNDRLLGGT\RLGSKGDTAVGGDACSOSKLQWGKVLSS PNLWTDMTLVH GOPFGHHTDSFRWLYDDAGVPISAMFITPGVTPWKTTLPGVVDW GANNPAIRVFEVDRATLSLKDMVTYFMLQANAQCTPRWELEY QLTEAYGVPDASAHSMHTVLDRIAGDGSTQRYYVNNSVYSAG VCDEACSMGHVCAMRQVDIDAYTTCLVASGTTPVPQLFLLIMAL LGLCT FPDIVR/EVGGEFVPVTRDDSSNGFPRTQGGPSFTVHPLGSPON RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSEPSSIT FFAFSLIRGYI\SIVMDAETQKKFPSDLLLTSSSGELMMWVRIG GQPLGFDEGGIVAQIAGPLAAADISAYYISTNFFDHALVPEDGI GSVIEVLQRRQEGLAS FFDIYR/EVGGFFVVTRDDSSNGFPRTQGGPSFTVHPLQSPON RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSEPPSSIT FFAFSLIRGYI\SIVMDAETQKKFPSDLLLTSSSGELMMWVRIG GQPLGFDEGGIVAQIAGPLAAADISAYYISTNFFDHALVPEDGI GSVIEVLQRRQEGLAS FFDIYR/EVGGFFVVTRDDSSNGFPRTQGGPSFTVHPLQSPON RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPPSSIT FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSSGELWMVRIG GQPLGFDEGGIVAQIAGPLAAADISAYYISTNFFDHALVPEDGI GSVIEVLQRRQEGLAS FFDIYR/EVGGFLAS FFAFSLIEGYI\SIVMDAETQKKPPSDLLLTSSSGELWMVRIG GPPLGFDEGGIVAQIAGPLAADISAYYISTNFFDHALVPEDGI GSVIEVLQRRQEGLAS LILRGGVALAKIERFFFYERAKAFAVVATGETALYGNI VESLURRAGCVALAKIERFFFYERAKKAFAVVATGETALYGNI LILRGGVALANPLL LLAQRWGWGVCFFSLAVSVKMNVLLFAGGLLFLLLLTQFGFRG ALPKLGICAGLQVVIGLPFILLENDSGYLSFSLIPLGRQFLFHHTV NMRFLPEALFLHRAFHLALLTAHLTLLLLFALCRWHRTGESILS LLRDPSKRKVPPQPLTPNQTVSTFTNFFIGIGFSRSHYQPYV WYPHTLPYLLMAMPARWITHLLRLLVLGLIELSWNTYPSTSCSS AALHI-CHAVILLDLUBLGPGPOFTGMSTGNSKYFPHLQ NCLAGGSSLLBETTMANATGCDLIEEFYGGTETGLTCMVSKTM KIKPGYMGTAASCYDVGI IDDKGNVLPPGTEGDIGIRVRPIRPD GIFSGVVDNDPKTAANIRGGPFULLGDRGKLFGEDGFYGPMGRADI GIRSGVVDNDPKTAANIRGGPFULLGDRGKLFGEDGFYGPMGRADI GIRSGVVDNDPKTAANIRGGPFULLGDRGKLFGEDGFYGPMGRADI TINSGGYNDRDKTAANIRGGPFULLGDRGKLFGEDGFYGPMGRADI TINSGGYNDRDKTAANIRGGPULLGDRGKLFGEDGFYGPMGRADI TUTCKIQRANKLGRANKARBAPCAVRHLEDILDSSELSLSIS	6819	1	961	CIDCTEMONEDNAMITGETERS THEORY TO THE CONTROL OF THE
YQVAPAQLVTRQLQVSVWHLGTLARRYLGEVIIPLATMOFEDS TTOSFRWHPLIKARANKYEDSVQGNGELTVRAKUVLPSRPRKLQ EAQEGTDQPSLHGQLCLVVLGAKNLPVRPGTINSFVKGCLTLF DQQKLRLKSPVLRKQACPQWKHSFVFSGVYPAQLRQSSLELTVW DQALFGMDRILGGT\RIGGT\R	0015	_	761	GEFERENCE DISTRICT L DESCOCRET CONTROL
TTGSFRWHPLRAKADKYEDSVPGSNELTVRAKLULPSRPRIKLQ EAQEGTODPSHGOLCLUVUGARNLPVRPBGTLNSPVKGCLTLP DQQKLRKSPVLRKQACPQWKHSFVPSGVTPAQLRQSSLELTVW DQALFGMNDRLLGGTTRLGSKGDTAVGGDACSQSKLQMQKVLSS PNLWTDMTLVH 340 GDWYIVGHVPPGFFFKDTAGKPGFPREKYLKVVRKHRVITA GOFFGHHHTDSFRMLXDAGVPISAMFITPGTPVBKTLTLDGVN GANNPAIRVFEYDRATLSLKDMVTYFMNLSQANAQGTPRWELEY QLTEAYGVPDASAHSMHTVLDRIAGDGTLQRYYVYNSVYSSAG VCDEACSMQHVCAMRQVDIDAYTTCLYASGTTPVPQLPLLLMAL LGLCT 6821 1088 518 EFDIYR/EVGGEFVPVTRDDSSNGFPRTQHGPSPTVHPIQSPQN RFCVLTLDPETLPAIATTLIDULFYSHSTPKRAASSSPEPSSIT FFAFSLIEGYI\SIVMDAFTQKKFPSDLLITSSSGELWRMVRIG GQPLGFDEGGIVAQIAGPLAAADISAYYISTNFDHALVPEDGI GSVIEVLQRQSGLAS 6822 1088 518 EFDIYR/EVGGEFVPVTRDDSSNGFPRTQHGPSPTVHPIQSPQN RFCVLTLDPETLPAIATTLIDULFYSHSTPKRAASSSPEPSSIT FFAFSLIEGYI\SIVMDAFTQKKFPSDLLITSSSGELWRMVRIG GQPLGFDEGGIVAQIAGPLAAADISAYYISTNFDHALVPEDGI GSVIEVLQRQGELAS 6823 654 221 PFKLLSRWRMGHGDEIV\LSDLNFPGLHLPVVGPWRSVQTAC GIPQLLEAVLKLLPLDTYVESPAAVMELVPSDKERGLQTPVWTE YSSILRRAGCVRALAKIEFFFFFRAKKAFAVVATGETALYGNL LILKGGVLALNPLL 6824 858 104 LLLAQRWGWGVCAFFSLAVSVKMNVLLFAGLLFLLTQFGFRG ALPKLGICAGLQVVIGLPFLLENPSGYLSRSFDLGQCFLFHITV NNRFLPEALFLHRAFHLALLTHAHLTLLLLFALCRHHRTGESILS LLERDPSKRKVPQPUTPNGTUSTFSNFGIGTGFSRSHVQFYV WYFHTLPYLLWMMPARWLTPHLLRLLVLGLIELSWMTYPSTSCSS AALHCHAVILLQLAULGPPPKSTQHSKKMH 6825 3 1173 SSGEFGLQASDIMWTISDTGWILTILCSLMEPWALGACTFVHLL PKFPDFLVILKTLSSYPIKSMMGAPLYVRMLQQOLSSYKFPHLQ NCLAGGESLLPTLENMRAQTGLDIRFFYGGTGTTGLTCMVSKTM KIKGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRPI GIFSGYVONDPKTAANIRGDVILADRGIKGDGGYFQFMGRADD IINSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAP VILALQFLSHDPPGLTKRICKSCHAPAVYRMEPVUNDLSLLSLS	1			VOVADAGI VEDGI OVCUMUL CELI ADDUM GUNTUDPTEQETEK
EAQEGTOQPSLHGOLCLVVLGARNLPVRDGTLNSFVKGCLTLP DQQKLRLKSPVLRKQACPQWKHS FVSGGYTPAQLRQSSLELTVW QQALFGMNDRLLGGT\RLGSKGDTAVGGDACSOSKLQWGKVLSS PNLWTDMTLVLH 6820 1014 340 GDWYIVGHVPPGFFFKTQNKAWFREGFNEKYLKVVRKHRVIA GQFFGHHHTDSFRMLYDDAGVPISAMFITPGYTPMKTTLDGVVN GANNPAIRVPEYDRATLSLKDMYTYFMNLSQANAQGTPRWELEY QLTEAYGVPDASAHSMHTVLDRIAGDQGTLQRYYVYNSVSYSAG VCDEACSMGHVCAMRQVDLDAYTTCLYASGTTPVPQLPLLLMAL LGLGT 6821 1088 518 EFDIYR/EVGGEFVPVTRDDSSNGFPRTQHGPSPTVHF1QSPQN RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT FFAFSLIEGYI\SIVMDAETQKKFPSDLLITSSSGELMRMVRIG GQPLGFBCGIVAQITAGPLAAADISAYYISTNFDHALVPEDGI GSVIEVLQRRQGELAS RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT FFAFSLIEGYI\SIVMDAETQKKFPSDLLITSSSGELMRMVRIG GQPLGFBCGIVAQITAGPLAAADISAYYISTNFDHALVPEDGI GSVIEVLQRQGELAS RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT FFAFSLIEGYI\SIVMDAETQKKFPSDLLITSSGELMRMVRIG GQPLGFBCGIVAQITAGPLAAADISAYYISTNFDHALVPEDGI GSVIEVLQRQGELAS GGPLGFBCGIVAQITAGPLAAADISAYYISTNFDHALVPEDGI GSVIEVLQRQGGLAS GGPLGFBCGIVAQITAGPLAAADISAYYISTNFDHALVPEDGI GSVIEVLQRQGGLAS GGPLGFBCGIVAQITAGPLAAADISAYYISTNFDHALVPEDGI GSVIEVLQRQGGLAS GGPLGFBCGIVAQITAGPLAAADISAYYISTNFDHALVPEDGI GSVIEVLQRQGGLAS GGPLGFBCGIVAQITAGPLAAADISAYYISTNFDHALVPEDGI GSVIEVLQRQGGLAS GGPLGFBCGIVAQITAGPLAAADISAYYISTNFDHALVPEDGI GSVIEVLQRQGGLAS GGPLGFBCGIVAQITAGPLAAADISAYYISTNFDHALVPEDGI GSVIEVLQRQGGLAS LLLAQRWGMQQCGFSLAVGVKMVVLLFAGGLTPLLLTQFGFRC ALPKLGICAGLQVULGLPFLLENDSGYLGRGETALYGNL LLRAGGVRALAKIERFFFYERAKKAFAVVATGETALLYGNL ILRKGVLALNPLL LLRDPSKRVPPQPLTPMQIVSTLFTSNFIGICFRSLHYQFYV WFHTLPYLLWAMPARMLTHLLTLLLLFALCRWHRTGESILS LLRDPSKRVPPQPLTPMQIVSTLFTSNFIGICFRSLHYQFYV WFHTLPYLLWAMPARMLTHLLRLLVLGLIELSWMYYFSTSCSS AALMICHAVILLQLWLGGPPFPKSTQHSKKMA LLAGGESLLPETLENWRAQTGLDIRFFYGTETGLTCMVSKTM KIKGYMTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPTRPI GFFSGYVDNDBVKTAANIRGDFWLLGDRGIKDEDGYFQFMGRADD IINSGGYRIGPSEVENALMENBHVAVETAVISSPPPVRGEVVKAP VILALQFLSHDPEQLTKELGRGUKSVTAPKYPKRIETVILNEU TVTCKICRAVALKRDEWMSCKAPCAVEHREDIHLDSPLSLSIF				TOVAPAQUATROLOS VWHLGTLARRAFIGEATIPLATWOFEDS
DQQKLEKSPVLRKQACPQWKHSFVSGVTPAQLRQSSLELTVW DQALFGMNDRLLGGT\RLGSKGDTAVGGDACSQSKLQWQKVLSS PNLWTDMTLVLH 6820 1014 340 GDMYYYUGHVPPEFFEKTONKAWFREGFNEKYLKVVRKHHRVIA GCFFGHHHTDSFRMLYDDAGVPISAMFITPGUTPWKTTLGVVN GANNPAIRVFEYDRATLSLKDMYTYFMNLSQANAQGTPRWELEY QLTEAYGVPDASAHSMHTVLDRIAGDGTIQRYYYNSVYSAG VCDEACSMQHVCAMRQVDIDAYTTCLYASGTTPVPQLPLLLMAL LGLCT 6821 1088 518 EFDIYR/EVGGEFVPVTRDDSSNGFPRTQHGPSPTVHPQSPQN RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSSGLWRMVRIG GQPLGFDEGGIVAQIAGPLAADISAYYISTFNFDHALVPEDGI GSVIEVLQRRQEGLAS 6822 1088 518 EFDIYR/EVGGEFVPVTRDDSSNGFPRTQHGPSPTVHPQSPQN RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSSGELWRMVRIG GQPLGFDEGGIVAQIAGPLAADISAYYISTFNFDHALVPEDGI GSVIEVLQRRQEGLAS 6823 654 221 PFKLSERARRMGHGBEIV\LSDLNFPGLLHLEVVGPWRSVQTAC GIPQLEAVLKLLPLDTYVESPAAVMELVPSDKREGLGTPVWTE YESILRRAGCVRALAKIERFEFYERAKKAFAVVATGETALYGNL LIKKGVLALNPLL 6824 858 104 LLLAQRWGWG\CCFFSLAVSVKMNVLLFAPGLLFLLTQFGFRG ALPKLGICAGLQVVLGLPFLLENPSGYLSRSFDLGRQFLFHHTV NWRFLPEALFLHRAFHLALLTLLLLFALCRHHRTGESILS LLRDPSKRKVPPOPLTPNQIVSTLFTSNFIGICFSRSLHYQFYV WYFHTLPYLLWAMPARWITHLTLLLLFLACRHHRTGESILS LLRDPSKRKVPPOPLTPNQIVSTLFTSNFIGICFSRSLHYQFYV WYFHTLPYLLWAMPARWITHLTLLLLFLACRHHRTGESILS LLRDPSKRKVPPOPLTPNQIVSTLFTSNFIGICFSRSLHYQFYV WYFHTLPYLLWAMPARWITHLTLLLLFLACRHHRTGESILS LLRDPSKRKVPPOPLTPNQIVSTLFTSNFIGICFSRSLHYQFYV WYFHTLPYLLWAMPARWITHLTLLLLGLIELISMTYPSTSCSS AALHICHAVILLQLWLGPQPFPKSTQHEKKAH KIKRGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPTRPL NCLAGGESLLPETLENWRAQTGLDIREFYGQTETGLITCMVSKTM KIKRGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPTRPL OKLAGGESLLPETLENWRAQTGLDIREFYGQTETGLITCMVSKTM KIKRGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPTRPL GIFSGYVDNPBVKTANIRGDFWLLGDRGIKDEGGYFORGADD IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAF KIKRGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPTRPL TVTKKIQRA NICKERSSCHERDIHLDDSPLISLSSF	1			FACECTRODEL UCOLOL VILLE CANON PURPOSE NORTH NOR
DOALFGMNDRLIGGT\RIGSKGDTAVGGDACSQSKLQWQKVLSS PRIMITDMITULH 6820 1014 340 GDMVYIVGHVPPGFFEKTQNKAWFREGFNEKYLKVVRKHHRVIA GOFFGHHHTDSFRMLYDDAGVPI SAMFITPGUTPWKTTLFGVVN GANNPAIRVFEYDRATILSLKDMVTYFMLSQANAQGTPRWELEY QLTEAYGVPDASAHSMHTVLDRIAGDGSTLQRYVYNNSVSYSAG VCDEACSMQHVCAMRQVDIDAYTTCLYASGTTPVPQLFLLLMAL LGLCT 6821 1088 518 EFDIYR/EVGGEFVPVTRDDSSNGFPRTQHGPSPTVHPIQSPQN RFCVLTLDPETLPAIATTLLIDVLFYSHSTPKEAASSSEPEPSIT FFAFSLIEGYI\SIVMDAETQKKFPSDLLITSSSGELMRWNVIG GOPLGFDECGIVAQIAGPLAAADISAYYISTFNPDHALVPEDGI GSVIEVLQRRQGGLAS 6822 1088 518 EFDIYR/EVGGEFVPVTRDDSSNGFPRTQHGPSFTVHPIQSPQN RFCVLTLDPETLPAIATTLLDVLFYSHSTPKEAASSSPEPSSIT FFAFSLIEGYI\SIVMDAETQKKFPSDLLITSSSGELMRWRIG GQPLGFDECGIVAQIAGPLAAADISAYYISTFNPDHALVPEDGI GSVIEVLQRRQEGLAS GOPLGFDECGIVAQIAGPLAAADISAYYISTFNPDHALVPEDGI GSVIEVLQRRQEGLAS GOPLGFDECGIVAQIAGPLAAADISAYYISTFNPDHALVPEDGI GSVIEVLQRRQEGLAS GSVIEVLQRRQEGLAS 654 221 PPKLJSRWARMGHGDEIV\LSDLNFPGLLHLPVVGPWRSVQTAC GIPQLLEAVLKLLPLDTYVESPAAVMELVPSDKERGLQTPVWTE YESILRRAGCVRALAKIERFEFYERAKKAFAVVATGETALVGNL ILRKGVLALNPLL 6824 858 104 LLLAGRWGWG\CCFFSLAVSVKMNVLLFAPGLLFLLLTQFGFRG ALPKLGICAGLQVVLGLPFILLENPSGYLSRSFDLGRQFLFHMTV WRFLPEALFLHRAFFHLALLTAHLTLLLLALTQLELESHNTYPSTSCSS AALHICHAVILLQLWLGPPPPKSTQHSKKAH 6825 3 1173 SSGEFGLQASDIMWTISDTGWILITLCSIMEPWALGACTFVHLL NCLAGGESLLPETLENWRAQTGLDIRFFYGQTETGLTCMVSKTM KIKPGYMGTAASCYDVQIIDDKGNVLPPGTEGGIGIRVKPIRPI GIFSGYVONPDKTAANIRGDFWLLGDRGIKDEOGYPGFMGRADD IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAF VILALOFISHDPEQLIKELGQDVKSVTAPYKYPRKIEFVILNIPK TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF				DOOKLEI KERVI BKOA GROWKIIGITHEGUMBA OF BOOK TEP
6820 1014 340 GDMYYUGHVPGFFEKTONKAWFREGFNEKYLKVURKHHRVIA GQFFGHHHTDSFRMLYDDAGVPISAMFITPGVTPWKTTLPGVVN GANNPAIRVFEYPRATI.SLKDMVYTPMNLSQANAGGFFRWELEY GUTEA/GVPDASAHSMTVLDRIAGDGTLQRYYVYNSVYSAG VCDEA/GMVPDASAHSMTVLDRIAGDGTLQRYYVYNSVYSAG VCDEA/GMVPDASAHSMTVLDRIAGDGTLQRYYVYNSVYSAG VCDEA/GMVPDASAHSMTVLDRIAGDGTLQRYYVYNSVYSAG VCDEA/GMVPDASAHSMTVLDRIAGNAGGFFRVDGLPLLIMAL LGLCT FROULTLD FTLPAIATTLIDVLPYSHSTPKEAASSSEPSIT FFAFSLIEGYI\SIVMDAETOKKPSDLLITSSGELWMVRIG GQPLGFDEGIVAQIAGPLAAADISAYYISTFNPHALVPEDGI GSVIEVLQRRQEGLAS FFOIYR/EVGGEFVPVTRDDSSNGFPRTQHGPSPTVHPIQSPQN RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT FFAFSLIEGYI\SIVMDAETOKKPSDLLITSSGELWMWRIG GQPLGFDEGIVAQIAGPLAAADISAYYISTFNPHALVPEDGI GSVIEVLQRRQEGLAS FFAFSLIEGYI\SIVMDAETOKKPSDLLITSSGELWMVRIG GGPLGFDEGIVAQIAGPLAAADISAYYISTFNPHALVPEDGI GSVIEVLQRRQEGLAS FFAFSLIEGYI\SIVMDAETOKKPSDLLLTSSGELWMWRIG GGPLGFDEGIVAQIAGPLAAADISAYYISTFNPHALVPEDGI GSVIEVLQRRQEGLAS FFAFSLIEGYI\SIVMDAETOKKPSDLLLTSSGELWMWRIG GGPLGFDEGIVAQIAGPLAAADISAYYISTFNPHALVPEDGI GSVIEVLQRRQEGLAS FFAFSLIEGYI\SIVMDAETOKKPSDLLTSSGELWMRVEIG GSVIEVLQRRQEGLAS FFAFSLIEGYI\LSPAAVMELVPSDKERGLQTPWTTE YESILRRAGCVRRLAKLEPEFFYERAKKAFAVVATGETALYGNL ILRKGVIALNPLL LIRKGVIALNPLL LIRKGVIALNPLL LILRBSGVIALNPLL LILRBSGVIALNPLLEBUSGVISSFDLGRQFLFHWTV WMFHTLPYLLMAMPARWLTHLIRLLVIGLILESWNTYPSTSCS AALHICHAVILLQLWLGPOFFPKSTQISKKAH FFKFDLVILLWAMPARWLTHLIRLLVIGLIELSWNTYPSTSCSS AALHICHAVILLQLWLGPOFFPKSTQISKKAH PFKFDLVILLWAMPARWLTHLIRLLVIGLIELSWNTYPSTSCSS AALHICHAVILLQLWLGPOFFPKSTQISKKAH KIKRGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRPI GIFSGYVNDMPKTAANIRGDFWLIGDRGIKDGOGYPGMGADD NCLAGGESLLPFTLENWRAQTGLDIREFYGQTETGLTCMVSKTM KIKRGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRPI GIFSGYVNDMPKTAANIRGDFWLIGDRGIKDEOGYPGMGADD IINSSGYRIGPSEVENALMEHPAVVETAVISSPPVRGEVVKAF VILALOFISHDPEQLTKELQQHVKSVTAPYKYPRKIEFVILNIPK TVTGKIQRA\KLRDKEWKNGSKAFCAVRHLRDIHLDSPLLSLSF	1 1			DOM ECHNIDAL COM DI COMODENTICADA COMO DE COMODENTICADA COMO DE COMODENTICADA COMO DE COMODENTICADA COMO DE COMODENTICADA COMO DE COMODENTICADA COMO DE COMODENTICADA COMO DE COMODENTICADA COMODENTICADA COMO DE COMODENTICADA COMO DE COMODENTICADA COMO DE COMODENTICADA COMO DE COMODENTICADA COMO DE COMODENTICADA COMO DE COMODENTICADA COMO DE COMODENTICADA COMO DE COMODENTICADA COMODENTICADA COMO DE ICADA COMODENTICADA CO
GB20				
GGFFGHHHTDSFRNLYDDAGUPISAMFITGUTPWKTTLEGUVN GANNPAIRVFFYDRATLSLKUMVTYFMNLSQANAQGTPRWELEY QLTEAYGUVPDASAHSMHTVLDRIAGDQSTLQRYYVYNSVYSAG VCDEACSMQHVCAMRQVDIDATTCLYASGTTDVPQLPLLIMAL LGLCT FFDYR/EVGGEFVPVTRDDSSNGFPRTQHGPSPTVHPIQSPQN RFCVLTLDPETLPAIATTLIDVLFYSHSTKRAASSSPEPSSIT FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSSGELMRMVRIG GGPLGFDECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI GSVIEVLQRRQEGLAS FFDYR/EVGGEFVPVTRDDSSNGFPRTQHGPSPTVHPIQSPQN RFCVLTLDPETLPAIATTLIDVLFYSHSTFKEAASSSPEPSSIT FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSSGELMRWVRIG GSVIEVLQRRQEGLAS FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSSGELWRVRIG GGPLGFDECGIVAQIAGPLAAADISAYYISTFMFDHALVPEDGI GGPLGFDECGIVAQIAGPLAAADISAYYISTFMFDHALVPEDGI GGPLGFDECGIVAQIAGPLAAADISAYYISTFMFDHALVPEDGI GGPLGRDECGIVAQIAGPLAAADISAYYISTFMFDHALVPEDGI GGPLGRDECGIVAQIAGPLAAADISAYYISTFMFDHALVPEDGI GSVIEVLQRRQEGLAS 6823 654 221 PPKLLSRWARMGHGDEIV\LSDLNFPGLLHLPVVGPWRSVQTAC GIPQLLEAVLKLIPLDTYVESFAAVMELVPSDKERGLQTPWTTE YSSILRRAGCVRALKAKIERFFFYERAKKAFAVVATGETALYGNU LIRKGVLALNPLL LLAQRWGWG\CCFFSLAVSVKMNVLLFAPGLLFLLLTQFFRG ALPKLGICAGLQVVLGLPFFLENPSGYLSRSPDLGRGFLFHWTV NNRFLPEALFLHRAFHLALLTAHLTLLLLFALCRWHRTGESILS LLRDPSKRKVPPQPLTPNQIVSTLFTSNPIGIGFSKEHYGFYV WFFHTLPYLLWAMPRARHITHLIRLLVLGLIELSWNTYPSTSCSS AALHICHAVILLQLWLGPQPFPKSTQHSKXAH FKFPPLVILKTLSSYPIKSMMGAPIVYRMLQQDLSSYKFFHLQ NCLAGGESILPETLENNRAQTGLDTREFYGGTETGLTCMVSKTM KIKPGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRPI NCLAGGESILPETLENNRAQTGLDTREFYGGTETGLTCMVSKTM KIKPGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRPI INSSGYRIGPSEVENALMEHPAVVETAVISSPDPVGGGVVKAF VILALQFLSHDPEQLTKELQQHVKSVTAPYKYPRKIEFVILNLPK VILALQFLSHDPEQLTKELQQHVKSVTAPYKYPRKIEFVILNLPK VILALQFLSHDPEQLTKELQQHVKSVTAPYKYPRKIEFVILNLPK TVTGKIQRA\KLEDKEMMSGKAPCAVRHIRDIHLDSPLLSLSSF	6820	7014	340	
GANNPATRVFETDRATLSLKDMVTYFMNLSQANAQGTPRWELEY QLTEAYGVPDASAHSMHTVLDRIAGDQSTLQRYYVNNSVSYAG VCDEACSMQHVCAMRQVDIDAYTTCLYASGTTPVPQLPLLLMAL LGGCT EFDIYR/EVGGEFVPVTRDDSSNGFPRTOHGPSPTVHPIQSPQN RCVLTLDPETLPATATTLIDVLFYSHSTPKEAASSSPEPSSIT FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSSGELWRMVRIG GQDLGFPECGIVAQIAGPLAAADISAYYISTFNPDHALVPEDGI GSVIEVLQRRQECLAS FEDIYR/EVGGEFVPVTRDDSSNGFPRTOHGPSPTVHPIQSPQN RFCVLTLDPETLPATATTLIDVLFYSHSTPKEAASSSPEPSSIT FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSSGELWRMVRIG GQPLGFPECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI GSVIEVLQRRQEGLAS 6823 654 221 PPKLLSRWARMGHGDBIV\LSDLNFPGLLHLPVVGFWRSVQTAC GIPQLLEAVLKLLPLDTYVESPAAVMELVPSDKERGLQTPVWTE VESILRRAGCVRALKILEPLDTYVESPAAVMELVPSDKERGLQTPVWTE VESILRRAGCVRALKILEPLDTYVESPAAVMELVPSDKERGLQTFVWTE VESILRRAGCVRALKILEPLDTYLESPSGYLSRSFDLGRQFLFHHTV NWRFLPEALPLHRAPHLALLTAHLTLLLFALCRWHRTGESILS LLRDPSKRVPPQPLTPNQIVSTLFTSNFIGICFSRSLHVQFYV WYFHTLPYLLWAMPARWLTHLLELLVGLIELSWNTYPSTSCSS AALHICHAVILLQLWLGPQPFPRSTQHSKKAH WYFHTLPYLLWAMPARWLTHLLELLVGLIELSWNTYPSTSCSS AALHICHAVILLQLWLGPQPFPRSTQHSKKAH SGEFGLQASDIMWTISDTGWILITLCSLMEPWALGACTFVHLL PKFDPLVILKTLSSYPIKSMMGAPIVVRMLLQQDLSSYKFPHLQ NCLAGGESLLPETLENWRAQTGLDIREFYGGTETGLTCMVSKTM KIKPGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRPI GIFSGYDNBPKTAANIRGDFWLLGDRGIKDEDGYPQFMGRADD IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAF VILALQFLSHDPEGLTKELQQHVKSVTAPYKYPRKIEFVINLPK TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF		707.7	240	GOPECHHUPDGEDMI YDDAGUDIGANDIRGUMDUWWWW.
GUTEAYGVPDASAHSMHTVLDRIAGDGSTLQRYYVYNSVSYSAC VCDEACSMQHVCAMRQVDIDAYTTCLYASGTTPVPQLFLLLMAL LGLCT FERSTLIEGYT RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT FFAFSLIEGYT\SIVMDAETQKKFPSDLLLTSSSGELMRMVRIG GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI GSVIEVLQRRQEGLAS FFDIYR/EVGGEFVPVTRDDSSNGFPRTOHGPSPTVHPIQSPQN RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSSGELMRMVRIG GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI GSVIEVLQRRQEGLAS GGPLGFTDCGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI GSVIEVLQRRQEGLAS 6823 654 221 PFKLLSRWARMGHGDEIV\LSDLNFPGLLHLPVVGPWRSVQTAC GIPQLLEAVLKLLPLDTYVESPAAVMELVPSNKERGLQTPVWTE YESILRRAGCVRALAKIERFEFYERAKKAFAVVATGETALYGNL ILRKGVIALMPLL LLLAQRGWG\CCFFSLAVSVKMNVLLFAPGLLFLLLTQFGFRG ALPKLGICAGLQVVLGLPFLLENPSGYLSRSFDLGRQFLFHWTV NWRFLPEALFLHRAFHLALLTAHLTLLLLFALCRWHRTGESILS LLRDPSKRKVPPQPDPIPNQIVSTLFTSNFIGICFSRSLHYQFYV WYFHTLPYLLWAMPARWLTHLLRLVLGLIELSWNTYPSTSCSS AALHICHAVILLQUWLGPQFPFRSTQHSKKAH WYFHTLPYLLWAMPARWLTHLLRLVGLIELSWNTYPSTSCSS AALHICHAVILLQUWLGPQFPFRSTQHSKKAH NCLAGGESLLPETLENWRAQTGLDIRFFYGGTETGLTCMVSKTM KIKPGFWGTAASCVZDVQIIDDKGKNVLPPGTEGDIGIRVKPIRPI GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDEDGYFQFFWGRDD IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAF VILALQFLSHDPEQLTKELQQHVKSVTAPYKYPRKIEFVINLPK TVTGKIQRA\KLRDKEWKMSGKAPCAVRHKRDIHLDSPLLSLSF]			CAMIDATOUREVDDATE OF NDWARFTIPGVILLE CONTROL OF THE
VCDEACSMQHVCAMRQVDIDAYTTCLYASGTTPVPQLPLLLMAL LGLCT FFD1YR/EVGGEFVPVTRDDSSNGFPRTQHGPSPTVHPIQSPQN RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSSGELWRMVRIG GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI GSVIEVLQRRQECLAS FD1YR/EVGGEFVPVTRDDSSNGFPRTQHGPSPTVHPIQSPQN RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSSGELWRMVRIG GSVIEVLQRRQECLAS FFD1YR/EVGGEFVPVTRDDSSNGFPRTQHGPSPTVHPIQSPQN RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSSGELWRMVRIG GGPLGFDECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI GSVIEVLQRRQEGLAS 6823 654 221 PFKLLSRWARMGHGDEIV\LSDLNFFGLLHLPVVGPWRSVQTAC GIPQLLEAVLKLLPLDTYVESPAAVMELVPSDKERGLQTPVWTE YESILRRAGCVRALAKIERFFFYERAKKAFAVVATGETALYGNL ILKRQVLALNPLL 6824 858 104 LLLAQRWGWG\CCFFSLAVSVKMNVLLFAPGLLFLLLTQFGFRG ALPKLGICAGLQVVLGLPFLLENPSGYLSRSFDLGRQFLFHWTV NNFFLDPALFLHAPHLALLTAHLTLLLAPACRWHRTGESILS LLRDPSKRKVPPQPLTPNQIVSTLFTSNFIGICFSRSLHYQFYV WYFHTLPYLLWAMPARWLTHLLRLLVLGLIELSWMTYPSTSCSS AALHICHAVILLQLWLGPQPFPKSTQHSKKAH FKFDPLVILKTLSSYPIKSMMGAPIVYRMLLQQDLSSYKFPHLQ NCLAGGESLLPETLENWRAQTGLDIREFYGQTETGLTCMVSKTM KIKPGYMGTAASCYDVQIIDDKGNVLPPGFEGDIGIRVRFIRPI GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDEDGYFQFMGRADD IINSGGYRIGPSEVENALMSHPAVVETAVISSPDPVRGEVVKAF VILALQFISHDPGUTKELQQHVKSVTAPYKYPRKIEFVLINLPK TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF	į i			OLTPA VCUPDA CAUCHUTUI DEL ACCOUNT CAUCHTONICA
6821 1088 518 EFDIYR/EVGGEFVPVTRDDSSNGFPRTQHGPSPTVHPIQSPQN RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSSGELWRMVRIG GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFHALVPEDGI GSVIEVLQRRQEGLAS FFDIYR/EVGGEFVPVTRDDSSNGFPRTQHGPSPTVHPIQSPQN RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSSGELWRMVRIG GSVIEVLQRRQEGLAS FFDIYR/EVGGEFVPVTRDDSSNGFPRTQHGPSPTVHPIQSPQN RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSSGELWRMVRIG GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI GSVIEVLQRRQEGLAS FPELLSRWARMHGDBIV\LSDLNFPGLLHLPVVGPWRSVQTAC GIPQLLEAVLKLLPLDTYVESPAAVVELVPSDKERGLQTPVWTE YESILRRAGCVRALAKIERFEFYERAKKAFAVVATGETALYGNL LILKGVLALNPLL LILKGVLALNPLL LLRAGWGWG\CCFFSLAVSVKMNVLLFAGLLFILLTQFGFRG ALPKLGICAGLQVVLGLPFLLENPSGYLSRSFDLGRQFLPHWTV NWFFLPPALFFLHRAFHLALLTALLTLLLLFALCRWHRTGESILS LLRAGSKRKVPPQDLTPNQIVSTLFTSNFIGICFSRSLHYQFYV WYFHTLPYLLWAMPARWLTHLLRLLVLGLIELSWNTYPSTSCSS AALHICHAVILLQLWLGPQPFPKSTQHSKKAH NCHAGESLLPETLENWRAQTGLDIREFYCQTETGLTCMVSKTM KIKPGYMGTAASSPIKSMMGAPIVYRMLLQQDLSSYKFPHLQ NCLAGGESLLPETLENWRAQTGLDIREFYCQTETGLTCTVSKTM KIKPGYMGTAASSPIVQIIDDKGNVLPPGFGGDIGIRVFINPI GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDEDGYFQFMGRADD IINSGGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAF VILALQFISHDPGUTKELQQHVKSVTAPYKYPRKIEFVLINLPK TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF			,	VCDEA COMONICAMPOVIDED A VOIDE A COMPRISE SE
6821 1088 518 EFDIYR/EVGGEFVPVTRDDSSNGFPRTQHGPSPTVHPIQSPQN RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPBESSIT FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSSGELWRMVRIG GQPLGFDECGIVAQIAGPLAAADISAYYISTFNPDHALVPEDGI GSVIEVLQRRQEGLAS 6822 1088 518 EFDIYR/EVGGEFVPVTRDDSSNGFPRTQHGPSPTVHPIQSPQN RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPBPSSIT FFAFSLIEGYI\SIVMDAETQKKPPSDLLLTSSSGELWRMVRIG GGPLGFDECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI GSVIEVLQRRQEGLAS 654 221 PPKLLSRWARMGHGDEIV\LSDLNFPGLLHLPVVGPWRSVQTAC GIPQLLERVLKLLPLDTYVESPAAVMELVPSDKERGLQTPVWTE YESILRRAGCVRALAKIERFEFYERAKKAFAVVATGETALYGNL ILRKGVLALNPLL 6824 858 104 LLLAQRWSWG\CCFFSLAVSVKMNVLLFAPGLLFLLLTQFGFRG ALPKLGICAGLQVVLGLFFILENPSGYLSRSFDLGRQFLFHWTV WMRFLPEALFLHRAFHLALLTAHLTLLLIFALCRWRTTGESILS LLRDPSKRKVPPQPLTPNQIVSTLFTSNFIGICFSRSLHYQFYV WYFHTLPYLLWAMPARHLTHLLELLVLGLIELSWNTYPSTSCSS AALHICHAVILQDWLGGPPFKSTQHSKKAH 6825 3 1173 SSGEFGLQASDIMWTISDTGWILIILCSLMEPWALGACTFVHLL PKFDPLVILKTLSSYPIKSMMGAPIVYRMLLQQDLSSYKFPHLQ NCLAGGESLLPETLENWRAQTGLDIREFYGGTETGLTCMVSKTM KIKPGTMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRPI GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDEDGYFQFMGRADD IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAF VILALQFISHDPEQLTKELQQPHKSVTAPKYPRKIEFVLNLPK TVTGKIQRA\KLRDKEWKMSGKAFCAVRHLRIHLDSFLLSLSF				LGLOT
RECVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSSGELWRMVRIG GQPLGFDECGIVAQIAGHAAADISAYYISTFNPDHALVPEDGI GSVIEVLQRRQEGLAS FFDIYR/EVGGEFVPVTRDDSSNGFPRTQHGSPSTVHPIQSPQN RECVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSSGELWRMVRIG GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI GSVIEVLQRRQEGLAS 6823 654 221 PFKLLSRWARMCHGDBIV\LSDLNFFGLLHLPVVGPWRSVQTAC GIPQLLEAVLKLLPLDTYVESPAAVMELVPSDKERGLQTPVWTE YESILRRAGCVRALAKIERFEFYERAKKAFAVVATGETALYGNL ILKKGVLALNPLL LLAQRWGWG\CCFFSLAVSVKMNVLLFAPGLLFLLTQFGFRG ALPKLGICAGLQVVLGLPFLLENPSGYLSRSFDLGRQFLFHWTV NWRFLPEALFLHRAFHLALLTAHLTLLLLFALCRWHRTGESILS LLRDFSKRKVPPQPLTPNQIVSTLFTSNFIGICFSRSLHYQFYV WYPHTLPYLLWAMPARWLHTHLLRLLVLGLIELSWNTYPSTSCSS AALHICHAVILLQLWLGPQPFPKSTQHSKKAH SSGEFGLQASDIMWTISDTGWILIILCSLMEPWALGACTFVHLL PKFDPLVILKTLSSYPJKSMMGAPJVYRMLLQQDLSSXKFPHLQ NCLAGGESLLPFTLENWRAQTGLDIREFYGQTETGLTCMVSKTM KIKPGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRPI GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDEDGYFQFMGRADD IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAF VILALQFLSHDPEQLTKELQQHVKSVTAPYKYPRKIEFVLNLPK TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF	6821	1088	518	
FFAFSLIEGYI\SIUMDAETOKKFPSDLLLTSSSGELWRMVRIG GQPLGFDECGIVAQIAQPIAADISAYYISTFNFDHALVPEDGI GSVIEVLQRRQEGLAS FFDIYR/EVGGEFVPVTRDDSSNGFPRTQHGPSPTVHPIQSPQN RFCVLTLDPETLPATATTLIDVLFYSHSTPKEAASSSPEPSSIT FFAFSLIEGYI\SIVMDAETQKKFPSDLLTSSSGELWRMVRIG GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI GSVIEVLQRRQEGLAS 6823 654 221 PFKLLSKWARMGHGDEIV\LSDLNFPGLLHLPVVGPWRSVQTAC GIPQLEBAVLKLLPLDTYVESPAAVMELVPSDKERGLQTPVWTE YESILRRAGCVRALAKIERFEFYERAKKAFAVVATGETALYGNL ILKKGVLALNPLL 6824 858 104 LLLAQRWGWG\CCFFSLAVSVKMNVLLFAPGLLFLLTQFGFRG ALPKLGICAGLQVVIGLPFLLENPSGYLSRSFDLGRQFLPHWTV NWRFLPEALFLHRAFHLALLTAHLTLLLFALCRWHRTGESILS LLRDPSKRKVPPQPLITPNQIVSTLFTSNFIGICFSRSLHYQFYV WYFHTLPYLLWAMPARWLTHLLRLVGLIELSWNTYPSTSCSS AALHICHAVILLQLWLGPQPFPKSTQHSKKAH 6825 3 1173 SSGEFGLQASDIMWTISDTGWILIILCSLMEPWALGACTFVHLL PKFDPLVILKTLSSYPIKSMMGAPIVYRMLQODLSSYKFPHLQ NCLAGGSSLLPETLENWRAQTGLDIREFYGQTETGLTCMVSKTM KIKPGYMGTAASCYDVQIIDDKGNVLPPGTESDIGIRVKPIRPI GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDEDGYFQFMGRADD IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAR VILALGFILSHDPEQLTKELQOHVKSVTAPYKYPRKI EFVLNLPK TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF	1		323	PECVI-TI-DDETI-DALATTI-TOVI-EVOUCTBURDA ACCORDACATO
GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI GSVIEVLQRRQEGLAS EFDIYR/EVGGEFVPVTRDDSSNGFPRTQHGPSPTVHPIQSPQN RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSGGELWRWRIG GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI GSVIEVLQRRQEGLAS 654 221 PPKLLSRWARMGHGDEIV\LSDLNFPGLLHLPVVGPWRSVQTAC GIPQLLEAVLKLLPLDTYVESPAAVMELVPSDKERGLQTPVWTE YESILRRAGCVRALAKIERFEFYERAKKAFAVVATGETALYGNL ILRKGVLALMPLL 6824 858 104 LLLAQRWGWG\CCFFSLAVSVKMNVLLFAFGLLFLLLTQFGFRG ALPKLGICAGLQVVIGLPFLLENPSGYLSRSFDLGRQFLFHWTV NWRFLPEALFLHRAFHLALLTAHLTLLLFALCRWHRTGESILS LLRDPSKRKVPPQPLTPNQIVSTLFTSNPIGICFSRSLHYQFYV WYPHTLEYLLWAMPARWLTHLLRLLVLGLIELSWNTYPSTSCSS AALHICHAVILLQLWLGPQPFPKSTQHSKKAH 6825 3 1173 SSGEFGLQASDIMWTISDTGWILIILCSLMEPWALGACTFVHLL PKFDPLVILKTLSSYPIKSMMGAPIVYRMLLQQDLSSYKFPHLQ NCLAGGESLLPETLENWRAQTGLDIREFYGQTETGLTCMVSKTM KIKPGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRPI GIFSGYVDNPDKTAANIRGDFWILLGDRGIKDEDGYPGFMGRADD IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAF VILALQFLSHDPEQLTKELQQHVKSVTAPYKYPRKIEFVLNLPK TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF				REAESIJEGVI \ SIMMAETOKKEDEDI I I TECCOTE MUMIDIO
6822 1088 518 EFDIYR/EVGGEFVPVTRDDSSNGFPRTQHGPSPTVHPIQSPQN RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSGELWRMVRIG GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI GSVIEVLQRRQEGLAS 654 221 PPKLLSRWARMGHGDEIV\LSDLNFPGLLHLPVVGPWRSVQTAC GIPQLLEAVLKLLPLDTYVESFAAVMELVPSDKERGLQTPVWTE YESILRRAGCVRALAKIERFEFYERAKKAFAVVATGETALYGNL ILRKGVLALNPLL 6824 858 104 LLLAQWGWG\CCFFSLAVSVKMNVLLFAPGLLFLLLTQFGFRG ALPKLGICAGLQVVLGLPFLLENPSGYLSRSFDLGRQFLFHWTV NWRFLPEALFLHRAFHLALLTAHLTLLLLFALCRWHRTGESILS LLRDPSKRKVPPQPLTPNQIVSTLFTSNFIGICFSRSLHYQFYV WYPHTLPYLLWAMPARWLTHLLRLLVLGLIELSWNTYPSTSCSS AALHICHAVILLQLWLGPQPFPKSTQHSKKAH 6825 3 1173 SSGEFGLOASDIMWTISDTGWILTILCSLMEPWALGACTFVHLL PKFDPLVILKTLSSYPIKSMGAPIVYRMLLQDLSSYKFPHLQ NCLAGGESLLPETLENWRAQTGLDIREFYGQTETGLTCMVSKTM KIKPGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRPI GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDEDGYFQFMGRADD IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAF VILALQFISHDPEQLTKELQQHVKSVTAPYKYPRKIEFVLNLPK TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF	l i			GOPLGFDECGTVAOTAGDLAAADTGAVVICTENEDUALUDEDOT
6822 1088 518 EFDIYR/EVGGEFVPVTRDDSSNGFPRTQHGPSPTVHPIQSPQN RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT FFAFSLIEGYI/SIVMDAETQKKFPSDLLLTSSGELWRMVRIG GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI GSVIEVLQRRQEGLAS 654 221 PPKLLSRWARMGHGDEIV\LSDLNFPGLLHLPVVGPWRSVQTAC GIPQLLEAVLKLLPLDTYVESPAAVMELVPSDKERGLQTPVWTE YESILRRAGCVRALAKIERFEFYERAKKAFAVVATGETALYGNL ILKKGVLALNPLL 6824 858 104 LLLAQRWGWG\CCFFSLAVSVKMNVLLFAFGLLFLLLTQFGFRG ALPKLGICAGLQVVLGLPFILLENPSGYLSRSFDLGRQFLFHWTV NWRFLPEALFLHRAFHLALLTAHLTLLLLFALCRWHRTGESILS LLRDPSKRKVPPQPLTPNQIVSTLFTSNPIGICFSRSLHYQFYV WYFHTLPYLLWAMPARWLTHLLRLLVLGLIELSWNTYPSTSCSS AALHICHAVILLQLWLGPQFFPKSTQHSKKAH PKFDPLVILKTLSSYPIKSMMGAPIVYRMLLQDLSSYKFPHLQ NCLAGGESLLPETLENWRAQTGLDIREFYGQTETGLTCMVSKTM KIKPGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRPI GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDEDGYFQFMGRADD IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAF VILALQFISHDPEQLTKELQQHVKSYTAPYKYPRKIEFVLNIPK TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF	1 1			
RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSSGELWRMVRIG GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI GSVIEVUQRRQEGLAS 654 221 PPKLLSRWARMGHGDBIV\LSDLNFPGLLHLPVVGPWRSVQTAC GIPQLLEAVLKLLPLDTYVESPAAVMELVPSDKERGLQTPVWTE YESILRRAGCVVALAKIERFEFYERAKKAFAVVATGETALYGNL ILRKGVLALNPLL 6824 858 104 LLLAQRWGWG\CCFFSLAVSVKMNVLLFAPGLLFLLLTQFGFRG ALPKLGICAGLQVVLGLPFLLENPSGYLSRSFDLGRQFLFHWTV NWRFLPEALFLHRAFHLALLTAHLTLLLLFALCRWHRTGESILS LLRDPSKRKVPPQPLTPNQIVSTLFTSNFIGICFSRSLHYQFYV WYFHTLPYLLWAMPARWLTHLLRLLVLGLIELSWNTYPSTSCSS AALHICHAVILLQLWLGPPPFKSTQHSKKAH PKFDPLVILKTLSSYPIKSMMGAPIVYRMLQQDLSSYKFPHLQ NCLAGGESLLPETLENWRAQTGLDIREFYGQTETGLTCMVSKTM KIKPGYMGTAASCYDVQIIDDKGNVLPPGTEEDIGIRVKPIRPI GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDEDGYFQFMGRADD IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAF VILALQFLSHDPEQLTKELQHVKSVTAPYYYPRKIEFVLNLPK TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF	6822	1088	518	
FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSSGELWRMVRIG GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI GSVIEVLQRRQEGLAS 6823 654 221 PPKLLSRWARMGHGDEIV\LSDLNFPGLLHLPVVGPWRSVQTAC GIPQLLEAVLKLLPLDTYVESPAAVMELVPSDKERGLQTPVWTE YESILRRAGCVRALAKIERFEFYERAKKAFAVVATGETALYGNL ILRKGVLALNPLL 6824 858 104 LLLAQRWGWG\CCFFSLAVSVKMNVLLFAPGLLFLLLTQFGFRG ALPKLGICAGLQVVLGLPFLLENPSGYLSRSFDLGRQFLFHWTV NWRFLPEALFLHRAFHLALLTAHLTLLLLFALCRWHRTGESILS LLRDPSKRKVPPQPLTPNQIVSTLFTSNFIGICFSRSLHYQFYV WYPHTLPYLLWAMPARWLTHLLRLLVLGLIELSWNTYPSTSCSS AALHICHAVILLQUWLGPQPFPKSTQHSKKAH SGEFGLQASDIMWTISDTGWILIILCSLMEPWALGACTFVHLL PKFDPLVILKTLSSYPIKSMMGAPIVYRMLLQQDLSSYKFPHLQ NCLAGGESLLPETLENWRAQTGLDIREFYGQTETGLTCMVSKTM KIKPGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRPI GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDEDGYFQFMGRADD IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAF VILALQFLSHNPEQLTKELQQHVKSVTAPYKYPRKIEFVLNLPK TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF				RECVITIONETIPATATTITOVI. FYCHCTDERA ACCORDEDCET
GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI GSVIEVLQRRQEGLAS 6823 654 221 PPKLLSRWARMGHGDEIV\LSDLNFFGLLHLPVVGFWRSVQTAC GIPQLLEAVLKLLPLDTYVESPAAVMELVPSDKERGLQTPVWTE YESILRRAGCVRALAKIERFEFYERAKKAFAVVATGETALYGNL ILRKGVLALNPLL 6824 858 104 LLLAQRWGWG\CCFFSLAVSVKMNVLLFAPGLLFLLTQFGFRG ALPKLGICAGLQVVLGLPFLLENPSGYLSRSFDLGRQFLFHWTV NWRFLPEALFLHRAFHLALLTAHLTLLLLFALCRWHRTGESILS LLRDPSKRKVPPQPLTPNQIVSTLFTSNFIGICFSRSLHYQFYV WYPHTLPYLLWAMPARWLTHLLRLLVLGLIELSWNTYPSTSCSS AALHICHAVILLQLWLGPQPFPKSTQHSKKAH 6825 3 1173 SSGEFGLQASDIMWTISDTGWILIILCSLMEPWALGACTFVHLL PKFDPLVILKTLSSYPIKSMMGAPIVYRMLLQQDLSSYKFPHLQ NCLAGGESLLPETLENWRAQTGLDIREFYGQTETGLTCMVSKTM KIKPGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRPI GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDEDGYFQFMGRADD IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAF VILALQFLSHDPEQLTKELQQHVKSVTAPYKYPRKIEFVLMLPK TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF	1 1			FFAFSIJEGYT\STVMDAETOKKEDSDIJIJEGGGGELMDMUDTO
GSVIEVLQRRQEGLAS 6823 654 221 6824 6824 6828 6828 6824 6828 6828 6829 6829 6829 6829 6820 6820 6820 6820 6820 6820 6820 6820	1		•	GOPLGFDECGIVAOIAGPLAAADISAYYISTENEDHALVDEDGT
6823 654 221 PPKLLSRWARMGHGDEIV\LSDLNFPGLLHLPVVGPWRSVQTAC GIPQLLEAVLKLLPLDTYVESPAAVMELVPSDKERGLQTPVWTE YESILRRAGCVRALAKIERFEFYERAKKAFAVVATGETALYGNL ILRKGVLALNPLL 6824 858 104 LLLAQRWGWG\CCFFSLAVSVKMNVLLFAPGLLFLLTQFGFRG ALPKLGICAGLQVVLGLPFLLENPSGYLSRSFDLGRQFLFHWTV NWRFLPEALFLHRAFHLALLTAHLTLLLLFALCRWHRTGESILS LLRDPSKRKVPPPQPLTPNQIVSTLFTSNFIGICFSRSLHYQFYV WYFHTLPYLLWAMPARWLTHLLRLLVLGLIELSWNTYPSTSCSS AALHICHAVILLQLWLGPQPFPKSTQHSKKAH 6825 3 1173 SSGEFGLQASDIMWTISDTGWILIILCSLMEPWALGACTFVHLL PKFDPLVILKTLSSYPIKSMMGAPIVYRMLLQDLSSYKFPHLQ NCLAGGESLLPETLENWRAQTGLDIREFYGQTETGLTCMVSKTM KIKPGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRPI GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDEDGYFQFMGRADD IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAF VILALQFLSHDPEQLTKELQQHVKSVTAPYKYPRKIEFVLNLPK TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF				
GIPQLLEAVLKLLPLDTYVESPAAVMELVPSDKERGLQTPVWTE YESILRRAGCVRALAKIERFEFYERAKKAFAVVATGETALYGNL ILRKGVLALNPLL 6824 858 104 LLLAQRWGWG\CCFFSLAVSVKMNVLLFAPGLLFLLTQFGFRG ALPKLGICAGLQVVLGLPFLLENPSGYLSRSFDLGRQFLFHNTV NWRFLPEALFLHRAFHLALLTAHLTLLLLFALCRWHRTGESILS LLRDPSKRKVPPQPLTPNQIVSTLFTSNFIGICFSRSLHYQFYV WYFHTLPYLLWAMPARWLTHLLRLLVLGLIELSWNTYPSTSCSS AALHICHAVILLQLWLGPQPFPKSTQHSKKAH 6825 3 1173 SGEFGLQASDIMWTISDTGWILIILCSLMEPWALGACTFVHLL PKFDPLVILKTLSSYPIKSMMGAPIVYRMLLQQDLSSYKFPHLQ NCLAGGESLLPETLENWRAQTGLDIREFYGQTETGLTCMVSKTM KIKPGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRPI GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDEDGYFQFMGRADD IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAF VILALQFLSHDPEQLTKELQQHVKSVTAPYKYPRKIEFVLNLPK TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF	6823	654	221	
YESILRRAGCVRALAKIERFEFYERAKKAFAVVATGETALYGNL ILRKGVLALNPLL 6824 858 104 LLLAQRWGWG\CCFFSLAVSVKMNVLLFAPGLLFLLLTQFGFRG ALPKLGICAGLQVVLGLPFLLENPSGYLSRSFDLGRQFLFHWTV NWRFLPEALFLHRAFHLALLTAHLTLLLLFALCRWHRTGESILS LLRDPSKRKVPPQPLTPNQIVSTLFTSNFIGICFSRSLHYQFYV WYPHTLPYLLWAMPARWLTHLLRLLVLGLIELSWNTYPSTSCSS AALHICHAVILLQLWLGPQPFPKSTQHSKKAH 6825 3 1173 SSGEFGLQASDIMWTISDTGWILIILCSLMEPWALGACTFVHLL PKFDPLVILKTLSSYPIKSMMGAPIVYRMLLQQDLSSYKFPHLQ NCLAGGESLLPETLENWRAQTGLDIREFYGGTETGLTCMVSKTM KIKPGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRPI GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDEDGYFQFMGRADD IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAF VILALQFLSHDPEQLTKELQQHVKSVTAPYKYPRKIEFVLNLPK TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF	1 1			GIPQLLEAVLKLLPLDTYVESPAAVMELVPSDKERGLOTPVWTE
ILRKGVLALNPLL 6824 858 104 LLLAQRWGWG\CCFFSLAVSVKMNVLLFAPGLLFILLTQFGFRG ALPKLGICAGLQVVLGLPFLLENPSGYLSRSFDLGRQFLFHWTV NWRFLPEALFLHRAFHLALLTAHLTLLLLFALCRWHRTGESILS LLRDPSKRKVPPQPLTPNQIVSTLFTSNFIGICFSRSLHYQFYV WYPHTLPYLLWAMPARWLTHLLRLLVLGLIELSWNTYPSTSCSS AALHICHAVILLQLWLGPQPFPKSTQHSKKAH 6825 3 1173 SSGEFGLQASDIMWTISDTGWILIILCSLMEPWALGACTFVHLL PKFDPLVILKTLSSYPIKSMMGAPIVYRMLLQQDLSSYKFPHLQ NCLAGGESLLPETLENWRAQTGLDIREFYGQTETGLTCMVSKTM KIKPGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRPI GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDEDGYFQFMGRADD IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAF VILALQFLSHDPEQLTKELQQHVKSVTAPYKYPRKIEFVLNLPK TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF				YESILRRAGCVRALAKIERFEFYERAKKAFAVVATGETALYGNI.
ALPKLGICAGLQVVLGLPFLLENPSGYLSRSFDLGRQFLFHWTV NWRFLPEALFLHRAFHLALLTAHLTLLLLFALCRWHRTGESILS LLRDPSKRKVPPQPLTPNQIVSTLFTSNFIGICFSRSLHYQFYV WYFHTLPYLLWAMPARWLTHLLRLLVLGLIELSWNTYPSTSCSS AALHICHAVILLQLWLGPQPFPKSTQHSKKAH 6825 3 1173 SSGEFGLQASDIMWTISDTGWILIILCSLMEPWALGACTFVHLL PKFDPLVILKTLSSYPIKSMMGAPIVYRMLLQQDLSSYKFPHLQ NCLAGGGSLLPETLENWRAQTGLDIREFYGQTETGLTCMVSKTM KIKPGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRPI GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDEDGYFQFMGRADD IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAF VILALQFLSHDPEQLTKELQQHVKSVTAPYKYPRKIEFVLNLPK TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF	1			
ALPKLGICAGLQVVLGLPFLLENPSGYLSRSFDLGRQFIFHWTV NWRFLPEALFLHRAFHLALLTAHLTLLLFALCRWHRTGESILS LLRDPSKRKVPPQPLTPNQIVSTLFTSNFIGICFSRSLHYQFYV WYFHTLPYLLWAMPARWLTHLLRLVLGLIELSWNTYPSTSCSS AALHICHAVILLQLWLGPQPFPKSTQHSKKAH 6825 3 1173 SSGEFGLQASDIMWTISDTGWILIILCSLMEPWALGACTFVHLL PKFDPLVILKTLSSYPIKSMMGAPIVYRMLLQQDLSSYKFPHLQ NCLAGGESLLPETLENWRAQTGLDIREFYGQTETGLTCMVSKTM KIKPGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRPI GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDEDGYFQFMGRADD IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAF VILALQFLSHDPEQLTKELQQHVKSVTAPYKYPRKIEFVLNLPK TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF	6824	858	104	LLLAQRWGWG\CCFFSLAVSVKMNVLLFAPGLLFLLLTOFGFRG
NWRFLPEALFLHRAFHLALLTAHLTLLLLFALCRWHRTGESILS LLRDPSKRKVPPQPLTPNQIVSTLFTSNFIGICFSRSLHYQFYV WYFHTLPYLLWAMPARWLTHLLRLLVLGLIELSWNTYPSTSCSS AALHICHAVILLQLWLGPQPFPKSTQHSKKAH 6825 3 1173 SSGEFGLQASDIMWTISDTGWILIILCSLMEPWALGACTFVHLL PKFDPLVILKTLSSYPIKSMMGAPIVYRMLLQQDLSSYKFPHLQ NCLAGGESLLPETLENWRAQTGLDIREFYGQTETGLTCMVSKTM KIKPGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRPI GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDEDGYFQFMGRADD IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAF VILALQFLSHDPEQLTKELQQHVKSVTAPYKYPRKIEFVLNLPK TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF	í I	ļ		ALPKLGICAGLQVVLGLPFLLENPSGYLSRSFDLGRQFLFHWTV
LLRDPSKRKVPPQPLTPNQIVSTLFTSNFIGICFSRSLHYQFYV WYFHTLPYLLWAMPARWLTHLLRLVLGLIELSWNTYPSTSCSS AALHICHAVILLQLWLGPQPFPKSTQHSKKAH 6825 3 1173 SSGEFGLQASDIMWTISDTGWILIILCSLMEPWALGACTFVHLL PKFDPLVILKTLSSYPIKSMMGAPIVYRMLLQQDLSSYKFPHLQ NCLAGGESLLPETLENWRAQTGLDIREFYGQTETGLTCMVSKTM KIKPGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRPI GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDEDGYFQFMGRADD IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAF VILALQFLSHDPEQLTKELQQHVKSVTAPYKYPRKIEFVLNLPK TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF	i I	1	İ	NWRFLPEALFLHRAFHLALLTAHLTLLLLFALCRWHRTGESILS
WYFHTLPYLLWAMPARWLTHLLRLLVLGLIELSWNTYPSTSCSS AALHICHAVILLQLWLGPQPFPKSTQHSKKAH 6825 3 1173 SSGEFGLQASDIMWTISDTGWILIILCSLMEBWALGACTFVHLL PKFDPLVILKTLSSYPIKSMMGAPIVYRMLLQQDLSSYKFPHLQ NCLAGGESLLPETLENWRAQTGLDIREFYGQTETGLTCMVSKTM KIKPGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRPI GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDEDGYFQFMGRADD IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAF VILALQFLSHDPEQLTKELQQHVKSVTAPYKYPRKIEFVLNLPK TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF	[[]		LLRDPSKRKVPPQPLTPNQIVSTLFTSNFIGICFSRSLHYOFYV
AALHICHAVILLQLWLGPQPFPKSTQHSKKAH 6825 3 1173 SGEFGLQASDIMWTISDTGWILIILCSLMEPWALGACTFVHLL PKFDPLVILKTLSSYPIKSMMGAPIVYRMLLQQDLSSYKFPHLQ NCLAGGESLLPETLENWRAQTGLDIREFYGQTETGLTCMVSKTM KIKPGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRPI GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDEDGYFQFMGRADD IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAF VILALQFLSHDPEQLTKELQQHVKSVTAPYKYPRKIEFVLNLPK TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF	ļ [WYFHTLPYLLWAMPARWLTHLLRLLVLGLIELSWNTYPSTSCSS
PKFDPLVILKTLSSYPIKSMMGAPIVYRMLLQQDLSSYKFPHLQ NCLAGGESLLPETLENWRAQTGLDIREFYGQTETGLTCMVSKTM KIKPGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRPI GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDEDGYFQFMGRADD IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAF VILALQFLSHDPEQLTKELQQHVKSVTAPYKYPRKIEFVLNLPK TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF				
NCLAGGESLLPETLENWRAQTGLDIREFYGQTETGLTCMVSKTM KIKPGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRPI GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDEDGYFQFMGRADD IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAF VILALQFLSHDPEQLTKELQQHVKSVTAPYKYPRKIEFVLNLPK TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF	6825	3	1173	SSGEFGLQASDIMWTISDTGWILIILCSLMEPWALGACTFVHLL
KIKPGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRPI GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDEDGYFQFMGRADD IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAF VILALQFLSHDPEQLTKELQQHVKSVTAPYKYPRKIEFVLNLPK TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF	į l			
KIKPGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRPI GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDEDGYFQFMGRADD IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAF VILALQFLSHDPEQLTKELQQHVKSVTAPYKYPRKIEFVLNLPK TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF	(l			
GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDEDGYFQFMGRADD IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAF VILALQFLSHDPEQLTKELQQHVKSVTAPYKYPRKIEFVLNLPK TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF	Į !			KIKPGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRPI
VILALQFLSHDPEQLTKELQQHVKSVTAPYKYPRKIEFVLNLPK TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF				GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDEDGYFQFMGRADD
VILALQFLSHDPEQLTKELQQHVKSVTAPYKYPRKIEFVLNLPK TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF				IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAF
				VILALQFLSHDPEQLTKELQQHVKSVTAPYKYPRKIEFVLNLPK
1 DECCT 3 - DAM - 11 -	1			TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF
				PFGPLALPMDGYGDSLWEEHEYKFCLALVISTKLYHVRC
6826 2304 954 LKTESFKPW/VNIALAFHLLGERASPNSFWQPYIQTLPREYDTP	6826	2304	954	LKTESFKPW/VNIALAFHLLGERASPNSFWQPYIQTLPREYDTP
LYFEEDEVRYLQSTQAIHDVFSQYKNTARQYAYFYKVIQTHPHA		1		LYFEEDEVRYLQSTQAIHDVFSQYKNTARQYAYFYKVIQTHPHA
NKLPLKDSFTYEDYRWAVSSVMTRQNQIPTEDGSRVTLALIPLW		ł		NKLPLKDSFTYEDYRWAVSSVMTRQNQIPTEDGSRVTLALIPLW
DMCNHTNGLITTGYNLEDDRCECVALQDFRAGEQIYIFYGTRSN	(l	1	l	DMCNHTNGLITTGYNLEDDRCECVALQDFRAGEQIYIFYGTRSN
AEFVIHSGFFFDNNSHDRVKIKLGVSKSDRLYAMKAEVLARAGI		1	į	AEFVIHSGFFFDNNSHDRVKIKLGVSKSDRLYAMKAEVLARAGI
PTSSVFALHFTEPPISAQLLAFLRVFCMTEEELKEHLLGDSAID	1	ì		
RIFTLGNSEFPVSWDNEVKLWTFLEDRASLLLKTYKTTIEEDKS	į <u>I</u>	1		
VLKNHDLSVRAKMAIKLRLGEKEILEKAVKSAAVNREYYRQQME	ļ 1	J		
EKAPLPKYEESNLGLLESSVGDSRLPLVLRNLEEEAGVQDALNI	1	[
REAISKAKATENGLVNGENSIPNGTRSENESLNQESKRAVEDAK	1			
GSSSDSTAGVKE				GSSSDSTAGVKE

	T		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine
	location	corresponding	H=Histidine, I=Isoleucine, K=Lvsine
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion
6827	sequence		\=possible nucleotide insertion) .
6827	1	779	SSVVEFGLSVLGGLFLLFVLENMLGLLRHRGLRPRCCRRKRRNL
			ETRNLDPENGSGMALQPLQAAPEPGAQGQREKNSOHPPALAPPG
			HQGHSHGHQGGTDITWMVLLGDGLHNLTDGLAIGAAFSDGFSSG
		i	LSTTLAVFCHELPHELGDFAMLLQSGLSFRRLLLLSLVSGALGL
1	}		GGAVLGVGLSLGPVPLTPWVFGVTAGVFLYVALVDMLPALFPSS
(000			GAPAYA\HVLLQGLGLLLGGCLMLAITLLEERLLPVTTEG
6828	3	1654	KSQHG/WILQLMHSCKEGYVKDLKGNPGLHRAMLDLDNGTRPSE
l l	1		LGHLSQTASLKRGSSFQSGRDDTWRYKTPHRVAFVEKLTKLVLS
			QLPNFWKLWISYVNGSLFSETAEKSGQIERSKNVRORONDFKKM
	1		IQEVMHSLVKLTRGALLPLSIRDGEAKOYGGWEVKCELSGOWLA
i	ŀ		HAIQTVRLTHESLTALEIPNDLLQTIQDLILDLRVRCVMATLOH
]		TAFEIKRLAEKEDWIVDNEGLTSLPCQFEQCIVCSLOSLKGVLE
1			CKPGEASVFQQPKTQEEVCQLSINIMQVFIYCLEOLSTKPDADI
.}	1		DTTHLSVDVSSPDLFGSIHEDFSLTSEQRLLIVLSNCCYLERHT
1	-		FLNIAEHFEKHNFQGIEKITQVSMASLKELDQRLFENYIELKAD
			PIVGSLEPGIYAGYFDWKDCLPPTGVRNYLKEALVNIIAVHAEV
1			FTISKELVPRVLSKVIEAVSEELSRLMQCVSSFSKNGALOARLE
İ			ICALRDTVAVYLTPESKSSFKQALEALPQLSSGADKKLLEELLN
			KFKSSMHLQLTCFQAASSTMMKT
6829	1	782 .	MRMEAGEAAPPAGAGGRAAGGWGKWVRLNVGGTVFLTTRQTLCR
1			EQKSFLSRLCQGEELQSDRDETGAYLIDRDPTYFGPILNFLRHG
1 :	i		KLVLOKDMAEEGVLEEAEFYNIGPLIRIIKDRMEEKDYTVTOVP
1			PKHVYRVLQCQEEELTQMVSTMSDGWRFEOLVNIGSSYNYGSED
1 1			QAEFLCVVSKELHSTPNGLSSESSRKTKSTEEOLEEOOOGEETV
6030			EEVEVEQVQVEADAQEK/CCYKPEAPGCEAPDHLOGI.GVPT
6830	1	939	MEPGSVENLSIVYRSRDFLVVNKHWDVRIDSKAWRETLTLOKOL
1 1			RYRFPELADPDTCYGFRFCHQLDFSTSGALCVALNKAAAGSAYR
			CFKERRVTKAYLALLRGHIQESRVTISHAIGRNSTEGRAHTMCT
	Į.		EGSQGCENPKPSLTDLVVLEHGLYAGDPVSKVLLKPLTGRTHOL
1 1	j		RV\HCSALGHPVVGDLTYGEVSGREDRPFRMMLHAFYIRTPTDT
			ECVEVCTPDPFLPSLDACWSPHTLLQSLDQLVQALRATPDPDPE
1 1	j		DRGPRPGSPSALLPGPGRPPPPPTKPPETEAQRGPCLQWLSEWT
6033			LEPDS
6831	3	1087	SLFFGSSTPDNKVAEQEDLETQPSPSVEKAVTVIDPEGTIPTNF
1 1	1		NVAEKPADHSLSEVKLKTADEPRGTLVKSGDGQNVKEKSMILSN
1	!		VEDLQQPKFISEVSREDYGKKEISGDSEEMNINSVVTSADGENT.
1 1	į		EIQSYSLIGEKLVMEEAKTIVPPHVTDSKRVOKPAIAPPSKWNT
	1		SIFKEEPRSDQKQKSLLSFDVVDKVPQQPKSASSNFASKNITKE
1 1			SEKPESIILPVEESKGSLIDFSEDRLKKEMONPTSLKISEEETK
1 [J		LRSVSPTEKKDNLENR\SYTL\AEKKVLAEKONSV\ADT.ELDDC
, ,	1		NEIGKTQITLGSRSTELKESKADAMPQHFYQNEDYNERPKIIVG
6832	1000	· · · · · · · · · · · · · · · · · · ·	SEKEKDEKKKK
0032	1809	412	MGSGLISGPPQDNSGEALKEPERAQEHSLPNFAGGQHFPEYLLV
}		ļ	VSLKKKRSEDDYEPIITYQFPKRENLLRGOOEEEERLLKAIPI.F
] [ì	CFPDGNEWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG
]		ļ	PRLPKVYCIISCIGCFGLFSKILDEVEKRHQISMAVIYPFMOGI.
1 1			REAAFPAPGKTVTLKSFIPDSGTEFISLTRPLDSHLEHVDFSSL
		ĺ	LHCLSFEQILQIFASAVLERKIIFLAEGLSTLSOCIHAAAALLY
			PFSWAHTYIPVVPESLLATVCCPTPFMVGVQMRFQOEVMDSPME
1 1	ļ	j	EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGOGINELKT
1	1		AEQINEHVSGPFVQFFVKIVGHYASYIKREANGOGHFOERSFCK
	1	ĺ	ALTSKTNRRFVKKFVKTQLFSLFIQEAEKSKNPPAGYFOOKILE
			YEEQKKQ/TETKGKNCEIRAVVNKND
6833	1	1129	PLMTLSQCGGIPGHGHSHGGHGHGHGLPKGPRVKSTRPGSSDIN
	1		VAPGEQGPDQEETNTLVANTSNSNGLKLDPADPENPRSGDTVEV
			QVNGNLVREPDHMELEEDRAGQLNMRGVFLHVLGDALGSVIVVV

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	I INTERTALLIE, CECVSCEINE DEAGNAPHIE NALL N
1	location	corresponding	Gradamic Acid, F=Phenylalanine C_Cl
	corresponding	to first	
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
i	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
ļ	sequence	1	\=possible nucleotide insertion)
İ			NALVFYFSWKGCSEGDFCVNPCFPDPCKAFVEIINSTHASVYEA
	1		GPCWVLYLDPTLCVVMVCILLYTTYPLLKESALILLQTVPKQID
ſ	1	Ì	IRNLIKELRNVEGVEEVHELHVWQLAGSRIIATAHIKCEDPTSY
i		1	I ME VARI I ROVEHNEGIHATTIOPEFASVIGGEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
	}		CADACCCG TEPOAPSGKDAEKTPAVSTSCI.EL.CAMILEVERDEDEN
6834			AENIPA (VVIEIKN (IPNK (OPESSI,
0034	78	1151	AGQERPAPIWRLLWLPTPSVSRKAEPAHIDIND+GA+B+DGGV
1		i	DCGSSASAIGWH*RLTPWSPGGS*HM*SSKADVTOADEULUAGD
			CORDINASGARGIVGTTVOVLVEACODI.I.I.FTGIMGINI DA COD
1	1		SKAD DIEEVIQVRDAHLGNAVVGCAOCI.SOCOVCGAY AVALLE
			AAAAVRDCKEVLTVSGDKOOAEVSVRI.*VRDVCVERACCVERGO
- 1	1		ARGREGIALAKGRGGTNEVEEOVOVDGVOKLVI.GAUECUET UAG
			QUOGEDQAARTRLLOAGAHSVAHGRROGOADCPDUOEACUGGUD
l	1		LQQVVGDAL*ARE*APQIIVLLLLEDVAQLRTGKKA*DLVVDVE
6835	1	834	
· ·	1		GIPAADR\EASLELIKLDISRTFPNLCIFQQGGPYHDMLHSILG
	1		AYTCYRPDVGYVQGMSFIAAVLILNLDTADAFIAFSNLLNKPCQ MAFFRVDHGLMLTYFAAFEVFFEENLPKLFAHFKKNNLTPDIYL
1	1 1		IDWIFTLYSKSLPLDLACRIWDVFCRDGEEFLFRTALGILKLFE
ĺ			DILTKMDFIHMAQFLTRLPEDLPAEELFASIATIQMQSRNKKWA
			QVLTALQKDSREMREGKSVPPTLRLQREFALGTNQSPMPRPLCC
6836			FRHIPGOPRIDAL
0036	1	850	MSCGRPPPDVDGMITLKV\DNLTYRTSPDSLRRVFEKYGRVGDV
	1		I I PRESHTKAPRGFAFVRFHDRRDAODAFAAMDCAFI DODDE DE
1	1		VARIGRADLERSROGRRHAAGPEAA / PVCPDCPCVCPDCPCPC
1	1 1		KKIRSKSRGPSUSKSRSRSRYRGSRYSRSPYSRSPYSRSPYGRSPYGRS
1	1 1		FISKSKIKESKYGGSHYSSSGYSNSDVSDVHGSDGUGVGGGGG
j	1		SKSASTSKSSSARRSKSSSVSRSRSRSRSRSRSRSRSRSRSRSRSRSRSRSR
6837	1	1369	NONDREARPERSPEEEGOMSS
1		1303	TDGAAVAGNPGSDYFPGGTAP/GGPRTRRP\SGTSSSGSKASGP
Į.	1		PNPPAQGDGTSLSPNYTLESTSGNDGKPVSGGGGRGRRKRDS
ſ	1		GHVSPGTFFDKYSAAPDSGGAPGVSPGQQQASGAAVGGSSAGET
ſ	1		RGAPTPHEKALTSPSWGKGAELLLGDQPDLIGSLDGGAKSDSSS PNVGEFASDEVSTSYANEDEVSSSSDNPQALVKASRSPLVTGSP
1	1		KLPPRGVGAGEHGPKAPPPALGLGIMSNSTSTPDSYGGGGGPGH
	1		PGTPGLEQVRTPTSSSGAPPPDEIHPLEILQAQIQLQRQQFSIS
	İ		EDQPLGLKGGKKGECAVGASGAQNGDSELGSCCSEAVKSAMSTI
]	DDDSDMAEHSAAWYMPADKALVDSADDDKTI.ADWEKA KDONDNO
1 .		j	REAHDLPANKASASOPGSHLOCI, SVHCTDDUGDA KADA CUDUUD
6838	16		SURSDISHREGTE VAALT
	10	499	LTDTPPPKTHMIHHSISDYKATLRCWALGFYPMEITLTWQQDEE
		i	DOIRDHED VETRPAGIGTFORWAAVANDSGER / O / DVM CTUTOUR
		}	GLEEPLI LRWEQSSQPTIPIVGTVAGIVI.GAMUTGAMICAMICA
6839	1	7105	RRANSDRVS1SEAASSDHAOGSDVS1.TACKV
	_	1195	AAPAGGGPDPEALSAFPGRHLSGLSWPOVKPLDALLSERIDIVE
1 1	1	F	RGNFPTLSVQPRQIRAGGPOHPGGAG\ THUHPUPI.UCCAA CITIT
j	1	1	TESSES I RULDLVERMDLRSEASFOLTKAWT, ACLI, DELDACU
] /		i	SKAKI I PLILIKEAY VOKLVKVCTDSDRWSLISI SNKGCVNDET V
ļ [1	<u> </u>	F VDS VRRQFEFSIDSFOIILDSLLLFGOCSSTPMSF3 PURTURO
] [ESLYGDFTEALEHLRHRVIATRSPEEIRGGGLLKYCHLLVRGFR
		i	PRPSTDVRALQRYMCSRFFIDFPDLVEQRRTLERYLEAHFGGAD
1 1		1	AARRYACLVTLHRVVNESTVCLMNHERROTLDLIAALALQALAE QGPAATAALAWRPPGTDGVVPATVNYYVTPVQPLLAHAYPTWLP
		1	CN CN
6840	4254		ELQGDFSVPDVPKSMAWCENSICVGFKRDYYLIRVDGKGSIKEL
<u> </u>			FPTGKQLEPLVAPLADGKVAVGQDDLTVVLNEEGICTQKCALNW
			TO THE PROPERTY OF THE PROPERT

SEQ	T 75	1 =	
ID	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide	(A=Alanine, C=Cvsteine, D=Aspartic Acid P-
1.0.	location	location	Glutamic Acid, F=Phenylalanine, G=Glyging
1	corresponding	corresponding	H=H1Stidine, I=Isoleucine, K=Lvsine
	to first	to first amino acid	L=Leucine, M=Methionine, N=Asparagine,
Ì	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
			\=possible nucleotide insertion)
	1		TDIPVAMEHQPPYIIAVLPRYVEIRTFEPRLLVQSIELQRPRFI
ļ		İ	TSGGSNIIYVASNHFVWRLIPVPMATQIQQLLQDKQFELALQLA
	į		EMKDDSDSEKQQQIHHIKNLYAFNLFCQKRFDESMQVFAKLGTD
		İ	PTHVMGLYPDLLPTDYRKQLQYPNPLPVLSGAELEKAHLALIDY
1	l I		LTQKRSQLVKKLNDSDHQSSTSPLMEGTPTIKSKKKLLQIIDTT
1			LLKCYLHTNVALVAPLLRLENNHCHIEESEHVLKKAHKYSELII
1	1		LYEKKGLHEKALQVLVDQSKKANSPLKGHERTVQYLQHLGTENL
ł	i i		HLIFSYSVWVLRDFPEDGLKIFTEDLPEVESLPRDRVLGFLIEN
į	:		FKGLAIPYLEHIIHVWEETGSRFHNCLIQLYCEKVQGLMKEYLL
1	f I		SFPAGKTPVPAGEEEGELGEYRQKLLMFLEISSYYDPGRLICDF
1			PFDGLLEERALLLGRMGKHEQALFIYVHILKDTRMABEYCHKHY DRNKDGNKDVYLSLLRMYLSPPSIHCLGPIKLELLEPKANLQAA
	İ		LQVLELHHSKLDTTKALNLLPANTQINDIRIFLEKVLEENAQKK
			RFNQVLKNLLHAEFLRV\QEERILHQQVKCIITEEKVCMVCKKK
L			IGNSAFARYPNGVVVHYFCS\KEVNPADT
6841	1	3206	TPSTTGTKSNTPTSSVPSAAVTPLNESLQPLGDYGVGSKNSKRA
			REKRDSRNMEVQVTQEMRNVSIGMGSSDEWSDVQDIIDSTPELD
1			MCPETRLDRTGSSPTQGIVNKAFGINTDSLYHELSTAGSEVIGD
			VDEGADLLGEFSGMGKEVGNLLLENSQLLETKNALNVVKNDLIA
1 .			KVDQLSGEQEVLRGELEAAKQAKVKLENRIKELEEELKRVKSEA
] :			IIARREPKEEAEDVSSYLCTESDKIPMAORRRFTRVEMARVLME
l	I		RNQYKERLMELQEAVRWTEMIRASREHPSVOEKKKSTIWOFFSB
f .			LFSSSSSPPPAKRPYPSGNIHYKSPTTAGFSORRNHAMCDISAC
1			SRPLEFFPDDDCTSSARREOKREOYROVREHVRNDDCPLOACCW
1	1		SUPAKYKQLSPNGGQEDTRMKNVPVPVYCRPLVEKDPTMKLWCA
]			AGVNLSGWRPNEDDAGNGVKPAPGRDPLTCDREGDGEPKSAHTS
1 .	ŀ		PEKKKAKELPEMDATSSRVWILTSTLTTSKVVIIDANOPGTVAD
			QFTVCNAHVLCISSIPAASDSDYPPGEMFLDSDVNPEDDGADGV
]			LAGITLVGCATRCNVPRSNCSSRGDTPVLDKGOGEVATIANGKV
]	j		NPSQSTEEATEATEVPDPGPSEPETATLRPGPLTEHVFTDPAPT
	i		PSSGPQPGSENGPEPDSSSTRPEPEPSGDPTGAGSSAAPTMWI.C
ĺ	Ì		AQNGWLYVHSAVANWKKCLHSIKLKDSVLSLVHVKGRVLVALAD
! !			GTLAIFHRGEDGQWDLSNYHLMDLGHPHHSIRCMAVVYDRVWCG
ľ			YKNKVHVIQPKTMQIEKSFDAHPRRESQVRQLAWIGDGVWVSIR
			LDSTLRLYHAHTHQHLQDVDIEPYVSKMLGTGKLGFSFVRITAL
1			LVAGSRLWVGTGNGVVISIPLTETVVLHRGQ\LLG\LRANKTSP
	1		TSGEG\ARPGG\IIHVYG\DDSSDRAARSFIPYCSMAQAQLCFH
		ĺ	GHRDAVKFFVSVPGNVLATLNGSVLDSPAEGPGPAAPASEVEGQ
_	1	ŀ	KLRNVLVLSGGEGYIDFRIGDGEDDETEEGAGDMSQVKPVLSKA ERSHIIVWQVSYTPE
6842	3	926	RCQQLSATILTDHQYLERTPLCAILKQKAPQQYRIRAKLRSYKP
ł			RRLFQSVKLHCPKCHLLQEVPHEGDLDIIFQDGATKTPDVKLQN
1	į		TSLYDSKIWTTKNQKGRKVAVHFVKNNGILPLSNECLLLIEGGT
1			LSEICKLSNKFNSVIPVRSGHEDLELLDLSAPFLIQGTVHHYGC
l	ł		KQWST*RSIQNLNSLVDKTSWIPSSVAEALGIVPLQYVFVMTFT
ļ	ľ	1	LDDGTGVLEAYLMDSDKFFQIPASEVLMDDDLQKSVDMIMDMFC
		1	PPGIKIDAYPWLECFIKSYNVTNGTDNQICYQIFDTTVAEDVI
6843	2	851	NHRKVLSGAKRYECNECGKSFAYTSSLIKHRRIHTGERPYECSE
İ		}	CGRSFAENSSLIKHLRVHTGERPYECVECGKSFRRSSSLLQHQR
		· I	VHTRERPYECSECGKSFSLRSNLIHHQRVHTGERHECGQCGKSF
}	İ	ļ	SRKSSLIIHLRVHTGERPYECSDCGKSFAENSSLIKHLRVHTGE
1		ļ	RPYECIDCGKSFRHSSFRRHQRVHTGMRPYK*SKFWKFSCPGF
-	ļ		LLLQGQRVHTGSRCYECDKWGIFFS*NASFFT*KSAPTEEVPFE
			CNECEKAFSPLSLVTTIFT
6844	244	642	EHQLAGFELRKTQTSMSLGTTREKTDRVKSTAYLSPQELEDVFY
			QYDVKSEIYSFGIVLWEIATGDIPFQGCNSEKIRKLVAVKRQQE
		·	- TOUR TOUR TOUR TOUR TOUR TOUR TOUR TOUR

SEQ	Predicted	Predicted end	l Designation of the Control of the
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ſ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
İ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ı	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1			PLGEDCPSELREIIDECRAHDPSVRPSVDEILKKLSTFSK*CIK
6845			±
0043	3	1519	VAVRDECYWRHVFWDQDLWMLLFILMCHPETARARLEYRIRTLD
	1		GALENAQNLGYOGAKFAWESADSGLEVCDEDTYGYODIUUDGAA
- 1	1		GLAFELIYHTTQDLOLFREAGGWDVVRAVAEFWCGDVDWGDDDD
			RIBURGVMSPDEYHSGVNNSVYTNVI,VONSI,PFAAAI,AODI CLD
	l .		1 PSQWLAVADKIKVPFDVEONFHPEFDGVFDGFIAIVOADIBRIG
	J		1 PVPFSLSPDVRRKNLEIYEAVTSPOGPAMTWSMEAVGWMET VD
- 1	-		AVRARGLLDRSFANMAEPFKVWTENADGSGAVNELTGMCGELOR
ł	1		VVFGCTGFRVTRAGVTFDPVCLSGISRVSVSGTFVOGNKINEGE
			SEDSVIVEVTARAGPWAPHLEAELWPSOSPISI.PCHYVCEPPC
			AGRIQMSPPKLPGSSSSEFPGRTFSDVRDPLQSPLWVTLGSSSP
}	1		TESTIVDPASE*SGTGASETSLGPSIWPRIHDDLIGHTIACUDG
6846	213	1258	PAARLSGKVHAAWPEFKAFCL
1		1230	LYFLKTIK*LNRLAEHP*YENEKLTKLRNTIMEQYTRTEESARG
İ			IIFTKTRQSAYALSQWITENEKFAEVGVKAHHLIGAGHSSEFKP
			MTQNEQKEVISKFRTGKINLLIATTVAEEGLDIKECNIVIRYGL
ĺ	[[VTNEIAMVQARGRARADESTYVLVAHSGSGVIEHETVNDFREKM
	1		MYKAIHCVQNMKPEEYAHKILELQMQSIMEKKMKTKRNIAKHYK
		•	NNPSLITFLCKNCSVLACSGEDIHVIEKMHHVNMTPEFKELYIV
	l i		RENKTLQKKCADYQINGEIICKCGQAWGTMMVHKGLDLPCLKIR NFVVVFKNNSTKKQYKKWVELPITFPNLDYSECCLFSDED
6847	1450	348	SMCWNSDRLEMPLIDLALILYPPSYVPYTGHLSDDSLSRKYCLT
	[WFEDALNGVL*RAEAIQPHCVNAGDRMEKFRQKYWNKLQTLRQQ
i			PFAYGTLTVRSLLDTREHCLNEFNFPDPYSKVKQRENGVALRCF
			PGVVRSLDALGWEERQLALVKGLLAGNVFDWGAKAVSAVLESDP
	l f		YFGFEEAKRKLQERPWLVDSYSEWLQRLKGPPHKCALIFADNSG
			1 1011LGVFPFVRELLLRGTEVILACNSCPALMDVFDCFC1 TITE T
			RIAGMDPVVHSALREERLLLVOTGSSSPCIDI.Spr.DYCL NATUR
1	!		ERGADLVVIEGMGRAVHTNYHAALRCESLKLAVIKNAWLAERLG
6848			GRLFSVIFKYEVPAE
0040	19	16	AMWWNSLDGIRNIVLSNPKKRNTLSLAMLKSLQSDILHDADSND
			LKVIIISAEGPVFSSGHDLKELTEEOGRDVHAEVEOTCGVIRNIN
			IKNHPVPVIAMVNGLATAAGCOLVASCDIAVASDVGSEAMDGIB:
1]			VGLFCSTPGVALARAVPRKVALEMI,FTGEDISAOPALI UGI I NIK
			VVPEAELQEETMRIARKIASLSRPVVSI GKATEVKOLDODI GED
6849	70	821	IILISQAMVDNLALRDGOEGITAFI.OKRKPVWSUFDV+VFII
		021	SLGVDGSCLEQGSPAPRPOTDTSP*PVGNWATOOFDLVHOGVEG
[VCVLFASVPDFKEFYSESNINHEGLECIRLINETTADEDELTON
1	ł		PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM
	į		VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVIGAQKPQ
1			YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG
6850	2	1235	VIKVKGKGQLCTYFLNTDLTRTGPPSATLG
1		7777	ARGENHEWTFEKERQHISRNAQDKQELHLFMLSGVPDAVFDLTD
		1	LDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL
		i	RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI GLESLPEIPHLKII INVENITENDEN
1		İ	GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT KLLVLNSLKKMMNVAPLEL ONGELED TOWN TO THE
1		ł	KLLVLNSLKKMMNVAELELQNCELERIPHAIFSLSNLQELDLKS
			NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL
	ł	i	YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ
]			HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ
<u> </u>		İ	LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI
6851	1765	660	VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD
			LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA
			CYCVYKLTIGRDDSEKLEEGGEEWDDDQELDEEEPDIWFDFET
		 <u>l</u> .	

Deginning Cocation Cocation Cocati	SEO	Predicted	Predicted end	I Design and I was a second as
No:	, –		1	Amino acid segment containing signal peptide
corresponding to first amino acid	NO:		i e	Glutamic Acid F-Phenylalaning C-Classic
to first amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid sequence seq		location		H=Histidine T=Tsoleucine K=Tucine
amino acid residue of amino acid PIGGKLLFAEPKDAGFFPSYE HHATWASAGNCKNSCV_LDLSKCLPIGGKLLFAEPKDAGFFPSYE HHATWASAGNCKNSCV_LDLSKCLPIGGKLLFAEPKDAGFFPSYE HHATWASAGNCKNSCV_LDLSKCLPIGGKLLFAEPKDAGFFPSYE HHATWASAGNCKNSCV_LDLSKCLPIGGKLLFAEPKDAGFFPSYE HHATWASAGNCKNSCV_LDLSKCLPIGGKLLFAEPKDAGFFPSYE HHATWASAGNCKNSCV_LDLSKCLPIGGKLLFAEPKDAGFFPSYE HHATWASAGNCKNSCV_LDLSKCLPIGGKLLFAEPKDAGFFPSYE HATWASAGNCKNSCV_LDLSKCLPIGGKLLFAEPKDAGFFPSYE HATWASAGNCKNSCV_LDLSKCLPIGGKLLFAEPKDAGFFPSYE HTAGESTAAPKHCHSCNSCV_LDLSKCLPIGGKLTAEPKDAGFFPSYE ASSCALANCETTERPLEEPKDAGTSVTNSIAGSTBEACHWAGHTAEPKDAGFFTSAGNCSV_LDLSKCLPIGGKLTAEPKDAGFTSAGNCSV_LDLSKCLPIGGKLTAEPKDAGFTSAGNCSV_LDLSKCLPIGGKLTAEPKDAGFTSAGNCSCNSCLPUGGENGTAEPKDAGFTSAGNCSCNSCLPUGGENGTAEPKDAGFTSAGNCSCNSCLPUGGENGTAEPKDAGFTSAGNCSCNSCLPUGGENGTAEPKDAGFTSAGNCSCNSCLPUGGENGTAEPKDAGFTSAGNCSCNSCLPUGGENGTAEPKDAGFTSAGNCSCNSCLPUGGENGTAEPKDAGFTSAGNCSCNSCLPUGGENGTAEPKDAGFTSAGNCSCNSCLPUGGENGTAEPKDAGFTSAGNCSCNSCLPUGGGNAGTAGNAGTSAGNAGTSAGNAGTSAGNAGTSAGNAGTSAGNAGTSAGNAGTSAGNAGTSAGNAGTSAGNAGTSAGNAGTSAGNAGTSAGNA		corresponding		L=Leucine. M=Methionine N=Asparagine
amino acid residue of amino acid sequence KHEDKKNIFYAARTFATLFAWFAWHIAKSASDIK FPLISKOSGGCAKVQULKPLMGLISKEVPLAGELVGAQMLFSFNSL FIRMGREILLEFTAP 87RGEETTANFIKHEDKKNIFYAARTFATLFAWFAWHIAKSASDIK FPLISKOSGGCAKVQULKPLMGLISKEVPLAGELVGAQMLFSFNSL FIRMGREILLEFTAP 87GGEVETANFIKHEDKKNIFYAARTFATLFAWFAWHIAKSGEV GRIGHARIAKSASDIK FPLISKOSGGCAKVQULKPLMGLISKEVPLAGELVGAQMLFSFNSL FRANCE FRANCESTANFIKHEDKANTIFYATLFAWFATAFAWFAWHIAKSGERGE GRIGHARIAKSASDIK FPLISKOSGGCAKVQULKPLMGLISKEVPLAGELVGAQMLFSFNSL FRANCESTANFIKHEN FRANCESTANFIKHENDEN FRANCESTANFIKHEN FRANCESTANFIKHEN FRANCESTANFIKHENDEN FRANCESTANFIKHEN FRANCESTANFIKHEN FRANCESTANFIKHEN FRANCESTANFIKHENDERSTANFIKHEN FRANCESTANFIKHEN FRANCESTANFIKHEN FRANCESTANFIKHENDERSTANFIKHEN FRANCESTANFIKHEN FRANCESTANFIKHENDERSTANFIKHEN FRANCESTANFIKHEN FRANCESTANFIKHEN FRANCESTANFIKHEN FRANCESTANFIKHENDERSTANFIKHEN FRANCESTANFIKHEN FRANCESTANFIKHEN FRANCESTANFIKHENDERSTANFIKHENDERSTANFIKHEN FRANCESTANFIKHEN FRA	1	to first	amino acid	P=Proline, O=Glutamine, R=Arginine
### amino acid sequence codon, /possible nucleotide deletion, /possible nucleotide deletion, /possible nucleotide deletion, /possible nucleotide insertion) #### Approximate to the codon, /possible nucleotide insertion ###################################		amino acid	residue of	S=Serine, T=Threonine, V=Valine
Sequence (Codon, /-possible nucleotide deletion, /-possible nucleotide dinsertion) RAPPWTEDGDWTEFGAFFGTTEDFSGGGKANRAHEIRORFFFYE HKNYWSAGNCKONSCVLOLSKCHIJGKALFJAFPCDAGFFFSGD INSALASLSMARNTSFTDETTVERALCAFDNIANSIESGGGKKM YINSVCRHTVSKCNSFYLOGGGINLLISHTVILAFPCDAGFFFSGD INSALASLSMARNTSFTDETTVERALCAFDNIANSIESGGGKKM YINSVCRHTVSKCNSFYLOGGGINLLISHTVILAFPCDAGFFFSGD FIRMORRELLEFTAP FRINGNRELLEFTAP 6852 1 407 RTRGBETYANFIKHNOGKNIFYAARTPATUFAVWFAMYITSUTA GFIGLMSIAVYCHWGALDIHCTWAYWXTSGFFREIGTVIDQ IABTLWEOVLKPLGNUNLWERNIEGSVTNSIKAGLTDQVSHHARL KTD 6853 3 469 GDSCAVCIELVKPLDIVEILTCMHIPKKTVDPMLEHRTCHM KUDLASLIEVDVEGGSVSLOVPVSNEINSASKHEDNRSET ASSCYASVQGTYEPPLBEHVQSTNSSIAGLUNDENHAVDUPH VDMPTTEEDEFMQETAVREIK SASSCYASVQGTYEPPLBEHVQSTNSSIAGLUNDENHAVDUPH VDMPTTEEDEFMQETAVREIKS FESYIGTFPGGELCVCAAIONLODSSASYFLMRKLVYEBFTOM PVNRTLRMMTYSHHIVQOLDKRKILDVKRKULDVEGTCHTKKPC ILCVEGFKEHCEEPWHITRYPMKHISCKHARSVETEGNGEDLR LFHSFEELLEABGFOGGRANDVANILAGUTEFLVKKKSEHVFOI LFGISKSSDS 1913 1148 GRVGGRVGRIGSPLSGARMEVIASTDTIKTEFULLFTDOTDDLAK EEPTSLFORDSETKGESGLVLEGDKEIHQIFFDLDKKALMSRF YIPRGGIGNAAMWAVALDALMREGIVCRDINFNNILLADRGHI OLITYFSRMSEVEDSCDSDATERMYCAPFGVGATTEETACDWMSL GAVLFFELLTGKTLVSCHAFGINHTHTUNDEWEBERRSLIQOL LQVINFLERGKTVLVSCHAFGINHTHTUNDEWEBERRSLIQOL LQVINFLERGKVVSCHARGHVERTVSCHAFGINHTHTUNDEWEBERRSLIQOL LQVINFLERGKVVSCHARGHVERTVSCHAFGINHTHTUNDEWEBERRSLIQOL LQVINFLERGKVVSCHARGHVERTVSCHAFGINHTHTUNDEWEBERRSLIQOL LQVINFLERGKVVSCHARGHVERTVSCHAFGINHTHTUNDEWEBERRSLIQOL LQVINFLERGKVVSCHARGHVERTVSCHAFGINHTHTUNDEWEBERRSLIQOL LQVINFLERGKVVSCHARGHVERTVSCHAFGINHTHTUNDEWEBERRSLIGBLESKALWR KKFKIGGSWMTWINNINFQELIQDEFEDSGGSKTFSAKDYMARTP HWALFGASBERGFPDATTHGRNSKAISGC 6857 1 617 KGPEATAWVCVCSHBNCRQMHKFSHASAQTWCGSPTASADNI KLAMAMGOKHTLASATGARGHVARDLOFGIRFLDSGGIRFLGSLALDSGIRTSSVFASPA LRCVOTAALILEELLEKKIKKRPRCGSSGARSPTASADNI KLAMAMGOKHTLASATGARGHVARHUNGSGSSARSPTASADNI KLAMAMGOKHTLASATGARGHVARHUNGSGRAAFFYRMWITS SAGSWANGSSPVSPDVVDLRTINGSLLDSGIRTSSVFASPA LRCVOTAALILEELLIGERKSKKALGKGRAFTFANGRAAFFYRMWITS SAGSWANGSSPVSPDVVDLRTINGSLLDSGIRTSSVFASPAN VARYTHASAUVERVSGRAFTS		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Ston
Nepossible nucleotide insertion		amino acid	sequence	Codon, /=possible nucleotide deletion
MARPWTEDDMTERGAFGGTEDRESGGGKANRAHETIGDREFFYE HINTWISAGNCKUNSCVLLDSKCLFTGGKLIFTGGKLFTGGFTFYE HINTWISAGNCKUNSCVLLDSKCLFTGGKLFTGGKLFTGGKLFTGGKLFTGGKLFTGGKLFTGGKLFTGGKLFTGGKLFTGGKLFTGGKLFTGGKTFTGGKTGFTGGGGTKM YINSVCRETVSKCCNSFLGGGGKINLLISMVLAGSGLKK FPLISBGSGCAKVQVLKPLMGLSERPVLAGELVGAQMLFSFMSL FPLISBGSGCAKVQVLKPLMGLSERPVLAGELVGAQMLFSFMSL FPLISBGSGCAKVQVLKPLMGLSERPVLAGELVGAQMLFSFMSL FPLISBGSGCAKVQVLKPLMGLSERPVLAGELVGAQMLFSFMSL FPLISBGSGCAKVQVLKPLMGLSERPVLAGELVGAQMLFSFMSL FPLISBGSGCAKVQVLKPLMGLSERPVLAGELVGAQMLFSFMSL FPLISBGSGCAKVQVLKPLMGLSERPVLAGELVGAQMLFSFMSL FPLISBGSGCAKVQVLKPLMGLSERPVLAGELVGAQMLFSFMSL FPLISBGSGCAKVQVLKPLMGLSERVAGAMAYTISGLT GFIGLANSIAVLCALVAGAULTACKTAGATAGATAGATAGATAGATAGATAGATAGATAGATAG		sequence .	ļ	\=possible nucleotide insertion)
HKNYWSAQNCKNGSCVLDLSKCLPJQGKLFAPERDAGPFFSQD INSHLASLSKANRTNSTPTPTVTREALCAPINASTESGGGIKM YINSUCRETVSRCCNSFLQQAGIALLISMTVINMILASSASDLK FPLISBGSCARQUVLKPMGLSKEVPLAINASSASDLK FPLISBGSCARQUVLKPMGLSKEVPLAINASSASDLK FPLISBGSCARQUVLKPMGLSKEVPLAINASSASDLK FIRMGREILLETPAP 6852 1 407 RTRGEETYANPIKHNDOKNIFYAARTPATLFAVMFAMYITSGLT GFIGLASIAVLCNLVMGLALIFLCTWAYVKYSGEPREIGTVIDG IAFTLMEGVLKPLAUMMELALIFLCTWAYVKYSGEPREIGTVIDG IAFTLMEGVLKPLAUMMELALIFLCTWAYVKYSGEPREIGTVIDG KTD GPIGLASIAVLCNLVMGLALIFLCTWAYVKYSGEPREIGTVIDG IAFTLMEGVLKPLAUMMELENGTONNINSHAPART KTD GPIGLASIAVLCNLVMGLALIFLCTWAYVKYSGEPREIGTVIDG KCDILKALGIEVDUPGOSVSLQVUVSNEIFRSASSHEEDINSET ASSCYASVQGYTEPPLEBEVUVSTESGLOVENGTHEANSVAVDVIPH VDNPTFEEDETPNCETAVREIKS 6854 1148 585 HESYTGTFPGFGLCVCARJONGSASYFLARSHVYEFSTQAK PVKNTFLRRWIYSHHYQODLRKKILDVGKELDUTGFCMTGKOF ILVEGFKEHCERWHITISYPDMKHISGCHEANSVAVDVIPH VDNPTFEEDETPNLOFTGAVLGUNGSASYFLARSHVYEFSTQAK PVKNTFLRRWIYSHHYQODLRKKILDVGKELDUTGFCMTGKOF ILVEGFKEHCERWHITISYPDMKHISGCHEANSVADDLALARF PVKNTFLRRWIYSHHYQODLRKKILDVGKELDVFTQTDLAK LAFGESESDS 6855 1913 1148 GRVGGRVGGFIGSPLSGANSYIASTDTLKTESVLLFTPQTDLAK LAFGESESDS GRVGGRVGGFIGSPLSGANSYIASTDTLKTESVLLFTPQTDLAK LAFGESESDS GRVGGRVGGFIGSPLSGANSYIASTDTLKTESVLLFTPQTDLAK LAFGESESDS GRVGGRVGGFIGSPLSGANSYIASTDTLKTESVLLFTPQTDLAK CHYFICKSCAS GRVGGRVGGFIGSPLSGANSYIASTDTLKTESVLLFTPQTDLAK LAFGESESDS GRVGGRVGGFIGSPLSGANSYIASTDTLKTESVLLFTPQTDLAK LAFGESESDS GRVGGRVGGFIGSPLSGANSYIASTDTLKTESVLLFTPQTDLAK GRVGGRVGGFIGSPLSGANSYIASTDTLKTESVLLFTPQTDTLAK GRVGGRVGGFIGSPLSGANSYIASTDTLKTESVLLFTPQTDTLAK GRVGGRVGGFIGSPLSGANSYIASTDTLKTESVLLFTPQTDTLAK GRVGGRVGGFIGSPLSGANSYIASTDTLKTESVLLFTPQTDTLAK LALALAR GRVGGRVGGFIGSPLSGANSYIASTDTLKTESVLLFTPQTDTLAK LALALAR GRVGGRVGGRVGGFIGSPLSGANSYAGNUNGANTAGRCGSPTPASAPNH KLMANDGGRTLPSATTDAKEGCLAGFTWGGTASKANVANTAT HKALPTLAGASCANGTAGASTATAGACTAGASTPASAPNH KLMANDGGRTLPSATTDAKEGCLAGAGISRLAGLIGGENAGAGNUNGANTAGAT GRVGGRVGGRVGGRVGGGRAGAGNUNGANGAANTAGAGAAYSPAGAAYSPAGAATASTPAM GRGGGRVGGRVGGRVGGGRAGAGAATASTAGANAA GRVGFVAGGAATATAGAGAAATAGAA GRCGGRVGGAATATAGAGAAATAGAAATAGAAATAGAAATAGAAATAGA				MARPWTEDGDWTEPGAPGGTEDRPSGGGKANRAHPIKORPFPYE
INSILASISMARNISPTPPPTVRRALICAPDHLINASIESGGIKM YINSVCRETYSCKOS FLOQOSIALLISTUMMLAKSASIDLK FPLISBGSCAKUQULKPILMGLSKEVILAGELVGAQMLFSFMSL FPLISBGSCAKUQULKPILMGLSKEVILAGELVGAQMLFSFMSL FPLISBGSCAKUQULKPILMGLSKEVILAGELVGAQMLFSFMSL FPLISBGSCAKUQULKPILMGLSKEVILAGELVGAQMLFSFMSL GREETYANFIKKINDGKRIFYAARTPATLFAVMFAMYITSGLT KTD GPIGLMSIAVLCNLVMGLALFICTMAYTGSFMBIGTVIDO LAETLMEQOVLRPLGANLFICTMAYTSKAGLTDQVSCHIRATUM KTD GBSCAVCIELYKPADLUFILTCMITFFKTCVDPBLLEHRTCDMC KTD LAETLMEQOVLRPLGADLWGTTMSCAGPHBIGTVIDO LAETLMEQOVLRPLGADLWGTTMSCAGPHBIGTVIDO LAETLMEQOVLRPLGADLWGTTMSCAGPHBIGTVIDO LAETLMEQOVLRPLGADLWGTMSCAGPHBIGTVIDO LAETLMEQOVLRPLGADLWGTMSCAGPHBIGTVIDO LAETLMEQOVLRPLGADLWGTMSCAGPHBIGTVIDO LAETLMEQOVLRPLGAGAGAGULFTCMITFFKTCMCD LAETLMEQOVLRPLGAGAGAGULFTCMITFFKTCMCD ASSCAVASVQCTYEPPLEBUVQCTMSCAGPHBIGTVIDO LAETLMEQOVLRPLGAGAGAGULFTCMITFFKTCMCD LAETLMEQOVLRPLGAGAGAGAGULFTCMITFFKTCMCD LAETLMEQOVLRPLGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	1	1	1	HKNTWSAQNCKNGSCVLDLSKCLFIQGKLLFAEPKDAGFPFSOD
### STINUTURE TYPE AND THE PROPERTY OF THE PRO				INSHLASLSMARNTSPTPDPTVREALCAPDNLNASIESOGOIKM
6852 1 407 RTRGEREYANFIKHDGKNIFYAARTPATLFAVMFAMYIISGLT GFIGLMSIAVLCNLVMGLALIFLCTWAYVXYSGEFREIGTVIDG LAFILMSOVIRS LIKAGLTDOVSHARL KTD 6953 3 469 GDSCAVCIELYKPNDLVEILTCMHTENTCVDPRLLEHRTCDMC KCDLLKALGIEUTVEDGGSVELOUPVSNEIPNSASSHEEDNRSET ASSGYASVGOTTEPPLEBHVOSTNESLQLVMHEANSVAVDVIPH VDNPTFEEDETPNOETAVREIKS 6854 1148 585 HESYIGTFDFGELCVCAAIQMICDNSASYFLERKLVYEPSTOAK FORTH TO THE STATE OF THE STATE O				YINEVCRETVSRCCNSFLQQAGLNLLISMTVINNMLAKSASDLK
6852 1 407 PRRGEETYANPY KINDOKNI PAARTPATLEAUWFANY I ISGLE OF IGLANI JAVLCAL WALALI PLCTWAY VY SGEPREIGT TVO IAET LINEQVLKPLGDNIMBENI RGS VYTAS I KAGLITQUSHIARL KTD GDSCAVCIEL YKPNDLVRILTCHNI FIKTCVDFWLLEHRTCPMC KCDILKALGI EUVDEDGSVSLQVPVSNSI INSASSHEEDINSSET ASSGVARVGOTTEPPLEBHVQSTNSSLIGLVNHEANSVAUD I PH VDNPTTEEDETFNOETAAVREI KS 6854 1148 585 HESYIGTFPPGELCVAALQWLGDWSASY FIANKLIVYEPSTOAK PVKNTFLRRWI YSHHI YQODLKKKI LDVGKRLDVTGFCMTGKPG I CLVEGFKEHCEEFWHTH I KYPNWKI SKHEASVET GENGEDLE LFHSFEELLLEAHGDYGLRNDKKKLIDVGKRLDVTGFCMTGKPG I CLVEGFKEHCEEFWHTH I KYPNWKI SKHEASVET GENGEDLE LFHSFEELLLEAHGDYGLRNDKKKLIDVGKRLDVTGFCMTGKPG I CLVEGFKEHCEEFWHTH I KYPNWKI SKHEASVET GENGEDLE LFHSFEELLLEAHGDYGLRNDKKKLEADSKET GENGEDLE LFHSFEELLLEAHGDYGLRNDKKKLEADSKET VYFPGCI QRWAREWVALDALHREGI VCRCIMPINI LINDRGHT OLLTYFRENSE VEDECDSDAI ERMIVACAPEVGAL TETELACUWWSI. CLTYFRENSE VEDECDSDAI ERMIVACAPEVGAL TETELACUWWSI. CANUFELLIGHT SKEELLI		l		FPLISEGSGCAKVQVLKPLMGLSEKPVLAGELVGAQMLFSFMSL
GPIGLNSIAVLENLYMGLALIFICTWATEVAKYSGERELIGTVIDO IABTLMEQVLRPLGDNIMEENIRGSVTNSIKAGLITOVSHHARL KTD 6853 3 469 GDSCAVCIELYKPHDLVRILTCHIFFHKTCUPPHLLEHRTCHK KTD CKDILKALGIEVPUDGSVSLQVPVSNSIKNSASSHEEDNRSET ASSGYASVQGTYEPPLEHVQSTNESLQLVNHEANSVAVDVIPH VDNFTFEEDEFTNQETAVREIKS 6854 1148 585 HESYIGTFDFGELCVCAAIGMIGDNSASYFINRKLVYEPSTOAK PVKNTPLRAMIVSHHIVODLRKKILDVGKRLDVTGFCMTGKP PVKNTPLRAMIVSHHIVODLRKKILDVGKRLDVTGFCMTGKP IICVEGFKEHCEEFWHTIRYPMWHIISCKRARESVETEGNGEDLR LFHSFEELLLEARGDYGLRNDVHNNLGGFLEFLKKHKSEHFFQI IICVEGFKEHCEEFWHTIRYPMWHIISCKRARESVETEGNGEDLR LFHSFEELLLEARGDYGLRNDVHNNLGGFLEFLKKHKSEHFFQI IICVEGFKEHCEEFWHTIRYPMWHIISCKRARESVETEGNGEDLR LFHSFEELLLEARGDYGLRNDVHNNLGGFLEFLKKHKSEHFFQI IICVEGFKEHCEEFWHTIRYPMWHIISCKRARESVETEGNGEDLR LFHSFEELLLEARGDYGLRNDVHNNLGGFLEFLKHKKSEHFFQI IICVEGFKEHCEFWHTIRYPMWHIISCKRARESVETEGNGEDLR LFHSFEELLLEARGDYGLRNDVHNNLGGFLEFLAKHKKEEHFGDI IICVEGFKEHCEFWHTIRYPMWHIISCKRARESVETEGNGEDLR LFHSFEELLLEARGDYGLRNDVHNNLGGFLEFLAKHKKEEHFGDLAKH CHTFSFRWEVEDSCSDADITEMTCAFEVGAITESTEACHWEL GRUMPHLERGAVGAVGDUKSHPFTTVAMPHENDITURGHTIL GRUMPHLERGAVGAVGDUKSHPFTTVAMPHENDITURGWHSKALAVAQQA SISLTMAHUVEWHEEVVQPVRELUDLIPEYEIACEHHEHSKCLLIAH RKFKIGGEWMTWINNTRFQELIOFFDRGGSKTFSAKDYWARTF DLQQRISSEDGTNMHLQLVRQBMAVCPEQLSFFLDSKQTLKFT KKFKIGGEWTWINNTRFQELIOFFTVYTFFWERBYRKHILGSPLCKAF RHVKVDTLSQFEALSRILVPAAWCTVGRD 6857 1 617 KGPEATAMVCVSHENGRONHKFSHSAAQTWGESFFTASANYWARTF DLQQRISSEDGTNMHLQLVRQBMAVCPEQLSFFLDSKQTLKFT TGYRNCFHITAVRLSDGFFTYTYFFWERBKKRILGSFTASANY LKAMMEGGKTIPSATEDARECLEARJSRILGELIGERLESKALMF DLQQRISSEDGTNMHLQLVRQBMAVCPEQLSFFLOKAGAT KHAMPHTATAVARUSGF TFYTTYFFWERMKRINGLSPLCKAF RHVKVDTLSQFEALSRILVPAAWCTVGRD 6858 2 669 RSGRIKDFENDPLSSGGFTSGTATGADALDSGIFTSSVFASBA LRCVOTAKLILEELKLEKKIK RVEPGIFFWTKMEAGKTTPTIM KLEELKEAMFNIDTDTVBAFFDLARDVARVYFKRGIEN SAAWVASSFFYNDPVUNKFUNFNAKGGFTFYTTTHRAKRINGUNGATHVANV VARSSLHSVSSFFFREDLEKKSVTHSSRQCATHVSKILGT VSHGVALSQKGRWIALITTKENNGRNSMETVLFTPSKARKPUN ANASSLHSVSSFFREDLEEKKSVTHSSRCHCATHVSKILGT VSHGVALSQKGRWIALITTRENNGRNSMETVLFTPSKARKPUN NAPSHHSVSSSFFREDLEEKKSVTHSSRCHCATHVSKILGT VSHGVALSQKGRWIA	COFO			
ASTUMENOVLEPIGENIMEERINGSVTMS IKAGLTDOVSHHARL	6852	1	407	RTRGEETYANFIKHNDGKNIFYAARTPATLFAVMFAMYIISGLT
6853 3 469 GDSCAVCIELYKPNDLVRILICNNIFPKTCVDPNLLEHRTCPMC KCDILKALGIEVDVEDGSVSLQVDVSNEIPNSASHEDNNSET ASSGYASVQGTVEPPLEHRVGSTREQLVNHHARNSVAVDVIPH VDNPTFEEDETPNQETAVREIKS 6854 1148 585 HESYIGTFDPGELCVCAAIQMLQDNSASYFLNRKLVVEPSTQAK PVRNTPIRMMISHIVIQQLRKKILDVCKRLDVTGFCMTGKPG IICVEGFKERLCEERWHITIRYDNWKHISCKHARSVETEGNGEDLR LFHSFEELLLEARIGYGLGKNINHALGQFIEFLKKKKEHVFQI LFGIESKSSDS 6855 1913 1148 GRVGGRVGRICSPLSGANEYTASTDTIKTEEVLLEFTQTDDLAK EEPTSLEGRDSETKGESGLVLEGDKEIHQIFFDLDKKLALASRF YIPSGCIGRNAAEMVALDALHREG GRVGGRVGRICSPLSGANEYTASTDTIKTEEVLLEFTQTDDLAK EEPTSLEGRDSETKGESGLVLEGDKEIHQIFFDLDKKLALASRF YIPSGCIGRNAAEMVALDALHREG GRVGGRVGRICSPLSGANEYTASTDTIKTEEVLLEFTQTDDLAK EEPTSLEGRDSETKGESGLVLEGDKEIHQIFFDLDKKLALASRF YIPSGCIGRNAAEMVALDALHREG GRVGGRVGRICSPLSGANEYTASTDTIKTEEVLLEFTQTDDLAK EEPTSLEGRDSETKGESGLVLEGDKEIHQIFFDLDKKLALASRF YIPSGCIGRNAAEMVALDALHREGVERDEHDENDFIEVKGVTYCGESSA SSLTMAHUSWHEEVVQEVRELUVLIFEVETBLACHEHGNCLLIAH RKFKIGGEWATHINTNRFQELICGSSGGSKTSAACHVACQOR TVVRLUTLVKAMWVDELQAYAQULEDSGGSKTSAACHVACQOR HKALFGASERGPDRYDTRHCRNNKSKAISGC KGPEATAMVCVCSHDHORGNNITKSBAGGTVGGSPTPASAPHH KLMAMRCGKTLDSATEDAKEEGLEAQISKLAELIGRLESKALMF DLQQRLSDEGTNMHLQLVRQEMAVCDEQLESFLDSIRQYLRGT TGVRNCFHITAVRLSDGFTFVITWETEEBAKKHLOSPLCKAF RHVKVDTLSQPFALSTLIDPAACTVGRB 6858 2 669 RSGG IKDFENDPLSSGGFTFOSTAGDALLDSGTRISSVFASFA LRCVQTAKLILEELKLEKKKKRVBGGIFENTKWEAGKTTPTLM SLEELKEANFNITDTDYRPAFPLSAAHDASVGCMBCTASMVQ IVMTCPQDTGVTLVSRIGSTLDSCTRPLLGLPPBECCDFAQLUR KYSLGMCFCEENKEEGKWELVNPPVKTLTIGANAAFNRNNMIS GN 6859 1 1 1150 GETMFKKAKKKPRKSDSGGYNLSDTIGSFSTGLLKSG KTINSVESLPELLITSDSEGSYAGVGSFROLGSPDTTGFISDKIE AKVKPYVNGTSPVSRGDLKFWEKSPLLSGADPKKVSHGLICKT VSRGVKLSQKGRKMIALTTKENSGAMSMETVLFTPSKAPKPVD AAASSLANGSSFSVSPDFLLEEKKSTLALIQIEBSGVFAGNEHGKT VSRGVKLSQKGRKMIALTTKENSGAMSMETVLFTPSKAPKPVD AAASSLANGSSFSVSPDLLEEKKSTLALIQIEBSGRVFSHLICKT VSRGVKLSQKGRKMIALTTKENSGAMSMETVLFTPSKAPKHCKT VSRGVKLSQKGRKMIATTKENSGAMSMETVLFTPSKAPKHCHT VSRGVKLSQKGRKGIFFFKVATNIMEAMLFOULTHPFYSEEQKKQLATSPBCQP MSSPVLDGQQIMGTRPAQEMSKAMINMAMCGCHYMM				GFIGLNSIAVLCNLVMGLALIFLCTWAYVKYSGEFREIGTVIDQ
6853 3 469 GDSCAVCIELYKENDLVRLITCHNI FHRTCVDFWLLEHRTCPMC KCDILKALGIEVVKENDLVRLITCHNI FHRTCVDFWLLEHRTCPMC KCDILKALGIEVVKENDSVAQVVVENEIPRASASHEDNINSET ASSCYASVGGTVEPPLEEHVOSTINSASSHEDNINSET ASSCYASVGGTVEPPLEEHVOSTINSASSHEDNINSET ASSCYASVGGTVEPPLEEHVOSTINSASSHEDNINSET ASSCYASVGGTVEPPLEEHVOSTINSSIQUVNIEANSVAVDVIPI VONPTFEEDETINGETAVREIKS BESTIGTPPDELLCVAAIOMLONSASYFLNRKLVYEPSTOAK PVKNTFLRMWITSHHIYQQULKKILDVSKRLDVSGFCMTCKPG IICVEGFKEHCESFFWHITRYPNMKHISCKHABSVSTEENGEDLR LFHSFEELLLEAHGDYGLRNDYHMNIGGFLEFLKKHKSEHVPGI LFGIESKSDS 1913 1148 GRVGGRVGRICSPLSGANEYIASTDTLKTEEVLLFTDQTDLAK EEPTSLFQRDSETKGESGLVLEGDKEIHGIFFDDLKKLALASRF YIPSGCIGNAAARMVALDALHREICHCENBEIHGIFFDDLKKLALASRF YIPSGCIGNAAARMVALDALHREICHCENBEIHGIFFDDLKKLALASRF YIPSGCIGNAAARMVALDALHREICHCENBEIHGIFFDDLKALAVKOQR TVIRTUSCHSPASTAGAVACVEDIKSHPFFTPUDWAALMR UTGLYVSVDASTYGBLKKIDFEPPFOOPPLDSLKALAVKXQQR TVVRLTLVKAMWVDBLQAXAQLVSLGNPDFIEVKGVTYCGESSA SSLTMAHVPWHEEVVQFTVELVDLIPETFLAEHENNCLLIAH RKFKIGGEWMTMINNRFQELIGEYBDGGGKTFSAKDYMACRP HWALFGASSRGDPROTRHCRKNKSKAISGC 6857 1 617 KGPEATAWVCVSEIBPHCRONHIFFSHOOPFLDSLKALAVKXQQR TVVRLTLVKAWWDBLQAXAQLVSELGHDGIEVKGVTYCGESSA SSLTMAHVPWHEEVVQFTVELVDLIPETFLAEHENNCLLIAH KLMAMSCGKTLPSATEDAKEGLEAQISSLABLIGGRESKALMP DLQQRISCHDTHNHILQLUKQEMAVCPECLSEFLDSLRQVLRGT TGVRNCFHTTAVRLSDGFTFVIYEFBETEAWKHLQSPLCKAF RHVKVDTLSQPBALSRALIVDAAACTUSAQTGSFTPASAPNH KLMAMSCGKTLPSATEDAKEGLEAQISSLABLIGGLESKALMP DLQQRISCHLIADAVCPECLSEFLDSLRQVLRGTT TGVRNCFHTTAVRLSDGFTFVIYEFBETEAWKHLQSPLCKAF RHVKVDTLSQPBALSRALIVDAAACTVXTLTIGANAAFNWRNMIS GN 6858 2 669 RSRGIKDFENDPPLSSCGIFGSRIGDALLDSGIRISSVFASPA LRCVOTAKLILEELKLEKKIKIRVBGIFFENTKWEAGKTTPTUM SSEENKERANFNITOTRAPAFPLSALFVXTLTIGANAAFNWRNMIS GN 6859 11 1150 GETMFKKAKKKRPKRSDSSGGYNLSDLIOSPSTGLLKSG KTMSVESLBELLTSDSGSYAGVGSPRDLQSPDTTGFHISDKIE AKVKPYVNGTSPVYSREDLKYTLTGANAAAFNWRNMIS GN GETMFKKAKTKAKKKPRKRSDSSGGYNLSDLIOSPSTGLLKSG VANVESTBELGVSKASTPDFLLEEKKYLLTDFDSKAPKPON AMASSLHALTTKENSGMMSMETVLTFTPSKAPKPON AMASSLHALTTKENSGMMSMETVLTFTPSKAPKPON VAPVTTASIVEELOGAAALTSTKENSGMTMMWHGG GN AMASSLHALDVSKASTPDFLLEEKKYLLALIGIEERGKCATPS		!		IAETLWEQVLKPLGDNLMEENIRQSVTNSIKAGLTDQVSHHARL
RODICKALGIEVVERGESVELQVPSMEITPSASPHEDINSET ASSCYASVGOTTEPPLEEHVOSTRESLQLVMIEANSVAVDVIPH VONPTTFEDETPNGETAVREIKS 6854 1148 585 HESYIGTFDFGELCVCAATOWLODNSASYELRKKUVYEPSTOAK PVNTPTFEDETPNGELLVCAATOWLODNSASYELRKKUVYEPSTOAK PVNTPTFEDETPNGELCVCAATOWLODNSASYELRKKUVYEPSTOAK PVNTPTLRMMIYSHHIYOODLRKALDVGRLDVTGFCMTGKPG IICVEGFKERUCEFWHTIRYPNWKHISCKHAESVETERNGEDLR LFHSTEELLLEAHGDYGLRNDYHMNIGCFLEFLKKHKSEHVPGI LFGIESKSSDS 6855 1913 1148 GRVGGRVGRICSFLESGANEYIASTDTLKTEEVLLFTDGTDDLAK EEPTSLFQCRSETKGESGLVLEEGKEIHGIFFDLDKKLALASRF YIPBGCIORNAAEMVVALDALHREGIVCHDIFTDGTDDLAK EEPTSLFQCRSETKGESGLVLEEGKEIHGIFFDLDKKLALASRF YIPBGCIORNAAEMVVALDALHREGIVCHDIFTDTDLAK GAVLFELLTOKKTLVECHPAGINTHTTLNMPEWISEEARSLIQQL LOPPPLERLGAGVACUEDIXSHPFFTPUDWALLAR GAVLFELLTOKKTLVECHPAGINTHTTLNMPEWISEEARSLIQQL LOPPPLERLGAGVACUEDIXSHPFFTPUDWALLAR RKFRIGGEWHINTNRROELIGEYEDSGGSKTFSAKDYMARTP HWALFGASERGEDPWGVFRELIVOLPEYELGCEHEHOSILLIAH RKFRIGGEWHINTNRROELIGEYEDSGGSKTFSAKDYMARTP HWALFGASERGEDPWGVFRELIVOLPEYELGCEHEHOSILLIAH RKFRIGGEWHINTNRROELIGEYEDSGGSKTFSAKDYMARTP HWALFGASERGEDPWGVFRELIVOLPEYELGCEHEHOSILLIAH RKFRIGGEWHINTNRROWCPEGLEFIDGLERGYLRGT TGVRNCFHTTAVRLSDGFTFVIYEFWETEEAWKHLGSPLCKAF RKVKUTTLSQPEALSRALDGVFROEDGINGLEGGSTPSASPANH KLMAMEGGKTLPSATEDAKEEGLAGISILABLIGRLESKALWF DLQQRLSDEDGTNMHLQLVRQEMACVPEGLEFIDGLERGYLRGT TGVRNCFHTTAVRLSDGFTFVIYEFWETEEAWKHLGSPLCKAF RKVKUTTLSQPEALSRALDGVFROEDGINGSTRISSVFASPA LRCVTAKLIBELKLEKKIKIRVBGTFDSTRIDGTLING KTMSVESLFELLKEKKIKIRVBGSTGSTRIDGRPRCGDFAQLUR KYPSLGMCCFCEENKEBCKWELVMPPVKTLTHGANAAFNWRMIS GN GETMFKKAKTKAKKKPRKRSDSSGGYNLSDIIGSPSTGLLKSG KTMSVESLFELLITSDSGGSYAGGSPRLLOSPPTTGFHSDLYE AKVEYVVNCTSPVVSREDLKPMEKSPILKISADPPTTGFHSDLYE SAASWAGSPSPVSPPVVDLRTIMEIEESRCKCCATPKSHLGKT VSHGVKLSGKGRRHIATTYKENSGMNSMETVLFTPSKAPKPVN AAASSLABSVSKKSTGFDLLEEKKSTASGADVKKVSFKGIEN SQAPKLVRCSTHGTFGGEGAALTSRSGDLYKVKVSFKGIEN SQAPKLVRCSTHGTFGGEAALTATTKENSGADVKKVSFKGIEN SQAPKLVRCSTHGTFGGEAALTATTKENSGADVKKVSFKGIEN SQAPKLVRCSTHGTFGGEAALTATTKENSGADVKKVSFKGIEN SQAPKLVRCSTHGTFGGEAALTATHTHPYPSEEOKKQLAD DTGLTILLQVINNWINARRIUTGDHATHPYPSEEOKKQLAD DTGLTILLQVINNW	6953	ļ		
ASSYASYOCTYPPPLEBITYORELQLUNHEANSVAVDVIPH VDNPTPEBDETPROETAVREILS 6854 1148 585 HESYIGTPDGETAVERIK PVKNTTPREMIXTPROETAVERIK PVKNTTPREMIXTPROETAVERIK PVKNTTPREMIXTPROETAVERIK PVKNTTPREMIXTPROETAVERIK PVKNTTPREMIXTSHITYOODLRKKILDVGRRIDVTGPCMTGKED II CVEGFKENCEEFWHTIRYPNWKHISCKHAESVETEGNGEDLR LFHSFEELLEARGDYGRRNDYHNNILGYLEFILKKHKSERVFOI LFGIESKSSDS 6855 1913 1148 GRVGGRYGRICSFLGSANEYIASTDTLKTEEVLLFTDOTDDLAK EEPPTSLORDSFTKGSEGULVELGDKEIHQIFEDLDKKIALASRR YIPEGCIORNAARMVVALDALHREGIVCRDLNFNNILLNDRGHI OLITYSRWSSVEDSCDSDAIERVACAPEVGAITEETEACDWSL GAVLFELLTCKTLVECHPAGINTHTTLNMPEWUSEEARSLIQOL LOPNPLERLGAGVAGVEDIKSHPFTDFVDQFLDSLKALAVKQOR TVYRLTLVKAMVUDELQAVAQLVSLGNPDFIFVKGVTYCGESSA SSLTMAHVPHEEVVQFVRELUPIPFETERGHSNCLLIAH RKFRIGGEWMTNINTNRFOELLOFYEDSGSKTFSAKDYMARTP HVALLFGASERGFDPKDTHRIGNRIKSATSGC 6857 1 617 KGPEATAMVCVCSHPNCRONHIKFSHSAAQTWCGSPTPASAPNH KLMAMRGQSKLIPSATEDAKERGLEAQISRALELIGRLEKSALMF DLQQRLSDEDGTIMHLQUVRQEMAVCPCQUSEFILDSLRQYLRGT TGVRNCFHTTAVKLSDGFTFV1YEFWETERBWKRHLQSPLCKAF RHVKVDTLSQPEALGRILVPAMCTVGRD 6858 2 669 RSGIKDFENDPPLSSCGIFGSRIAGDALLDSGIRISSVASSBA LRCVQTAKLILEELLEKKIK INFEGFFFFVWEGFFENTWEAGKTTPTLM SLEELKEAMFNIDTDYRPAFPLSALMPAESYQEYMDRCTASMVQ IVNTCPQDTGVILIVSHOSTLDSCTRFLLLSPREGGPAQLUR KIPSLGMCFCEBNKEGGKELVINPVKTLTHGAMAFMWRNINIS GN KTRSVESLPELLITSDSGGSYAGVGSPRDLGSPPTTGFHSDKIE AKVKPYVNOTSSPVSTREDLKEWRSPILKERGRATPKSHLGKT VSHGVKLSGKRKMIALITKENNSGKMSMTVLFTPSKARKEVN AAASSLISVSKSFRPDFLLEEKKSVTSHSSGDHVKKVSFKGIEN SASWVAGSPSPVSPPVVDLRTIMEIEERGRCGGATPKSHLGKT VSHGVKLSGKGRKMIALITKENNSGKMSMTVLFTPSKARKEVN VAPVTFASILVEELQOGAALIRSEKFLALIQLEPHAIQDLLVF YERGMPEEFVIVERTPGGPLAVPMMKHGC 6860 1889 1515 DKOKKROKKGIFPKVVATNIMRAMLFOHLTHPYPSEEQKKQLAO DGGLTILGVNNWFINARRITVOPMIDOSNRAVSGGAAYSPRQO PMGPVLDGQCHIGTRPAGPMSGMMMMGHOGWHYM MGSPVLDGQCHIGTRPAGPMSGMMMMGHOGWHYM MGSPVLDGQCHIGTRPAGPMSGMMMMGHOGWHYM	1 0033	1 -3	469	GDSCAVCIELYKPNDLVRILTCNHIFHKTCVDPWLLEHRTCPMC
6854 1148 585 HESYIGTPD/GECVCAA GWILODNSASYFINRKLVVEFSTOAK PVKNTPIRMMIYSHHIYQOLLRKK LLDVGKRLDVTGPCMTGKPG IICVEGFKEHCEBFWHTIRYPNWKILGDGLEKKKAESVETGGNGEDLR LFHSFEBLLLEARGDYGLRNDYHNNLGGFLEFLKKHKSEHVFQI LFHSFEBLLLEARGDYGLRNDYHNNLGGFLEFLKKHKSEHVFQI LFGIESKSSDS GRVGGRVGRICSPLSGANEYIASTDTLKTEEVLLFTDQTDDLAK EEPPSLFORDSFTKGESGLVLECDKEIHQIFEDLDKKLALASRF YIPBGCORMAABMVVADDALHGEUVCHDLNPNNILLNDRGHI QAVLFELLTGKTLVECHPAGINTHTILNMEHWSEEARSLIQQL LQPNPLERLGAGAGGEDIKKSHFFTPVDWAELDR GAVLFELLTGKTLVECHPAGINTHTTUMBEWVSEEARSLIQQL LQPNPLERLGAGAGGEDIKKSHFFTPVDWAELDR GAVLFELLTGKTLVECHPAGINTHTUMBEWVSEEARSLIQQL LQPNPLERLGAGAGGEDIKKSHFFTPVDWAELDR GAVLFELLTGKTLVECHPAGINTHTUMBEWVSEEARSLIQQL LQPNPLERLGAGAGGEDIKKSHFFTPVDWAELDR GAVLFELLTGKTLVECHPAGINTHTHTUMBEWVSEEARSLIQQL LQPNPLERLGAGAGGEDIKKSHFFTPVDWAELDR GAVLFELLTGKTLVECHPAGINTHTHTUMBEWVSEEARSLIQQL LQPNPLERLGAGAGGEDIKSHFFTPVDWAELDR GAVLFELLTGKTLVECHPAGINTHTHTUMBEWVSEEARSLIQQL GAVLFELLTGKTLVECHPAGINTHTHTUMBEWVSEEARSLIQQL GAVLFELLTGKTLVECHPAGINTHTHTUMBEWVSEEARSLIQQL GAVLFELLTGKTLVECHPAGINTHTHTUMBEWVSEEARSLIQQL GAVLFELLTGKTLVECHPAGINTHTHEWSTEEARCHVAGVTCGSSA SSLTMAHVPHEEVVQFVEELVDLIPPSVEACHEHSNCLLIAH RKFKIGGEWHTWINTRPQELIQEYDEAGGSKYTFSAKDYMARTP HWALFGASERGPPDKUTRHQKRNKSKAISGC 6857 1 617 KGFEATAMVCVCSHDNCRQNHIKESHSAADTWACTYGTD KKMPACTAGEBENGCAGTTGSALDAGA KKMPACTAGEBENGCAGTTGSALDAGATAGATAGATAGATAGATAGATAGATAGATAGATAGA	1	į		ACCULARALGIEVDVEDGSVSLQVPVSNEIFNSASSHEEDNRSET
1148	1	į		ASSGYASVQGTYEPPLEEHVQSTNESLQLVNHEANSVAVDVIPH
FUNKTFERMITYSHLTYQQDERKILDVGRREDVTGFCMTGKPG FVKNTFERMITYSHLTYQDDERKILDVGRREDVTGFCMTGKPG IICVGGFKEHCEERWHTIRYPNIKHILGKHAESVETTGNGEDLER LFHSFEELLLEBARDYGLINDYHNILGGFLEFLKKHKSEHVFQI LFGIESKSSDS GRVGGRVGRICSPLSGANEYIASTDTLKTEEVLLFTDQTDDLAK EEPTSLFQRDSETKGESGLVLEGDKEIHQIFEDLDKKLALASRF Y1PGGCLQRWAAEMVVALDALHREGIVCRDLWFNILLADRGHI GAVLFELLTGKTLVECHPAGINTHTTLIMPEWYSEEARSLIQQL LQPHPLERLCGAVAGVEDIKSHFFTPVDWAELMR 6856 1617 997 VTQLYVSVDASTKDSLKKLDRFLFKDFWQOFLDSLKALAVKQQR TVVRLTLVKAWMVDELQAVAQLVSLGNPDFIEVKGVTYCGESSA SSLTMAHVPWHEEVVQFVRELVDLIPFEYSDFWGGFLGLKALAVKQQR RKKFKIGGEWMTLINYNRFGELIQEYSDGGSKTFSAKDYMARTP HWALFGASEBGFDFKDTRIGRKNKSKALSGC 6857 1 617 KGPEATAMVCVCSHPNCRONHIKPSHSAAQTWGGSFTPASANH KLMAMEGKSTLPSATEDAKECLAQISKLABLIGRLEBSKALMF DLQQRLSDEGGTMHLQLVRQEMAVCPEQLSEFLDSLRQYLRGT TGVRNCFHITAVRLSDGFTFVIYEFWETEBAKKRHLQSFLCKAF RHVKVDTLSQPEALSRILVPAAWCTVGRD 6858 2 669 RSRGIKDFENDPPLSSCGIFGSRIAGDALDSGIRISSVFASPA LRCVQTAKLILEBLKLEKKIVREPGIFEWKWEAGKSTPJTLM SLEELKEANFNIDTDYRPAFPLSAMPARSYQCYMDRCTASMVQ UNTCPODTOVILIVSHGSTLDCTRPLLGLPPRECGPPAQLVR KIPSLGMCFCEENKEEGKWELVNPPVKTLTHGANAAFAWRRNIS GN 6859 1 1150 GETMFKKAKTKAKKKPRKSDSSGGYNLSDIIQSFSTGLKKSG KTINSVESLEELLTSDSEGSYAGVGSPRDLQSPDFTTGFHSDKIE AKVKYPVNGTSPVYSREDLIKEKSPILKISADQPIPSNRIDTT SSASWJAGSFSPVSPPVDLVRTIMSIEESRQKCGATPKSHLGKT VSHGVKLSQKQRKMIALTTKENNSGMNMETVLFFPSKAPKPVN AMASSLHSVSSKSFRDFILLEERKSVTSHSSGDHVKKVSFKGIEN SQAPKLVRCSTHGTFGPEGNHISDLPLIDSENPHLSSSVTAPSM VAPVYTASIVEELQCAPALIRSREKPDALIQIEHACQDLLVF YEAFGMPEEFVIVERTPCGPLAVPMMNKIGC 6860 1889 1515 DKOKKROKKGG FFRVAATNIMRAWLFQULLTHPYSEEQKKQLAQ DTGLTILQVNNWFINARRIUTQMTDGSNRAVSGGAAYSPRQQP MGSPVLDGQQHMGIRPAGGMGMGMMCMCQQWHYM MGSFVLDGQQHMGIRPAGFMSGMGMMCMCQQWHYM MGSFVLDGQQHMGIRPAGGMGMGMCMCMCQCHYM	6854	7148	505	
IICVEGFKEHCEEWHTIRYPNMKHISCKHAESVETEGNGEDLR LFHSFEELLLERHGDYGLRNDYHMILGOFLEFLKKHKSEHVFQ1 LFGIESKSSDS GRVGGRUGICSPLSGANEYIASTDTLKTEVLLFTDQTDDLAK EEPTSLPCRDSETKGESGLVLEGDKEIHQIFEDLDKKLALASKF YIPEGCIQRWAAEMVVALDALHREG IVCRILMPNNILLNDRGHI CLTYFSRWSEVEDSCDSDAIERMYCAPEVOAITSETEACDWWSL GAVLFELLTGKTLVECHPAGINTHTTLNMPEWVSEERRSLIQOL LQFNPLERLGGAVAGVEDIKSHEFFTPVOWAELMR CAVITYSINDSTKIDSLKKIDEPLFKOFWOQPLDSLKALAVKQOR TVYRLTLVKAWNVDELQAVAQLVSLGNPDFIEVKGYTYCGESSA SILTMAHVPHREEVVQFVELDLIFPSELACHEHSINCLLIAH RKFKIGGEWWTINYNRFQELIQEYEDGGSKTFSAKDYMARTP HWALFGASERGFDFKDTRHQRKNSKAKISGC GAVERLAND GESTAMMUCVELQSHPACGNNIKFSHSAAQTMCGSFTPASAPNH KLMAMEGGRILPSATEDAKEEGLEAQISKLAELIGRLESKALWF DLQQRLSBEDGTMHLQLVRGWAVCFEQLSEFLDSLRQYLRGT TGVRNCFHITAVRLSDGFTFVIYEFWETEEAWKRHLQSFLCKAF RRKKVDTLSQFEALSRILVPAAWCTVGRD GRONG			363	PUKNTEI BMWIYCHUI YOODI BKKII DIGWEI BWWIYE BANGO
LFHSFEILLEAHGYGLRNDYHMNLGQFLEFLKKHKSEHVFQI LFGIESKSSDS 1913 1148 GRVGGRVGRICSPLSGANEYIASTDTLKTEEVLLFTDQTDDLAK EEPTSLFQRDSETKGESGLVLEGDKEIHQIFEDLDKKLALASFF YIPPGCIQRWAAEMVVALDHIRGEIVCRDLNYHNILLADRGHI OLTYFSRWSEVEDSCDSDAIRRMYCAPEVGAITEETEACDWWSL GAVLFELLTGKTLVECHPAGINTHTTLNMPEWVSEARSLIQOL LQFNPLERLGAGVAGVEDIKSHPFFTPVDWAELMR 6856 1617 997 VTOLYVSVDASTKOSLKKIDREPFFTPVDWAELMR TVVRLTLVKANNVDELQAYAQLVSLGNPDFIEVKGYTYGGESSA SSLTMAHVPWHEEVVQFVRELVDLIPEYEIACEHEHSNCLLILAH RKFKIGGEWMTWINNTRFQELIGEYEDGGGSKTFSAKDYMARTP HWALFGASERGFDPKDITHGRKNKSKAISGC 6857 1 617 KGPEATAMVCVCSHBNCRONNIKPSHSAAQTWCGSPTPASAPNH KLMAMEGGKTLPSATEDAKEELEAQISRLAELIGRLESKALWF DLQQRLSDEDGTNMHLQLVRQEMAVCPSQLSEFLDSLRQYLRGT TGYRNCFHITAVRLSDGFTFVIYSFWETEEAWKRHLQSPLCKAF RHVKVDTLSQPEALSRILVPAMCTVGRD ARCHITAVRLSDGFTFVIYSFWETEEAWKRHLQSPLCKAF RHVKVDTLSQPEALSRILVPAMCTVGRD LGRCHAFFENSTER STENSTER S	i			TTCVFCFKFUCFFFWUFTDVDWWWTTCCKTDVTGFCMTGKPG
1913 1148 GRYGGRVGRI CSPLSGANEYTASTDTLKTEEVLLFTDQTDLAK EEPTSLFQRDSETKGESGLVLEGDKEIHQIFEDLDKKLALASRF YIPEGCIQRWAAEMWVALDALHREGIVCRDLNFNNILLNDRGHI OLTYFSRWSEVEDSCOBSIREMYCAPEVGATTEETEACDWSLL GAVLFELLTGKTLVECHPAGINTHTTLMMPEWVSEEARSLIQQL LOPMPLERLGAGVAGVEHDUMASLMR 6856 1617 997 VTQLYVSVDASTKDSLKKIDRPFKDFWQQFLDSLKALAVKQOR TVYRLTLVKAWNVDELQAYAQLVSLGNPDFIEVKGVTYCGESSA SSITMAHVPWHEEVVQFYRELVDLIPEVEIACEHERSNCLLIAH RKFRIGGEWWTWINNTROELIQBYEDSGGSKTFSAKDYMARTP HWALFGASERGFDPKDTTRKRNKSKALSGC 6857 1 617 KGPEATAMVCVCSHPNCRQNHIKBSHSAAQTWCGSPTPASAPNH KLMAMEGGKTLPSATEDAKEEGLEAQISRLAELIGRLESKALWF DLQQRLSDEDGTNMHLQLVRQEMAVCPBQLSEFIDSLKGYLRGT TGVRNCHITAVRLSDGFTFVIYEFWETEEAWKRHLQSPLCKAF RHVKVDTLSQPEALSRILVPAAWCTVGRD 6858 2 669 RSRGIKDFENDPPLSSCGIFQSRTAGDALLDSGTRISSVFASPA LRCVQTAKLILBELKLEKKIKIRVEPGIFEMTKHEAGKTTPTLM SLEELKEANNFIDTDYRAPACTVGRD 6859 1 1150 GETMFKKAKKKPKRSDSSGYNLSDIIQSPSSTGLLKSG KINSVESLEPELLTSDESGYAGVGSPRDLQSPDFTTGFHSDKIE AKVKPYVNGTSPVYSREDLKPWEKSPILKISAPQPIFSNRIDTT SSASWVAGSFSPVSPPVVDLRTIMEIESSRCKCGATPKSHLGKT VSHGVKLSGVGRMMIALTURNSGMNSMETVLFTPSKEAPKPVN AWASSLHSVSSKSFRDFLLEKKSVTHSSGDHVKKVSFKGIEN SQAPKIVRCSTHGTPGPGENHISDLPLDSPNPWLSSVTAPSM VAPVTFASIVEEELQCEAALIRSREKFLALIQIEEHAIQDLLVF YEAFGMPEEFVIVERTPCGFLAVPMNKHGC 6860 1889 1515 DKOKKRGKIGFFFKVATHRAWLFGHLTHPYPSEECKKQLAQ DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP MGSFVLDGQCHMGIRPAGPMSMCMDGCWHYM	1			LEHSEET.LLEAHCDVGLDNDVHMMI COELEEL WELWODING
6855 1913 1148 GRVGGRVGRICSPLSGANEYIASTDTLKTEEVLLFTDQTDDLAK EEPTSLFQRDSETKESGLVLEGGBEINGIFEDLKKLALASRF YIPEGCIQRWAAEMVALDALHREGIVCRDINPNILLIADRGHI OLTYFSRWSEVEDSCDSDAIREMYCAPEVGAITEETEACDWMSL GAVLFELLITGRTUECHEDGINTHTTLMMPEWYSEEARSLIQOL LQFNPLERLGAGVAGVEDIKSHPFFTPVDWAELMR 6856 1617 997 VTQLYVSVDASTKDSLKKIDREPFTPVDWAELMR TVYRLTLVKANNVDELQAYAQLVSIGNPDFIEVKGYTYGGESSA SSLTMAHVPWHEEVVQFYRELVDLIPEYEIACEHEHSNCLLIAH RKFKIGGEWMTWINYNRFQELIOPFIEVKGYTYGGESSA SSLTMAHVPWHEEVVQFYRELVDLIPEYEIACEHEHSNCLLIAH RKFKIGGEWTWINNRFQELIOPFIEVKGYTYGGESA SSLTMAHVPWHEEVVQFYRELVDLIPEYEIACEHEHSNCLLIAH RKFKIGGEWTWINNYNRFQELIOPFIEVKGYTYGGESA SSLTMAHVPWHEEVVQFYRELVDLIPEYEIACEHEHSNCLLIAH RKFKIGGEWTWINNRFQELIOPFIEVGSTDSGASKTFSAKDYMARTP HWALFGASERGFDEKDTRHQRKNNSKAISGC 6857 1 617 KGPEATAMVCVCSHPNCRONNIKPSHSAAQTWCGSPTPASADNH KLMAMEGGKTLPSATEDAKEGELEAQISRLAELIGRLESKALWF DLQQRLSDEDGTNMHLQLVRQEMAVCPEQLSEFIDSLRQYLRGT TGYRNCFHITAVRLSDGFTFVIYSFWETEEAWKRHLQSPLCKAF RHVKVDTLSGDFAFFVIYSFWETEEAWKRHLQSPLCKAF RHVKVDTLSGPEALSRILVPAMCTVGRD 6858 2 669 RSSGIKDFENDPPLSGCIFGSRIAGDALLDSGIRISSVFASPA LRCVQTAKLILEELKLEKIKIVPAMCTVGRD SEELKEANNNIDTDVRHAPFPLSALMPAESYQEYMDRCTASMVQ IVNTCPQDTGVIIIVSHGSTLDSCTRPLLGIPPRECGPPAQLVR KIPSLGMCFCEENKEEGKWELVNPPVKTLTHGANAAPHWRNWIS GN 6859 1 1150 GETMFKKAKTKAKKKPRKRSDSSGYNLSDIIQSPSTGLLKSG KTMSVSSLSPELLTSDESGSYAGVUSPRDLQSPDFTTGFHSDKIE AKWLPYVNGTSPLYSREDLKPWEKSPILKISAPQPIPSNRIDTT SSASWVAGSPSPVSPPVVDLRTIMEIEESRCKCAATPKSHIGKT VSHGVKLSQKQRMIALITTENNSGMNSMETVLFTPSKAPRPVN AMASSLHSVSSKSFRPFLLEEKKSVTSHSSGDHVKKVSFKGIEN SQAPKIVGCSTHOTPOFGENHISDPLLDSPNPWLSSSVTAPSM VAPVTFASIVEEELQQEAALIRSREKPLALIQIBEHAIQDLLVF YEAFGMPEEPVIVERTPCGPLAVPMNKHGC 6860 1889 1515 DKDKKRQKRGIFPKVATNIMRAWLFOHLTHPYPSEEDKKQLAQ DTGLTILQVANWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP MGSPVLDGQOHMCIRPAGFMSGMCSMMMMCMCGMHYM	ì			LFGIESKSSDS
EEPTSLFQRDSETKGESGLVLEGKELHQIFEDLDKKLALASRF YIPEGCIQRWAAEMVALDALHREGIVCRDLNPNNILLNDRGHI QLTYFSRWSEVEDSCDSDAIERNYCAPEVGAITESTEACDWWSL GAVLFELLTGKTLVECHPAGISINTHTTLNMPEWSEEARSLIQOL LQFNPLERIGAGVAGUPUKSHPFFTPVDWAELMR 6856 1617 997 VTQLYVSVDASTKDSLKKIDRPLFKDFWQQFLDSLKALAVKQQR TVYRLTLVKANNVDELQAYAQUVSLGNPDFIEVKGVTYCGESSA SSITMAHVPWHEEVVQFYRELVDLIPFYETACEHEHSNCLLIAH RKFKIGGEWWTMINYNRFQELIGEYEDSGGSKTFSAKDYMARTP HWALFGASERGFDPKDTRHQRKNSKAISGC KGPEATAMVCVCSHPNCRONHIKPSHSAAQTWCGSPTPASAPNH KLMAMPGGKTLPSATEDARECGLEAQISRLAELIGRLESKALWF DLQQRLSDEDGTNMHLQLVQREMAVCPEQLEFLDSLRQFLRGF TGVRNCFHITAVRLSDGFTFVIYEFWETEEAWKHLOSPLCKAF RHVKVDTLSQFEALSRILVPAWCTVGRD 6858 2 669 RSRGIKDFENDPPLSSCGIFQSRIAGDALLDSGIRISSVFASPA LRCVQTAKLLLEELKLEKKIKURVEGIFEWTKWEAGKTTPTLM SLEELKEANFNIDTDYRPAFPLSALMPASSYQEYMDRCTASMVQ IVNTCPQDTGVILIVYSTLDSCTBLSCTRPHLGLPPRECGDFAQLVR KIPSLGMCFCEENKEEGKWELVNPPVKTLTHGANAAFNWRNWIS GN 6859 1 1150 GETMFKKAKTKAKKKPRKRSDSSGGYNLSDIIQSPSSTGLLKSG KTNSVESLPELLTSDSEGSYAGVGSPRDLQSPDFTTGFHSDKIE AKVKPYNGTSPVYSREDLKPWEKSPILKISAPQPIESNRIDTT SSASWVAGSFSPVSBPVDLRTFIMEIEERROKCGATPKSHLGKT VSHGVKLSQKQRKMIALTTKENNSGMNSMETVLFTPSKAPKPVN AWASSLHSVSSKSFRDFLLEEKKSVTSHSSGDHVKKVSFKGLEN SQAPKLVRCSTHGFPEGPEGNHISDLPLLDSPNPULSSSVTAPSM VAPVTFASIVEELQQEAALIRSREKPLALIQIEEHAIQDLLVF YEAFGNPEBFVIVERTPGGPLAVPMWNKHGG GROGSPVLLOGNGRANGHGMNGMGGGWHYM MGSFVLLOGNGHMSINPAGEFOHLTHPYPSEEOKKQLAQ DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP MGSFVLLOGNGHMSINFRAMEFOHLTHPYPSEEOKKQLAQ DTGLTILQVNNWFINARRIIVQPMLTHPYPSEEOKKQLAQ DTGLTILQVNNWFINARRIIVQPMLTHPYPSEEOKKQLAQ DDGLKRQKKRGIFFKVATNIMRAWLFOHLTHPYPSEEOKKQLAQ DDGLKRQKKRGIFFKVATNIMRAWLFOHLTHPYPSEEOKKQLAQ DDGLKRQKKRGIFFKVATNIMRAWLFOHLTHPYPSEEOKKQLAQ DDGLKRQKKRGIFFKVATNIMRAWLFOHLTHPYPSEEOKKQLAQ DDGLKRQKKRGIFFKVATNIMRAWLFOHLTHPYPSEEOKKQLAQ DDGLTLTLQVNNWFINARRIIVQPHTHPYPSEEOKKQLAQ DDGLTLTLQVNNWFINARRIIVQPHTHPYPSEEOKKQLAQ	6855	1913	1148	
STERGICRWAREMYVALDALHEGIUCRDINPNNILLDRGHI CLTYFSRNSEVEDSCSDAIERMYCAPPUGAITEETEACDWSL GAVLFELLTGKTLVECHPAGINTHTTLNMPEWUSEEARSLIQOL LQFNPLERLGAGVAGVEDIKSHFFTPVDUMAELMR CAVILFELLTGKTLVECHPAGINTHTTLNMPEWUSEEARSLIQOL LQFNPLERLGAGVAGVEDIKSHFFTPVDUMAELMR CAVILFELLTGKTLVECHPAGINTHTTLNMPEWUSEEARSLIQOL LQFNPLERLGAGVAGVEDIKSHFFTPVDUMAELMR CAVILFELLTGKTLVECHPAGINTHTTLNMPEWUSEEARSLIQOL LQFNPLERLGAGVAGVEDIKSHFFTPVDUMAELMR TVTQLIYSVDASTKOSLKKIDRPLPKUPWQOPIDSIKALAVKQOR TVTRLTLVKAMWIDELQAYAQUVSLGNPDFIEVKGVTYCGESSA SSLTMAHVPWHEEVVQFVRELDVIPFESGGKKTFSAKDYMARTP HWALFGASERGFDFKDTRRGRNHKSKAISGC	-			EEPTSLFORDSETKGESGLVLEGDKETHOTEEDLDKKIALAGDE
GUTTFSRWSEVEDSCDSDATERMYCAPEVGAITEETEACDWWSL GAVLIFELLIGKTILVECHPAGINTHTILNMPEWVSEARSLIQOL LQFNPLERLGAGVAGVEDIKKHPFFTPVDWABLMR 1617 997 VTQLYVSVDASTKDSLKKIPRPLFRDFWQQFLDSLKALAVKQQR TVYRLITLVKAWNVDGAYAQLVSLGNPDFIEVKGVTYCGESSA SSLTMAHVPWHEEVVQFVRELVDLIPEYELACEHEHSNCLLIAH RKFKIGGEWWTHINYNRFQELIQEYEDGSGSKTFSAKDYMARTP HWALIFGASERGFDPKDTRHQRKNKSKAISGC 6857 1 617 KGPEATAMVCVCSHPNCRQNHIKFSHSAAQTWCGSPTPASAPNH KLMAMEGGKTLPSATEDAKEEGLEAQISRLAELIGRLESKALWF DLQQRLSEDGGTNMHLQLVRQEMAVCPEQLISFIDISLRQYLRGT TGVRNCFHITAVRLSDGFTFVIYEFWETEEAWKRHLQSPLCKAF RHVKVDTLSQFEALSRILVPAAMCTVCRD 6858 2 669 RSRGIKDFENDPPLSSGGIFOSRLAEDGGIRISSVFASPA LRCCVOTAKLILBELKLEKKIKIRVEPGIFEWTKWEAGKTTPTLM SLEELKEANFNIDTDYRPAFPLSALMPAESYQEYMDRCTASMVQ IVNTCPQDTGVILIVSHGSTLDSCTRPLLGLPPRECGDFAQLVR KIPSLGMCFCEENKEEGKWELVNPPVKTLTHGANAAFNWRNWIS GN 6859 1 1150 GETMFKKAKTKAKKKPRKRSDSSGGYNLSDIIQSPSSTGLLKSG KINSVESLPELLISDSEGSYAGVGSPRDLQSPDFTTGFHSDKIE AKVKPYVNGTSPVYSREDLKPWEKSPILKISAPQPIPSNRIDTT SSASWVAGSFSPVSPVVDLRTIMEIEESRQKCGATPKSHLIGKT VSHGVKLSQKQRKMTALTTKENNSGMISMETVLFTBSKAPKPVN AWASSLHSVSSKSFRDFLLEEKKSVTSHSSGDHVKKVSTKGIEN SQAPKLVRCSTHGTTGPEGNHISDLPLLDSPNPWLSSSVTAPSM VAPVTFASIVEELQQEAALIRSREKPLALIQIEHAIQDLLVF YEAFGNPEEFVIVERTTPQGPLAVPMWNKHGC 6860 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFGHLTHPYPSEEQKKQLAQ DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP MGSPVLDGQQHMGIRPAGPMSGMGMNMGMDGWHYM GSPVLDGQQHMGIRPAGPMSGMGMNMMGMDGWHYM 6861 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFGHLTHPYPSEEQKKOLAQ				YIPEGCIQRWAAEMVVALDALHREGIVCRDINPNNTLINDRGHT
GAVIFELLTGKTLVECHPAGINTHTTLIMPEWVSEERSLIQOL LOFMPLERLGAGVAGVEDIKSHPFFTPVDWAELMR 16856 1617 997 VTQLYVSVDASTKDSLKKIDRPLFKDFWOOFLDSLKALAVKQQR TVYRLTLVKAWNVDELQAYAQLVSLGNPDFIEVKGVTYCGESSA SSLTMAHVPWHEEVVQFYRELVDLIPEYELACEHEHSNCLLIAH RKFKIGGEWWTHINYNRFQELIGEYEDSGGKFFSAKDYMARTP HWALFGASERGFDPKDTRHCRKNKSKAISGC 6857 1 617 KGPEATAMVCVCSHPNCRQNHIKFSHSAAQTWCGSPTPASAPNH KKMAMEQGKTLPSATEDAKEEGLEAQISRLAELIGRLESKALWF DLQQRLSDEDGTNMHLQLVRQEMAVCPEQLSEFLDSLRQYLRGT TGVRNCFHITAVRLSDGFTV1YEFFETEBAWKHLQSPLCKAF RHVKVDTLSQFEALGRILVPAWCTVGRD 6858 2 669 RSRGIKDFENDPPLSSCGIFQSRIAGDALLDSGIRISSVFASPA LRCVQTAKLILEELKLEKKIKRVEPGIFEWTKWEAGKTTPTLM SLEELKEANFNIDTDYRPAFPLSALMPAESYQSYMDRCTASMVQ IVNTCPQDTGVILIVSHGSTLDSCTRPLLGLPPRECGDFAQLVR KIPSLGMCFCEENKEEGKWELVNPPVKTLTHGANAAFNWRNWIS GN 6859 1 1150 GETMFKKAKTKAKKKPRKRSDSSGGYNLSDIIQSPSTTGILKSG KTNSVESLPELLTSDSEGSYAGVGSPRDLQSPDFTTGFHSDKIE AKVKPYVMGTSPVYSBEDLKPWEKSPILKISRAPQTFSNRIDTT SSASWVAGSFSPVSPPVDLRTIMEIEESRQKCGATPKSHLGKT VSHGVKLSQKQRKMTALTTKENNSGMMSMETVLFTPSKAPKPVN AMASSLINSVSSKFRDLLEEKKSVTSHSSGDHVKKVSFKGIEN SQAPKIVRCSTHGTPGPGNHISDLPLLDSSNFWLSSSVTAPSM VAPVTFASIVEELQQEAALIRSREKPLALIQIEEHAIQDLLVF YEAFGRIPEEFVIVERIPQGPLAVPMMKHGC 6860 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFCHLTHPYPSEEQKKQLAQ DTGLTTLQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP MGSPVLDGQQHMGIRPAGPMSGMGMNMGMDCGWHYM 686FVLDGQQHMGIRPAGPMSGMGMNMMGMDCGWHYM	ļ			QLTYFSRWSEVEDSCDSDAIERMYCAPEVGAITEETEACDWWSI
LOFMPLERIGAGVAGVEDIKSHPFFTPVDWARLMR 16856 1617 997 VTQLYVSVDASTKDLKKIDRPLFKDFWQOFLDSLKALAVKQOR TVYRLTLVKAWNVDELQAYAQLVSLGNPDFIEVKGTTYGESSA SSLTMAHVPWHEEVVQFYRELVDLIPEYEIACEHENSCLLIAH RKFKIGGEWWTWINYNRFOELLQGYSEDSGSKTFSAKDYMARTP HWALIFGASERGFPDFKDTRHQRKNKSKAISGC 6857 1 617 KGPEATAMVCVCSHPNCRQNHIKFSHSAAQTWCGSPTPASAPNH KLMAMEQGKTLPSATEDAKEEGLEAQISRLAELIGRLESKALWF DLQQRLSDEDGTMHLQLVRQEMAVCPEQLSEFLDSLRQYLRGT TGVRNCFHITAVRLSDGFTFVIYEFWETEEAWKRHLQSPLCKAF RHVKVDTLSQPEALSRILVPAAWCTVGRD 6858 2 669 RSRGIKDFENDPPLSSCGIFQSRIAGDALLDSGIRISSVFASPA LRCVQTAKLILEELKLEKKIKIRVBEGIFEWTKWEAGKTTPTLM SLEELKEANFNIDTDVRPAFPLSALMPAESYQEYMDRCTASMVQ IVNTCPQDTGVILIVSHGSTLDSCTRPLLCLPPRECGDFAQLVR KIPSLGMCFCEENKEEGKWELVNPPVKTLTHGANAAFNWRNWIS GN KIPSLGMCFCEENKEEGKWELVNPPVKTLTHGANAAFNWRNWIS GN 6859 1 1150 GETMFKKAKTKAKKKPRKRSDSGGYNLSDIIQSPSSTGLLKSG KTINSVESLPELLISDSEGSYAVGSPRDLQSPDFTTGFHSDKIE AKVKPYNGTSPVYSREDLKPWEKSPILKISAPQPIPSNRIDTT SSASWVAGSFSPVSPPVVDLRTIMEIEESRQKCGATPKSHLGKT VSHGVKLSQKQRKMIALTTKENNSGMNSMETVLFTPSKAPKPVN AAASSLHSVSSKSFRDFLLEEKKSVTSHSSGDHVKKVSFKGIEN SQAPKIVRCSTHGTPGPEGNHISDLPLLDSPNPWLSSSVTAPSM VAPVTFASIVEELQQEAALIRSREKPLALIQIEEHAIQDLLVF VERAFGNPEEFVIVERTPOGPLAVPMWNKHGC SQAPKIVRCSTHGTPGGPEGNHISDLPLLDSPNPWLSSSVTAPSM VAPVTFASIVEELQQEAALIRSREKPLALIQIEEHAIQDLLVF VERAFGNPEEFVIVERTPOGPLAVPMWNKHGC TRAFGNPEEFVIVERTPOGPLAVPMWNKHGC DTGLTTLQVNNWFINARRIIVQPMIDQSNRAVSGGAAYSDEGQP MGSFVLDGQQHMGIRPAGPMSGMGMMMMGMGQWHYM MGSFVLDGQQHGIRPRAGPMSGMGMMMMGMGQWHYM 6860 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ DTGLTTLQVNNWFINARNITQHTHTPYPSEEQKKQLAQ				GAVLFELLTGKTLVECHPAGINTHTTLNMPEWVSEEARSLIOOL
TVYRLTLVKANNVDELQAYAQLVSLGNPDFIEVKGYTYCGESSA SSLTMAHVPWHEEVVQFVRELVDLIPEYEIACEHEHSNCLLIAH RKFKIGGEWWTWINYNRFQELIQEYEDSGGSKTFSAKDYMARTP HWALFGASERGFDPKDTRHQRKNKSKALSGC 6857 1 617 KGPEATAMVCVCSHPNCRQNHIKFSHSAAQTWCGSPTPASAPNH KLMAMEQGKTLPSATEDAKEGGLEAQISRLAELIGRLESKALWF DLQQRLSDEDGTMMHLQLVRQEMAVCPEQLSEFLDSLRQYLRGT TGVRNCFHITAVRLSDGFTFVIYEFWETEEAWKRHLQSPLCKAF RHVKVDTLSQPEALSRILVPAAWCTVGRD 6858 2 669 RSRGIKDFENDPPLSSCGIFQSRIAGDALLDSGIRISSVFASPA LRCVQTAKLILEELKLEKKIKIRVEPGIFEWTKWEAGKTTPTLM SLEELKEANFNIDTDYRPAFPLSALMPAESYQEYMDRCTASMVQ IVNTCPQDTGVILIVSHGSTLDSCTRPLLGLPPRECGFPAQLVR KIPSLGMCFCEENKEEGKWELVNPPVKTLTHGANAAFNWRNWIS GN 6859 1 1150 GETMFKKAKKKAKKPRKRSDSSGGYNLSDIIQSPSTGLLKSG KTNSVESLPELLTSDSEGSYAGVGSPRDLQSPDFTTGFHSDKIE AKVKPYVNGTSFVYSREDLKPMEKSPILKISAPQPIPSNRIDTT SSASWVAGSFSPVSPPVVDLRTIMEIEFSRQKCGATPKSHLGKT VSHGVKLSQKQRKMIALTTKENNSGMNSMETVLFTPSKAPKPVN VSHGVKLSQKQRKMIALTTKENNSGMNSMETVLFTPSKAPKPVN VSHGVKLSQKQRKMIALTTKENNSGMNSMETVLFTPSKAPKPVN VSHGVKLSQKQRKMIALTTKENNSGMNSMETVLFTPSKAPKPVN VAPVTFASIVEEELQCBAALIRSREKPLALIQIEEHAIQDLLVF VSHGVKLSQKQRKMIASREPCHALIQIEEHAIQDLLVF VSHGVKSTHOTPGGPBGNHISDLPLLDSPNPWLSSSVTAPSM VAPVTFASIVEEELQCBAALIRSREKPLALIQIEEHAIQDLLVF VSHGVKRGVKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ DTGLTILQVNNNFINARRIIVQPMIDQSNRAVSGGAAYSPEGQP MGSFVLDGQQHMGIRPAGPMSGMMMMMCDQWHYM 6860 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKOLAQ DTGLTILQVNNNFINARRIIVQPMIDQSNRAVSGGAAYSPEGQP MGSFVLDGQQHMGIRPAGPMSGMMMMMCMDQWHYM				LQFNPLERLGAGVAGVEDIKSHPFFTPVDWAELMR
SSLTMAHVPHHEEVVQFVRELVDLIPEYEIACEHEHSNCLLIAH RKFKIGGEWATUNYNRFQELIQEYEDSGGSKTFSAKDYMARTP HWALFGASERGFDPRDTRHQRKNKSKAISGC 6857 1 617 KGPEATAMVCVCSHPMCRQNHIKPSHSAAQTWCGSPTPASAPNH KLMAMEQKTLPSATEDAKEEGLEAQISRLAELIGRLESKALWF DLQQRLSDEDGTNMHLQLVRQEMAVCPSQLSEFLDSLRQYLRGT TGVRNCFHITAVRLSDGFTFVIYEFWETEEAWKRHLQSPLCKAF RHVKVDTLSQFEALSRILVPAAWCTVGRD 6858 2 669 RSRGIKDFENDPPLSSCGIFQSRIAGDALLDSGIRISSVFASPA LRCVQTAKLILEELKLEKKIKIRVEPGIFEWIKWEAGKTTPTLM SLEELKEANFNIDTDYRPAFFLSALMPAESYQEYMDRCTASMVQ IVNTCPQDTGVILIVSHGSTLDSCTRPLLGLPPRECGDFAQLVR KIPSLGMCFCEENKEEGKWELVNPPVKTLTHGANAAFNWRNWIS GN 6859 1 1150 GETMFKKAKKKPRKRSDSSGGYNLSDIIQSPSSTGLLKSG KINSVESLPELLTSDSEGSYAGVGSPRDLQSPDFTTGFHSDKIE AKVKPYVNGTSPVYSREDLKPWEKSPILKISAPQPIPSNRIDTT SSASWAGSFSPVSPPVVDLRTIMEIEESROKGGATPKSHLGKT VSHGVKLSQKQRKMIALTTKENNSGMNSMETVLFTPSKAPKPVN AMASSLHSVSSKSFRDFLLEEKKSVTSHSSGDHVKKVSFKGIEN SQAPKIVRCSTHGTFGPEGNHISDLPLLDSPNPWLSSSVTAPSM VAPVTFASIVEEELQQEAALIRSREKPLALIQIEEHAIQDLLVF YEAFGNPEEFVIVERTPCGPLAVPMMKHGC 6860 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ DTGLTILQVNNWFINARRIIVQPMTDQSNRAVSQGAAYSPEGQP MGSFVLDGGQQHMGIRPAGPMSGMMMMGMDGQWHYM 6861 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEOKKOLAO	6826	1617	997	VTQLYVSVDASTKDSLKKIDRPLFKDFWQQFLDSLKALAVKQQR
RKFKIGGEWNTWINYNRFQELIQEYEDSGSKTFSAKDYMARTP HWALFGASERGFDPKDTRHQRKNKSKAISGC 6857 1 617 617 618 KGPEATAMVCVCSHPNCRQNHIKPSHSAAQTWCGSPTPASAPNH KLMAMEQGKTLPSATEDAKEEGLEAQISRLAELIGRLESKALWF DLQQRLSDEDGTNMHHQLVRQEMAVCPEQLSEFIDSLRQYLRGT TGVRNCFHITAVRLSDGFTFVIYEFWETEEAWKRHLQSPLCKAF RHVKVDTLSQPEALSRILVPAAWCTVGRD 6858 2 669 RSRGIKDFENDPPLSSCGIFQSRIAGDALLDSGIRISSVFASPA LRCVQTAKLILEELKLEKKIKIRVEPGIFEWTKWEAGKTTPTLM SLEELKEANPINDTDYRPAFPLSALMPAESYQEYMDRCTASMVQ IVNTCPQDTGVILIVSHGSTLDSCTRPLLGLPPRECGPFAQLVR KIPSLGMCFCEENKEEGKWELVNPPVKTLTHGANAAFNWRNWIS GN 6859 1 1150 GETMFKKAKTKAKKKPRKSDSSGGYNLSDIIQSPSSTGLLKSG KTNSVESLPELLTSDSEGSYAGVGSPRDLQSPDFTTGFHSDKIE AKVKPYVNGTSPYVSREDLKPWEKSPILKISAPQPIPSNRIDTT SSASWVAGSFSPVSPVVDLRTIMEIEESRQKCGATPKSHLGKT VSHGVKLSQKQRKMIALTTKENNSGMNSMETVLFTPSKAPKPVN AWASSLHSVSSKSFRDFLLEEKKSVTSHSSGDHVKKVSFKGIEN SQAPKIVRCSTHGTPGPEGNHISDLPLLDSPNPWLSSSVTAPSM VAPVTFASIVEEELQQEAALIRSREKPLALIQIEEHAIQDLLVF YEAFGNPEEFVIVERTPQCPLAVPMWNKHGC 6860 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ DTGLTILQVNNWFINARRIIVQPMTDQSNRAVSQGAAYSPEGQP MGSPVLDGQQHMGIRPAGPMSGMMMMGMDGQWHYM 6861 1889 1515 DKDKKRQKRGIFPKVATNIMRAWLFQHLTHPYPSSEEOKKOLAO				TVYRLTLVKAWNVDELQAYAQLVSLGNPDFIEVKGVTYCGESSA
HWALFGASERGFDPKDTRHQRKNKSKAISGC KGPEATAMVCVCSHPNCRQNHIKPSHSAAQTWCGSPTPASAPNH KLMAMEQGKTLPSATEDAKEEGLEAQISRIAELIGRLESKALWF DLQQRLSDEDGTNMHLQLVRQEMAVCPEQLSEFLDSLRQYLRGT TGVRNCFHITAVRLSDGFTFVIYEFWETEEAWKRHLQSPLCKAF RHVKVDTLSQPEALSRILVPAAWCTVGRD 6858 2 669 RSRGIKDFENDPPLSSCGIFQSRIAGDALLDSGIRISSVFASPA LRCVQTAKLILEELKLEKKIKIRVEPGIFEWTKWEAGKTTPTLM SLEELKEANFNIDTDYRPAFPLSALMPAESYQEYMDRCTASMVQ IVNTCPQDTGVILIVSHGSTLDSCTRPLLGLPPRECGDFAQLVR KIPSLGMCFCEENKEEGKWELVNPPVKTLTHGANAAFNWRNWIS GN 6859 1 1150 GETMFKKAKTKAKKKPRKRSDSSGGYNLSDIIQSPSSTGLLKSG KTINSVESLFELLTSDSEGSYAGGSPRDLQSPDFTTGFHSDKIE AKVKPYVNGTSPVYSREDLKPWEKSPILKISAPQPIFSNRIDTT SSASWAGSSPSPVSPPVVDLRTIMEIEESRQKCGATPKSHLGKT VSHGVKLSQKQRKMIALTTKENNSGMNSMETVLFTPSKAPKPVN AWASSLHSVSSKSFRDFLLEEKKSVTSHSSGDHVKKVSFKGIEN SQAPKIVRCSTHGTPGPEGNHISDLPLLDSPNPWLSSSVTAPSM VAPVTFASIVEELQQEAALIRSREKFLALIQIEEHAIQDLLVF YEAFGNPEEFVIVERTPQGPLAVPMWNKHGC 6860 1889 1515 DKDKKRQKRGIFFKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSGCAAAYSPEGQP MGSPVLDGQQHMGIRPAGPMSGMGMNMMGDQWHYM 6861 1889 1515 DKDKKRQKRGIFFKVATNIMRAWLFQHLTHPYPSEEQKKGLAQ	1			SSLTMAHVPWHEEVVQFVRELVDLIPEYEIACEHEHSNCLLIAH
6857 1 617 KGPEATAMVCVCSHPNCRQNHIKFSHSAAQTWCGSPTPASAPNH KLMAMEQGKTLPSATEDAKEEGLEAQISRLAELIGRLESKALWF DLQQRLSDEDGTNMHLQLVRQEMAVCPEQLSEFLDSLRQYLRGT TGYRNCFHITAVRLSDGFTFVIYEFWETTEAWKRHLQSPLCKAF RHVKVDTLSQPEALSRILVPAAWCTVGRD 6858 2 669 RSRGIKDFENDPPLSSCGIFQSRIAGDALDSGIRISSVFASPA LRCVQTAKLILEELKLEKKIKIRVEPGIFEWTKWEAGKTTPTLM SLEELKEANFNIDTDYRPAFPLSALMPAESYQEYMDRCTASMVQ IVNTCPQDTGVILIVSHGSTLDSCTRPLLGLPPRECGDFAQLVR KIPSLGMCFCEENKEEGKWELVNPPVKTLTHGANAAFNWRNWIS GN 6859 1 1150 GETMFKKAKTKAKKKPRKRSDSSGGYNLSDIIQSPSSTGLLKSG KTINSVESLPELLTSDSEGSYAGVGSPRDLQSPDFTTGFHSDKIE AKVKPYVNGTSPVYSREDLKPWEKSPILKISAPQPIPSNRIDTT SSASWVAGSPSPVSPPVVDLRTIMEIEESRQKCGATPKSHLGKT VSHGVKLSQKQRKMIALTTKENNSGMNSMETVLFTPSKAPKPVN AWASSLHSVSSKSFRDFLLEEKKSVTSHSSGDHVKKVSFKGIEN SQAPKIVRCSTHGTFGPEGNHISDLPLLDSPNEWLSSSVTAPSM VAPVTFASIVEEELQQEAALIRSREKPLALIQIEEHAIQDLLVF YEAFGNPEEFVIVERTPOGPLAVPMWNKHGC 6860 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPRGQP MGSPVLDGQQHMGIRPAGPMSGMMMMGMDQWHYM 6861 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPRGQP MGSPVLDGQQHMGIRPAGPMSGMMMMGMDQQWHYM	İ			RKFKIGGEWWTWINYNRFQELIQEYEDSGGSKTFSAKDYMARTP
KKMAMEQKKTLPSATEDAKEGLEAQISRLAELIGRLESKALWF KKMAMEQKKTLPSATEDAKEGLEAQISRLAELIGRLESKALWF DLQQRLSDEDGTNMHLQLVRQEMAVCPEQLSEFLDSLRQYLRGT TGVRNCFHITAVRLSDGFTFVIYEFWETEEAWKRHLQSPLCKAF RHVKVDTLSQPEALSRILVPAAWCTVGRD 6858 2 669 RSRGIKDFENDPPLSSCGIFQSRIAGDALDSGIRISSVFASPA LRCVQTAKLILEELKLEKKIKIRVEPGIFEWTKWEAGKTTPTLM SLEELKEANFNIDTDYRPAFPLSALMPAESYQEYMDRCTASMVQ IVNTCPQDTGVILIVSHGSTLDSCTRPLLGLPPRECGDFAQLVR KIPSLGMCFCEENKEEGKWELVNPPVKTLTHGANAAFNWRNWIS GN 6859 1 1150 GETMFKKAKTKAKKKPRKRSDSSGGYNLSDIIQSPSSTGLLKSG KTINSVESLPELLITSDSEGSYAGVGSPRDLQSPDFTTGFHSDKIE AKVKPYVNGTSPVYSREDLKPWEKSPILKISAPQPIPSNRIDTT SSASWVAGSFSPVSPPVVDLRTIMEIEESRQKCGATPKSHLGKT VSHGVKLSQKQRKMIALTTKENNSGMNSMETVLFTPSKAPKPVN AWASSLHSVESKSFRDFILEEKKSVTSHSSGDHVKKVSFKGIEN SQAPKIVRCSTHGTPGPEGNHISDLPLLDSPNPWLSSVYTAPSM VAPVTFASIVEEELQQEAALIRSREKPLALIQIEHAIQDLLVF YEAFGNPEEFVIVERTPQGPLAVPMWNKHGC 6860 1889 1515 DKDKKRQKRRGIFPKVATNIMRAMLFQHLTHPYPSEEQKKQLAQ MGSFVLDGQQHMGIRPAGPMSGMMMMGDGQWHYM 6861 1889 1515 DKDKKRQKRGIFPKVATNIMRAMLFQHLTHPYPSEEQKKQLAQ	6857			
DLQQRLSDEDGTMMHLQLVRQEMAVCPEQLSEFLDSLRQYLRGT TGYRNCFHITAVRLSDGFTFVIYEFWETEEAWKRHLQSPLCKAF RHVKVDTLSQPEALSRILVPAAWCTVGRD RSRGIKDFENDPPLSSCGIFQSRIAGDALLDSGIRISSVFASPA LRCVQTAKLILEELKLEKKIKIRVEPGIFEWTKWEAGKTTPTLM SLEELKEANFNIDTDYRPAFPLSALMPAESYQEYMDRCTASMVQ IVNTCPQDTGVILIVSHGSTLDSCTRPLLGLPPRECGDFAQLVR KIPSLGMCFCEENKEEGKWELVNPPVKTLTHGANAAFNWRNWIS GN GN GETMFKKAKTKAKKKPRKSDSSGGYNLSDIIQSPSSTGLLKSG KTNSVESLPELLTSDSEGSYAGVGSPRDLQSPDFTTGFHSDKIE AKVKPYVNGTSPVSREDLKPWEKSPILKISAPQPIPSNRIDTT SSASWVAGSFSPVSPPVVDLKTIMEIEESRQKCGATPKSHLGKT VSHGVKLSQKQRKMIALTTKENNSGMISMETVLFTPSKAPKPVN AWASSLHSVSSKSFRDFLLEEKKSVTSHSSGDHVKKVSFKGIEN SQAPKIVRCSTHGTPGPEGNHISDLPLLDSPNPWLSSSVTAPSM VAPVTFASIVEEELQQEAALIRSREKPLALIQIEEHAIQDLLVF YEAFGNPEEFVIVERTPQGPLAVPMWNKHGC DKDKKRQKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP MGSFVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM MGSFVLDGQQHIGIRPAGPMSGMGMNMGMDGQWHYM 6861 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ			61.7	KGPEATAMVCVCSHPNCRQNHIKPSHSAAQTWCGSPTPASAPNH
TGVRNCFHITAVRLSDGFTFVIYEFWETEEAWKRHLQSPLCKAF RHVKVDTLSQPEALSRILVPAAWCTVGRD RSRGIKDFENDPPLSSCGIFQSRIAGDALLDSGIRISSVFASPA LRCVQTAKLILEELKLEKKIKIRVEPGIFEWTKWEAGKTTPTLM SLEELKEANFNIDTDYRPAFPLSALMPAESYQEYMDRCTASMVQ IVNTCPQDTGVILIVSHGSTLDSCTRPLLGLPPRECGDFAQLVR KIPSLGMCFCEENKEEGKWELVNPPVKTLTHGANAAFNWRNWIS GN 6859 1 1150 GETMFKKAKTKAKKKPRKRSDSSGGYNLSDIIQSPSSTGLLKSG KTNSVESLPELLTSDSEGSYAGVGSFRDLQSPDFTTGFHSDKIE AKVKPYVNGTSPVYSREDLKPWEKSPILKISAPQPIPSNRIDTT SSASWVAGSFSPVSPPVVDLRTIMEIEESRQKCGATPKSHLGKT VSHGVKLSQKQRKMIALTTKENNSGMNSMETVLFTPSKAPKPVN AWASSLHSVSSKSFRDFLLEEKKSVTSHSSGDHVKKVSFKGIEN SQAPKLVRCSTHGTPGPEGNHISDLPLLDSPNPWLSSSTTAPSM VAPVTFASIVEEELQEAALIRSREKPLALIQIEEHAIQDLLVF YEAFGNPEEFVIVERTPQGPLAVPMWNKHGC 6860 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ MGSFVLDGQQIMGIRPAGPMSGMGMNMGMDGQWHYM 6861 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKOLAQ				DI CORI CDEDCEMMUS OLUBORANICO DE CONTROL DE
RHVKVDTLSQPEALSRILVPAAWCTVGRD 6858 2 669 RSRGIKDFENDPPLSSCGIFGSRIAGDALLDSGIRISSVFASPA LRCVQTAKLILEELKLEKKIKIRVEPGIFEWTKWEAGKTTPTLM SLEELKEANFNIDTDYRPAFPLSALMPAESYQEYMDRCTASMVQ IVMTCPQDTGVILIVSHGSTLDSCTRPLLGLPPRECGDFAQLVR KIPSLGMCFCEENKEEGKWELVNPPVKTLTHGANAAFNWRNWIS GN 6859 1 1150 GETMFKKAKTKAKKKPRKRSDSSGGYNLSDIIQSPSSTGLLKSG KTNSVESLPELLTSDSEGSYAGVGSPRDLQSPDFTTGFHSDKIE AKVKPYVNGTSPVYSREDLKPWEKSPILKISAPQPIPSNRIDTT SSASWVAGSFSPVSPPVVDLRTIMEIEESRQKCGATPKSHLGKT VSHGVKLSQKQRKMIALTTKENNSGMNSMETVLFTPSKAPKPVN AWASSLHSVSSKSFRDFLLEEKKSVTSHSSGDHVKKVSFKGIEN SQAPKIVRCSTHGTPGPEGNHISDLPLLDSPNPWLSSSVTAPSM VAPVTFASIVEELQQEAALIRSREKPLALIQIEEHAIQDLLVF YEAFGNPEEFVIVERTPQGPLAVPMWNKHGC 6860 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP MGSFVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM 6861 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKOLAQ				TCVPNCEHITANDI ODCUMPNIANDI CONTROLLERANDI
6858 .2 669 RSRGIKDFENDPPLSSCGIFQSRIAGDALLDSGIRISSVFASPA LRCVQTAKLILEELKLEKKIKIRVEPGIFEWTKWEAGKTTPTLM SLEELKEANFNIDTDYRPAFPLSALMPAESYQEYMDRCTASMVQ IVNTCPQDTGVILIVSHGSTLDSCTRPLLGLPPRECGDFAQLVR KIPSLGMCFCEENKEEGKWELVNPPVKTLTHGANAAFNWRNWIS GN GETMFKKAKTKAKKKPRKRSDSSGGYNLSDIIQSPSSTGLLKSG KTINSVESLPELLTSDSEGSYAGVGSPRDLQSPDFTTGFHSDKIE AKVKPYVNGTSPVYSREDLKPWEKSPILKISAPQPIPSNRIDTT SSASWVAGSFSPVSPPVVDLRTIMEIEESRQKCGATPKSHLGKT VSHGVKLSQKQRKMIALTTKENNSGMNSMETVLFTPSKAPKPVN AWASSLHSVSSKSFRDFLLEEKKSVTSHSSGDHVKKVSFKGIEN SQAPKIVRCSTHGTPGPEGNHISDLPLLDSPNPWLSSSVTAPSM VAPVTFASIVEEELQQEAALIRSREKPLALIQIEEHAIQDLLVF YEAFGNPEEFVIVERTPQGPLAVPMWNKHGC 6860 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP MGSFVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM 6861 1889 1515 DKDKKRQKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKOLAQ				PHYKADAT CORF TEATH A WOLLD BE AN KKHT OS BECKYLE
LRCVQTAKLILEELKLEKKIKIRVEPGIFEWTKWEAGKTTPTLM SLEELKEANFNIDTDYRPAFPLSALMPAESYQEYMDRCTASMVQ IVNTCPQDTGVILIVSHGSTLDSCTRPLLGLPPRECGDFAQLVR KIPSLGMCFCEENKEEGKWELVNPPVKTLTHGANAAFNWRNWIS GN 6859 1 1150 GETMFKKAKTKAKKKPRKRSDSSGGYNLSDIIQSPSSTGLLKSG KTNSVESLPELLTSDSEGSYAGVGSPRDLQSPDFTTGFHSDKIE AKVKPYVNGTSPVYSREDLKPWEKSPILKISAPQPIPSNRIDTT SSASWVAGSFSPVSPPVVDLRTIMEIEESRQKCGATPKSHLGKT VSHGVKLSQKQRKMIALTTKENNSGMNSMETVLFTPSKAPKPVN AWASSLHSVSSKSFRDFLLEEKKSVTSHSSGDHVKKVSFKGIEN SQAPKIVRCSTHGTPGPEGNHISDLPLLDSPNPWLSSSVTAPSM VAPVTFASIVEELQQEAALIRSREKPLALIQIEEHAIQDLLVF YEAFGNPEEFVIVERTPQGPLAVPMWNKHGC 6860 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP MGSFVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM 6861 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ DKDKKRQKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKOLAO	6858	2	669	PSRCINDEENDORISCGIEGGDIAGDALI DOGIDIO
SLEELKEANFNIDTDYRPAFPLSALMPAESYQEYMDRCTASMVQ IVNTCPQDTGVILIVSHGSTLDSCTRPLLGLPPRECGDFAQLVR KIPSLGMCFCEENKEEGKWELVNPPVKTLTHGANAAFNWRNWIS GN 6859 1 1150 GETMFKKAKTKAKKKPRKRSDSSGGYNLSDIIQSPSSTGLLKSG KTMSVESLPELLTSDSEGSYAGVGSPRDLQSPDFTTGFHSDKIE AKVKPYVNGTSPVYSREDLKPWEKSPILKISAPQPIPSNRIDTT SSASWVAGSFSPVSPPVVDLRTIMEIEESRQKCGATPKSHLGKT VSHGVKLSQKQRKMIALTTKENNSGMNSMETVLFTPSKAPKPVN AWASSLHSVSSKSFRDFLLEEKKSVTSHSSGDHVKKVSFKGIEN SQAPKIVRCSTHGTPGPEGNHISDLPLLDSPNPWLSSSVTAPSM VAPVTFASIVEEELQQEAALIRSREKPLALIQIEEHAIQDLLVF YEAFGNPEEFVIVERTPQGPLAVPMWNKHGC 6860 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP MGSFVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM 6861 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP MGSFVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM	1			LRCVOTAKI I I EEL KI EKKI KI DURDCI PRODUNDA CUMBANI
IVNTCPQDTGVILIVSHGSTLDSCTRPLLGLPPRECGDFAQLVR KIPSLGMCFCEENKEEGKWELVNPPVKTLTHGANAAFNWRNWIS GN GETMFKKAKTKAKKKPRKRSDSSGGYNLSDIIQSPSSTGLLKSG KTNSVESLPELLTSDSEGSYAGVGSPRDLQSPDFTTGFHSDKIE AKVKPYVNGTSPVYSREDLKPWEKSPILKISAPQPIPSNRIDTT SSASWVAGSFSPVSPPVVDLRTIMEIEESRQKCGATPKSHLGKT VSHGVKLSQKQRKMIALTTKENNSGMNSMETVLFTPSKAPKPVN AWASSLHSVSSKSFRDFLLEEKKSVTSHSSGDHVKKVSFKGIEN SQAPKIVRCSTHGTPGPEGNHISDLPLLDSPNPWLSSSVTAPSM VAPVTFASIVEEELQQEAALIRSREKPLALIQIEEHAIQDLLVF YEAFGNPEEFVIVERTPQGPLAVPMWNKHGC BKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP MGSFVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM 6861 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ DKGSFVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM 6861 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKOLAO	1 1		ł	SLEELKEANFNIDTDYRPAFPI.CALMDAFEVORVMDDCOMA CARROL
KIPSLGMCFCEENKEEGKWELVNPPVKTLTHGANAAFNWRNWIS GN 6859 1 1150 GETMFKKAKTKAKKKPRKRSDSSGGYNLSDIIQSPSSTGLLKSG KTNSVESLPELLTSDSEGSYAGVGSPRDLQSPDFTTGFHSDKIE AKVKPYVNGTSPVYSREDLKPWEKSPILKISAPQPIPSNRIDTT SSASWVAGSFSPVSPPVVDLRTIMEIEESRQKCGATPKSHLGKT VSHGVKLSQKQRKMIALTTKENNSGMNSMETVLFTPSKAPKPVN AWASSLHSVSSKSFRDFLLEEKKSVTSHSSGDHVKKVSFKGIEN SQAPKIVRCSTHGTPGPEGNHISDLPLLDSPNPWLSSSVTAPSM VAPVTFASIVEEELQQEAALIRSREKPLALIQIEEHAIQDLLVF YEAFGNPEEFVIVERTPQGPLAVPMWNKHGC 6860 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ MGSFVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM 6861 1889 1515 DKDKKRQKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP MGSFVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM 6861 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKOLAQ				IVNTCPODTGVILIVSHGSTLDSCTRPI.I.CI.DDDFCCDPACTED
GN GETMFKKAKTKAKKKPRKRSDSSGGYNLSDIIQSPSSTGLLKSG KTNSVESLPELLTSDSEGSYAGVGSPRDLQSPDFTTGFHSDKIE AKVKPYVNGTSPVYSREDLKPWEKSPILKISAPQPIPSNRIDTT SSASWVAGSFSPVSPPVVDLRTIMEIEESRQKCGATPKSHLGKT VSHGVKLSQKQRKMIALTTKENNSGMNSMETVLFTPSKAPKPVN AWASSLHSVSSKSFRDFLLEEKKSVTSHSSGDHVKKVSFKGIEN SQAPKIVRCSTHGTPGPEGNHISDLPLLDSPNPWLSSSVTAPSM VAPVTFASIVEEELQQEAALIRSREKPLALIQIEEHAIQDLLVF YEAFGNPEEFVIVERTPQGPLAVPMWNKHGC 6860 1889 1515 DKDKKRQKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP MGSFVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM 6861 1889 1515 DKDKKRQKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKOLAO	, ,			KIPSLGMCFCEENKEEGKWELVNPPVKTLTHGANAAPNWDMUTG
KTINVESLPELLTSDSEGSYAGVGSPRDLQSPDFTTGFHSDKIE AKVKPYVNGTSPVYSREDLKPWEKSPILKISAPQPIPSNRIDTT SSASWVAGSFSPVSPPVVDLRTIMEIEESRQKCGATPKSHLGKT VSHGVKLSQKQRKMIALTTKENNSGMNSMETVLFTPSKAPKPVN AWASSLHSVSSKSFRDFLLEEKKSVTSHSSGDHVKKVSFKGIEN SQAPKIVRCSTHGTPGPEGNHISDLPLLDSPNPWLSSSVTAPSM VAPVTFASIVEELQQEAALIRSREKPLALIQIEEHAIQDLLVF YEAFGNPEEFVIVERTPQGPLAVPMWNKHGC 6860 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP MGSFVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM 6861 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ	<u> </u>			
KTNSVESLPELLTSDSEGSYAGVGSPRDLQSPDFTTGFHSDKIE AKVKPYVNGTSPVYSREDLKPWEKSPILKISAPQPIPSNRIDTT SSASWVAGSFSPVSPPVVDLRTIMEIEESRQKCGATPKSHLGKT VSHGVKLSQKQRKMIALTTKENNSGMNSMETVLFTPSKAPKPVN AWASSLHSVSSKSFRDFLLEEKKSVTSHSSGDHVKKVSFKGIEN SQAPKIVRCSTHGTPGPEGNHISDLPLLDSPNPWLSSSVTAPSM VAPVTFASIVEEELQQEAALIRSREKPLALIQIEEHAIQDLLVF YEAFGNPEEFVIVERTPQGPLAVPMWNKHGC 6860 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP MGSFVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM 6861 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKOLAO	6859	1	1150	GETMFKKAKTKAKKKPRKRSDSSGGYNLSDI10SPSSTGLLVGG
AKVKPYVNGTSPVYSREDLKPWEKSPILKISAPQPIPSNRIDTT SSASWVAGSFSPVSPPVVDLRTIMEIEESRQKCGATPKSHLGKT VSHGVKLSQKQRKMIALTTKENNSGMNSMETVLFTPSKAPKPVN AWASSLHSVSSKSFRDFLLEEKKSVTSHSSGDHVKKVSFKGIEN SQAPKIVRCSTHGTPGPEGNHISDLPLLDSPNPWLSSSVTAPSM VAPVTFASIVEEELQQEAALIRSREKPLALIQIEHAIQDLLVF YEAFGNPEEFVIVERTPQGPLAVPMWNKHGC DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP MGSFVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM 6861 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP MGSFVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM 6861 0KDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ]	İ		KTNSVESLPELLTSDSEGSYAGVGSPRDLQSPDFTTGFHSDKIE
SSASWVAGSFSPVSPPVVDLRTIMEIEESRQKCGATPKSHLGKT VSHGVKLSQKQRKMIALTTKENNSGMNSMETVLFTPSKAPKPVN AWASSLHSVSSKSFRDFLLEEKKSVTSHSSGDHVKKVSFKGIEN SQAPKIVRCSTHGTPGPEGNHISDLPLLDSPNPWLSSSVTAPSM VAPVTFASIVEELQQEAALIRSREKPLALIQIEEHAIQDLLVF YEAFGNPEEFVIVERTPQGPLAVPMWNKHGC BKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP MGSFVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM 6861 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ] !			AKVKPYVNGTSPVYSREDLKPWEKSPILKISAPOPIPSNRIDTT
VSHGVKLSQKQRKMIALTTKENNSGMNSMETVLFTPSKAPKPVN AWASSLHSVSSKSFRDFLLEEKKSVTSHSSGDHVKKVSFKGIEN SQAPKIVRCSTHGTPGPEGNHISDLPLLDSPNPWLSSSVTAPSM VAPVTFASIVEELQQEAALIRSREKPLALIQIEEHAIQDLLVF YEAFGNPEEFVIVERTPQGPLAVPMWNKHGC BKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP MGSFVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM 6861 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ		j		SSASWVAGSFSPVSPPVVDLRTIMEIEESRQKCGATPKSHLGKT
AWASSLHSVSSKSFRDFLLEEKKSVTSHSSGDHVKKVSFKGIEN SQAPKIVRCSTHGTPGPEGNHISDLPLLDSPNPWLSSSVTAPSM VAPVTFASIVEEELQQEAALIRSREKPLALIQIEEHAIQDLLVF YEAFGNPEEFVIVERTPQGPLAVPMWNKHGC 6860 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP MGSFVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM 6861 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ	Į J	. }	j	VSHGVKLSQKQRKMIALTTKENNSGMNSMETVLFTPSKAPKPVN
SQAPKIVRCSTHGTPGPEGNHISDLPLLDSPNPWLSSSVTAPSM VAPVTFASIVEEELQQEAALIRSREKPLALIQIEEHAIQDLLVF YEAFGNPEEFVIVERTPQGPLAVPMWNKHGC 6860 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP MGSFVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM 6861 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ	1 1	I	Í	AWASSLHSVSSKSFRDFLLEEKKSVTSHSSGDHVKKVSFKGIEN
VAPVTFASIVEEELQQEAALIRSREKPLALIQIEEHAIQDLLVF YEAFGNPEEFVIVERTPQGPLAVPMWNKHGC 6860 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP MGSFVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM 6861 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKOLAO	<u> </u>	1		SQAPKIVRCSTHGTPGPEGNHISDLPLLDSPNPWLSSSVTAPSM
6860 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP MGSFVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM 6861 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ	<u> </u>	1	ļ	VAPVTFASIVEEELQQEAALIRSREKPLALIQIEEHAIQDLLVF
DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP MGSFVLDGQQHMGIRPAGPMSGMMNMGMDGQWHYM 6861 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKOLAO	6860	1000		
MGSFVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM 6861 1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAO	6000	1003	1515	
1889 1515 DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKOLAO	1			
DADARROKRGIFPRVATNIMRAWLFQHLTHPYPSEEOKKOLAO	6861	7000		MGSFVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM
DIGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP		4007	1212	DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ
	<u> </u>			DIGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP

SEQ	Predicted	Predicted end	Amino agid gogmont
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S≃Serine, T=Threonine, V=Valine,
İ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\=possible nucleotide insertion)
			MGSFVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM
6862	2	471	EEIDREFHNKLKLKEDKLEKQEKPVNGEDKGDSGVDTQNSEGNA
ł			DEEDPLGPNCYYDKTKSFFDNISCDDNRERRPTWAEERRLNAET
ì			FGIPLRPNRGRGGYRGRGGLGFRGGRGGGRGGTFTAPRGFRG
			GFRGGRGGREFADFEYRKTTAFGP
6863	2216	487	PQEPALKSEFSQVASNTIPLPLPQPNTCKDNGPCKQVCSTVGGS
			AICSCFPGYAIMADGVSCEDQDECLMGAHDCSRRQFCVNTLGSF
1	ì		YCVNHTVLCADGYILNAHRKCVDINECVTDLHTCSRGEHCVNTL
1			GSFHCYKALTCEPGYALKDGECEDVDECAMGTHTCQPGFLCQNT
			KGSFYCQARQRCMDGFLQDPEGNCVDINECTSLSEPCRPGFSCI
ì	{		NTVGSYTCQRNPLICARGYHASDDGTKCVDVNECETGVHRCGEG
			QVCHNLPGSYRCDCKAGFQRDAFGRGCIDVNECWASPGRLCOHT
			CENTLGSYRCSCASGFLLAADGKRCEDVNECEAORCSOECANIY
1			GSYQCYCRQGYQLAEDGHTCTDIDECAQGAGILCTFRCLNVPGS
1			YQCACPEQGYTMTANGRSCKDVDECALGTHNCSEAETCHNIOGS
l .			FRCLRFECPPNYVQVSKTKCERTTCHDFLECQNSPARITHYQLN
ľ			PQTGLLVPAHIFRIGPAPAFTGDTIALNIIKGNEEGYFGTRRLN
			AYTGVVYLQRAVLEPRDFALDVEMKLWRQGSVTTFLAKMHIFFT
			TFAL
6864	2	2933	LADSSPSNLQIIIKELLSMHHQPDPALTKEFDYLPPVDSRSSSG
1			FVGLRNGGATCYMNAVFQQLYMQPGLPESLLSVDDDTDNPDDSV
			FYQVQSLFGHLMESKLQYYVPENFWKIFKMWNKELYVREQQDAY
			EFFTSLIDQMDEYLKKMGRDQIFKNTFQGIYSDQKICKDCPHRY
1			EREEAFMALNLGVTSCQSLEISLDQFVRGEVLEGSNAYYCEKCK
1	ļ		EKRITVKRTCIKSLPSVLVIHLMRFGFDWESGRSIKYDEQIRFP
			WMLNMEPYTVSGMARQDSSSEVGENGRSVDQGGGGSPRKKVALT
			ENYELVGVIVHSGQAHAGHYYSFIKDRRGCGKGKWYKFNDTVIE
1	i		EFDLNDETLEYECFGGEYRPKVYDQTNPYTDVRRRYWNAYMLFY QRVSDQNSPVLPKKSRVSVVRQEAEDLSLSAPSSPEISPQSSPR
			PHRPNNDRLSILTKLVKKGEKKGLFVEKMPARIYQMVRDENLKF
}			MKNRDVYSSDYFSFVLSLASLNATKLKHPYYPCMAKVSLQLAIQ
	i		FLFQTYLRTKKKLRVDTEEWIATIEALLSKSFDACQWLVEYFIS
			SEGRELIKIFLLECNVREVRVAVATILEKTLDSALFYQDKLKSL
1			HQLLEVLLALLDKDVPENCKNCAQYFFLFNTFVQKQGIRAGDLL
			LRHSALRHMISFLLGASRQNNQIRRWSSAQAREFGNLHNTVALL
J i			VLHSDVSSQRNVAPGIFKQRPPISIAPSSPLLPLHEEVEALLFM
·			SEGKPYLLEVMFALRELTGSLLALIEMVVYCCFCNEHFSFTMLH
			FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFETEN
,			GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH
}	ļ		WSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAODTLA
}	i		YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSESPMMIGEL
6055			RSDLDDVDP
6865	1820	1242	DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSQGSMMPSCNRS
			CSCSRGPSVEDGKWYGVRSYLHLFYEGYAVPPKLEGIGEGEFLV
]	J		LDQRAADYNQALGTCRLAGTALCVAAGVLLAICLFWAMIGWLSQ
	1		DTKAEPLDPEADSHVEVFGDEPEQQLSPIFRNASGQSWFSPPAS
6866	1571	40=	PFGQSSVQTIQPKRDS
5550	13/1	495	DCPRPRYTLYGLRATCMRDLDWAWINAVSAFKALEQDLPVNIKF
	!		IIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKP
) l	Í		AITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLG
[[1		SLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLEEYRNSSR
	Ì		VEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRV
	1		IGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTL
1	Ī		GLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMF
	į		QEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLFAAFFL EMAQLH
	- - L		FUMERU

SEO	Drodi et a	I Been did not not	
ID	Predicted beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid R-
NO.	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l .	sequence	sequence	Codon, /=possible nucleotide deletion,
6867	2833	1704	\=possible nucleotide insertion)
] ""	2033	1704	GTRIMSQPKQKELAGFVRQKMLLDYSVYMGRCVPQESRSPQRSP
1			LQSAESSPTAGKKLPEVPPSEEEEQEAWVNALLGRIFWDFLGEK
i,	1	}	YWSDLVSKKIQMKLSKIKLPYFMNELTLTELDMGVAVPKILQAF
			KPYVDHQGLWIDLEMSYNGSFLMTLETKMNLTKLGKEPLVEALK
ł			VGEIGKEGCRPRAFCLADSDEESSSAGSSEEDDAPEPSGGDKOL
1	ł		LPGAEGYVGGHRTSKIMRFVDKITKSKYFQKATETEFIKKKIEE
1	ł		VSNTPLLLTVEVQECRGTLAVNIPPPPTDRVWYGFRKPPHVELK
			ARPKLGEREVTLVHVTDWIEKKLEQEFQKVFVMPNMDDVYITIM
6868			HSAMDPRSTSCLLKDPPVEAADOP
0000	1	346	RPTRPPTRPEEIKNLILPYISDMNFVQDLCEDFYELFKTDKGFD
1			KATFESQMSVMRGQILNLTQALRDGKSPFQLVQIPCVIVERSQG
6869			GSQGRIVHLSNSFTQTVNCRKPFFSSW
6869	3	1619	MYMERMDKRALISFWESVEHLKNANKNEIPQLVGEIYQNFFVES
! I			KEISVEKSLYKEIQQCLVGNKGIEVFYKIOEDVYETIKDRYVDS
] [FIVSDLYEKLLIKEEEKHASQMISNKDEMGPRDEAGREAVDDGT
1			NQINEQASFAVNKLRELNEKLEYKROALNSIONAPKPDKKTVSK
			LKDEIILIEKERTDLQLHMARTDWWCENLGMWKASITSGEVTEE
1 1			NGEQLPCYFVMVSLQEVGGVETKNWTVPKRLSEFHNLHBKLSEC
1			VPSLKKDQLPSLSKLPFKSIDHTFMEKFENOLNKFLONLLSDER
i l			LCQSEALYAPLSPSPDYLKVIDVOGKKNSFSLSSFLERI,PRDFF
1 1			SHQEEETEEDSDLSDYGDDVDGRKDALAEPCFMLTGETEELPCM
1 1			FKWVRRTLIALVQVTFGRTINKQIRDTVSWIFSEOMLVYYTNIF
ŀ			RDAFWPNGKLAPPTTIRSKEQSOETKORAOOKLLENIPDMLOSI.
1 1			VGQQNARHGIIKIFNALQETRANKHLLYALMELLLIELCPELRV
6870	<u> </u>		HLDQLKAGQV
0070	- 1	1566	MAAVVAATRWWQLLLVLSAAGMGASGAPQPPNILLLLMDDMGWG
	j		DLGVYGEPSRETPNLDRMAAEGLLFPNFYSANPLCSPSRAALLT
<u> </u>	}		GRLPIRNGFYTTNAHARNAYTPQEIVGGIPDSEQLLPELLKKAG
	Ţ		YVSKIVGKWHLGHRPQFHPLKHGFDEWFGSPNCHFGPYDNKARP
	i		NIPVYRDWEMVGRYYEEFPINLKTGEANLTQIYLQEALDFIKRQ
			ARHHPFFLYWAVDATHAPVYASKPFLGTSQRGRYGDAVREIDDS
	i		IGKILELLQDLHVADNTFVFFTSDNGAALISAPEQGGSNGPFLC
			GKQTTFEGGMREPALAWWPGHVTAGQVSHQLGSIMDLFTTSLAL
ì	1		AGLTPPSDRAIDGLNLLPTLLQGRLMDRPIFYYRGDTLMAATLG
1	ł	ł	QHKAHFWTWTNSWENFRQGIDFCPGQNVSGVTTHNLEDHTKLPL
į	i		IFHLGRDPGERFPLSFASAEYQEALSRITSVVQQHQEALVPAQP
6871	209	1126	QLNVCNWAVMNWAPPGCEKLGKCLTPPESIPKKCLWSH
	200	1126	RMSLNPPIFLKRSEENSSKFVETKQSQTTSIASEDPLQNLCLAS
1			QEVLQKAQQSGRSKCLKCGGSRMFYCYTCYVPVENVPIEQIPLV
Į.	İ		KLPLKIDIIKHPNETDGKSTAIHAKLLAPEFVNIYTYPCIPEYE
ľ			EKDHEVALIFPGPQSISIKDISFHLQKRIQNNVRGKNDDPDKPS
i			FKRKRTEEQEFCDLNDSKCKGTTLKKIIFIDSTWNQTNKIFTDE
ł			RLQGLLQVELKTRKTCFWRHQKGKPDTFLSTIEAIYYFLVDYHT
6872	880		DILKEKYRGQYDNLLFFYSFMYQLIKNAKCSGDKETGKLTH
	990	459	FGLLMVVLSLIFMKGNCVREDLIFNFLFKLGLDVRETNGLFGNT
1	1		KKLITEVFVRQKYLEYRRIPYTEPAEYEFLWGPRAFLETSKMLV
1		J	LRFLAKLHKKDPQSWPFHYLEALAECEWEDTDEDEPDTGDSAHG
6873	1929		PTSRPPPR
· · · · · · · · · · · · · · · · · · ·	1323	955	DEQAVLCSKDKTYDLKIADTSNMLLFIPGCKTPDQLKKEDSHCN
1		i	IIHTEIFGFSNNYWELRRRRPKLKKLKKLLMENPYEGPDSQKEK
1	į.	ĺ	DSNSSKYTTEDLLDQIQASEEEIMTQLQVLNACKIGGYWRILEF
ſ		1	DYEMKLLNHVTQLVDSESWSFGKVPLNTCLQELGPLEPEEMIEH
			OT VOVOVVIOR PORTER PARTY AND A PARTY AND
1			CLKCYGKKYVDEGEVYFELDADKICRAAARMLLQNAVKFNLAEF
			QEVWQQSVPEGMVTSLDQLKGLALVDRHSRPEIIFLLKVDDLPE
			CENCIGARIVOEGEVIFELDADKICRAAARMLLQNAVKFNLAEF QEVWQQSVPEGMVTSLDQLKGLALVDRHSRPEIIFLLKVDDLPE DNQERFNSLFSLREKWTEEDIAPYIQDLCGEKQTIGALLTKYSH SSMQNGVKVYNSRRPIS

SEO	Predicted	Predicted end	I Amino and I
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
}	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
-	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	i *	\=possible nucleotide insertion)
6874	1	307	DSIADHVNSAAVNVEEGTKNLGKAAKYKLAALPVAGALIGGMVG
			GPIGLLAGFKVAGIAAALGGGVLGFTGGKLIQRKKQKMMEKLTS
			SCPDLPSQTDKKCS
6875	1688	349	VIGTGERGNSASEKWEIMFNEELGDPFIIIHSISLLNAEEHSIA
1			TLLLRIEKEELDMKGSGFYVSLEWVTISKKNQDNKKYEIIKRDI
{	i		LRGKSVPHYAAIEPDGNGLMIVSYKSLTFVQAGQDLEENMDEDI
			SEKIKEPLYYWQQTEDDLTVTIRLPEDNTKEDIQIQFLPDHINI
ſ	1		VLKDHQFLEGKLYSSIDHESSTWIIKESNSLEISLIKKNEGLTW
	!		PELVIGDKQGELIRDSAQCAAIAERLMHLTSEELNPNPDKEKPP
			CNAQELEECDIFFEESSSLCRFDGNTLKTTHVVNLGSNOYLFSV
	1		IVDPKEMPCFCLRHDVDALLWOPHSSKODDMWEHTATFNALGVV
	•		QASKRDKKFFACAPNYSYAALCECLRRVFIYROPAPMSTVI,VNP
ł]		KEGRQVGQVAKQQVASLETNDPILGFQATNERLFVLTTKNLFLI
6876	41		KVNTEN
"""	41	1285	VGEMTLIWRHLLRPLCLVTSAPRILEMHPFLSLGTSRTSVTKLS
1			LHTKPRMPPCDFMPERYQVIFLVNSGSEANELAMLMARAHSNNI
			DIISFRGAYHGCSPYTLGLTNVGIYKMELPGGTGCQPTMCPDVF
			RGPWGGSHCRDSPVQTIRKCSCAPDCCQAKDQYIEQFKDTLSTS
			VAKSIAGFFAEPIQGVNGVVQYPKGFLKEAFELVRARGGVCIAN
1			EVQTGFGRLGSHFWGFQTHDVLPDIVTMAKGIGNGFPMAAVITT
1			PEIAKSLAKCLOHFNTFGGNPMACAIGSAVLEVIKEENLOENSO
l i			EVGTYMLLKFAKLRDEFEIVGDVRGKGLMIGIEMVQDKISCRPL PREEVNQIHEDCKHMGLLVGRGSIFSQTFRIAPSMCITKPEVDF
			AVEVFRSALTQHMERRAK
6877	1	778	GTSPSPARAYAPPTERKRFYQNVSITQGEGGFEINLDHRKLKTP
1 1	J		QAKLFTVPSEALAIAVATEWDSQQDTIKYYTMHLTTLCNTSLDN
}			PTQRNKDQLIRAAVKFLDTDTICYRVEEPETLVELQRNEWDPII
1 1			EWAEKRYGVEISSTSIMGPSIPAKTREVLVSHLASYNTWALQG
1			IEFVAAQLKSMVLTLGLIDLRLTVEOAVLLSRLEEEYO1OKWGN
			IEWAHDYELQELRARTAAGTLFIHLCSESTTVKHKIJKE
6878	931	263	QTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEOGON
1	1		LEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCODKEGNDAD
1	[EYTWFKDGIRLLENPRLGSOSTNSSYTMNTKTGTLOFNTVCKLD
i I	1		TGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVALVIS
] }			VCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSF
6879	3	945	II
		845	IRVIGESDIMQEFLSESDENYNGVSDVELRVALPDGTTVTVRVK
			KNSTTDQVYQAIAAKVGMDSTTVNYFALFEVISHSFVRKLAPNE
	,		FPHKLYIONYTSAVPGTCLTIRKWLFTTEEEILLNDNDLAVTYF
) i	Į		FHQAVDDVKKGYIKAEEKSYQLQKLYEQRKMVMYLNMLRTCEGY
	1		NEIIFPHCACDSRRKGHVITAISITHFKLHACTEEGQLENQVIA FEWDEMQRWDTDEEGMAFCFEYARGEKKPRWVKIFTPYPNYMHE
	İ		CFERVFCELKWRKEEY
6880	2110	1437	RKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISS
			MANIYNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRS
			NRDQIKNCGFFYGHRAFSVALIFVTAFQGLSVAFILKFLDNMFH
	!	Ī	VLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFIYNAS
			KPQVPEYAPRQERIRDLSGNLWERSSGDGEELERLTKPKSDESD
			EDTF
6881	2638	2244	NDSKWEDIHVITGALKMFFRELPEPLFTFNHFNDFVNAIKQEPR
		ŀ	QRVAAVKDLIRQLPKPNQDTMQILFRHLRRVIENGEKNRMTYQS
			IAIVFGPTLLKPEKETGNIAVHTVYQNQIVELILLELSSIFGR
6882	1	850	GIPEAQLWIYPVKSCKGVPVSEAECTAMGLRSGNLRDREWLVIN
		.]	QEGNMVTARQEPRLVLISLTCDGDTLTLSAAYTKDLLLDIKTPT
		1	TNAVHKCRVHGLEIEGRDCGEATAQWITSFLKSOPYRLVHFEPH
			MRPRRPHQIADLFRPKDQIAYSDTSPFLILSEASLADLNSRLEK

		T =	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
J	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	residue of	residue of	S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
-		sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1		1	KVKATNFRPNIVISGCDVYAEDSWDELLIGDVELKRVMACSRCI
1	1		LTTVDPDTGVMSRKEPLETLKSYRQCDPSERKLYGKSPLFGQYF
6883	2794	2255	VLENPGTIKVGDPVYLLGQ
""	4/34	2256	NSKLKLNONLKLFITLTYQVLSLHGWGPGIHLQKEGAFPVTQNR
ľ			ALQLLYDLRYLNIVLTAKGDEVKSGRSKPDSRIEKVTDHLEALI
,		1	DPFDLDVFTPHLNSNLHRLVQRTSVLFGLVTGTENQLAPRSSTF
	<u> </u>		NSQEPHNILPLASSQIRFGLLPLSMTSTRKAKSTRNIETKAQYD
6884	2	99	ANC
6885	297		EFERVTAEAVKPRETSEPRAAAQRFCEKFPFL
5505	231	1554	STGQFWHVTDLHLDPTYHITDDHTKVCASSKGANASNPGPFGDV
			LCDSPYQLILSAFDFIKNSGQEASFMIWTGDSPPHVPVPELSTD
			TVINVITNMTTTIQSLFPNLQVFPALGNHDYWPQDQLSVVTSKV
	1		YNAVANLWKPWLDEEAISTLRKGGFYSQKVTTNPNLRIISLNTN
			LYYGPNIMTLNKTDPANQFEWLESTLNNSQQNKEKVYIIAHVPV
ł	1		GYLPSSQNITAMREYYNEKLIDIFQKYSDVIAGQFYGHTHRDSI
į			MVLSDKKGSPVNSLFVAPAVTPVKSVLEKQTNNPGIRLFQYDPR DYKLLDMLQYYLNLTEANLKGESIWKLEYILTQTYDIEDLQPES
1			LYGLAKQFTILDSKQFIKYYNYFFVSYDSSVTCDKTCKAFQICA
			IMNLDNISYADCLKOLYIKHNY
6886	2	1341	QCGGIPGREGGSSRPLEEGTGSSPACVRGAAPGSEDAFYPTRAK
1			QARVSQELKKAAKRTVSISEGPDTLGDGMRERRETLALAPEPEP
			LEKEACEKWKRPFRSASATSLTLSHCVDVVKGLLDFKKRRGHSI
	1		GGAPEQRYQIIPVCVAARLPTRAQDVLDAHLSEVNAVRFGPNSS
į.	!		LLATGGADRLIHLWNVVGSRLEANQTLEGAGGSITSVDFDPSGY
1			QVLAATYNQAAQLWKVGEAQSKETLSGHKDKVTAAKFKLTRHQA
1	}		VTGSRDRTVKEWDLGRAYCSRTINVLSYCNDVVCGDHIIISGHN
1			DQKIRFWDSRGPHCTQVIPVQGRVTSLSLSHDOLHLLSCSRDNT
			LKVIDLRVSNIRQVFRADGFKCGSDWTKAVFSPDRSYALAGSCD
			GALYIWDVDTGKLESRLQGPHCAAVNAVAWCYSGSHMVSVDQGR
			KVVLWQ
6887	1047	116	WTARPSQKPFWEAGAVPGDPLSTGCSQAQLGGCCPRGPWGPQHG
1			GQQRAAGPTLPRGERGGPQQSGPGLAAQTPPTSKQVAWRAFLTG
J			TYRSQSPRSPAGPFRGGTGWWPEPAVCLCVAVGPORLSSPGLVY
1 1	1		NASGSEHCYDIYRLYHSCADPTGCGTGPDARAWDYOACTEINLT
			FASNNVTDMFPDLPFTDELRQRYCLDTWGVWPRPDWLLTSFWGG
			DLRAASNIIFSNGNLDPWAGGGIRRNLSASVIAVTIQGGAHHLD
	!		LRASHPEDPASVVEARKLEATIIGEWVKAARREQQPALRGGPRL
<u></u>			SL
6888	1	992	FVAYVKKEIPHIVVTHCLLNPHALVIKTLPTKLRDALFTVVRVI
1			NFIKGRAPNHRLFQAFFEEIGIEYSVLLFHTEMRWLSRGQILTH
1			IFEMYEEINQFLHHKSSNLVDGFENKEFKIHLAYLADLFKHLNE
			LSASMORTGMNTVSAREKLSAFVRKFPFWQKRIEKRNFTNFPFL
			EEIIVSDNEGIFIAAEITLHLQQLSNFFHGYFSIGDLNEASKWI
		ĺ	LDPFLFNIDFVDDSYLMKNDLAELRASGQILMEFETMKLEDFWC
]			AQFTAFPNLAKTALEILMPFATTYLCELGFSITFTFQNKVPEAA
6889		15-	LILSDDIRVAISKKVPSFLGHH
0009	1	1534	LTLENQIKEEREQDNSESPNGRTSPLVSQNNEQGSTLRDLLTTT
1			AGKLRVGSTDAGIAFAPVYSMGAPSSKSGRTMPNILDDIIASVV
1	,		ENKIPPSKTSKINVKPELKEEPEESIISAVDENNKLYSDIPHSW
, l	1		ICEKHILWLKDYKNSSNWKLFKECWKQGQPAVVSGVHKKMNISL
J	 		WKAESISLDFGDHQADLLNCKDSIISNANVKEFWDGFEEVSKRQ
]			KNKSGETVVLKLKDWPSGEDFKTMMPARYEDLLKSLPLPEYCNP
			EGKFNLASHLPGFFVRPDLGPRLCSAYGVVAAKDHDIGTTNLHI
į į	1		EVSDVVNILVYVGIAKGNGILSKAGILKKFEEEDLDDILRKRLK
1			DSSEIPGALWHIYAGKDVDKIRBFLQKISKEQGLEVLPEHDPIR
L			DQSWYVNKKLRQRLLEEYGVRTWTLIQFLGDAIVLPAGALHQVQ

SEQ	Predicted	Predicted end	I ami no poid
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	•	\=possible nucleotide insertion)
			NFHSCIQVTEDFVSPEHLVESFHLTQELRLLKEEINYDDKLQVK
1	}		NILYHAVKEMVRALKIHEDEVDDMEEN
6890	3	667	THACGMWIPLYLHRALVVHKTAETCNSPPCGAKDSLIFGAITCF
			TGFLGVDTGAGATRWCRLKTQRADPLVCAVGMLGSAIFICLIFV
1	ł		AAKSSIVGAYICIFVGETLLFSNWAITADILMYVVIPTRRATAV
			ALQSFTSHLLGDAGSPYLIGFISDLIRQSTKDSPLWEFLSLGYA
[LMLCPFVVVLGGMFFLATALFFVSDRARAEQQVNQLAMPPASVK
1			A SEMANDINA SOCIAL APPROPRIATION OF A SEMANDINA SOCIAL DESCRIPTION OF A SE
6891	1980	1262	LRIHQELLSKELKLLRGITIESIIHIGLAAGKEQFMQDASNVMQ
			LLLKTQSHLYNMEDNNPEVRQAAAYGLGVMAQFGGDDYRSLCSE
1			AVPLLVKVIKRAHSKTKKNVIATENCISAIGKILKFKPNCVNVD
1			EVLPHWLSWLPLHEDKEEAIQTLSFLCDLIESNHPVVIGPNNSN
1			LPKIISIIAEGKINETINYEDPCAKRLANVVRQVQTSEDLWLEC
		L	VSQLDDEQQEALQELLNFA
6892	3	876	RSVAAASGPGAWGTDHYCLELLRKRDYEGYLCSLLLPAESRSSV
			FALRAFNVELAQVKDSVSEKTIGLMRMQFWKKTVEDIYCDNPPH
			QPVAIELWKAVKRHNLTKRWLMKIVDEREKNLDDKAYRNIKELE
			NYAENTQSSLLYLTLEILGIKDLHADHAASHIGKAOGIVTCLRA
1.	[TPYHGSRRKVFLPMDICMLHGVSQEDFLRRNODKNVRDVIYDIA
İ			SQAHLHLKHARSFHKTVPVKAFPAFLQTVSLEDFLKKIQRVDFD
			IFHPSLQQKNTLLPLYLYIQSWRKTY
6893	1	842	DGERKSMSVERTFSEINKAEEQYSLCQELCSELAQDLQKERLKG
			RTVTIKLKNVNFEVKTRASTVSSVVSTABEIFAIAKELLKTEID
			ADFPHPLRLRLMGVRISSFPNEEDRKHQQRSIIGFLQAGNQALS
	1		ATECTLEKTDKDKFVKPLEMSHKKSFFDKKRSERKWSHQDTFKC
1	[]		EAVNKQSFQTSQPFQVLKKKMNENLEISENSDDCQILTCPVCFR
1			AQGCISLEALNKHVDECLDGPSISENFKMFSCSHVSATKVNKKE
6894	1742	1463	NVPASSLCEKQDYEAH
3331	1742	1403	TTLCKPLVPREHQFYETLPAEMRKFTPQYKGKSQLLEGLPHWRG
1			DVRDRGHGRPWQPSLEPSLPPTLCFPSLSSFSSSWPSAQHLTPS VFNPW
6895	2379	478	
	-3.3	410	VTYVELCDLASPTALLIMRTVLDLIVEDLQSTSEDKEQQYTSQT
1	!		TRLLALLYALASHKACKLAILHLINGTIKGDERYAEIFQDLLAL VRSPGDSVIRQQCVEYVTSILQSLCDQDIALILPSSSEGSISEL
[]			EQLSNSLPNKELMTSICDCLLATLANSESSYNCLLTCVRTMMFL
}	ļ		AEHDYGLFHLKSSLRKNSSALHSLLKRVVSTFSKDTGELASSFL
			EFMRQILNSDTIGCCGDDNGLMEVEGAHTSRTMSINAAELKQLL
			QSKEESPENLFLELEKLVLEHSKDDDNLDSLLDSVVGLKOMLES
1 1	}		SGDPLPLSDQDVEPVLSAPESLQNLFNNRTAYVLADVMDDQLKS
	Ì		MWFTPFQAEEIDTDLDLVKVDLIELSEKCCSDFDLHSELFPSFT.
]		SEPSSPGRTKTTKGFKLGKHKHETFITSSGKSEYIEPAKRAHVV
ļ †	l.		PPPRGRGGGGGGGIRPHDIFRQRKQNTSRPPSMHVDDFVAAES
1	ļ		KEVVPQDGIPPPKRPLKVSQKISSRGGFSGNRGGRGAFHSQNRF
			FTPPASKGNYSRREGTRGSSWSAQNTPRGNYNESRGGQSNFNRG
1 1	1		PLPPLRPLSSTGYRPSPRDRASRGRGGLGPSWASANSGSGGSRG
<u>l</u>			KFVSGGSGRGRHVRSFTR
6896	1	. 555	GNIVIQKKKYNKQHIIPLENVTIDSIKDEGDLRNGWLIKTPTKS
1 1	ļ		FAVYAATATEKSEWMNHINKCVTDLLSKSGKTPSNEHAAVWVPD
ļ l	ſ		SEATVCMRCQKAKFTPVNRRHHCRKCGFVVCGPCSEKRFLLPSO
i 1			SSKPVRICDFCYDLLSAGDMATCQPARSDSYSQSLKSPLNDMSD
			DDDDDDSSD
6897	3	920	GDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHY
1 1			AGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVL
1		ļ	SLAWGFIADVDLESEKYRRLGEMRFTLGTFLRLAALRTYRGRLA
[ľ	YLPVGRVGSKTPASPVVVQQGPVDAHLVPLEEPVPSHWTVVPDE
<u> </u>			DFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAML

Sto	CEC	Dwo dis at - 3		
No: nuclectide location corresponding to first samino acid corresponding to first samino acid residue of amino acid sequence sequ	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
corresponding to first to firs				M=Alanine, C=Cvsteine
corresponding to first amino acid amino acid amino acid sequence s	140:		1	Giutamic Acid. F=Phenylalanine G_Cluster
Lo first amino acid am	ł			H=H1SCIGINE, I=Isoleucine, K=Tysine
amino acid residue of amino acid amino acid amino acid sequence Part Part Part	1	corresponding		L=Leucine, M=Methionine N-Asparagine
residue of amino acid sequence	- [P=Proline, Q=Glutamine, R=Arginine
amino acid sequence s	j			S=Serine, T=Threonine, V=Valine
Sequence Codon, /-possible nucleotide deletion, -possible nucleotide dinection -possible nucleotide nucleotide dinection -possible nucleotide nucleotide nucleotide nknown * Gb				
Tell-lamerighemeyscrivity provaries production Tell-lamerighemeyscrivity provaries productive Tell-lamerighemeyscrivity provaries productive Tell-lamerighemeyscrivity provaries productive Tell-lamerighemeyscrivity provaries Tell-lamerighemeyscrivity provaries Tell-lamerighemeyscrivity provaries Tell-lamerighemeyscrivity provaries Tell-lamerighemeyscrivity Tell-lamerigheme			sequence	Codon, /=possible nucleotide deletion
LELE-AMERIKRIEMBYSCP/LVVVVPAFRLEPROGKOVFAVEDED AWSEAW/GGVPAPFERD	<u> </u>	sequence		\=possible nucleotide insertion\
6898 919 346 OKTITANASLLKGROGITYENERMEMOLITER LENGTH LITCH LENT INESLIFILEMOTDINGSSKPURTAAKTWIPKILLICG LENT INESLIFILEMOTDINGSSKPURTAAKTWIPKILLICG LENT INESLIFILEMOTDINGSSKPURTAAKTWIPKILLICG OCPILISLAFYGNTOSSIGSOSPKREQUENSKITTSAAEGAHPSPL MPHENDASGKVSQVGQGTSDEALSMLSEGSDASTIBIHTASESC NINSEGDPALPTHGDL 827 MKVKKNINDAYLLDKIKNINDCFISCFFKKMLTTLMFSHEGILSL LEHGESYTSJLCAYARSILTYPWELGGVWCAKTGYSASI TFHTKPYYGGKLHEVTABVKINITINTVUCUCGENSVLEFTYS NGETKYVDLYKLAPTKKRYPLEKODPFSSRLWKNYTDSIJRES SIDKATEHKHTLEERGRTEERHETETGTPWKTKYFIKEGDGWY HKPLMKI IPTTOPAB 6900 3 451 FEVIGSKGIHBLRSTSTALHHALESSSLLMFFRRALDSTHIF VLPGKWGESTERELLELITKYSOGCOLOSTIBIHKNANQKS MEGFIVSQLITRTHDVIKKARTINLEVRKLLHQSEAPSLPFYSK MEGFIVSQLITRTHDVIKKARTINLEVRKLLHQSEAPSLPFYTHHH LADLVCUSWPALKROFFVLLOGS FEVRARQFILKMSFYRVHLOFS 6901 1 201 DDNNVGRLETDFKWITLOGOSTLEGMAAWLDNVMMQALKPYEGRP SFPKARAGPLIKMSFYRVHLOFS 6902 2 267 GAPPFPFSQDPEROPDGARPSSHHHSDLFFRESSALEGQAGAGA SADMEPSSLUDLIPLINTUPDELISVLDDP DLIPRINNDLSLFLENN HILK HILK HILK MESSLDVSLSCVLACCDVECKFDILLNEVQAIQKKSGNFDLLLC VGNFFGSTODABESENVERI KKAPIQTYVUGANNGETKYFQDA DGCELAENITYLGRAGIFYSSSCLOIVVLGANNGETKYFQDA DGCELAENITYLGRAGIFYSSSCLOIVVLGANNGETKYFQDA DGCELAENITYLGRAGIFYSSSCLOIVVLGANNGETKYFQDA DGCELAENITYLGRAGIFYSSSCLOIVVLGANNGETKYFQDA DGCELAENITYLGRAGIFYSSSCLOIVVLGANNGETKYFQDA DGCELAENITYLGRAGIFYSSSCLOIVVLGANNGETKYFQDA DGCELAENITYLGRAGIFYSSSCLOIVVLGANNGETKYFQDA DGCELAENITYLGRAGIFYSSCESPERHLWWIGHT REPFSSRGKWPPPOPOPOPOPOPOPOPICHERSSGEWD TKKCGSALVSSLATLANVGURERFRALIKNYTYERLPYRNSILLOGN AGRIFTER LAALDVGURERFTILLDFENNAVENEEVKAPL REPFSSRGKWPPPDLAGATKYRIJAFFVELDTGKKHHR REPFSSRGKWPPPDLAGAFFVELDTGKGRKRSS TGGSKSSGNAGGORDFENNAKHHRITAAR TRUDPETTILD 6905 1 226 VSKTGRETTTSSHYLFALGVERTLYLFNWINSTHERFODLIKDAF TEVRKTKIRNGISFTIDBRATKKRSSNMKRLSPAPOLGFSS DAHTSYYSESTHULMSFPRSSLEELHGANFTNILLAPIVVFTET TEVRKTKIRNGISFTIDBRATKKRSSNMKRLSPAPOLGFSS DAHTSYYSESTHULMSFPRSSLEELHGANGELRVERKYGG SSSGSSVAGSOSTLFGOPPRTYKSGEDLFUKTKYGGDDDGS SSGGSSVAGSOSTLFGOPPRTYKSGELFLIKARNAGETTREVTCUTTA SLLDVFULTRRSSLLKFLAPRILLDLLUTCUTAGAFFYPGLG THAALUSUNAGARPSSLEELHGANGERSLERGERDE	1			LRLFLAMEKGRHMEYECPYLVYVPVVAFRLEDKDGKGVEAUTOR
OKTYTAVASLIKGROGIYTENERMIGAVIKIRFFKIMULIICG LENIINSELFYLEMTOINGSLKEVPIKATTVEIMSLINDA QCFILISLAPYGNICCSLGFQSPRKETQMESITTSAAGAHPSPL MPHENPASKVSQVGQGTDERLSMLSEGSDATIBHTASESC NINISGDPALPTHGDL 827 MEVEKINDAYLDENKINDCFISCFFKGMLTTLMESHSGILSL LEHGESYTSJPCAYARSILTVPBVSLGGKVSVANCANCTYGASI THYKTRYVADAYLDENKINNDCFISCFFKGMLTTLMESHSGILSL LEHGESYTSJPCAYARSILTVPBVSLGGKVSVANCANCTYGASI THYKTRYVADAYLDENKINNDCFISCFFKGMLTTLMESHSGILSE EIDAATEHHTLISERGRISHINITVAVVGCGHNISULEFTYS NGETKAVDLITKLAVIKRVRPLERGOPFESSRLWKNVTDSIRBS EIDAATEHHTLISERGRISTERHTETGTPWKTYFYIKRGDGWVY HERUMKIIPTTQABA 6900 3 451 TEVUGSKGHELBERSTSALHHALEESASLLIMFNRAALPSTHIP VLPKKVGESTERELLELRTKVSOOGOLLOGTTEHLKONANQGKS HERDIVISULTRIHVULKCARTNLEVYKLLGGSBAPSLEPTHHPI LADLVGDSRPALRFON LADLVGDSRPALRFON LADLVGDSRPALRFON LADLVGDSRPALRFON LADLVGDSRPALRFON GFFGARQPLIKNSPYRTHLOFS 6901 1 201 DORNVORLITTIFKWTTQQGTTLEQWAAWLDNVMMQALKPYEGRP SPENARQPLIKNSPYRTHLOFS 6902 2 267 GAPPFPSGPFGPPGAPSSHHBSDLTFNESSALEGOAGAGA GAPPFPFSGLPFWHTQGGSTLEQWAAWLDNVMMQALKPYEGRP GFFGARQPLIKNSPYRTHLOFS 6903 1 149 RINGVYRGGFTGIHTLVICMWCNNCDDSCFLESTVKAESSDGI HILL GFFGARGVENSPHELSSVLDPSCHOOKHDLISTSPWEDSADEGOAGAGA AGARTEFLALALANGAPEKKRYLDASILVGANANGETVKYPQDA DGCELABHITYLGRKGIFTGSSGLQIVYLSGTTSINEVPGYSF SPENDVSSLRWMLCTTGSFKOUTDLLTSSFWEGHTDLLUCK VGMFFGSTQDAEWEYKGGIKKAPLGTVULGANNGETVKYPQDA DGCELABHITYLGRKGIFTGSSGLQIVYLSGTTSINEVPGYSF SPENDVSSLRWMLCTTGSFKOUTDLLTSSFWEGHTLVVGNCBKRSS TGRDSKSPHENKOTTGSFKOUTDLLTSSFWEGHTLVVGNCBKRSS TGRDSKSPHENKOTTGSFKOUTDLLTSSTUDIKOAP TKKCGSALVSSLATGLKFRYHFAALKTYYERLPYRNHILLOR AGARTEFLALANGAPEKKRYLDASILVFTGSTDDILKOAP TITAQGQGIELLEIFERSDIKGIAAPGAAFFVELDTGSTDDILKOAP TITAQGCQIELLEIFERSDIKGIAAPGAAFFVELDTGSTDDILKOAP TITAQGCQGIELLEIFERSDIKGIAAPGAAFFVELDTGSTDDILKOAP TTALAKGSLONDHALLIFTGSFTLIMINFRRYBETGFFDLIAT VAGLUOTYLVCDFFYLVITKVLKKKKLSLDA SYDDINGHIDFTTAASNICARSHILOOUT PURTYTEKTYOLDTG TEVRTYIKINGISFTLIMINFRAFTEGFFDLIAT VAGLUOTYLVCDFFYLVTTRVBLITTAKSCHUTHEKTYTGGDDDGS SSGGSSVAGSGSTAGGGIAFRTSGGEFTLIMINFRRYGGLTGKTVOLTTCAAWFFTYNGL DATTTYSGLVALBERGFFTSALTIGETHELLUCTUGAWFTYNGLUTTAA SLLDVFVLTRRSSLLTFL	6890	910		LMVSEAVQGQVHPNYFWMVSGCVEPPPSWKPOOMPDBEED
GSESSASGUAGKARTERIELDER LENN LINESULFYLENGTDINGSSIKPURTAAKTTWEIMGLINDA GOFFLISLAFYGMTCGLIGGOSPKEKEUMSTGABGARPSPL MHENDRAGKVSQVGGGTSDEALSMLSGGSDASTIEHTRASESC MKVKKNDAYLLDENKINNDCFISCFFKKMLTTLMFSHIGGLISL LEHGESYTESJDCAYARS LITYPWPELGGVWACKTGYSASI TFHTKPYGGKLHRVTASVKINITITNTVVCRVGGGWSVLEFTYS NGETKYVDLYKLAUTKKRYPLEKODPTESRLWKRVTDSIRGE EIDKATEHKHTLSERGRTEEHHRTETGTPWKTKYFIKEGGGWVY HKPLMKILFTTOPAB FILVINGSKGIHELRSSTSALHHALESSASLLMFWFRAADSTHIF FULGSKGIHELRSSTSALHHALESSASLLMFWFRAADSTHIF FULGSKGIHELRSSTSALHHALESSASLLMFWFRAADSTHIF FORD 1 201 DDNNVQRLETDFKMTLOGGSTLEGWAANLDNVMMQALKPYEGRP SFPKAARGFLIKMSFYRVHLGOSS GODO 1 1 201 DDNNVQRLETDFKMTLOGGSTLEGWAANLDNVMMQALKPYEGRP SFPKAARGFLIKMSFYRVHLGOS GODO 2 2 267 GAPPFPFSGPFROPDAAPSSHHHSDLAFFNSSALLKGAARAGA GOO 3 1 149 RINGVYRGGPTGHILVIDOMVQNFQDESCFLFSTVKARESSDGI HILIK 6904 464 2092 MEASLDVSLSCVLACGDVERKFDILFNRVOALGKKSGNFDLLLC WENFESSTOADBEBESKLDLAFSLSVLDPLOAGTRSSALLKOFTKYFQDA GGCLAENITYLGRKGIFFGSSGLOTYVLGANNOSTVKFGOA GGCLAENITYLGRKGIFFGSSGLOTYVLGANNOSTVKFOA GARTRFTLALAUNGPBEKKNFURABLKTVTRARPTWFHTHILOGN AGARTRFTLALAUNGPBEKKNFURABLKTVTRARPTVFHDENSGSGEVD TKKCGSALVSSLATGLKOFTHPARICHTSREVEWGYSF TGREKSSPHRKOPTKNFOADSTOKTVLGAPSVERHLVWIGTH CYTALAKGGLSDDHVLLTGTGVGVVELGAPSVERHLVWIGTH CYTALAKGGLSDDHVLLTGTGVGVVELGAPSVERHLVWIGTH CYTALAKGGLSDDHVLLTGTGVGVVELGAPSVERHLVWIGTH CYTALAKGGLSDDHVLLTGTGVGVVELGAPSVERHLVWIGTH REFFESRGKNCVVPERNYSHTELD GTGTGVFVVELGAPSVERHLVWIGTH CYTALAKGGLSDDHVLLTGTGTGVGVVELGAPSVERHLVWIGTH CYTALAKGGLSDDHVLLTGTGTGVGVVELGAPSVERHLVWIGTH CYTALAKGGLSDDHVLLTGTGTGVGVVELGAPSVERHLVWIGTH CYTALAKGGLSDDHVLLTGTGTGVGVVELGAPSVERHLVWIGTH CYTALAKGGLSDDHVLLTGTGTGVGVVELGAPSVERHLVMTGTGT CYTALAKGGLSDDHVLLTGTGTGVGVVELGAPSVERHLVMTGTGT CYTALAKGGLSDDHVLLTGTGTGVGVVELGAPSVERHLVMTGTGT CYTALAKGGLSDDHVLLTGTGTGVGVVELGAPSVERHLVMTGTGT CYTALAKGGLSDDHVLTKGTGTGTGTGTGTGTTGTTGTTTGTTGTTTTTTTTTT	0000	319	346	QKTVTAVASLLKGROGIYTENERRMGAVIKIRFFKIMIJU ITOW
GOPLISLAFYGNIGGSLGYGNGESLTABAEGAHPSPL	ļ	1	}	LSNIINESLLFYLEMOTDINGGSLKPVRTAAKTTWFTMGTINDA
6899 120 827 MKVEKDRAPTFIGDL EHRESYTSJECANSKILTIMERSISGILSK EHRESYTSJECANSKILTIVMEVLIGKVSVNICAKTOYSASI TFHTKPFYGGKLHRVTAEVKHNITTVUCRVQGEMISULEPTYS SIEDATEHHHTLERQKTEERHRTTGTPMKTKYFIKEGDGWY HEPLMKI IPTTOPAB 6900 3 451 FEVIGSKGIHERTSSTSALHHALESSASLITMFWRAALPSTHIP ULPKVGGSTSRELLELERTKVSOGEQLLGSTTEHHKNANOQKES MEGPIVSOLTRTHIPVLKKARTRLEVRKLEGGEASSTPHHIP LADLVOLSWPALRROEK MEGPIVSOLTRTHIPVLKKARTRLEVRKLEGGEASSTPHHIP LADLVOLSWPALRROEK MEGPIVSOLTRTHIPVLKKARTRLEVRKLEGGEASSTPHHIP LADLVOLSWPALROEK MEGPIVSOLTRTHIPVLKKARTRLEVRKLEGGEASSTSPHHIP LADLVOLSWPALROEK MEGPIVSOLTRTHIPVLKKARTRLEVRKLEGGEASSTSPHHIP LADLVOLSWPALROEK MEGPIVSOLTRTHIPVLKKARTRLEVRKLEGGEASSTSPHHIP LADLVOLSWPALROEK MEGPIVSOLTRTHIPVLKKARTRLEVRKLEGGEASSTSPHHIP LADLVOLSWPALROEK MEGPIVSOLTRTHIPVLKKARTRLEVRKLEGGEASSTSPHHIP LADLVOLSWPALROEK MEGPIVSOLTRTHIPVLKKARTRLEVRKLEGGEASSTSPHHIP LADLVOLSWPALROEK MEGPIVSOLTRTHIPVLKKARTRLEVRKARTLEVRKESPHHIP LADLVOLSWPALROEK MEGPIVSOLTRTHIPVLKKARTRLEVRKARTRLEVRKLEGGAGAGAA SIDMEBISLOLLEFETDRHITLOGGUSTLEGWAAWLDNVMMQALRYPEGRP SFPKAROFELLEFTTRHILOGWOFFDESSACHESTVKAESSDGT HILK LADLVOLSWPALROEK MEGPIVSOLTARGERSPENSTLESSAGAGAGAA SIDMEBISLOLLEFTTRHILOGWOFFDESSAGAGAGAAA SIDMEBISLOLLEFTTRHILOGWOFFDESSAGAGAGAAAA MEASLEVSLSCVLACGDVEGKEPLLFRRVOATGKKSGENDELLC VGMFFGSTQDAEMEEYKTOIKKARIQTYVLGANNOFTVKYPODA DGCELAENITTLIGKGIFTGSSGGLOTYCTSENINEPUNGTS SPKNOSSLRMLCTTSGYKGVDILLITSPMKVVGNFGNSSGEVD TKKCGSALVSSLATGLKERTYSGESGETSINLERGGKKKSS TGRBSKSSPHKONFRYPOPPGEMINGTELSFTVRHILLOGRED AGHATFTALANVONPEKKKYLAPSIVPRHLAURGTEKKYNNICH CYTALAKGLSDBVVLIKDPFTHASTRANGENINEGGEKSENITKART RROFFSGGGASIGKARTSHOPPKSCHARGENGGGGAAYFYVLOTOFT TRYRTKIKRGGFTIMARKMYSTEHPALDFTNAKKKYGTE FREDEFYDETLIDD SYDDHROETHFTAASNIKARMISTERDABFKTGRIAGKITBAI ATTATVSGLVALEMIKVTGYTPFRAYKNWELNILATIVVFTET TSVRTKIKRIGISFTIMARKAMTSTEHPALDFTNAKKYGTE FREDEFYDETTLAD ATTATVSGLVALEMIKVTGYTPFRAYKNWELNILATIVVFTET TSVRTKIKRIGISFTIMARKAMTSTEHPALDFTNAKKYGTE FREDEFYDELLERGEARABENGOGGGGGGGGGGGSSSRAGGSGSTLFMANTAFSGREFTTATTYGGDDDGS SSSGGSSRAGGSUTFKORARSFORFETTATTYGGEDDGGGGGGGGGSGSSRAGGSGGGGGGALAHD TAALLEGLUARRAA	- [QGFLLSLAFYGWTGCSLGFOSPRKEIOWESI.TTSAAFGAUDEDI
REPRESENTED REPRESENTED REPRESENTED REPRESENTED REPRESENTED REPRESENTED REPRESENTED REPRESENTED REPRESEN				MPHENPASGKVSQVGGQTSDEALSMLSEGSDASTIEIHTASESC
BROWNINDAY LIDON TISCPPEKNELT TUMENS GILST EHRGESTYSSLCYMAS LITUPWEUGS WSVINCAKTYSASI TFHTKPPYGGKLHRUTAEVKHHITTUVCRUGEWISVINCAKTYSASI TFHTKPPYGGKLHRUTAEVKHHITTUVCRUGEWISVILETTYS NGETKYUDLTKLAUTKKRUPLEKQDFESRELWINVIDSLIRES EIDKATEHHRITLERQATEERIRTETGTPMKTKYFIKEGDGWY KPLWKI IPTTOPAB 1	6899	120	-	NKNEGDPALPTHGDL
LEHGESTTSLPCAVARSILITVPMVELIGGKUSVNICAKTGYSASI TFHTKTPFYGKLHRVTRASVRINITUVCRVIGGEMSVELFTYS NGETKYVDLTKLAVTKRAVRPLEKOPPFSSRLHWINVTDSLIRS EIDRATTHKHTLEERGRTEERHRTETGTPWKTKYFIKEGGGWY HKPLWKIIPTTOPAB TOVLGGKGITHEIRSSTSALHHALEESASLLTMFWRAALPSTHIP VLPGKVGESTERELLELRTKVSOOEOLLQSTITHLKNANQOKES MEOPIVSOLTRITHDVLKKARTNILEVRKLLEGGEAPSLSPTHHIP LADLVGDSWPALRTQEK 6901 1 201 DDNNVQRLETDPKMTLQQOSTLEQMAAULDNVMMQALKPYEGRP SFFKARAGPLLKWSTYRYHLGFS GAPPPPPSOPPROPPQAAPSSHHSDLTTNPSSALEGOAGAOGA SDMPEDSLDLIPELTINPELLSTUDPPDLPSNSNDDLLSLFPENN 6903 1 149 RINGVYRQGPTGIHLUVIDOMVONFQDESCFLPSTVKAESSDGI HIILK 6904 464 2092 MEASLPVSLSCVLACGDVEGKFDILFNRVOAIGKKEGNPDLLLC VGMPFGSTDDAWBERYNTGIKKAPIOTYVLGANNQETVKYPQDA DGCELAENTTYJGRKGIPTGSSGLQIVVLSGTSELBEPVPGVSF SPKNOVSLEMMLCTTSGPKOVOILLTSPWRCVONFGNSSGEVD TKKCGSALVSLAMGLCTTSGPKOVOILLTSPWRCVONFGNSSGEVD TKKCGSALVSLAMGLCTSGPKOVOILLTSPWRCVONFGNSSGEVD TKKCGSALVSLAMGLCTSGPKOVOILLTSPWRCVONFGNSSGEVD TKKCGSALVSLAMGLCTSGPKOVOILLTSPWRCVONFGNSSGEVD TKKCGSALVSLAMGLCTSGPKOVOILLTSPWRCVONFGNSSGEVD TKKCGSALVSLAMGLCTSGPKOVOILLTSPWRCVONFGNSSGEVD TKKCGSALVSLAMGLCTSGPKOVOILLTSPWRCVONFGNSSGEVD TKKCGSALVSLAMGLCTSGPKOVOILLTSTBWRCVONFGNSSGEVD TKKCGSALVSLAMGLCTSGPKOVOILLTSTBWRCVONFGNSSGEVD TKKCGSALVSLAMGLGTLARFYTHALGTVYRGRLPKHILLOR AGHATEFIALANVGNPEKKYLYARSIVPRHLILOR TKKCGSALVSLAMGLCTSGPKOVOILLTSTBWRCVONFGNSSGEVD TKKCGSALVSLAMGLCTSGPKOVOILLTSTBWRCVONFGNSSGEVD TKKCGSALVSLAMGLCTSGPKOVOILLTSTBWRCVONFGNSSGEVD TKKCGSALVSLAMGLCTSGPKOVOILLTSTBWRCVONFGNSSGEVD TKKCGSALVSLAMGLCTSGPKOVOILLTSTBWRCVONFGNSSGEVD TKKCGSALVSLAMGLCTSGPKOVOILLTSTBWRCHTARFTTALTURATIVERLAPT RRFFSSGCKMCVVPERNYKSHILDGOVILLTSTBWRCHTARFTTALTURATIVERLAPT RRFFSTOPTITLD TRANGTATURATIVERSGCAPTFTURATIVERLYRTTURATIVERLYRT RRFFKSGCKMCVVPERNYKSHILDGOVILLTGRKLFHR IKNNFLOFGRBVLASSAILTNPDKYDHOKGAMFTEGKLFHA ATTTATVSGLVAMAGNATTENDRAVTHGEDFKTKRIAGKITPAI TSVRTKITRNGISFTITDMWTVHCKEDFFTLLDFITNVKEKYGIE PTMVVQGVMLVVPWPGHAKKLKLTHHKLVKFTEKKYVDLTV SPAPDIDDDEDLEGPPVYYSSHOTUSDFFVORGOVINGUNG SSSGGSSVAGSGSTLEKSDPLFTTSGGGGGGGGISHBO THALLUSWWAARGSRANGENDEWFFORSSWRCHERPLE BRIEBLAABFSSNWGKBAN	0099	120	827	MKVRKNNDAYLLDKNKINMDCFISCFFKKMLTTLMFSHSGILSL
THINKPYGKLHRVTARVERPLEKOPPESRRIMENVIDGLIRES	ļ		1	LEHGEEYTFSLPCAYARSILTVPWVELGGKVSVNCAKTCVCACT
SINGTRANDERMAND AND SINGTRAND	ŀ			TFHTKPFYGGKLHRVTAEVKHNITNTVVCRVOGEWNGVI FETVE
6900 3 451 TEVIGSKGIHELESSTSALHMALEESASLLIMPFORALPSTHITP VLPGKKGIHELESSTSALHMALEESASLLIMPFORALPSTHITP VLPGKKGIHELESSTSALHMALEESASLLIMPFORALPSTHITP VLPGKKGUESSTERELLELRTKYSOOFOLLOSTTEHLKNANQKKES MEOFIVSOLTRTHUNLKKARTNLEVRKLLIGSEAPSLSPTHHED LADLUGDSWPALBEFORK 6901 1 201 DDNNVQRLETDFKMTLQQGSTLEQWAAWLDNVMMQALKPYEGRP SFFKARQFLLKWSFYRYHLGFS GAPPPPSOPPROPPOAPSSHPHISDLTFNESSALEGOAGACGA SDWEPSLOLLPELTNPDELLSYLDPPDLESNSNDDLLSLFENN HILK 6904 464 2092 MEASLPYSLSCVLACCDUEGKPDILFNNVQAIQKKEGNFPLLC VGNPFGSTODAEWEYKTGIKKAPIGTYVLGANNQSTVKYFGDA DGCELAENTTYLGRKGIFTGSSGGLQIVYLGGTESLMEPVPGVSF SPKDVSSLRMMLCTTSOPKGVDILLTSPWFKCVGNFGNSGSVD TKKCGSALVSSLATGLRERYHFAALEKTYYERLPYKNHILLOEN AGHATFIALANVGPPEKKYLVFGLAPPEVEKHLVVNIGTH CVIALAKGGLSDHVLILPIGHTOSVVELISAEVVEEVEKYKATL RRFKSGKWCVYPERNYKSHLUQUIPVFIGSSTTDIKDAF ITQAGEQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFFLOFGREVLASSALINVPDKSDWRQCJISKEDEETLARR FRKDPEPYDFTLDB 6905 1 226 VSKTGEAETITSHYLFALGYRTLYLFNNIWRYHFEGFFDLIAI VGKUGVTVLYCDFFVLYITKVLKKKLSLPA 6906 3 611 SYDDNINGHIPFTAASSLARKWSIEPADFFKTKRIAGKITPAI ATTTATVSGLVALBURIKVTGGYPSKYNIWRYHFEGFFDLIAI VGKUGVTVLYCDFFVLYITKVLKKKLSLPA 6907 2 2228 IRGVPVMAGAFFESSGEESTSHLIMPRKGQLTTYSQGDDDGS SSGSSSVAGSGSTLFROSPLETLIKKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPRSSLEELHGDANWGDLEVRRRRGT GGSESSRAGGLOKKATEPPLGSSYSSEDDVYSDVOQSS SSRLRSAVSRAGSLLMWATSPGRLFFLLYWMAGTTWYRLITTAA SLLDVFVLTRRFFSSLEELHGDANWGEDLEVRRRRGT GGSESSRAGGLOKKATEPPLGSSYSSEDDVYSDVOQSS SSRLRSAVSRAGSLLMWATSPGRLFFLLYWMAGTTWYRLITTAA SLLDVFVLTRRFFSSLEELHGDANWGEDLEVRRRRGT GGSESSRAGGLOKKATEPPLGSGYSSEDDVYSDVOQSS SSRLRSAVSRAGSLLMWATSPGRLFFLLYWMAGTTWYRLITTAA SLLDVFVLTRRFFSSLEELHGDANWGEDLEVRRRRGT GGSESSRAGGLOKKATEPPLGSGYSSEDDVYSDVOQSS SSRLRSAVSRAGSLLMWATSPGRLFFLLYWMAGTTWYRLITTAA SLLDVFVLTRRFFSSLVFFSSLEELHGRAGGPGGGGGGSHBD DLFKKIVPASQESEARIQQUKSEVGLEFORSSVKELRRLE BRIEBALAAFFSSNWCKEARREPELERGGRFGFGESSKERLERLE BLFKKEALAAFFSSNWCKEARREPELERGGRFGFGESSKERLERLE BLFKKEALAAFFSSNWCKEARREPELERGGRFGFGFSSVKELRRLE BRIEBALAAFFSSNWCKEARREPELERGGRFGFGFSSCKELRRLE BLOQLAGGOEAALKOSVAREFUCHOOTOSPGOPDA		ľ	1	NGETKYVDLTKLAVTKKRVRPLEKODPFESRRI WKMUTDGI DEC
HREMMITIPTOPADE				EIDKATEHKHTLEERQRTEERHRTETGTPWKTKYFIKEGDGWVY
TEVIGSKGI HEIRSTSTALHHIALEESABLITMFRRAALPSTHIP VLPGKVOESTERBLELERTVSQOEOLLOSTTEHLKNANQQKES MEOFIVSQLTRTHDULKKARTNILEVRKLLHQSEAPSLSPTHHHP LADLUGDSWPALRFORK 6902 2 267 GAPPPPSOPRROPPLARPSHPHEDLITFNESALESQAGACGA SDMEDESLOLLPELTNPDELLSYLDPPDLESNENDDLLSLPENN 6903 1 149 RINGVYRQGPTGIHLVIDQMVQNFQDESCFLFSTVKAESSDGI HILK HILK 6904 464 2092 MEASLEVSLSCVLACGDVEGKFDLLFNRVQAIQKKEGNFDLLLC VGNFFGSTQDABWESYKTGIKKAPIQVYLGANNQSTVKYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESIMEPVPGYSF SPKDVSSLRMMCTTSOPKGVDLITSPMRKVQNGSTVKSYFQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESIMEPVPGYSF SPKDVSSLRMMCTTSOPKGVDLITSPMRKVQNGSMSSGEVD TKKCGSALVSSLATGLRERYHFAALRKTYYERLPYRNHILLQEN AOHATFILLANVGNEKKKYLYAFSI VYMKMDAABLUKQPPD VTENPYRKSGQEASIGKQILAPVESACOFFFDLERKQORKRSS TGRBKSSSHPKQPRKPPQPPGCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDBVLLIFIGHTVGSVVELSAEVVEEVEKKKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPAPSCSTDDIKDAF ITQAQCQIELLEIPEIDIKQQRAAYFYVELDTGEKLFHR IKKNFPLOFGREVLASEAILNVPDKSDMRQCQISKEDBETLARR FRKDPEPTDFTLDD 4906 3 611 226 VSKTGEAETITSHYLFALGVYRTLYLFNNINRYHFEGFFDLIAI VAGLVQTVLYCDFFYLVITKKKKLISLPA STODMIGHIDFITAASNLRAKWSIEPADFFKTKRIAGKITPAT ATTTATVSGLVALEMIKVTGGYPFEAYKNIFLNALIPIVVFTET TEVRKTKINNGISFTIMDENTVHGKEDFTLLDFINAVEEKYGIE PTWVVQGVKMLYVVPWGGHAKRIKLITMHKLVRPTTEKKYVDLTV SPAPDIDDDEDLPGPPVYYFFSDDT 4007 2 2228 LEGVVPWAAGAFRSSGEETSLLMSRRSQRLTRYSQGDDDGS SSGGSSVAGSGSTLARGSGTLFKRSSMLTRRROF GGSESSRRSGLVGRKATEPFLGSSGYSSEDDYVGSDVOQGS SSRLRSAVSRAGSLLMWANTSPGRLFRLLYWMAGTTWFRITTAA SLLDVFVLTRFFSSLTFHMELLLTLTTCTYGAWYFPYGLO TFHPALVSWMAKDSRRADEGGEARDSSPHFQAEQRYMSRVHSL ERRLEALAEFSSNWOKEMMRLERELERGGAPGGGGGGGISHBD TLALLEGLVSRRBAALKGDFRRETTAARIQELSALRAEHQODEE BLFKKIVRASGESEARIQQUKSGEWGSMTGSFORSSVELERRLE DQLAGLQCELAALALKQSSVABEVGLLDOOLOGSSOKSLERRLE DQLAGLQCELAALALKGSVABEVGLLDOOLOGSPOSSVELERRLE DQLAGLGQELAALALKGSVABEVGLLDOOLOGSPOSSVELERRLE	6900		457	HKPLWKIIPTTQPAE
### ADDRIGHT OF THE PRINCE OF	""		451	TEVLGSKGIHELRSSTSALHHALEESASLLTMFWRAALPSTHIP
6901 1 201 DDNNVQRETDFKNTLQQGSTLEQMAMLDNVMMQALKPYEGRP 6902 2 267 GAPPPPSQPPRQPPQAPSSHPHSDLTFNPSALEGQAGAGGA 6903 1 149 RINGVYRQGFGHILWSPYRYHLGPS 6904 464 2092 MEASLPYLSCVLACGDVEGKFDILFNRVQAIQKKSGNPDLLSLFENN 6904 464 2092 MEASLPYLSCVLACGDVEGKFDILFNRVQAIQKKSGNPDLLLC 6904 VAGA 2092 MEASLPYLSCVLACGDVEGKFDILFNRVQAIQKKSGNPDLLLC 6904 VAGA 2092 MEASLPYLSCVLACGDVEGKFDILFNRVQAIQKKSGNPDLLLC 6905 VAGA 2092 MEASLPYLSCVLACGDVEGKFDILFNRVQAIQKKSGNPDLLLC 6906 VAGA 2092 MEASLPYLSCVLACGDVEGKFDILFNRVQAIQKKSGNPDLLLC 6907 VAGA 2092 MEASLPYLSCVLACGDVEGKFDILFNRVQAIQKKSGNPDLLLC 6908 VAGA 2092 MEASLPYLSCVLACGDVEGKFDILFNRVQAIQKKSGNPDLLLC 6908 VAGA 2092 MEASLPYLGRAGAVEGKFKYSTERPYPGYSF 6908 VAGA 2092 VAGA 2	i		i	VLPGKVGESTERELLELRTKVSOOEOLLOSTTEHI,KNANOOVES
DDNNVQRLETDFKMTLQQQSTLEQWAAWLDNVMMQALKPYEGRP SFPKARAQFILKWSFYRYHLGFS GAPPFPSQPRQFQAAPSHPHISDLTFNPSALEGQACAGGA SDMEPSJDLPELTNPDELLSYLDPPDLPSNSNDDLLSLFENN 6903 1 149 RINOVYRQBPGHILVIDQWVQNFQDESCFLFSTVKAESSDGI HILK 6904 464 2092 MEASLPVSLSCVLACGDVEKKFDLFNRVQAIQKKSGNPDLLLC VGMPFGSTQDAEWEYKRG KKAPIQTYVLGANNQETVKYPQDA DGCELABNITYLGRKGIFTGSGLQIVYLGGTESLNEPVPGYSF SPKUVSSLRMHLCTTSQFKGVDLLISPWPKCVONFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AQHATRFIALANVGNPEKKKYLVAFSIVPMKLMDAAELVKQPPD VTENPYKKSGQEASIGKGLDAVESSVELGFFDLNEKQGRKRSS TGRDSKSSPHPKQPRKPPQDPGPCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RAFFKSRGKWCVVFENNYKSHHLQLQVIPVPIGSSTTDIKDAF ITQAGQQIELLEIPEHSDIKQIAQPGAAVFYVELDTGEKLFHR IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDEBTLARR FRKDFSPYDFTLDD 4 VSKTGEAETITSHYLFALGVYTRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCPFFYLYITVKLKKKKLSLPA 4 SYDDRINGHTDFTTAASNLERKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFBAKTKWFLIALPIVVFTET TEVRKTKIRNGISFTIWDRWTHGKEDFTLLDFINAVEKYGIE FFTMVVQGVMLVYPVMPGHAKRLKITMHLLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVWYYSPHDTD 5 SSGGSSVAGSGSTLFKDSPLRTLKRKSSNMKRLEPAPQLGPSS SSGSSSVAGSGSTLFKDSPLRTLKRKSSNMKRLEPAPQLGPSS SSGSSSVAGSGSTLFKDSPLRTLKRKSSNMKRLEPAPQLGPSS SSGSSSVAGSGSTLFKDSPLRTLKRKSSNMKRLEPAPQLGPSS SSRLESAVSRAGSLUMWATSFFGLIFFLLYWMAGTTWYRLITTAA SLLDVFVUTRRFSSLKTTLWFLIPLLLLICTTTGAWYFYPYGLQ TFHPALUSWMAAKDSRRADEGWEARDSSPHFQAEQRYMSRVHSL ERRLEALAAEFSSMWOKEARDSSPHFQAEQRYMSRVHSL ERRLEALAAEFSSMWOKEARDSSPHFQAEQRYMSRVHSL ERRLEALAAEFSSMWOKEARDSSPHFQAEQRYMSRVHSL ERRLEALAAEFSSMWOKEARDSSPHFQAEQRYMSRVHSL ERRLEALAAEFSSMWOKEARDERLELERQGAPQGGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQODSE DLFKKIVRASGESEARIQOLKSEWOSMTQESFGSSVKELRRLE DDLALGQQELAAALLKGSVGATGGSFGSVKELRRLE DDLALGQQELAAALLKGSVGATGGSFGSVKELRRLE DDLALGQQELAAALLKGSVGATGGSFGSSVKELRRLE DDLALGQQELAAALLKGSVGATGGSFGSVKELRRLE DDLALGQQELAAALLKGSVGATGGSFGSSVKELRRLE DDLALGQQELAAALLKGGSVAGGGGGLANDDVSGSP	-		į	MEQFIVSQLTRTHDVLKKARTNLEVRKLLHOSEAPSLSDTHHUD
6902 2 267 GAPPPPPSQPPROPPGAAPSHPHEDLTFNPSSALEGQAGAGGA GAPPPPSQPPROPPGAAPSHPHEDLTFNPSSALEGQAGAGGA GAPPPPSQPPROPPGAAPSHPHEDLTFNPSSALEGQAGAGGA GAPPPPSQPPROPPGAAPSHPHEDLTFNPSSALEGQAGAGGA GAPPPPSQPPROPPGAAPSHPHEDLTFNPSSALEGQAGAGGA GAPPPPSQPPROPPGAAPSHPHEDLTFNPSSALEGQAGAGGA GAPPPPSQPPROPPGAAPSHPHEDLTFNPSSALEGQAGAGGA GAPPPPSQPPROPPGAAPSHPHEDLTFNPSSALEGQAGAGGA GAPPPPSQPPROPPGAAPSHPHEDLTFNPSSALEGQAGAGGA GAPPPPSQPPROPPGAAPSHPHEDLTFNPSSALEGQAGAGGA GAPPPPSQPPROPPGAAPSHPHEDLTSLIDEPUNDSALEGAGAGAGAGA GAPPPPSQPPROPPGAAPSHPHEDLTSLIDEPUNDSALEGAGAGAGAGA GAPPPPSQPPROPPGAAPSHPHEDLTSLIPEPUNDAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	6901	 	203	LADLVGDSWPALRFQEK
GAPPPPSQPPRQPPQAAPSSHPHSDLTFNPSSALEGQAGAGGA GP03 1 149 RINQVYRQGPTGIHLUVDQWVQNPQDESCFLFSTVKAESSGI HILLK 6904 464 2092 MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLC VGMPFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYPQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLINEPVPGYSF SPRUVSSLRWMLCTTSQPKGVDILLTSPMPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHILLQEN AQHATRFIALLANVGNPEKKKYLYAPSIVPMKKMDAAELUKQPPD VTENPYRKSGQEASIGKQILAPVEESACCFFFDLINERQGRKRSS TGRDSKSSPMPKQPRPPQPPPGWFCLASPEVEKHLVVMIGTH CYLALANGGLSDBHVLILIFIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPLSCSTTDDIKDAF ITQAQEQQIELLEIPEHEDIKQIAQFGAAYFFVELDTGEKLFHR IKNNFLQFGREVLASEALINVPDKSDWRQCQISKEDETLARR FFKDFPFYDFTLDD 3 611 SYDDINGHIDFITAASSLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKUTGYPFFAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHARKLKTHHKLVKPTTEKKYVDLTV SFAPPIDGBEDLFGPPWYYFSHDTD 6907 2 2228 LEGVPVWAAGAFRFSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSGSTIFKDSPLRTLKRKSSMNKRLSPAPQLGPSS DAHTSYYSESLVHESMFPRSSLEELHIGDANWGEDLFVRRRRGT GGSESSRAGGLVGRKATEDPLGSSGYSSEDDVYGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWMACTTWYKLITAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLICLTYGAWYFYPYGLQ FFREDALABALSGERRARERGERGAGGGGGGSLHED TLALLEGLVSRREAALKEDFRRETAARIGEELSALRAEHQQDSE DLFKKIVRASGSEEARIQQLKSEWGSMTQESPGSSVKELRRLE DQLAGLQQELAALALKKYSAEVEREVELIPOOIOAWRDDVESORPA		_	201	DDNMVQRLETDFKMTLQQQSTLEQWAAWLDNVMMQALKPYEGRP
GAPPPPSQPPKOPQAAPSSIPHSDLTFNPSSALEGGAGGA SDMPEPSLDLIPELINPDELLSYLDPPDLPSNNNDDLISLPENN RINGVYRGGPTGIHILVIDQMVQNPQDESCFLFSTVKAESSDGI HI 149 RINGVYRGGPTGIHILVIDQMVQNPQDESCFLFSTVKAESSDGI MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNPDLLC VGNPFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYPQDA DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLBEPVPGYSF SPKDVSSLRMMLCTISGPKGVDILLTSPMPKCVGNFGNSSGEVD TKKCGSALVSSLARGLKPRYHFBALEKTYYERLPYRNHIILQEN AOHATRFIALANVCNPERKKKYLYAPSIVPMKLMDAAELVKQPPD VTENPYRKSGQBASIGKQILAPVEESACQFFFDLNEKQGRKRSS TGRDSKSSPHPKQPRKPPQPPSCPCFCLASPSVEKHLVVNIGTH RRFFKSRGKMCVVFERNYKSHLLQLQVIPVLSGSEVEEVEKKKATL RRFFKSRGKMCVVFERNYKSHLLQLQVIPVLSGSEVEEVEKKKATL RRFFKSRGKMCVVFERNYKSHLLQLQVIPVLSGSEVEEVEKKKATL RRFFKSRGKMCVVFERNYKSHLLQLQVIPVLSGSEVEEVEKKKATL RRFFKSRGTTISHVLFALGVYRTLYLFNWWFYHFEGFFDLIAT VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA 6905 1 226 VSKIGERETTISHVLFALGVYRTLYLFNWWFYHFEGFFDLIAT VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA ATTTATVSGLVALEMIKKLTHHKLVKPTTEKKYVDLTV SFAPDIDGDEDLFGPPVYYFSHDTD ATTTATVSGLVALEMIKKLTHHKLVKPTTEKKYVDLTV SFAPDIDGDEDLFGPPVYYFSHDTD 6907 2 2228 LRGVPVWAAGAFFFSGEESTSHLIMSRRSQRLTRYSQGDDGS SSSGGSSVAGSQSTLFKDSPLTKKRSSMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPRSSLEELHGDANWGEDLFVRRRGGT GGSESSRAGGLVGRKATEDFLGSSGYSSEDDVYGYSDVDQQSS SSRLRSAVSRAGSLLWMATSPGRLFFRLLYWMGTTTWTLITAA SLLDVFVLTRRFSSLXTFLWFLLPLLLLICLTYGAWYFPYSLQ ERREALAAREFSSNMQKRATEDFLGSSGYSSEDDVYGYSDVDQQSS SSRLRSAVSRAGSLLWMATSPGRLFFRLLYWMGTTWYRLITAA SLLDVFVLTRRFSSLXTFLWFLLPLLLLICLTYGAWYFPYSLQ ERREALAAEFSSNMQKRRAEFSLEELGGAPGQGGGGLSHED THALLUSWWAAKDSRRADGEWBARDSPHFQAEQGWGRGLHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKURASGESEARIQQLKSEWOGSMTQESFDESVKELRRLE DQLAGLQCLAALALKKGSMEREVELLRQGAPGQOGGGGLSHED DLFKKURASGESEARIQQLKSEWOGSMTQESFDESVKELRRLE DQLAGLQCLAALALKKGSMEGSFCOORDON OND OND OND OND OND OND OND OND OND	6902	2	367	SFPKAARQFLLKWSFYRYHLGFS
RINGVYRGGPTGIHILVIDGMVQNFQDESCFLFSTVKAESSDGI HIILK MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC VGMFFGSTQDAEWEEYKTGI KKAPIQTYVLGANNQETVKYFQDA DGCELABNITYLGRKGIFTGSSGLOIVYLSGTESLMEPVPGYSF SPKDVSSLRMMLCTTSQPKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYBELPYRNHIILQEN AOHATRFIALANVGMPEKKKYLYAFSIVPMKIMDAAELUKQPPD VTENPYRKSGGEASIGKQILAPVEESACQFFFDLMEKQGRKRSS TGRDXKSSPHPKQPRKPPQPPGWFCLASPEVEHLVUNIGTH CYLALAKGGLSDDHVLILFIGHYQSVVELSAEVVEEVEKYKATL RAFFKSRGKMCVVFERNYKSHHLQQVIPVPISCSTTDDIKDAF IYQAQEQQIEILEIPSINKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASEAILNVPDKSDWRCCQISKEDEETLARR FRKDFEPYDTILDD 4 SYNDEMHOHIDFITAASNLRAWSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNHFLLAIPIVVFTET TEVRKYKIRNGISFTIWDRWTYHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRKLIMMKLVKPTTEKKYVDLTV SFAPDIDGDEDLEGPPVRYYSHDTD 5907 2 2228 LRGVPVWAAGAFFFSGGESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVASGQSTLFKDSPLRTLKKKSNMKRLSPAPQLGPSS SSGGSSVASGQSTLFKDSPLRTLKRKSSMKRLSPAPQLGPSS SSGGSSVASGQSTLFKDSPLRTLKRKSSMKRLSPAPQLGPSS SSRLFKANVARGSLEWMATSPGRIFFCLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPULLLTCLTYGAWYFYPGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRYMSRVHISL ERRLEALAAEFSSNMOKAMREBELELRGQAPAGGGGGGLSHED TLALLEGLVSRRAAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQBSEARIQQLKSWOSMCGSFGESSVKELRRLE DQLAGLQQCELAALALKQSSVAEGGGLLPOOLOAVRDDVSSGPA	_	_	207	GAPPPPPSQPPRQPPQAAPSSHPHSDLTFNPSSALEGQAGAQGA
6904 464 2092 MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKGGNFDLLLC VGNFFGSTQDAEWEYYKIT KKAPIQTYVLGANNQETVKYFQDA DGCELAENITYLGRKGIFTGSSGLQTYVLSGTESLMEPVPGYSF SPKDVSSLRMMLCTTSOPKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYKHHILLQEN AQHATRFIALANVGNPEKKKYLLYAFSIVPMKLMDAAELVKQPPD VTENPYKKSGGEASIGKQILLAPVESSACOFFFDLMEKQGRKRSS TGRDXSSSPHPKQPRKPPQPPGCCVFCLASPEVEKHLVUNIGTH CYLALAKGGLSDDHVLILFIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFRNYKSHHLQLQVIPVEISCSTTDDIKDAF IKNAFPLOFGRRVLASEAILNVPDKSDWRQCQISKEDETLARR FRKDPEPYDFTLDD 6905 1 226 VSKTGERETTSHYLFALGVYRTLYLFNWWRYHFEGFFDLIAI VAGLVQTVLVCOFFYLYITKVLKGKKLSLPA 6906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPADFFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNNFLNLAIPIVVFTET TEVRKYKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMKKLVKPTTEKKYVDLTV SFAPDIDGDEDLEGPPVRYYFSHDTD 6907 2 2228 LRGVPVWAAGAFFFSGEESTHLMSRRSGRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS SSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS SSGLKSAVSRAGSLLWMATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRFFSSLKTFLWFLLDFLLLUTCLTVGAWYFYPGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEGRWRRVHSL ERRLEALAAEFSSNWOKAMRLERLELERGGAPGGGGGLSHED TLALLEGLVSRRAAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSRWOSMTGESFGESSVKELRRLE DQLAGLQQCELAALALKGSSVAEGVGLLPOOLOGNDDVSSGPA	6903	1	149	SUMPEPSEDELPEETNPDELESYLDPPDEPSNSNDDLESEFENN
MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNPDLLLC VGMFFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYFQDA DGCELAEMITYLGRKIFTGSSGLQIVYLSGTESLMEPVPGYSF SPKDVSSLRMMLCTTSQFKGVDILITSPWPKCVGMFGNSSGEVD TKKCGSALVSSLATGLKRRYHFAALEKTYYERLPYRNHILLQEN AQHATRFIALANVGMPEKKKYLVAFSIVPMKLMDAAELVKQPPD VTENPYRKSGQEASIGKQILAPVEESACQFFFDLMEKQGRKRSS TGRDSKSSPHPKQPRKPPQPPGCWFCLASPEVEKHLVVMIGTH CYTALAAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATI RRFFKSRGKWCVVFERNYKSHLUQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKNNFPLOFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDPEPYDFTLDD 3 611 SYDDHNGHIDFITAASNLRAKMYSTEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNMFLNLAIPIVVFTET TEVRKYKINGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVYWMPGHARKLKTMHKLVKPTIEKKYVDLTV SFAPDIDGDEDLFGPPVRYYFSHDTD 6907 2 2228 LRGVPVWAAGAFRFSGEESTSHLIMSRRQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSMMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRGT GGSESSRASGLVGRKATEGLSSSGYSSEDDVVGYSDVDQQSS SSRRRSAVSRAGSLLWWATSPFRLFFLYBWAGTTWFRLTTAA SLLDDVFULTRFFSSLKYFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWAAKDSRRADEGWERDSSFHFQAEQRYMSRVHSL ERRLEALAAEFSSNWOKAAMRLERLERGGAPGGGGGGLHED TLALLEGLVSRRBAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSRWOSMTGESFGESSVKERRELE DQLAGLQQELAALALKQSSVABEVGLLEQOIOOXPRDVFSGEPA	1	_	143	RINQVIRQGPTGIHILVIDQMVQNFQDESCFLFSTVKAESSDGI
VGNFFGSTQDABWEYKTG IKKAPINYQAIQKKSGNFDLLLC VGNFFGSTQDABWEYKTG IKKAPIQTYVUGANNOGTVKYPQDA DGCGLAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF SPKDVSSLRMMLCTTSGFKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AQHATRFIALANVGNPEKKKYLYAPSIVPMKLMDAAELUKQPPD VTENPYKKSGEASIGKQILAPVEESACQFFFDLNEKQGRKRSS TGRDSKSSPHPKOPROPPGPGCVGCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPBHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASEAILNVPDKSDMRQCQISKEDEETLARR FRKDFPPYDFTLDD 4 VSKTGEAETITSHYLFALGVYRTLYLFNWIMRYHFEGFFDLTAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA FRKDFSPYDFTLDD 5 SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKITPAI ATTTATVSGLVALEMIKVTGGYPFGAYINWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPWPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD 5 SSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANMGEDLRVRRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDDVQOYS SSRLRSAVSRAGSLLMMVATSFGRLFFLLYWMAGTTWYRLITAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHPQAEQRWMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIGUEKSEWGSMTQESFQESSVKELRRLE DQLAGLQQELAALAKQSSVABEVGLLPQOLOGVRDDVSGSPPA	6904	464	2092	
SPENDYSSIRMMLCTTSQPKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN AOHATRIFIALANVGNPEKKYLYAFSIVPMKLMDAAELUKQPPD VTENPYRKSGGEASIGKQILAPVESACQFFFDLNEKGGKKRSS TGRDSKSSPHPKQPRKPPQPPPGPCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVELSCTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAPTYVELDTGEKLFHR IKKNFPLOFGREVLASEAILNVPDKSDWRQCQISKEDETLARR FRKDFEPYFTLDD FRKDPEPYFTLDD 3 611 SYDDHNGHIDFITAASNIRAKMYSIEPADRFKTKRIAGKIIPAT ATTTATYGGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVGVKMLYVPWPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD 2228 LRGVFWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPRSSLEELHGDANWGEDLRVRRRRGT GGSESSRASGLVGGKATEDPLGSSGGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFOSSVKELRRLE DQLAGLQQRLAALALKQSSVAEEVGLLESOLOOLOOLONGDUVSSOFPA	1 :		1 2032	WEASTPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC
SPROVSSLAMMLCTTSOPKGVDILLTSPMPKCVGNFGMSSGEVD TKKCSGALVSSLATGLKPRYHFAALEKTYYERLPYRHHILQEN AQHATRFIALANVGNPEKKKYLYAFSI VPMKLMDAAELUKQPPD VTENPYRKSGQEASIGKQILAPVEESACQFFFDLNEKQGKKSS TGRDSKSSPHPKQPRKPPQPPGPCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVI PVPLSCSTTDDI KDAF ITQAQEQQIELLEI PERISDI KQIAQPGAAYFVVELDTGEKLFHR IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD 4 226 VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLTAI VAGLVQTVLYCDFFYLVITKVLKGKKLSLPA 5 YDDHNGHIDPITAASNLRAKWYSIEPADRFKTKRIAGKTIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKYKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTWVVQGVKMLYVPVWPGHAKRLKITMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD 2 2228 LRGVPVWAAGAFRFSSGEETSHLIMSRRSQRLTRYSQGDDGS SSSGGSSVAGSQSTLFKDSFLRTLKRKSSMKKLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLKSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRFFSSLKTFLWFLLPLLLLCLTYGAWYFYPYGLQ TFHPALVSWWAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLERGGAPGGGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQDLKSEWQSMTQESFGESSVKELRRLE DQLAGLQQELAALALKQSSVAEEVGLLPQOOOAVRDDVSSOFPA	4		1	DGCELAENIEVI GDVGIERGEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
TRKCGSALVSSLATGLERRYHFAALEKTYYERLPYRNHIILQEN AOHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAAELUKQPPD VTENPYRKSGQEASIGKQILAPVEESACQFFFDLNEKQGRKRSS TGRDSKSSPHPKQPRKPPQPPGPCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDHVLILFIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVEISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASSEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD 1 226 VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLTAI VAGLVQTVLYVCDFFYLYITKVLKGKKLSLPA 6906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPADFFKTKRIAGKITPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLVYPVWBCHAKKLKHTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPPPVRYYFSHDTD AHTSYYSESIVHESWFPPRSSLEELHGDANWGEDLRVRRRGT GGSESSRAGGSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESILVHESWFPPRSSLEELHGDANWGEDLRVRRRGT GGSESSRAGGLVGRKATEDFLGSSGGVSSEDDVYGYSDUDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLITAA SLLDVFVLTRRFSSLKFLWFLLPLLLLTCLTTGAWYFFYPGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMKLERLELRQGAPGGGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQEESPQESSVELRRLE DQLAGLQQELAALALKQSSVAEEVGLLPOOIOAVRDDVESORPA	1		ŀ	SPYDYSSI DMMI OFFICE PROPERTY TO THE DMMI OFFICE PROPERTY TO THE SPYDYSIA DMMI OFFICE PROPERTY TO THE SPYDYSIA DMMI OFFICE PROPERTY TO THE SPYDYSIA DMMI OFFICE PROPERTY TO THE SPYDYSIA DMMI OFFICE PROPERTY TO THE SPYDYSIA DMMI OFFICE PROPERTY TO THE SPYDYSIA DMMI OFFICE PROPERTY TO THE SPYDYSIA DMMI OFFICE PROPERTY TO THE SPYDYSIA DMMI OFFICE PROPERTY TO THE SPYDY TO THE SPYDYSIA DMMI OFFICE PROPERTY TO THE SPYDYSIA DMMI OFFICE PROPERTY TO THE SPYDY TO
AGHATIFIALANVGRPEKKKYLYAFSI UPMKLMDAAELUKQPPD VTENPYRKSGEASIGKQILAPVEESACQFFFDLNEKKGRKRSS TGRDSKSSPHPKQPKPPQPPGPCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD 226 VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD 2228 LRGVPWAAGAFFFSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGSSVAGSQSTLFKDSPLRTLKRKSSMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLTUMAGTTWYRLTTAA SLLDVFVLTRRFSSLKHFLUMFLLPLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRYMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQBELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DULAGLQGLAALALKQSSVAEEVGLLPOOIOAVRDDVESSOFPA	1		ſ	TKKCGSALVSSLATCI KDRVIERAL RVIEWINDE DATE
TGRDSKSSPHPKQPRKPQPPRPDGPCWFCLASPEVEKHLVVNIGTH TGRDSKSSPHPKQPRKPPQPPGCWFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFSPYDFTLDD 1 226 VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA 6906 3 611 SYDDHNGHIDFITAASNLEAKMYSIEPADRFKTKRIAGKIIPAI ATTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLFGPPVRYYFSHDTD LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWWAATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRFFSSLKTFLWFLLPLLLLTCLTYGAWYFYPFGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRYMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQBELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DOLAGLQQELAALALKQSSVAEEVGLLPOOIOAVRDDVESOFPA	ļ			AOHATRETALANGCHDERVRYL VARGINGWEIN TON TON TON TON TON TON TON TON TON TO
TGRDSKSSPHPKOPRFPOPPGCMFCLASPEVEKHLVVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKKYKATL RRFFKSRGWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKIFHR IKKNFPLOFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA 6906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYSHDTD LRGVPVWAAGAFRFSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLSAVSRAGSGLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVAEEVGLLPOOIOAVRDDVFSORPA			İ	VTENPYRKSGOEASIGKOILA DUEEGA GOERROA WILLIAM STORMAN AND ARELVKOPPD
CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL RRFFKSRGKWCVVFERNYKSHHLQLQVIFVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASEATLNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD 1 226 VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA 5906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMFGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD 2 2228 LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVAEEVGLLPOOLOAVRDDVESORPA			j	TGRDSKSSPHPKOPPKPPOPPGPGWPGC A GPRIMING A GROWN
RFFKSRGKWCVYFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQFGAAYFYVELDTGEKLIFHR IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD 5905 1 226 VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA 5906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVMLLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD 52 2228 LRGVPVWAAGAFFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKLVRASQESEARIQQLKSEWGSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVAEEVGLLPOOIOAVRDDVESSGPA	i			CYLALAKGGI.SDDHWI.TI.DIGUYOGURER CARRESTER
1 TYAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD 1 226 VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA 6906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD 6907 2 2228 LRGVPVWAAGAFRFSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRRGT GGSESSRASGLVGRKATEDFLGSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLERQGAPGQGGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVAEEVGLLRPOOLOAVRDDVESORPA				RRFFKSRGKWCVVFEPNVKGUULOLOVIDVDIGGGGGGGGGGGG
IKKNFPLOFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR FRKDFEPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLTAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAFFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVAEEVGLLPOOIOAVRDDVESOFPA	1 1			ITQAQEQQIELLEIPEHSDIKQIAQPQAAVPVUELDEGENT TUR
6905 1 226 VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA 6906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRGT GGSESSRASGLVGRKATEDFLGSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVAEEVGLLPOOIOAVRDDVESOFPA	1 1			IKKNFPLOFGREVIASEATIMUDDKSDWDOCOTCKEDERWARD
4 226 VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA 6906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD 6907 2 2228 LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVAEEVGLIPOOIOAVRDDVESOFPA				FRKDFEPYDFTLDD
6906 3 611 SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD LRGVPVWAAGAFRFSSGEETSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVAEEVGLIPOOIOAVRDDVESOFPA	6905	1	226	VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFFGFEDIIAI
SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTWVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVAEEVGLIPOOIOAVRDDVESOFPA				VAGLVQTVLYCDFFYLYITKVLKGKKI.SI.PA
ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTWVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVAEEVGLIPOOIOAVRDDVESOFPA	6906	3	611	SYDDHNGHIDFITAASNLRAKMYSTEDADDEVERDIAGVIIDA
TEVKKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRGGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVAEEVGLIPOOIOAVRDDVESOFPA	1		Ī	ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNT.AIDTIMETET
PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLITTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVAEEVGLIPOOIOAVRDDVESOFPA	1			TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFTNAVKEKVGIE
SFAPDIDGEDLPGPPVRYYFSHDTD LRGVPVWAAGAFRFSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLITTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVAEEVGLLPOOIOAVRDDVESOFPA	1 1			PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKVVDLTV
LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVAEEVGLLPOOIOAVRDDVESOFPA				SFAPDIDGDEDLPGPPVRYYFSHDTD
SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPRSSLEELHGDANWGEDLRVRRRGT GGSESSRASGLVGRKATEDFLGSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVAEEVGLLPOOIOAVRDDVESOFPA	6907	2	2228	LRGVPVWAAGAFRFSSGEESTSHLIMSRRSORLTRYSOGDDDCC
DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVAEEVGLLPOOIOAVRDDVESOFPA		ĺ		SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSDADOLGDGS
GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVAEEVGLLPOOIOAVRDDVESOFPA	1 1	1	1	DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVPPPRGT
SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVAEEVGLLPOOIOAVRDDVESOFPA	1 1	1	1	GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDOGS
SLLDVFVLTRRFSSLKTFLWFLLPLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVAEEVGLLPOOIOAVRDDVESOFPA]]	i		SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYPLTTAA
TFHPALVSWWAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVAEEVGLLPOOIOAVRDDVESOFPA	1		i	SLLDVFVLTRRFSSLKTFLWFLLPLLLTCLTYGAWYEVPVGTO
ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHED TLALLEGIVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVAEEVGLLPOOIOAVRDDVESOFPA	[[<u> </u>	TFHPALVSWWAAKDSRRADEGWEARDSSPHFOAFORVMSDUTTET
TLALLEGIVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVAEEVGLLPOOIOAVRDDVESOFPA		ļ	ŀ	ERRLEALAAEFSSNWQKEAMRLERLELROGAPGOGGGGGG GUPD
DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRLE DQLAGLQQELAALALKQSSVAEEVGLLPOOIOAVRDDVESOFPA				TLALLEGLVSRREAALKEDFRRETAARIOEELSALRAEHOODSE
DQLAGLQQELAALALKQSSVAEEVGLLPOOIOAVRDDVESOFPA				DLFKKIVRASQESEARIOOLKSEWOSMTOESFOESSVKEI.BDI.E
WISQFLARGGGRVGLLQREEMOAOLRELESKII.THVAFMOGKS			1	DQLAGLQQELAALALKQSSVAEEVGLLPOOIOAVRDDVESOFPA
	<u></u>			WISQFLARGGGGRVGLLQREEMQAOLRELESKILTHVAFMOCKS

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
ĺ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence	554	\=possible nucleotide insertion)
			AREAAASLSLTLQKEGVIGVTEEQVHHIVKQALQRYSEDRIGLA
ł			DYALESGGASVISTRCSETYETKTALLSLFGIPLWYHSOSPRVI
i			LQPDVHPGNCWAFOGPOGFAVVRLSARIRPTAVTLEHVPKALSP
			NSTISSAPKDFAIFGFDEDLQQEGTLLGKFTYDODGEPIOTFHF
			QAPTMATYQVVELRILTNWGHPEYTCIYRFRVHGEPAH
6908	3	780	QVPSAAWLMAVCGLGSRLGLGSRLGLQGCFGAARLLYPRFQSRG
1 0,00	1	/00	PQGVEDGDRPQPSSKTPRIPKIYTKTGDKGFSSTFTGERRPKDD
1		ļ	
		}	QVFEAVGTTDELSSAIGFALELVTEKGHTFAEELQKIQCTLQDV GSALATPCSSAREAHLKYTTFKAGPILELEQWIDKYTSOLPPLT
1		[AFILPSGGKISSALHFCRAVCRRAERRVVPLVOMGETDANVAKF
		İ	
6909	3	400	LNRLSDYLFTLARYAAMKEGNQEKIYKKNDPSAESEGL
\$303		409	GRLLAVGTDLYGQRSSAPEQELLVQDATPVSNSLLPEKAFSDIP
ŀ			SPYLRGTIKMMQAVRQAFQDQDDRRTWDGRPLTMAATFDDCLYA
1			LCVVDTIKRSSQTGEWQNIAIMTEEPELSPAYLISEAMRRSRMS
6910	1	1068	LYC
6310	1	1068	LVPVVVIDSYYYGKLVIAPLNIVLYNIFTPHGPDLYGTEPWYFY
			LINGFLNFNVAFALALLVLPLTSLMEYLLQRFHVQNLGHPYWLT
1		1	LAPMYIWFIIFFIQPHKEERFLFPVYPLICLCGAVALSALQHSF
		1	LYFQKCYHFVFQRYRLEHYTVTSNWLALGTVFLFGLLSFSRSVA
1			LFRGYHGPLDLYPEFYRIATDPTIHTVPEGRPVNVCVGKEWYRF
l			PSSFLLPDNWQLQFIPSEFRGQLPKPFAEGPLATRIVPTDMNDQ
			NLEEPSRYIDISKCHYLVDLDTMRETPREPKYSSNKEEWISLAY
ł	ł	ł	RPFLDASRSSKLLRAFYVPFLSDQYTVYVNYTILKPRKAKQIRK
6911	1184	966	KSGG
0,11	1104	700	GEDAEEMETGNVANLISIFGSSFSGLLRKSPGGGREEEEGEESG
6912	1	844	PEAAEPGQICCDKPVLRDMNPWSTAIVAF
0912	. •	044	AMKPVETHSFQMLFTILSTGSALKAQSYEDAYRCIKSSILLGSI
ł			SGGTDIISCFMGHNFSLPVYKGEIQARNLGMAVEAWNEEGKAVW
ŀ			GESGELVCTKPIPCQPTHFWNDENGNKYRKAYFSKFPGIWAHGD
			YCRINPKTGGIVMLGRSDGTLNPNGVRFGSSEIYNIVESFEEVE
	i		DSLCVPQYNKYREERVILFLKMASGHAFQPDLVKRIRDAIRMGL
		ļ	SARHVPSLILETKGIPYTLNGKKVEVAVKQIIAGKAVEQGGAFS
6913	1643	1000	NPETLDLYRDIPELQGF
		. 1558	KKSHEESHKEELSYGAQASLPLPCSDFR
6914	1251	615	ELAAECKSAGYPGTLIPYRCDLSNEEDILSMFSAIRSQHSGVDI
Ī	1		CINNAGLARPDTLLSGSTSGWKDMFNVNVLALSICTREAYQSMK
ĺ	1		ERNVDDGHIININSMSGHRVLPLSVTHFYSATKYAVTALTEGLR
1	1		QELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMK
F6015		650	CLKPEDVAEAVIYVLSTPAHIQIGDIQMRPTEQVT
6915	254	652	GRSLSFKTFLIWVLISIYQGGILMYGALVLFESEFVHVVAISFT
ĺ			ALILTELLMVALTVRTWHWLMVVAEFLSLGCYVSSLAFLNEYFD
<u> </u>	ļ		VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLAS
6916	254	652	GRSLSFKTFLIWVLISIYQGGILMYGALVLFESEFVHVVAISFT
1			ALILTELLMVALTVRTWHWLMVVAEFLSLGCYVSSLAFLNEYFD
	<u> </u>		VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLAS
6917	254	652	GRSLSFKTFLIWVLISIYQGGILMYGALVLFESEFVHVVAISFT
1			ALILTELLMVALTVRTWHWLMVVAEFLSLGCYVSSLAFLNEYFD
			VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLAS
6918	28	921	PEAGTRSWREPDPEDLRRFLLSAACRSFPQWLPGGGGGQVSSCS
1			DTDVPYLLLAVKSEPGRFAERQAVRETWGSPAPGIRLLFLLGSP
1			VGEAGPDLDSLVAWESRRYSDLLLWDFLDVPFNQTLKDLLLLAW
Í			LGRHCPTVSFVLRAQDDAFVHTPALLAHLRALPPASARSLYLGE
l			VFTQAMPLRKPGGPFYVPESFFEGGYPAYASGGGYVIAGRLAPW
]			LLRAAARVAPFPFEDVYTGLCIRALGLVPQAHPGFLTAWPADRT
i	1		ADHCAFRNLLLVRPLGPQASIRLWKQLQDPRLQC

Desiming nucleotide location corresponding contraining signal peptide location corresponding contraining contr	SEQ	Predicted	Predicted end	
No: nucleotide location corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid sequence		h .	1	Amino acid segment containing signal peptide
Cocation Corresponding Coffee Corresponding Coffee Cof				(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
corresponding to first amino acid residue of amino acid residue of amino acid sequence sequen			}	Grutamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of sequence control of the control of	1			hanstidine, laisoleucine, Kabysine,
amino acid residue of amino acid sequence sequen	ł			P=Proline O-Clutomine, N=Asparagine,
residue of amino acid sequence 6919 650 41 0GREELGSBYECF (GOEPFERLINGESTHEW) (COO.), *possible nucleotide deletion, *possible nucleotide insertion) (Coo.), *possi		amino acid		S-Serine T-Thronning Williamine,
Codon, /-possible nucleotide deletion, vepossible nucleotide dinsertion Codon, /-possible nucleotide dinsertion Codon, /-possible nucleotide dinsertion Codon, /-possible nucleotide insertion Codon, /-possible nucleotide Codon,	1	residue of		W-Trustophan V-Trustophan V-Trustophan
Sequence Name	ł	amino acid		Codon (-naggible
6919 850 41 GORRELJGGSYFOFFTGDEFERTUSEFHERVRSGGOLQQLQA ELDKLIKEVSTVRANSERVAKLUFGGIRISDEVERFYALSSVG ASIDLQKTSHDYADRITAY WINKFSFWINARPSTYVLLEHVPSF RCARFBOOQGOVIJOHORVOLSDITLGHPPPSVEHTGGANSAR RDFANFFLLSFFTHGGLQVTDETEVSIGKTFUKSETQTHFHL GORD PRAAFFKVKQILSDWERFSFWINARPSTYVLLEHPVPSKEHTGGANSAR RDFANFFLLSSFTHGGLQVTDETEVSIGKTFUKSETQTHFHL GORD PRAAFFKVKQILSDWERFSFWITCHSFETGANSAR RDFANFFLLSSFTHGGLQVTDETEVSIGKTFUKSETQTHFHL GORD PRAAFFKVKQILSDWERFSFWITCHSFETGANSAR GOSPH 6921 2 1711 MRATRSESCFFWITMIREGTLRKMENYLKEKQLCDVLLIAGHLRI PARHLUSANSDVFAAMFTNDVLEAKQBEVRHEGVODPALISIV QYAYTOVJQLKETTISSLIAAACLLQUTQVIDVCSNFLIKQLHP PARHLUSANSDVFAAMFTNDVLEAKQBEVRHEGVODPALISIV QYAYTOVJQLKETTISSLIAAACLLQUTQVIDVCSNFLIKQLHP SNCLGIRSFGDAQGCTELLAVARKYTHEHFISVIKNOGELGHLLS SNCLGIRSFGDAQGCTELLAVARKYTHEHFISVIKNOGELGHLLS SNCLGIRSFGDAQGCTELLAVARKYTHEHFISVIKNOGELGHLLS SNCLGIRSFGDAQGCTELLAVARKYTHEHFISVIKNOGELGHLLS SNCLGIRSFGDAGGCTELLAVARKYTHEHFISVIKNOGELGHLLSPR REISKLLCSDDINVDESTIFTHAMQWVERDVSROGELGHLLS SNCLGIRSFGDAAGCTERMANGGOVOVATYNGELVVLGTHVDGK TIRFPLDEPQLLADLETSSNFTCDLECOKLIMEAMKYHLLERRR SMMOSERTIKRFRGIGVATLEGDWAVAGGHDASYLINTVERRDD EGRONNVASMSTPRSTVGVVALDNKLYAVGGHDAPASNHL GEROPHTIKNSLGCAMBKKRGDVAAVAGHDASYLINTVERRDD EGRONNVASMSTPRSTVGVVALDNKLYAVGGHDAPASNHL SRISDCVERVDPKGDSMSTVAPLSVYGGHDAPASNHLVAVGG GORTHIKKSTVAPLATAGANARACHOVATYNGELVVVGGHDAPASNHL SRISDCVERVDPKGDSMSTVAPLSVYGGHRAVLDDKGFEDVYBVEV KGAQRELFVTPLSGMYNKSGGKVRITTKLEGDQLMTGTERETEK LPMGSTRAVVSEDIGGBEVVENTAGAGGSTINDVIA WYTPKDAAQQDAKABENKKEPLCRKCHRKVLDKAFBEVYBVEY GORTHALDVARACHOVATAGATAGA VATPAGAAQAAACHACHACHACHACHACHACHACHACHACHACHACHAC				\=nossible ruglectide deletion,
ELDELINEVSTYNDANDSENVALUPTORIEDEVSKYPTYALSSVO AS IDLOKTSIDYADRITA PRIMERS FINNYARPRYLLEHVER MINAFEDDOQUVIQLE OR VOLLDETT. TO PREVENTE GANSA PLOPATER PROPERTY OF THE MARKET OF THE MARKE	6919		41	OGPRELOCCUECOETOCERUS TO CONTROL OF THE CONTROL OF
ASIOLOKTSHDYADRITAYFWIRES FWINARPFTVILEHUPPEPG NCNAFEGOGQOVIOLDED TICH PSECHTGANNAP RDFAVFFLLS FFTHQGLQVYDETEVSLGKFTFDUSKES 107FHL ONDFPARFYKVIQILSNWGHPRFTCLYRVRAHGVRTSEGAEGS AQGPH 6920 1418 591 EAGGPSKVBLTLKKKK 6921 2 1711 MNATRSEEGFBUTINHAEGTLKRMENVIKEKQLCDVLLTAGHLRI FRAMELULSAVBUYRAMFTNUVLERAGERSUPPANLSIGU OYAYTGVLQLKEDTISSLLAAACLOLTQVIDVCSNFLLKGLHP SNCLGTRSFGDAGQCTELLANARKYTMEFUVROGELGMLLS YIRLPLLPPOLLADLETISSMFTGDLECGALBMENTYLTEKGLLEDURGN NEISKLLCSDDINVPDETIFHALMOWVCHDVONGGGELGMLLS YIRLPLLPPOLLADLETISSMFTGDLECGALBMENTYLTEKGLLEPDVK HIGTMAGGRIG-GPGAVILTNKLYVVGGGDABMKSTTTIEKTDLETSNUL HIGTMAGGRIG-GPGAVILTNKLYVVGGGDABMSTTTIEKTDLETSNUL HIGTMAGGRIG-GPGAVILTNKLYVVGGGDAGSSCLKMEN FDPHTKKMSLCAPMSKRRGGGVGVATTNGFLVVVGGDABASHNIST GROMBYVANSTRSTSVVALNALVANCHLOBGSSCLKMEN FDPHTKKMSLCAPMSKRRGGGVGVATTNGFLVVVGGDABASHNIST GLPPAGKTWKYSLAPENDFLORGERGEKKEKEKEKEFFDERDESEKKMIST GLPPAGKTWKYSLAPENDFLORGERGEKKEKEKEKEFFDURGESCLKMEN FDPHTKKMSLCAPMSKRRGGGVGVATTNGFLVVVGGDABASHNIST GLPPAGKTWKYSLAPENDFLORGERGEKKEKEKEKEFFDURGESCKMEN FDPHTKKMSLCAPMSKRRGGGVGVATTNGFLVVVGGBDABASHNIST GLPPAGKTWKYSEDIBCHEDVYNKAGLEDURGESCLKMEN FDPHTKKMSLCAPMSKRRGGGVGVATTNGFLVVVGGBROMV KGAQERLPTVULSGWNKSGGKVRLTFKLEODOLMIGTKGRTEK KGAQERLPTVULSGWNKSGGKVRLTFKLEODOLMIGTKGRTEK KGAQERLPTVULSGWNKSGGKVRLTFKLEODOLMIGTKGRTEK KGAQERLPTVULSGWNKSGGKVRLTFKLEODOLMIGTKGRTEK KGAQERLPTVULSGWNKSGGKVRLTFKLEODOLMIGTKGRTEK VDART KONTONION SERVENTERSTELFAVVWNAEAECORKO LDVTFONNOKVLKKALSLIRPILMTISTESCLFAVVWNAEAECORKO LDVTFONNOKVLKKALSLIRPILMTISTESCLFAVVWNAEAECORKO NOTHEN STORT SERVENTERSTENDAV SERVENTERSTENDAV SGTSDBIFFTVINERTSIVGSFRANKGTSILEGOLDSREV VDART KONTONION SERVENTERSTENDAV SERVENTERSTENDAV SGTSDBIFFTVINERTSIVGSFRANKGTSILEGOLDSREV VDART KONTONION SERVENTERSTENDAV SGTSDBIFFTVINERTSIVGSFRANKGTSILEGOLDSREV VDART KONTONION SERVENTERSTENDAV SGTSDBIFFTVINERTSIVGSFRANKGTSILEGOLDSREV VDART KONTONION SERVENTERSTENDAV SGTSDBIFFTVINERTSIVGSFRANKGVYCLOFTENDATE FRYTIDTILPVTPKRTSIVGSGKVSINGAVATGEGULKLE HEER VYTILPSAYARSILTITAWSTELGGKVSINCATCATCHAND BERNOTON SERVENTERSTENDAV SCHOOLT SERVENTERSTE	ŧ			ELDKI-HKENGTURA ANGERMAN URORI MER TENENGGOOLOOLOA
NCMAPSEDOGOVIQLPGRVQLSDITLQHPPPSVEKSEIQTPHL RDFAVFFLLSFTRIGGLQVYDETEVSLGERFTDVEKSEIQTPHL ONDPPAAFFKVKIQLISNMGHPRTCLYRVRAHGVRTSEGAEGS AGGH 6920 1418 591 EAGGPSKVBLTLKKKK 6921 2 1711 NATRSEGFBYINHAEGTLERMENVLREKQLCDVLLLAGHLRI PARKLULSAVSDVFAAMFTNOULEAKGEEVEMBEUVDPMALNSLV OVAYTGVLQLKEDTISSLLAAACLLGLTDVEGNFELLKQLHP SNCLGTRSFGDAQGCTELLNVARHYTWEHFIEVIKNGEFLLFA NEISKLLCSDINVPDEST IPPALMONVGHOVON ROGELGHLLS SNCJGTRSFGDAQGCTELLNVARHYTWEHFIEVIKNGEFLLFA NEISKLLCSDINVPDEST IPPALMONVGHOVON ROGELGHLLS YIRLPLLPPQLLADLETSSMFTGDLECOKLMENMKYHLLBERR SNMGSPRTTRPKSTVGALVALNAKLYTWEHFIEVIKNGEFLLFAN HIGTMAGRRLOPGVAVIDEKLYVVGGROGLIKTLNTVECCHNVCK I WITWDPMSTRHENGLOVATLEGPHAVOGEHGMISTTUREKDPVCK HIGTMAGRRLOPGVAVIDEKLYVVGGROGLIKTLNTVECCHNVCK I WITWDPMSTRHENGLOVATLEGPHAVOGEHGMSTYNVERND EGROWNYVASNSTPRSTVGVALNNIKLAJGGRGGSCLKRMEY PDPHTNKMSLCAPMERRREGEGEREFEREVENEVENDAVCCHLODKLYVVGG SRLSDCVERTDPRKODMSTRADLSVERDAVAVCHLODKLYVVGG SRLSDCVERTDPRKODMSTRADLSVERDAVAVCHLODKLYVVGG SRLSDCVERTDPRKODMSTRADLSVERDAVAVCHLODKLYVVGG VDHTALATVES VADRAVEKREREEREFEREFEREFEREVENEVENDAVCHLODKLAVVGG SRLSDCVERTDPRKODMSTRADLSVERDEGTGGERKONAVCHLODKLYVVGG SRLSDCVERTDPRKODMSTRADLSVERDEGTGGERKONAVCHLODKLYVVGG VDHTALATVES DRENGEREREFEREFEREFEREVENDAVCHLORKMEYER LEMGSIKNIVVSEDIEGHEDVALFERICKTORKAVERETASVYVVAVBPTOY VDAIROTHCKNOVER LEMGSIKNIVVSEDIEGHEDVALMAPGLOPTEASYYVVAVBUPTOY VDAIROTHCKNOVER VNIPHFANGAVLGKALSLIRFPLMTI EEFAAGPAGGILSDREV VNIPHFANGAVLGKALSLIRFPLMTI EEFAAGPAGGILSDREV VNIPHFANGAVLGKALSLIRFPLMTI EEFAAGPAGGILSDREV VNIPHFANGAVLGKALSLIRFPLMTI EEFAAGPAGGILSDREV VNIPHFANGAVLGKALSLIRFPLMTI EEFAAGPAGGILSDREV VNIPHFANGAVLGKALSLIRFPLMTI EEFAAGPAGGILSDREV VNIPHFANGAVLGKALSLIRFPLMTI EEFAAGPAGGILSDREV VNIPHFANGAVLGKALSLIRFPLMTI EEFAAGPAGGILSDREV VNIPHFANGAVLGKALSLIRFPLMTI EEFAAGPAGGILSDREV VNIPHFANGAVLGKALSLIRFPLMTI EEFAAGPAGGILDEFERG EEFTYTURTETA STADLEGGEMESTEKAVENTI EIFACGUALFTCANTOVATACATIKGD EEFTYTTIVAPPRKUR PITTUVEKAGGEMTATUVETAATIKGD EIFTT HITTUVEKAGAVAVAVATATAGAVAVAVATATAGATAVATATAGA DSHYCHTAATAGATAGATAGATAGATAGATAGATAGATAGATAGA	1			ASIDI OVTCUDVADDNEAVENING CONTRACTOR ASIDI OVTCUDVADDNEAVENING
RDFAVFFLLSFFTHQGLQVYDETEVSLGKFTFDVEKSEQTOFHL ONDFPARAFVKYQIJSNMGHRFTCLYRVRAHGVRTSEGAGG AQGH 6920 1418 591 EAGGPSKVBLTLKKKK RMATRSEEGFBVINHAEGTLRYMRNYLERKQLCDVLLAGHLRI OYAYTGVLQLKEDTISSLLAAACLLQLTQVIDVCSNFLIKQLHR SNCLGIRSFGAQCCFPLLVNAHKYTMEHFIEVIKQCHEVLAGHLRI SNCLGIRSFGAQCCFPLLVNAHKYTMEHFIEVIKQGLFBLLSG NCLGIRSFGAQCCFPLLVNAHKYTMEHFIEVIKQGLFBLLSG NCLGIRSFGAQCCFPLLVNAHKYTMEHFIEVIKQGLFBLLSG NCLGIRSFGAQCCFPLLVNAHKYTMEHFIEVIKQGLFBLLSG NCLGIRSFGAQCCFPLLVNAHKYTMEHFIEVIKQGLFBLLSG NCLGIRSFGAQCCFPLLVNAHKYTMEHFIEVIKGLTSSML HIGTMAGRILQFGVAVIDNKLYVVGGROGLKTLNTVECFNDVGK INTVMPDHSTRINGLOVATALGGPMAYAGGNALTNIFLEKVDLRTNSML HIGTMAGRILQFGVAVIDNKLYVVGGROGLKTLNTVECFNDVGK INTVMPDHSTRINGLOVATLGGPMAYAGGNALTNIFLEKVDLRTNSML HIGTMAGRILQFGVAVIDNKLYVVGGROGLKTLNTVECFNDVGK INTVMPDHSTRINGLOVATLGGPMAYAGGAVLAVVKLP PDHTNKMSCLAFMERKRGGVGVATYNGFLVVVGHDAPASNIC SRLSDCVERYDPKGDBWSTVAPLSVPRDAVAVCPLGDKLYVVG SRLSDCVERYDPKGDBWSTVAPLSVPRDAVAVCPLGDKLYVVG SRLSDCVERYDPKGDBWSTVAPLSVPRDAVAVCPLGDKLYVVG VLOCHTLLATVYSSVDAQNEMBEEVPUNIGAGVATVVKLP SRLSDCVERYDPKGDBWSTVAPLSVPRDAVAVCPLGDKLYVVG KGAGELLPTVSSVDAGNEMBEVPVNIGAGCVVVVKLP VNDFHADAQQDAKABENKEEVPLOSTGSELKGNISTI CEPPANGKWYKCLABENKEEVPLOSTGSELKGMSTSTELLVAV VNTPKDAQQDAKABENKEELCRGKORKVLDKKGBGVNTSVLA VNTPKDAQQDAKABENKEELCRGKORKVLDKKGBDVAPSV KGAGELLPTVLSGMYNNSGSKYRLTFKLEDQLUMGTKERTEK LPMGSTRAVVSEPIEGHBDYHMAFQLGFTEASYWVYWPDTQV VNLFLHFTVMPKKPVEYJLDRRCCLRGKCCCINRCQUESRMQY SGTSDBIEFTVHESTSI USGRYGSACVATIVATRABAECQNCQ SGTSDBIEFTVMRSTSI USGRYGSACQAGGILISDREV VNLFLHFTVMPKKPVEYJLDRRCCLRGKCCCINRCQUESRMQY SGTSDBIEFTVMRSTSI USGRYGSACQAGGAGGGILISDREV VNLFLHFTVMPKKPVEYJLDRRCCLRGKCCCINRCQUESRMQY SGTSDBIEFTVMRSTSI USGRYGSACQAGGAGGGILISDREV VNLFLHFTVVPKKRPVEYJLTAFHEGRKGALAKKPYNPI IGETFHCSWEVP KORVKYKKTASRSPASCHEHMADDPSKYKLRFVAGCUSHHEP ISCFYCECEBKRLCVNTHVVTKSKFMGMSUGVSMIGGECULRLLE HGEVYFTLDSAYABSILITHWELGKGMEVTSLACHGUNLTESMCLIKLL EMWETDYPVPKKRPULFENGGMMSTCLGARTGVSTATVFF DAMSSGDVEFFHILISMCHAUCHGFTVNG SLESTIMGLGVQSFPV DAMSSGDVEFVEHLISMCHAUCHGFTVNGSDGSILV LGMWSTDPLAKLLISMCHCHOHM INSVLKMUQDGFTTALP DAMSAGNTLISKVLOKARANVAVOTDPDKGKIKWDLGAALD	1			NCWARECDOCOUNTED BCDUOL CDTM OWNER PORTO
6920 1418 591 BAGGPSKVHLTLKKKK 6921 2 1711 MNATRSEGFFIVINHAROTLERMENYLEKGLCDVILLAGHLET PARKLULSAVSDYRAMFTINDULEAKGESVEMBEDYDRALISELV QYATTGYLOLKEDTISSLAAACLLOLTOVIDVCSNFLIKGLHET BARKLULSAVSDYRAMFTINDULEAKGESVEMBEDYDRALISELV QYATTGYLOLKEDTISSLAAACLLOLTOVIDVCSNFLIKGLHET SNCLGTRSFGDAGGCTELLNVARKYTHEFTEYLKNOGFFILLER NEISKLLCSDINVPDEETTERHALMOVLONGROGELGMILLS SNCLGTRSFGDAGGCTELLNVARKYTHEFTEYLKNOGFFILLER NEISKLLCSDINVPDEETTERHALMOVLONGROGELGMILLS SNCLGTRSFRGDAGGCTELLNVARKYTHEFTEYLKNOGFFILLER NEISKLLCSDINVPDEETTERHALMOVLONGROGELGMILLS YTRLPILPPOLLADLETSSMFTGOLUCOKLIMEAKYTHLEPRINVCK INTYMEPHSTKSTVCALLAVGKDDAMKGTTUTGETNNVCK INTYMEPHSTKSTVCALLAVGKDDAMKGTTUTGETNNVCK INTYMEPHSTKSTVCALLAVGKDDAMKGTTUTGETNNVCK INTYMEPHSTKSTVCALLAVGKDDAMKGTTUTGETNNVCK INTYMEPHSTKSTVCALLAVGKDAMKGTGOTALTNTGETNNVCK INTYMEPHSTKSTVCALLAVGKDAMKGTGOTALTNTGETNNVCK SRESDEVERYDPROGDMSTVARDISVROGGCSCLLKMEY PDPHTKMSCLAMPSKIRRGGGVGVALTNOFLVVGGGDSCLKKMEY PDPHTKMSCLAMPSKIRRGGGGVGALTNOFLAVCGLODKLYVVGG PDPHTKMSCLAMPSKIRRGGGGVGALTNOFLAVCGLODKLYVVGG PDPHTKMSCLAMPSKIRRGGGGVGALTNOFLAVCGLODKLYVVGG VLOGHTYLNTSTVARTSTANDETSTGELKGNINST GLEPAGGCVGARTENTERTSTANDETSTGELKGNINST GLEPAGGCVGARTENTERTSTANDETSTGELKGNINST GLEPAGGCVGARTENTERTSTANDETSTGELKGNINST GLEPAGGCCCALLAVGTENTALTERTSTANDETSTGELKGNINST GLEPAGGCCCALLAVGTENTALTERTSTANDETSTGELGGGGGG LEPTTFONKOKULGKALSLIRPPLMTIREFAAGGAGGGLISDREV VALFHHFTVARRTSIVGFGLVGSIHOPDVAVINIGITETSTANDET GGGGAGGAGGAMGTEGGCCGTANTFRAMPKEYPIFIGENFOY NUFFHALAVGAGGAGGAGGGGGGGGGGGGGGGGGGGGGGGGGGG	ì	i		PDEAURE I CERTIFICATION OF THE PROPERTY OF THE
6920 1418 591 EAGGPSKVBLTLKKKK 6921 2 1711 MNATRSEEGPHVINHARCTLRKMENYLERGLCDVLLAGHLRI PARHLULSAVSDYPRAAMFTDDVLEAKGREVRMEGVDPNALMSLV QYAATGVLGLKEDTIESLLAAACLLOLTQVIDVCSMFLIKGLHP PARHLULSAVSDYPRAAMFTDDVLEAKGREVRMEGVDPNALMSLV QYAATGVLGLKEDTIESLLAAACLLOLTQVIDVCSMFLIKGLHP SNCLGIRSFGDAGGCTELLAVARKYMHEHIEVIKNGEFLLPA NEISKLLCSDDINVPDEETIPHALMGWVGHDVONRGGELGMLLS YIRLPLIPPQLLADLETSSMPTGDLECCKLLMERHYHLLPERR NEISKLLCSDDINVPDEETIPHALMGWVGHDVONRGGELGMLLS YIRLPLIPPQLAALDETSSMPTGDLECCKLLMERHYHLLPERR NEISKLLCSDDINVPDEETIPHALMGWVGHDVONRGGELGMLLS YIRLPLIPPQLAALDETSSMPTGDLECCKLCHARKYHLLPERR NEISKLLCSDDINVPDEETIPHALMGWVGHDVONRGGELGMLLS YIRLPLIPPQLAALDETSSMPTGDLEGCKTLMTVEFTMPUCK INTVMPPMSTARHGLGYAATLEGPMWAGGRGAVUTVGFROPPUCK ROMMYVASHSTERSTVGVVALNKLYAIGGRGSCLKSMEY FDRITKMSLCAPMSKREGEVVALTNGFLYVGGHDAPASNHC SRLSDCVERYPPKGDSMSTVAPLSVPRDAVAVCPLGDKLYVVGG VDGHTALMTVESTPAGRANEKEEPVLAGKGAGGACVVVKLP FDRITKMSLCAPMSKREGEVVALTROFLYVGGHDAPASNHC SRLSDCVERYPPKGDSMSTVAPLSVPRDAVAVCPLGDKLYVVGG KGAQEBLPTVESGGMYNKGLAPEKSCHULTGKGACHWOKKLP KGAQEBLPTVESGGMYNKGLGGGACUTVUKLP KGAQEBLPTVESGGMYNKGLGGGACUTVUKLP KGAQEBLPTVESGGMYNKGLGGGACUTVUKLP KGAQEBLPTVESGGMYNKGLGGGACUTVUKLP KGAQEBLPTVESGGMYNKGLGGACUTVUKLP KGAQEBLPTVESGGMYNKGLGGACUTVUKLP KGAQEBLPTVESGGMYNKGLGGACUTVUKLP KGAQEBLPTVESGGMYNKGLGGACUTVUKLP KGAQEBLPTVESGGMYNKGGGVALTGGGGACUTVUKLP KGAQEBLPTVESGGMYNKGGGVALTGGGACUTVUKLP LDTGGACTATATTVUKSCGGULTGTATTVUKLP KGAQEBLPTVLGGTUKSGGTULTGTATTVUTCAGATTATTVUTCAGATTATTVUTCAGATTATTVUTCAGATTATTVUTCAGATTATTVUTCAGATTATTVUTCAGATTATTVUTCAGATTATTTATTTATTTTTTTTTTTTTTTTTTTTTTT	1]		ONDERA PROVINCIAL CONSCIENCE OF THE CONTRACT O
6920 1418 591 PAGGPEKVILITIKKKK 1 2 1711 MNATTSEEGFUVINHAEGTLRXMENYLKEKQLCDVLLIAGHLRI PAHRLVISAVSDYPAAMFTADVLEAKGEEVEMBGVDPMALNSLV OYAYTGVIQLKEDTIESILAAACLUQTOVIDVCSNFLIKQLHP SNCLGIRSFGDAQGCTELLMVAHKYMHEHIEVIKNOGFILDEN NEISKLLCSDDINVPDEETIFHALMQWWGBUVONRGGELGMLLS YIRLPLEPQLIADLETSSMFTGDLECKLMFAMKYHLJEERR SMMGSPRTKPRKSTVGALVAVGMDAMKGTTTIEKYDLRTNSWI, HIGTMMGRRLQGFUAVIDNIKLYVVGGHDARVANGFUGWISVLIMPVERMID EGROMMYVASMSTPERSTVGVALINKLYGGRDGSSCLKMENS FDPHTKKMSLCAPMSKRRGGVGVAYNOFLYVVGGHDAPASNHC GRUSDCVERYPDKGDBSSTVAPLSGPMYAVGFUGWISVLTVVG YDGHTYLNTVSSYDAQRNEWKEEVPVNIGRAGACVVVVKLD LTPPAGIRHEVVDEWERSFERENEREKFFDLEKQNIHSIT GLPPANGKWMYKGLAPEDKTIREIKVTSGAKIMGGSSTINDVLA VNTPKDAAQODAKAEENKKEPLCRKGHRKVLDKKKEPDVWPSV KGAQEELFVVBLGGMYNKSGGVKULTKOOLOMINISTT GLPPANGKWMYKGLAPEDKTIREIKVTSGAKIMGGSSTINDVLA VNTPKDAAQODAKAEENKKEPLCRKGHRKVLDOLMIGTKKETEK LPMGSTKRVVSEPEIGHEDYHMMFQLGPTEASYWWYWYPTCY VDAIKDTVIGKWGYF 6923 2469 1660 LGJFCILDITCAVLERDILSIRESKLFGAVVKNAREAECOKO LPYTFGNKOKVLGKALSILTRPLWTI EEPAAGPAGSGILSDREV VNLFLHFTVNPKKVLGKALSILTRPLWTI EEPAAGPAGSGILSDREV VNLFLHFTVNPKKVLGKALSILTRPLWTI EEPAAGPAGSGILSDREV VNLFLHFTVNPKKVLGKALSILTRPLWTI EEPAAGPAGSGILSDREV VNLFLHFTVNPKKVLGKALSILTRPLWTI EEPAAGPAGSGILSDREV VNLFLHFTVNPKKVLGKALSILTRPLWTI EEPAAGPAGSGILSDREV VNLFLHFTVNPKKVLGKALSILTRPLWTI EEPAAGPAGSGILSDREV VNLFLHFTVNPKKVLGKALSILTRPLWTI EEPAAGPAGSGILSDREV VNLFLHFTVNPKKVLGKALSILTRPLWTI EEPAAGPAGSGILSDREV VNLFLHFTVNPKKVLGKALSILTRPLWTI EEPAAGPAGSGILSDREV VNLFLHFTVNPKKVLGKALSILTRPLWTI EEPAAGPAGSGILDSMCML EIFYT 6924 2210 1235 PEERVICKVLCVTHVWTTSKFMMSVCVSWIGGVURLEL HGEEVVPTLPSATARSILTITUMVELGGKVSINCAKTVSKATVIF HTKP FYGGKVHRVTAEVKHNPTNTIVCKAAGGMRTLEFTYNNG ETKVLDTTTILVYVKKIGHTSKYLDRAMSVCGCNINGESULLLE HGEEVVPTLPSATARSILTITUMVELGGKONGTLECHWKLI EMWSTDPLAKGLGSERGRODOYLEKNRPTTGPBPHSFYRSLYRK OKCHSANGMENDSVIECHUNGSSONGTLECHWKLI EMWSTDPLAKGLGSERGRODOYLEKNRPTDGPPHSFYRSLYRK LOOSISDDVSFVBILISMCHYOHGHINSYLKPHLORDPTTALP DOMSSDDVSFVBILISMCHYOHGHINSYLKPHLORDPTTALD EGGLUHTABRILSYLDARSLCAABLVCKORVISEOMKKILI EMWSTDPLAKGLGSERGRADOYLFKNRFNSHMVTCSKORSIAV WMAASATILTIRRVILN	1			ACCOU
6921 2 1711 MNATRSEEGFHVINHAEQTLRKMENYLKEKQLCDVILLTAGHLRI PAHHLVLSAVSDYPAAMFTDDVLEAKQEEVMENGUPVALNISLU QYAYTGVLQLKEDTIESLLAAACLLQUTQVIDVCSNFLLIKQLHH SNCLGIRSFGDAQGCTELLMVAHKYTMEHIEUVINGEFLLLIPA MEISKLLCSDINNVPBETIFHALMWGHBVUNGGGLGMLLS YIRLPLLFPGLLADLETSSMFTGDLECCKLLMEAMKYHLLEERR SMMOSPRTRPKRSTVGLAVAUGMGAMGTTTEKYDLETTSML HIGFMKGRELQFGVAVIDNELYVVGGRGGLKTLNTVECFNPVG INTVMPPMSTRHELGLGVATLAGDWAVYTHEKYNVGHDAPASNHC GROWNYVASNSTDRSTVGVVALNNKLYAIGGRGGSSCLKSMEY FDPHTNKWSLCAPMSKRRGGVAVTNGFLYVVGGDAPASNHC RUSDCVERYNPKOBWSTVAPLSVFRDAVAVCFLGDKLYVVGG YDOHTYLNTVESTDAGKNEKREVEVYNJGRAGCVVVVKLP 1075 369 LTFPAGIREVRDREBEREREEREKPLSTGSKLMGGGSTINDVLA NYTPKDAAQODAKAEBEREREREKEVLSTGSKLMGGGSTINDVLA NYTPKDAAQODAKAEBEREREREKEVLSTGSKLMGGGSTINDVLA NYTPKDAAQODAKAEBEREREREKEVLSTGSKLMGGGSTINDVLA NYTPKDAAQODAKAEBEREREREKEVLDSTGSLKGNGTSTT GLPFAMQKVMYKGLAPEDVTLEIGETSSELGFGAVVWAYWYWYDTQY VDAIKDTVLGKWQYF 6923 2469 1660 LGLFCTLDTCGAVERDTLSIRESSELFGAVVRWAEAECQRQQ LPVTFGNKGKVLGKALSLRTPLMTIEFSRLFGAVVRWAEAECQRQQ LPVTFGNKGKVLGKALSLRTPLMTIEFSRLFGAVVRWAEAECQRQQ CPVTFFONKGKVLGKALSLRTPLMTIEFSRLFGAVVRWAEAECQRQQ SGTSRRIPFTVNRKISIVTOFGVKSTGHKGPDVGVNIGITSFEKK QTLGONDTGFSCDGTANTFRVMFKEPIELIPNVCYTACATLKGP DSHYGTKGLKKVVHETPAASKTVFFFFSSPNNNOTSIEGGQIP EIIFYT 6924 2210 1235 PEERVICTVEYYLTAFHEGRKGALAKKPYNPIIGFTFCSWEVP KORVKPKRTASRSPASCHSHPMADDPSKSYKLRFVAEQUSHHPD ISCFYCECEGERILCVWTHWYTKSFKMGEWNGTLEFTYNNG ETKVIDTTLEVYPKKIRPLEKQGPMESRNLMREVTRYLELGDI DAATEGKKHLEEKQRVERGTSSVUSKRREVGSMIGGCUPLELE HGEFYFFLDFBAKKRINPNTIVGKGWSMIGGENGLUFSMCAL ETKVIDTTLEVYPKKIRPLEKQGPMESRNLMREVTRYLELGDI DAATEGKRHLEEKGRVERGTSVUSKRREVRYFETGEDGSGGILQ SPLESTIMGLEVQSFYV DOWSSDQUSFVEHLISMCHYOHGHINSYLKPBLGCRALVESMCAL GENAVETDERVINGTGSVUSKRREVTTSVICKRYBERGAVY LOPISTINGKKLIGERGRADDPSKYRLIVEKI IQDIETTESWRGGRINGGTGGTSVUSKRREGWTCGTOPDFSTTALP GCGLDHILABRILSYLLDAGRICATUCSKORGING UPANDAGATDTIRRVINGGRAVAVOUTPGDPNSFYRSLIVEKI IQDIETTESSWRGGRINGGTGGTSVUSKRREGWTCGTOPDFSTTALP GCGLDHILABRILSYLLDAGRICATUCSKORGINGRKLII ERNWSTOPLWRIGGELINGTLGTRGSVULCLYDERVITYGSSDS TWEWDDWATGELLVUTGGRAVAVOUTPGDFNITAWSSCORTIKW STSTCEFVRT	6920	1418	591	<u> </u>
PARRIVISAVS DIVRAMITATIONER (PROMEDY PILES) PARRIVISAVS DIVRAMITATIONER (PROMEDY PILES) PARRIVISAVS DIVRAMITATIONER (PROMEDY PILES) SINCIGITS (POLAR PILES) SINCIGITS (POLAR PILES) NEISKLICSDDINVPDETI PHALMQWEGDUNNGGELGMILLS YIRIPLIPPQLIADLETS SMYTOLECKLIMBANKYLHLERR SMMOSPRTEPRKSTYGALVAVGGMDAMKGTTI EKYDLRTNSWIL HIGTMNGRICDGYMAV JUNINLIVVYGGHLGKTINTVECHPOPUGK IWTYMPPMSTRHOLGVATLEG PMYAVGGEDGKSYLNTVERHOD EGROMNYUAS MSTPER STVGVALINKLY GGRDGSSCLKKMEY FDPHTKKMSLCAPMSKRRGGVGVATYNGFLYVYGGHDA PASNIC SRISDCURSPYDEKOBSTVAPLISVPRDAVAVCPLIGDRLYVYGG YDGHTYLNTVES YDAQRNERKEEV PVNIGRAGACVVVVLID 6922 1075 369 LTPPAGITRHEVYDERREREREREK FFLDETSLKONITISTT GLPPANGKWMYKGLAF EDWITLREI KVTSGAKIMGGSTINDVLA VNTPKDAAQODAKAEENKEPLICKGKHRKUPLOKKEPDVWPSV KGAQEELFVVBLGGMYNKSGGKVEITKELGOOLDHIGTKERTEK LPMGST KRIVVSEP I ECHEDYHIMMAPQLGPTEASYYWYWYPTCY VDAIKDTVLGKWQYF 6923 2469 1660 LGLFCILPIDTLCAVLERDILS IRESKLFGAVVKNARAEACCOKO LPTYTENKKVLGKALSLI TRPLMTI EEPAAGPAGSGILSDREV VNLFLHFTVNPKKVLGKALSLI TRPLMTI EEPAAGPAGSGILSDREV VNLFLHFTVNPKKVLGKALSLI TRPLMTI EEPAAGPAGSGILSDREV VNLFLHFTVNPKKVLSFFLIST LTSPLMTI EEPAAGPAGSGILSDREV VNLFLHFTVNPKKVLSFFLIST SPESKINGTSTEEDGQIP EIIFYT 6924 2210 1235 PEERVICEVEYYLTAPHEGRKGALAKKPYNPI I GETFHCSWEVF KDRVKYKKTARS PASCHEHPMADDPS KSYKLRVVAGCYSHHPP LISCFYCECEKKILCVNTHVWTISKFMMMSVGVSMIGGVURLLE HGEEVYPTLBSAYARS ILIT I WWELGKYSINGKNIGGVURLLE HGEEVYPTLBSAYARS ILIT I WWELGKYSINGKNIGGVURLLE HGEEVYPTLBSAYARS ILIT I WWELGKYSINGKNIGGVURLLE HGEEVYPTLBSAYARS ILIT I WWELGKOMNIEGVURLLE GEGLANTARGLEVOSFPV DOMSSDOUSFVURLLISKNCHYOHGHINSYLKPHLORDFITALP DOMSSDOUSFVURLLISKNCHYOHGHINSYLKPHLORDFITALP DOMSSDOUSFVURLLISKNCHYOHGHINSYLKPHLORDFITALP EMWSTDPLAKGLISERGOMDOYLFKNRPPTOGPPNS FYRSLYKI LODIETIESWRGGRHNLORI CORTOSSUSS VILCENDER SVILCENDE	6921			
OYAYTGYLOLKEDTIESLLAAGLLQLITQVIDVCSNFLLKQLIP SNLGIRSFGDAQGCTELLNVAKYTWEHFIEVIKNOFFLLLEA NEISKLLCSDDINVPDEETIFHALMOWOHDVORDGELGMLLS YRLPLLIPPOLLADILETSSMFTGCKLLLEAMKYHLLPERR SMMGSPRTKERKSTUGALYAVGGMDAMKGTTTIEKYDLRINSUL HIGTMNGRRLLGGVAVIDNKLYVUGGRDGLKTLATVEEFAPVCK IWTVMPPMSTHRHGLGVAVIDNKLYVUGGRDGLKTLATVEEFAPVCK IWTVMPPMSTHRHGLGVAVIDNKLYVUGGRDGLKTLATVEEFAPVCK IWTVMPPMSTHRHGLGVAVLDRALVVANKLYAIGGRDGSSCLKSMEY FDPHTKMSCLCAPMENKERGVAVANNKLYAIGGRDGSSCLKSMEY FDPHTKMSCLCAPMENKERGVAVANNKLYAIGGRDGSSCLKSMEY FDPHTKMSCLCAPMENKRIGGVAVANNKLYAIGGRDGSSCLKSMEY FDPHTKMSCLCAPMENKRIGGVAVANNKLYAIGGRDGSSCLKSMEY FDPHTKMSCLAPMENKRIGGVAVANNKLYAIGLAVVORG SRASDCURRYDPKODSWSTUAPLSVPROMAVACHGDKLYVUGG SRASDCURRYDPKODSWSTUAPLSVPROMAVACHGLKKINTY SRASDCURRYDPKODSWSTUAPLSVPROMAVACHGLKALTY SRASDCURRYDPKODSWSTUAPLSVPROMAVCHGLKLAVY GRADELPTVLSGANNKENGKVRLTFSALTMGGSTIMDVLA UNTPKNAAQODAKARENKKEPLCRQKOHRKVLDKGKPEDVURSV KGAGELPTVLSGMYNKSGGKVRLTFKLEGOLWIGTKERTEK LPMGSIKNVUSEPLEGHEDVHMARPGLGFTEASYWVWAPPTOY VADAIRDTVIGHKOVY VANLFHIFTUNPKPRUF LEGHEDVHMAPPGLGFTEASYWVWAPPTOY VANLFHIFTUNPKPRUF LORDFICKSCLINTPTOWN OF THE STANGORY SGTSDRIFFTUNRRISIVGFGLUSIHGPTDVONIOIITSVEKK OTLGONDTOFSCODTANTFFWINKSCCINNFQOVESRIGGY SGTSDRIFFTUNRRISIVGFGLUSIHGPTDVONIOIITSVEKK OTLGONDTOFSCODTANTFFWINKSCCINNFQOVESRIGGIP DISTYLCECEBERLCVNTHWNTKSKRMGMSUCVSMIGGGVIRLLE HGGEVYFTLPSAVARSILTIPWELGGKVSINCAKTGYSATVIF HTIPFYTGKGKWRUTVARVEKRMGMSUCVSMIGGGVIRLLE HGGEVYFTLPSAVARSILTIPWELGGKVSINCAKTGYSATVIF PLOWSESDOVEFVEHLISRNCHVQHCHINSVIKREVTRYLRLIGDI DAATEGKVHLEEKGVENERKRENLRTPWKRYFIGEGGGILQ SPLESTLMGLEVOSFPV SGGAAGAMEPDSVIEDKTIELMCSVPRSLMURGVIRLEFTYNNG ETKVJDTTTLVYPKKIRPLEGROSGILVGSMIKKLL ERMVETDPLMKGLSERRGMOVIFKNRPTORPNSFYRSLYPKI 1001STIESSMRCGRIBHLQRICCRESNGVYCLOVDEKIISG LKDNSIKTWDKTSLECLKVLTCHTGSVLCLOVDERVIVTGSSDS TURVBVWATGEVLATILHINEAVILLRRSNGLWYTCSKORSIAV WDMSSDOVEFVEHLISRNCHVQHCHINSVIKRNDCOPPITTLP EGGLDHALISHNGLSERRSGROWICHKOLGALDF RAPASTLCLATIVEHSGRVFRLQFDEPGIISSSHDDTILLWDIEC GACLRVLEGHBLIVGCIRPDNRTVSGAYDGKKKMCJAALDF RAPASTLCLATIVEHSGRVFRLQFDEPGIISSSHDDTILLWDIEC GACLRVLEGHBLIVRCIRR DNAR		, , ,	1/11	DANEL W. GALGOWALANDE TERMENYLKEKQLCDVLLIAGHLRI
SNCLGTRSFEDDAGGCTELLNVAHKYTMEHFIEVIKNOEFLLLEA NEISKLCSDDINVEDETITHALWOWEHDVONROELGMILLS YIRLPLLPPOLLADLETSSMTGDLEGOKLLMEANKYHLLPERR SMMSPRTKPRRSTVGALALWAGMAKGTTITEKYDLRTNSWL HIGTMNGRRLQGUAVIUNKLYVUGGROGIKTLNTVECFRPUGK IWTVMPPMSTHRHGLGVATLEGPMYAVGGHOGSYLATVERWDP EGROMNYVASMSTERSTVGVVALNNKLYAIGGROGSSCLKSMEY FDPHTMKWSLCAPMSKRRGGVGVATYNGELVVGGHDAPASING SRISDCUREYDPKGDSWSTVAPLSVPRDAVAVCHLGDKLYVVGG YDGHTYLNTVESYDAQNAEMEERPPUNGGRAGACVVVVKLP CLPPAMGKUMYKGLAPEDKTLREIKVTSGAKIMGGGSTINDVLA VNTPKDAAQQDAKAEENKKEPLCRGKQHRKVLDKKKEPDVMTGSV KGAQRELPTVELSGMYMKSGGKVGLTFKLEQDQLWIGTKRRTEK LPMGSIKNVVSEPIEGHEDVHMMAFQLGFTERSYWVYWYPTQY VDAIKNTVLJKKNQVY VDAIKNTVLJKKNQVY VDAIKNTVLJKKNQVY VDAIKNTVLJKKNQVY NDAIKNTVLJKKNQVY NDAIKNTVLJKKNQVY SGTSDELRFTVMRRSISIVGFGLYGSIHGVANGAEAECORQ LPVTFGNKOKVLJGKALSLIRFPUMTI BEFARGPAQSGILDDREV VNLFLHFTVMPKPRVEYIDPRCCLRGKSCCINRFQQVESRWGY SGTSDELRFTVMRRSISIVGFGLYGSIHGPVQVESRWGY SGTSDELRFTVMRRSISIVGFGLYGSIHGPVQNIQHIEYEKK QTLGQNDTGFSCDGTANTFRVMFKEPIBILENVCYTACATLKGD DSNYGTKGLKKVVHETPAASKTVFFFFSSEGNNNGTSIEDGGIP EIFYT FERVILOTTILEVYPKKTARSPASCHEHPMADDPSKSYKLRFVAGGVSHHPP KORVKPKRTARSPASCHEHPMADDPSKSYKLRFVAGGVSHHPP LSGFYCECEBRRLCVNTHVWTKSKFMGMSUGVSMIGEGVLRLLE HGGEVYPTLPSAVARSILTIPWELIGKVSINCAKTYSSATVIF HTKPFYGGKVHRVTARVKINPITTIVCKAHGENNGFLEFTYNNG ETKVLDTTTLEVYPKKIRPLEKGGMERSRLIMREVTRYLRLGDI DAATERJKMHLEEKGRWEERKRENLETPWKKPYFIGEGGSGILQ SPLESTLMGLEVOSFPV DGWSESDOVEPVERLISRMCHYGHGHINKHRUTRYLRLGDI DAATERJKMPUTSVYPKKIRPLEKGGFMESRLIMREVTRYLRLGDI DAATERJKMPUTSVYPKKIRPLEKGGFMESRLIMREVTRYLRLGDI DAATERJKMPUTSVYPKKIRPLEKGGFMESRLIMREVTRYLRLEDGI DAATERJKMPUTSVYPKKIRPLERGSSGILGKALLIKEPHLORDFITALP EGGLDHIABNILSVILGHRANDVUDFDDKYIVSASGDSTIKW LICHIETSSMMRCGBRINLQRICGRESNKGVYCLQVDGEKIRSG LEDNSIKHDKATSLECLKVLTCHTGSVLCCDYDERVIVTGSSDS TRYNDVANTGELINTLIHNEAULTRIHNEAULTRECHMYTCKSORSIAV WIDMASATDITLRRYLUGHRAANNVUDFDDKYIVASSGDSTIKWW STSTCEFVRTLINGHKGRIACLQYRDRILVSGSSDNTIKLMDIEC GACLRVLEGHBELVRCIRFDNKRTIVGGAYDGKKKWOLQAALDP RAPASTLCLATLVEHSGRVFRLQFDEPGIISSSHDDTILIMDFL	1	•		PARKLVLSAVSDYFAAMFTNDVLEAKQEEVRMEGVDPNALNSLV
NEISKLCSBDINVPDEETIFHALMOWVGHULS YIRLPLEPPOLLADILETSSMFTCHECKLIMEAMKYHLLPERR SMMGSPRIKPRISTUGALYANGGMDAMKGTTIIEKYDLPTUNSUL HIGTMINGRILOGGUAVIDNIKLYVGGHDGWSYLNTUERWDP EGROMYVASMSTPRSTUGUVALINNIKLYNGGRDGSSCLKSMSY FDPHTNKWSLCAPMSKRRGGGVGAVINTURGHVVGGHDAPASNIC SRLSDCUBRYDPKGDSWSTUAPLSVPROLAVACHGRIKLYVUGG YDGHTLINTURSYDAQNREWKEEVPVNIGRAGACUVVKLP 6922 1075 369 LITPRAGIRHEWADREREREREREREPLOSTGSELKGNIHSTI GLPPANGKWINKGLAPEDFENTLREIKTGAKIMGGSTINDULA UNTPKNAAQODAKABENKKEPLCROKOHRKULDKGKPEDWINPSV KGADELPTVPLSGNYRKSGGKVAFTHELGODUNIGTKERTER LPMGSIKNVVSEPIEGHEDYHMMAPQLGPTEASYYWVYWPTQY VDAIKNTULGKWOYF 6923 2469 1660 LGLFCTLPIDTLCAVLERDTLSIRESRLFGAVVRWAEAECQRQQ LPVTFGNKGKVUGGALSLIREPPMITEERAAGPAQSGILSDREV VNLFLHFTUNREPSEVIDERPMITEERAAGPAQSGILSDREV VNLFLHFTUNREPSEVIDERPMITEERAAGPAQSGILSDREV VNLFLHFTUNREPSEVIDERPMITEERAAGPAQSGILSDREV VNLFLHFTUNREPSEVIDERPMITEERAAGPAQSGILSDREV VNLFLHFTUNREPSEVIDERPMITEERAAGPAQSGILSDREV VNLFLHFTUNREPSEVIDERPMITEERAAGPAQSGILSDREV VNLFLHFTUNREPSEVIDERPMITEERAAGPAQSGILSDREV VNLFLHFTUNREPSEVIDERPMITEERAAGPAQSGILSDREV VNLFLHFTUNREPSEVIDERPMITEERAAGPAQSGILSDREV VNLFLHFTUNREPSEVIDERPMITEERAAGPAQSGILSDREV VNLFLHFTUNREPSEVIDERPMITEERAAGPAQSGILSDREV VNLFLHFTUNREPSEVIDERFUNTEERAAGPAQSGILSDREV VNLFLHFTUNREPSEVIDERFUNTEERAAGPAQSGILSDREV VNLFLHFTUNREPSEVIDERPMITEERAAGPAQSGILSDREV VNLFLHFTUNREPSEVIDERFUNTEERAAGPAQSGILSDREV VNLFLHFTUNREPSEVIDERFUNTEERAAGPAQSGILSDREV VNLFLHFTUNREPSEVIDERFUNTEERAAGPAQSGILSDREV VNLFLHFTUNREPSEVIDERFUNTEERAAGPAQSGILSDREV VNLFLHFTUNREPSEVIDERFUNTEERAAGPAQSGILSDREV VNLFLHFTUNREPSEVIDERFUNTEERAAGPAQSGILSDREV VNLFLHFTUNREPSEVIDERFUNTEERAAGPAQSGILDREV SGTSDRIFTUNRESSUNGERKERERERERERERERERERERERERERERERERERER	j	<u> </u>		CNCLCIPCEGERESTIESLLAAACLLQLTQVIDVCSNFLIKQLHP
YIRLPLIPPOLLADLETSSMFTGDLECOKLIMEAMKYHLIPERR SMMOSPRIFREKSTUGALVAVGGRDGLKTLATVECPHPUGK HIGTMNGRRLQFGVAVIDNKLYVVGGRDGLKTLATVECPHPUGK IWTVMPPMSTHRHGLGVATLEGWAVGGRDGLKTLATVECPHPUGK IWTVMPPMSTHRHGLGVATLEGWAVGGRDGLKTLATVECPHPUGK IWTVMPPMSTHRHGLGVATLEGWAVGGRDGWSYLMTVERWDP EGROMNYVASMSTPRSTVGUVALNNKLYALGGRDGSSCLKGMEY FDPHTNKWSLCAPMSKRRGGVGVATYNGFLYVVGGHDARSING SRLSDCVERYDPKGDSWSTVAPLSVPRDAVAVCPLGDKLYVVGG YDGHTYLNTVESYDAQRNEWKEEVPKNTGGRAGACVVVVKLP 1075 369 1075 1075 1075 1075 1075 1075 1075 1089 1089AMGKWYKGLAPEDKTLREIKVTSGRAIMGGGSTINDVLA VNTPKDAQODAKARENKKEPLOKOGKORKVLDKKKPEDVMPSV KGAQELLPTVPLSGMYNKSGGKVRLTFKLEODGLWIGTKERTEK LPMGSIKNVVSEPPIGHEDYHMMAFQLGPTEASYYWYWPYTQY VDAIKDTVLGKWQYF 1094 1094 1094 1094 1094 1094 1094 1094]		NEISKI CODDINIDDEEDINAHKYTMEHFIEVIKNQEFLLLPA
SMMSPRTIFERSTUGALAVGGMDAMEGTTI EKYDLERINSUL HIGTMORRELGEVGAVATUNKLYAVGGRDGLKITUTVECKHPUCK IWTMPPMSTHRHGLGVAVIDKLYAVGGRDGLKSLTVERWDP EGROWNVAMSTPRSTVGVVALINKLYAIGGRDGSSCLKGMEY FDPHTNKWSLCAPMEKRRGGVGVATYNGFLYVVGGHDAPASING SRLSDCVERYDPKGDSWSTVAPLSVPRDAVCCHGDKLYVVGG YDGHTVLNTVESYDAQRNEWREREVPVNIGRGAGCVVVKLP GLPPAMCKMYKGLAPEDKTLERVTGRAKIMGGGSTINDVLA VNTPKDAQODAKABENKKEPLCRQKQHRKVLDKGKPEDVMPSV KGAQERLPTVPLSGMYNKSGGKVRLITFKLEDDLWIGTKRETEK LPMGSIKNVVSEP IBGHEDYMMAPQLGPTEASYWVYWPTOY VDAIKDTVLGKWQYF 6923 2469 1660 LGLFCTLPJDTLCAVLERDTLSIRESRLFGAVVRWAEAECQRQO LFVTFGNKGKVLGKALSLIRPPLWTIEFFAAGPAQSGILSDREV VNLFHTVNPRYPRVEYIDRPRCCLRGKECCINFFQQVSRMGY SGTSDRIRPTVNRRISINGFGLYGSIHGPDTVONIQIIEYEKK QTLGONDTGFSCDGTANTFMFEPIELIPNVCYTACATLKGP EIIFYT 6924 2210 1235 PERVICFVEYYLTAFHEGRKGALAKKPYNPI IGETFHCSWEVP KDRVKKKRTASRSPASCHEHPMADDPSKSYKLRFVAEQVSHHPP ISCFYCEGEBKRLCVNTHVWTKSKFMGMSGVSMIGEGVLRLE HGEEYVFTLPSAYRARSILTIEWELGKKSINGAKARGYSATVIF HTKPFYGGKVRRVTAEVKHNPTNTIVCKARGEMNGTLEFTYNNG ETVLUDTTLEVYPKKRPLEVHTSTVINCKARGEMNGTLEFTYNNG ETVLUDTTLEVYPKKRPLEVHLISRMCHYDGHFSCHLAKLY SPLESTLMGLEVQSFPV 6925 2 1653 RGGAAGAAMBEDSVIEDKTIELMCSVPRSLWLGGANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVGRKPPSEGMYQKEKDLCIKYF DOMSSEDQVEFVEHLISRMCHYDGHFINSYLKWHQOFPFITALP EQGLDHIABNILSVLDARSLCAAELVCKEWQRVISEGMLWKKLI EMWYTDPLWKGLSCREGRWQVIFKNRPJOFPNSTKALF LDDIETIESNMRCGRRHQDQTLFRINSYLKWHQOFPFITALP EQGLDHIABNILSVLDARSLCAAELVCKEWQRVISEGMLWKLI EMWATDPLWKGLGCRSDNSKOVCLQYDDEKIISG LENDSIKTWDKTSLECLKVUTGHTGSVLCLQYDERVITYGSSDS TVRWDVNTGEVAUTLIHHERGHGNVIVSGSDDNTIRLWDIC GACLRVLEGHEELVRCIRFDNKRVSGSDNTIRLWDIC GACLRVLEGHEELVRCIRFDNKRVSGSDNTIRLWDIC GACLRVLEGHEELVRCIRFDNKRVSGSDNTIRLWDIC GACLRVLEGHEELVRCIRFDNKRVSGSDNTIRLWDIC GACLRVLEGHEELVRCIRFDNKRVSGSDNTILLINDFL	1			WEISKLLCSDDINVPDEETIFHALMQWVGHDVQNRQGELGMLLS
HIGTMNGRELQFGVAVIDNKLYVGGRDGLKTLMTVECFHPVGK IWTVMPPMSTHRHGLGVATLEGPMYVGGHDGWSYLMTVERWPP EGROWNYVASMSTPRSTVGVVALNNKLYAIGGRDGSSCLKSMEY FDPHTNKWSLCAPMSKRRGGVGVATYNGFLYVVGGHDASNING SRLSDCVBRYDFKGDSWSTVAPLSVPRRDAVAVCPLGDKLYVVGG SRLSDCVBRYDFKGDSWSTVAPLSVPRRDAVAVCPLGDKLYVVGG YDGHTYLNTVESYDAQRNEKEPVENTIGRAGACVVVVKLP 1075 169 1175 169 1175 169 1175 169 1175 169 1175 169 1175 169 1175 169 1175 169 1175 169 1175 169 1175 169 1175 169 1176 169 1176 169 1176 169 1176 169 1176 169 1176 169 1176 169 1176 1177 1177		1		EMMOS DETAPOLICATION TO SMITTED LECOKIL MEAMKYHLL PERR
INTYMPPMSTHRIGLGVATLEGMYANGGHDGMSYLNTVERMDP EGRONNIVASMSTPRSTYGVVALNNIKLYAIGGHDGSSCLKSMEY FDPHTNIKMSLCAPMSKRRGGGVGNATYNGPLYVVGGHDAPASHIC GRADCVERYDPKGDSMSTVAPHSVERDAVACYTEJGKLYVVGG YDGHTYLNTVESYDAGRNEWKEXPVNIGRAGACVVVVKLP 1075 369 LTPPAGIRHEVRORREREREKREKEKPLDSTGSELKØNIHSIT CLPPAMGKUMYKGLAPEDKTIEKIVYGGAKIMGGGSTINDULA VNTPKDAAQQDAKAEENKKEPLCRQKOHRKVLDKGKPEDVMPSV KGAQERLPTVPLGGMYMKSGKVRITFKLEODQLWIGTKERREK LPMGSIKNVVSEPIEGHEDYHMMAPQLGFTEASYYWVYWVPTQY VDAIKDTVLGKWQYF 1660 LGFCTLPIDTLCAVLERDTLSIRESRLFGAVVRWAEAECQRQQ LPVTFGNKOKVLGKALSLIRFPLMTIEEPAAGPAQSGILSDREV VNLFLHFTUMPKPRUEYIIDRCLBRECCLBRECCIRFQQVESRWGY SGTSDRIRFTVNRRISIVGFGLYGSIHGPTDYQVMIQIIEYEKK QTLGQNDTGFSCDGTANTFRVMFKEPIBLEMVCTTACATLKGP DSHYGTKGLKKVVHETPAASKCRIFFPSSPERNNOTSIEDGQIP EIFFYT 16924 2210 1235 PEERVICFVEYYLTAFHEGRKGALAKKFYNPIIGETFHCSWEVP KORVKFRTASRSPASCHEHPMADDPSKSYKLRFVAEQVSHHPP ISCFYCECEEKRLCVNTHWATKSKRMGSVGVSMGGGCVLRLLE HEGEVYFTLPSAYARSILTIPWELGGKVSINCAKTGYSATVIF HITKPFYGGKHBVTAEVKIRPINTIVCKAHGEWNOTLEFTVNNG ETKVIDTTLLFVYPKKIRFLEWGGMESRINKREVTRYLRIGDI DAATEGKRHLEEKQRVEERKRENLRTPWKYRYFIQEGDGSGILQ SPLESTIMGLEVOSPPV AGGAAGAAMEPDSVIEDKTIELMCSVPRSLWIGGANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKRPSENYQKEKOLCIKYF DOMSSEDQVEFVEHLISRMCHHOHINSYLKPBLORDFITALP EGGLDHIABNILSYLDARSLCABELVCLGVDDRVIVTGSSDS TVRWMDVNTGSVLNTLHHINSVLLORFSNENKGVYCLQVDDEKLISG LEDNSIKTMDKTSLECLKVLTGHTGSVVLCLQVDDRVIVTGSSDS TVRWDVNTGSVLNTLHHINSVLLORFSNENKTVSCANGSSIAV WDMASATDITLRRVLVGHRAAVNVUDGRRAAVNTVLGSDS TVRWDVNTGSVLNTLHHINSVLLORFSNENKTVSCANGSSIAV WDMASATDITLRRVLVGHRAAVNVUDGRSDNTTIRLWDIEC GACLRVLEGHEELVRCRFDWKRIVSGSADNTIRLWDIEC GACLRVLEGHEELVRCRFDWKRIVSGSADNTILIUMDFL NVPBSAQNETERSPSRTYTYLGPDEFQIISSSHDDTILIUMDFL NVPBSAQNETERSPSRTYTYLGPDEFQIISSSHDDTILIUMDFL		1 1		HIGHWORD COUNTY TOWN
EGROWNYVASMSTPRSTVGVVALNNKLYAIGGRDGSSCLKSMEY FDPHTNKWSLCAPMSKREGGVATYMGFLYVVGGHDAPASNHC SRLSDCVGRYDPKOBMSTVAPLSVPRDAVAVCPLGDKLYVVGG YDGHTYLNTVESYDAGRNEKKEEVPVNIGRAGACVVVVKLP CLPPAMGKVMYKGLAPEDKTLSEIKKON IHSIT GLPPAMGKVMYKGLAPEDKTLSEIKKON IHSIT GLPPAMGKVMYKGLAPEDKTLSEIKKON IHSIT GLPPAMGKVMYKGLAPEDKTLSEIKKON IHSIT GLPPAMGKVMYKGLAPEDKTLSEIKVTGGAKIMGGGSTINDVLA VNTPKDAQQDAKAEENKKEPLGOKOHRKVLDKGKPEDVMPSV KGAQERLPTVPLGGMYNKSGGKVRLTFKLEQOQLWIGTKERTEK LPMGSIKNVVSEPIEGHEDYHMMAFQLGFTEASYYWVYWPTQY VDAIKDTVLGKWQYF LEFTCHNOKOVLGKALSLIKFPLMTIESFREGAVVRWAEAECQRQQ LPVTFGNKGKVLGKALSLIKFPLMTIESFREGAVVRWAEAECQRQQ LPVTFGNKGKVLGKALSLIKFPLMTIESFRAGAPAQSGILSDREV VNLFLHFTVNPKPRVEYIDRPRCCLRGKSCCINRFQQVESRWGY SGTSDRIFRTVNRRISIVGFGLYGSIKGTDVQVNIQIEVEYEKK QTLGQNTGFSCCDGTANTFRVWKEPIBILPNVCTACATLKGP DSHYGTKGLKKVVHETPAASKTVFFFSSPGNNNGTSIEDGQIP EIFFYT SERVICFVEYYLTAFHEGRKGALAKKPYNPIIGETFHCSWEVP KORVKPKRTASRSPASCHEHPPAADDPKSYKLRFVAEQUSHHPP ISCFYCECESKRLCVNTHWYKSKFMGMSUGYSMIGEGULRLE HGEFYYFTLPSAYARSILTIPWBELGGKVSINCAKTGYSATVIF HTKPFYGGKUNVTASKERLCVNTHWYKSKFMGMSUGYSMIGEGULRLE HGEFYYFTLPSAYARSILTIPWBELGGKVSINCAKTGYSATVIF HTKPFYGGKUNVTASKERLCVNTHWYKSKFMGMSUGYSMIGEGULRLE HGEFYYFTLPSAYARSILTIPWBELGGKVSINCAKTGYSATVIF HTKPFYGGKUNVTASKERLCVNTHWYKSKFMGMSUGYSMIGEGULRLE HGEFYYFTLPSAYARSILTIPWBELGGKVSINCAKTGYSATVIF HTKPFYGGKUNVTASKERLCVNTHWYKSKFMGMSUGYSMIGEGULRLE HGEFYYFTLPSAYARSILTIPWBELGGKVSINCAKTGYSATVIF HTKPFYGGKUNVTASKERNENTYKFKRGDIL GANDATECKRHLEEKQRVERKKRILTIPWRKYFTLQEGDGSGILQ SPLESTIMGLEVGSPFV KIRPTDGPMSTKRSLV KIRPTDGPMSTKRSLV KIRPTDGPMSTKRSLV KIRPTDGPMSTKRSLV KIRPTDGPMSTKRSLV KIRPTDGPMSTKRSLV KIRPTDGPMSTKRSLV KIRPTDGPMSTKRSLV KIRPTDGPMSTKRSLV KIRPTDGPMSTKRSLV KIRPTDGPMSTKRSLV KIRPTDGPMSTKRSLV KIRPTDGPMSTKRSLV KIRPTDGPMSTKRSLV KIRPTDGPMSTKRSLV KIRPTDGPMSTKRSLV KIRPTDGPMSTKRSLV KIRPTDGPMSTKRSLAV KIRPTDGMSTATVITGSSDS TURWWDMTGSVILVGGRSSDNTTIRLWU KIRPTDGMAGALDFURGKGLACLQYRDRLVVGGSSDNTTIRLWDG GACLRVLEGHELVRCURFDRAVILVGBADDTLLINDFL KNDPSSANDTILLWOFLA	1	ì		THE THINGRED GEO AV I DIKLYVVGGRDGLKTLNTVECFNPVGK
FDPHTNKMSLCAPMSKRRGGGVUATYNGFLYVVGGHDAPASHIC SRISDCVERTPPKGSDSWSTVAPLSVPRDAVACPLGDKLYVVGG YDGHTYLNTVESYDAQRNEWKEEVPVNIGRAGACVVVKLP LTPFAGIRHEVRDREREEREREKEKFPLDSTGSELKQNIHSIT GLPPAMGKVMYKGLAPEKITERIKVTSGAKIMGGGSTINDVLA VNTPKDAAQQDAKAENKKEPLCRQKQHRKVLDKGKPEDVMPSV KGAQERLPTVPLSGMYNKKSGGKVRLTFKLEQDQLWIGTKERTEK LPMGSIKNVVSEPIEGHEDYHMMAPQLOFTEASYYWVYWYPYDY VDAIKDTVLGKWQYF 6923 2469 1660 LGLFCTLPIDTLCAVLERDTLSIRESRLFGAVVRWAEAECQRQQ LPVTFGKKQNVLGKALSLIRFPLMTIEFFAAGPAQSGILSDREV VNLFLHFTVNRFKRVEVIDRFRCCLRGKECCINRFQQVESRWGY SGTSDRIRFTVNRRISIVGFGLYGSIHGPTDYQVNIOLIEVEKK QTLGQNDTGFSCDGTANTFRVMFKEPIBILDNVCYTACATLKGP DSHYGTKGLKKVVHETPAASKTVFFFSSPGNNNGTSIEGQIP EIIFYT 6924 2210 1235 PEERVICFVEYYLTAFHEGRKGALAKKPYNPIIGETFHCSWEVP KORVKYKRTASRSPASCHEHPMADDPSKSYKLRFVARQVSHHPP ISCFYCECEBKRLCVWTHVWTKSKFMGMSVGVSMIGEGULRLLE HGEEYVFTLPSAYARSILTIEWELGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTABVKHNPTNTIVCKAKGEWNGTLEFTYNNG ETTAVIDTTTLPVYPKKIRPLEKGGFBRSRALWREVTFYLRLGDI DAATEQKRHLEEKGRVEERRERLRTPWKPKYFIQEGGSGILQ SPLESTLMGLEVQSFPV 6925 2 1653 RGGAAGAAMEPDSVIEDKTIELMCSVPRSLMLGCANLVESMCAL SCLOSMPSVRCLQISKGTSSVIVGRKRPSEGNYQKEKDLCIKYF DQMSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAENILSYLDARSLCAAELUCKEWQRVISEGMLMKKLI ERMWRTDPLWKGLSERRGMOVYLFKNRPTDEPNSFYRSLYPKI LQDIETIESMWRCGRINLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKHMDKTSLECLKVUTHGHGSVLCLQYDDERVIVTGSSDS TVRVWDVNTGEVLNTLIHRNEAVLHLRFSNGLMVTCSKDRSIAV WDMSASATDITLRRVLVGHRAAWWVDFDDKYIVSAGSDRTIKWW STSTCFFVRTINGHKRGIACQYNDRLVVSGSSDNTTRLWDIEC GACLEVLEGHERLVRCIRFDNKRVSGSDNTIKWW STSTCFFVRTINGHKRGIACQYNDRLVVSGSSDNTIKLWDIG RAPASTLCLRTLVEHGRRVFRLOFDBFQIISSSHDDTILIWDFI NVPPSAQNETRSPSKTYTLYGHGSGAYCLGSSDNTGLWDFI NVPPSAQNETRSPSKTYTLYGHGSGAYGKKVDLQAALDP RAPASTLCLRTLVEHGRRVFRLOFDBFQIISSSHDDTILIWDFI NVPPSAQNETRSPSKTYTLYEHGRRGAISSSHDDTILIWDFI				FCPOWNY AND DOWN THE GPMYAVGGHDGWSYLNTVERWDP
SRISDCVERTYDPKOBGNSTVAPLESYPEDAVAVCPIGDKLYVVGG YDGHTYLINTVESYDAQNAEWREEVPVIIGRAGACVVVKLP G922 1075 369 LTPPAGIRHEVRDREREREREREKFFLDSTGSELKQNIHSIT GLPPAMQKVMYKGLAPEDKTLREIKVTSGAKIMGGGSTINDVLA VMYPKDAAQODAKAEBENKELICRKQCHRKVLDKOKPEBUMPBV KGAQERLPTVPLSGMYMKSGGKVRLIFKLEQDQLWIGTKERTEK LPMGSIKNVVSEPIEGHDYMMAFQLGPTEASYYWVYWYDTQY VDAIKDTVLGKWQYF 1060 LGIFCILPIDTLCAVLERDTLSIRESRLFGAVVRWAEAECQRQQ LPVTFGMKQKVLGKALSLIRFPLMTIEBFAAGPAQSGILSDREV VNLFLHHTVMPKPRVEVIDRPRCCLRGKECCINRFQQVESRWGY SGTSDRIFFTVNRRISIVGFGJYGSIHGPTDYQVNIOTIEVEKK QTLQNDTGFSCDGTANTFRWMFKEPIEILDNVCYTACATLKGP DSHYGTKGLKKVVHETPAASKTVFFFSSPGNNNGTSIEDGQIP EIIFYT PEERVICFVEYYLTAPHEGRKGALAKKPYNPIIGETFHCSWEVP KDRVKPKRTARRSPACHEHPMAVGVSNHIGECVLRLLE HGEEYYFTLPSAYARSILTIEWELGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTAEVKHNPTNIVCKAHGEMBGTLEFTYNMG ETKVIDTTLPVYPKKIRPLEKQGPMESRNLWREVTRYLRLIGDI DAATEQKRHLEEKQRVEERKRENLRTEWKRYFIQEGDGSGILQ SPLESTLMGLEVQSFPV 1653 RGGAAGAMEPDSVIEDKTIELMCSVPRSLWLGGANIJVESMCAL SCLOSMPSVRCJQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSVLKDMCQRFTTALP EQGLDHIAENILSYLDARSLCABELVCKEWQRVISEGMLMKKLI EMMYTDPLIKKGLISERRGMYTCSVLCVYDDERVIVTGSSDS TVRVWDVNTGGVLNTLLHNEAVLHLRFSNGLMVTCKORSIAV WDMSASATDITLRRVLVGHRAAVWVUPFDDKYIVAGSGDNTIRKW STSTCEFVRTLNGHKRGIAGQYRDLLVVGSSDDNTIRLWDIEC GACLEVLEGHEELVRCIRFDNKRIVSGSDNTIRLWDIEC GACLEVLEGHEELVRCIRFDNKRIVSGSDNTIRLWDIEC GACLEVLEGHEELVRCIRFDNKRIVSGSDNTIRLWDIEC GACLEVLEGHEELVRCIRFDNKRIVSGSDNTIRLWDIEC GACLEVLEGHEELVRCIRFDNKRIVSGSDNTIRLWDIEC GACLEVLEGHEELVRCIRFDNKRIVSGSDNTIRLWDIEC GACLEVLEGHEELVRCIRFDNKRIVSGSDNTIRLWDIEC GACLEVLEGHEELVRCIRFDNKRIVSGSDNTIRLWDIEC GACLEVLEGHEELVRCIRFDNKRIVSGSDNTIRLWDEFI NVPPSAQNETERSPSKTYTLGFDEFGUISSSHDDTILIWDFI NVPPSAQNETERSPSKTYTLGFDEFGUISSSHDDTILIWDFI		}		EGROWNIVASMSTPRSTVGVVALNNKLYAIGGRDGSSCLKSMEY
6922 1075 369 LITPAGTHEWFUNDERSEREREKEFENDSTGSELKQNIHSIT GLPPAMQKVMYKGLAPEDKTUSEKELKGNIHSIT GLPPAMQKVMYKGLAPEDKTLREIKVTSGAKIMGGSTINDVLA VNTPKDAAQQDAKABENKKEPLCRQKQHRKVLDKGKPEDVMPSV KGAQERLPTVPLSCMYNKKSGKVRLITFKLEDQDLMIGTKERTEK LPMGSIKNVVSEPIEGHEDYHMMAFQLGPTEASYYWVYWPTQY VDALKDTVLGKWQYF 6923 2469 1660 LGLFCILPIDTLCAVLERDTLSIRESRLFGAVVRWAEAECQRQQ LPVTFGNKQRVLGKALSLIRFJLMTIEFFAAGPAQSGILSDREV VNLPLHFTVMYKPRVEVIDTBRCCLRGKECCINRFQQVESRWGY SGTSDRIRFTVNRRISIVGFGLYGSIHEPTDYQVNIQIIEVEKK QTLGQNDTGFSCDGTANTFRVMFKEPIEILDNVCYTACATLKGP DSHYGTKGLKKVVHETPAASKTVFFFFSSPGNNNGTSIEDGQIP EIIFYT 6924 2210 1235 PEERVICFVEYYLTAFHEGRKGALAKKPYNPIIGETFHCSWEVP KORVKKKTASRSPASCHEHPMADDPSKSYKLRFVAEQVSHHPP ISGFYCECEKKRLCVNTHVWTKSKFMGMSVQVSMIGEGVLKLLE HGEYVYFTLDSAVARSILTWEVELGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTAEVKHNPTNTIVCKAHGEMMGTLEFTTNNG ETKVIDTTLPVYPKKIRPLEKGGPMESRNLWREVTRYLRIGDI DAATEQKRHLEERQRVEERKELRTPWKKYFIQEGGSGILQ SPLESTLMGLEVQSFPV 6925 2 1653 RGGAAGANEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKDMLQRDFITALP EQOLDHIAENILSYLDDASLCAABLVCKEWQRVISEGMLMKKLI ERMVSTDPLWKGLSERRGWDOYLFKNRPTDGPPNSFYRSLYPKI LQDIETIESMWRCGRINLQRIQCRSENSKGVYCLQYDDEKIISG LADNSIKHDMSTSLECLANGTGTGSVLCLOYDERVIVTGSSDS TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAWVUVFDDKYIVASAGDRTIKWW STSTCEFVRTINGHKRGIAQVRDLVVSGSSDNTTRLWDIEC GACLEVLEGHERLVRCIRFDDKRIVSGSDNTKLWBILDDIEL GACLEVLEGHERLVRCIRFDDKRIVSGSDNTKLWDIEGAALDV NVPDSAQNETRSPSKTYTLYGESSDNTKLWDIEG GACLEVLEGHERLVRCIRFDDKRIVSGSADGKKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDFGIISSSHDDTILIWDFI.NVPPSAQNETRSPSKTYTLYGESSDNTTLTUDFEL	1			CPL CDCUEPADRADAY CHARACTER OF
GLPPAMGKWNKGLAPENTIREIKUTSGAKIMGGSTINDVLA GLPPAMGKWNKGLAPENTIREIKVTSGAKIMGGSTINDVLA KGAQERLPTVPLSGMYNKSGGKVRLTFKLEQDQLWIGTKERTEK LPMGSIKNVUSEPIEGHEDYHMMAPQLGPTEASYYWYWVPTQY VDAIKDTVLGKWQYF 6923 2469 1660 LGFCILPIDTLCAVLERDTLSIRESRLFGAVVRWAEAECCRQQ LPVTFGKKOKVLIGKALSLIRFPLMTI EEFAAGPAQSGILSDREV VNLFLHETVUPKPRVEYIDRPCCLRGKECCINRFQQVESRWGY SGTSDRIRFTVNRRISIVGFGLYGSIHGPPTDYOVNIQIIEVEKK QTLGQNDTGFSCDCTANTFVWPKEPIELLPNVCYTACATLKGP DSHYGTKGLKKVVHETPAASKTVFFFFSSPGNNNGTSIEDGQIP EIIFYT 6924 2210 1235 PEERVICFVEYYLTAFHEGRKGALAKKPYNPIIGETFHCSWEVP KORVKPKRTASRSPASCHEHPMADDPSKSYKLKFVABQVSHHPP ISCFYCECEEKRLCVNTHVWTKSKPMGMSVGVSMIGEGVLRLLE HGEEYVFTLPSAYARSILTIPWELGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTAEVKHNPTNTTVCKAHGBWGTLEFTYNNG ETKVIDTTTLPVYPKKIRFPLEKQGPMESRNLWREVTRYLRLGDI DAATEQKRHLEEKQRVEERKRENIRTPWKRKYFIQBGDGSGILQ SPLESTLMGLEVOSFPV AGGAAGAAMBPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYOGHINSYLKPMLQRDFITALP EQGIDHIARMILSYLDARSLCABELVCKEWQRVISEGLIKKLI ERMYRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKL IQDIETIESNWRGGRHNLQRICGASENSKGVCLQYDDEKIISG LRDNSIKINDKTSLECKLKVLTGHTGSVLCLQVDERVIVTGSSDS TVRVWDVNTGSVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRVVLVGHRAAVNVDFDDKYIVSASGDRTIKWW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDMTIRLMDIEC GACLRVLEGHEBLVRCTRFDNKRIVSGAYDGKIKWWDLQAALDP RAPASTLCLRTLVEHSGRVFRLIGDEFQIISSSHDDTILIMDFL	J.)		VDGHTVI NTVESVDA ODNENIVEDI DEL
GLPPAMQKVMYKGLAPEDKTIREIKVTSGAKIMGGGSTINDVLA VNTPKDAAQODAKABENKEPLCRQKOMRKVLDKGKPEDVMPSV KGAQERLPTVPLSGMYNKSGGKVRLTFKLEQDQLWIGTKERTEK LPMGSIKNVVSEPIEGHEDYHMAFQLGPTEASYYWVYWVPTQY VDAIKDTVLGKWQYF 1660 LGLFCILPIDTLCAVLERDTLSIRESRLFGAVVRWAEAECQRQQ LPVTFGNKQKVLGKALSLIRFPIMTIEEFAAGPAQSGILSDREV VNLFLHFTVMPKPRVEVY1DRPRCCLRGKECCINRFQQVESRWGY SGTSDRIRFTVNRRISIVGFGLYGSIHGPTDYQVNIQIIEYEKK QTLGQNDTGFSCDGTANTFRVMFKEPIEILPNVCYTACATLKGP DSHYGTKGLKKVVHETPAASKTVFFFFSSPGNNNGTSIEDGQIP EIIFYT 6924 2210 1235 PEERVICTVEYYLTAFHEGRKGALAKKPYNPIIGETFHCSWEVP KDRVKPKRTASRSPASCHEHPMADDPSKSYKLRFVAEQUSHHPP ISCFYCECEBKRLCVNTHVWTKSKMMMSUGSWINGEGVLRLLE HGGEYYFTLPSVAYARSILTIPWELGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTAEVKHNPTNTIVCKAHGEWNGTLEFTYNNG ETKVIDTTLLPVYPKKIRPLEKGGMESRILNEVTTYLRLGDI DAATECKRHLEEKGRVEERKRENLRTPWKPKYFIQEGDGSGILQ SPLESTIMGLEVQSFPV 6925 2 1653 RGGAAGAMEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNCTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRCHYOHHINSYLKPMLQRDFTTALP EGGADHILARHILSYLLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMYRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSYRSLYPKI IQDIETIESNWRGGRHNLQRIGCRSENSKGVVCLQVDDEKIIGG LRDDSIKKINGKTSLECLKVLTGHTGSVLCLQVDERVIVTGSSDS TVRVWDVNTGEVLNTLIHHNEAVLLLRFSNGLMVTCSKDRS IAV WDMASATDITLRRVLVGHRAAWNVDFDDKYIVSASGDRTIKWW STSTCEFVETLINGHKGGIACLQYRDRLVVSGSSDMTIRLWDIEC GACLRVLEGHBELVRCIRFDNKRIVSGAYDGKIKWDLQAALDP RAPASTLCLRTLVEHBGRVFRLGPDEFQIISSSHDDTILIWDFL	6922	1075	369	LTPPACTENTURDED ED ED ED ED EN
VNTPKDAAQODAKAEENKKEPLCRQKQHRKVLDKGKEPDVMPSV KGAQERLPTVPLSGMYNKSGKVRLTFKLEQOQLWIGTKERTEK LPMGSIKNVVSEPIEGHEDYHMMAPQLGPTEASYYWYYWPTQY VDAIKDTVLGKWQYF LGUFCILDIDTLCAVLERDTLSIRESRLFGAVVRWAEAECQRQQ LPVTFGNKQKVLGKALSLIRFPLMTIEEFAAGPAQSGILSDREV VNLFLHFTVNPKPRVEYIDRPRCCLRGKECCINRFQQVESRWGY SGTSDRIRFTVNRRISUGFGLYGSIHGFDYQVNIQIIEYEKK QTLGQNDTGFSCDGTANTFRVMFKEPIEILPNVCYTACATLKGP DSHYGTKGLKKVVHETPAASKTVFFFFSSPGNNNGTSIEDGQIP EIIFYT SCFYCECEBKRLCVNTHWWTKSKFMGMSUGVSMGEGVLRLLE HGEYVFTLPSAYARSILTIPWVELGGKVSINCAKTGYSATVIF HTKPFYGGKVHVTAEVKHIPPLEKGGPMESRNLWREVTRYLRLGDI DAATEGKRHLEEKQRVEERKRENLRTPWKPYFIQEGDGSGILQ SPLESTLMGLEVQSFPV 1653 RGGAAGAMBEDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAENILSVLDARSLCAAELVCKEWGRVISEGMUKKLI ERMVRTDPLWKGLSERRGWDQVJFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGYVCLQYDDEKIISG LRNDSIKIWDKTSLECLKVUTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTGEVLNTLIHHNEAVIHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVCHRARAVNVDFDDEVIVTGSSODSTIKWW STSTCEFVETLINGHKRGTACLQYRDRLVVSGSSDNTIRKWBIEC GACLRVLECHBELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR			005	GLPPAMOKIMAKCI ADEDKIII DEZIZIMOGA IZAKONIHSIT
KGAQERIPTVPLISGMYNKSGGKVRLTFKLEQDQLWIGTKERTEK LPMGSIKNVVSEPIEGHEDYHMMAFQLGPTEASYYWVYWYPTQY VDAIKDTVLGKWQYF 1660 LGLFCILPIDTLCAVLERDTLSIRESRLFGAVVRWAEAECQRQQ LPVTFGNKOKVLGKALSLIRFPLMTIEEFAAGPAQSGILSDREV VRLFLHFTVNPKPRVEYIDRPRCCLRGKECCINRFQQVESRWGY VRLFLHFTVNPKPRVEYIDRPRCCLRGKECCINRFQQVESRWGY SGTSDRIRFTVNRRISIVGFGLYGSIHGPTDVQVNIQIIEYEKK QTLGQNDTGFSCDGTANTFRVMFKEPIEILPNVCYTACATLKGP DSHYGTKGLKKVVHETPAASKTVFFFFSSPGNNNGTSIEDGQIP EIIFYT PEERVICFVEYYLTAFHEGRKGALAKKFYNPIIGETFHCSWEVP KORVKFRTASRSPASCHEHPMADDPSKSYKLRFVAEQUSHHPP ISCFYCECEEKRLCVNTHVWTKSKFMGMSVGVSMIGEGVLRLLE HGEEYVFTLPSAYARSILTIPWELGGKVSINCAKTGYSATVIF HTXPFYGGKVHRVTAEVKINPTTTIVCKAHGEWHOTLEFTYNNG ETKVIDTTTLPVYPKKIRPLEKQGPMESRNLWREVTRYLRLGDI DAATEQKRHLEEKGRVEEKKRELRTPWKPKYFIQEGGSGILQ SPLESTIMGLEVQSFPV 6925 2 1653 RGGAAGAAMEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVECLQISNGTSSVIVSRKPPSEGNYQKEKDLCIKYF DQWSESDOVFFVEHLISKNCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESMWCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDEKIIVGSSDS TVRVWDVNTGEVLNTLIHHNEAVIHLRFSNSLMVTCSKORSIAV WDMASATDITLRRVLVGHAAVWVDFDDKYIVSASSGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR				WALDED A DOUBLE BURNERS OF STREET STR
LPMGSIKNVVSEPIEGEBYHMMAFQLGPTEASYYWVYWVPTQY VDAIKDTVLGKWGF 6923 2469 1660 LGLFCILPIDTLCAVLERDTLSIRESRLFGAVVRWAEAECQRQQ LPVTFGNRQKVLGKALSLIRFPLMTI BEFAAGPAQSGILSDREV VNLFHHFTVNPKPVYPYIDRPRCCLRGKECCINRFOQVESRWGY SGTSDRIRFTVNRRISIVGFGLYGSIHGPTDYQWIQIIEYEKK QTLGQNDTGFSCDGTANTFVWFKEPIEILDNVCYTACATLKGP DSHYGTKGLKKVVHETPAASKTVFFFFSSPGNNNGTSIEDGQIP E11FYT 6924 2210 1235 PEERVICFVEYYLTAFHEGRKGALAKKPYNPIIGETFHCSWEVP KORVKVFRTASRSPASCHEHPMADDPSKSYKLRFVAEQVSHHPP ISCFYCECEBERLCVWTHVWTKSKFMGMSVGVSMIGEGVLRLLE HGGEYVFTLPSAYARSILTIEWVELGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTAEVKHNPTNTIVCKAHGEWNGTLEFTYNMG ETKVIDTTTLPVYPKKIRPLEKQGPMESRNLWREVTRYLRLGDI DAATEQKHLLEEKQRVEERKENLRTPWKPKYFIQEGDGSGILQ SPLESTLMGLEVGSFPV 6925 2 1653 RGGAAGAAMBEDSVIEDKTIELMCSVPRSLWLGGANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSKKRPSEGNYQKEKOLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAENILSYLDARSLCAAELVCKSWQRVISEGKLWKKLI ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHUQRIQCRSENSKGVYCLQYDDEKIISG LQDIETIESNWRCGRHUQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDDEKIITGSSDS TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKKW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHBELVRCIRFDNKRIVSGADDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFFLQFDEFQIISSSHDDTILIMDIEC				KGAOFDI.DTVDI.CCMVNVCCCGGTI TOVI TODOL TODOL TO
6923 2469 1660 LGLFCILPIDTLCAVLERDTLSIRESRLFGAVVRWAEAECQRQQ LEVTFGNRQKVLGKALSLIRFPLMTI EEFAAGPAQSGILSDREV VNLFLHFTVNPKPRVEYI DRPRCCLRGKECCINRFQQVESRWGY SGTSDRIRFTVNRRISIVGFGLYGS IHGPTDYQVNIQIIEYEKK QTLGQNDTGFSCDGTANTFRVMFKEPIBLIPNVCYTACATLKGP DSHYGTKGLKKVVHETPAASKTVFFFFSSPGNNNGTSIEDGQIP EIIFYT 6924 2210 1235 PEERVICFVEYYLTAFHEGRKGALAKKPYNPIIGETFHCSWEVP KDRVKPKTASRSPASCHEHPMADDPSKSYKLRFVAEQVSHHPP ISCFYCECEBKRLCVNTHWYTKSKFMGMSVGVSMIGEGVLRLLE HGEFYVFTLPSAYARS LITIPWYELGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTAEVKHNPTNTIVCKAHGEWNGTLEFTYNNG ETKVIDTTTLPVYPKKIRPLEKGGPMESRNLWREVTRYLRLGDI DAATEGVRHLEEKGVVEERKRENLRTPWKPKYFIQEGDGSGILQ SPLESTLMGLEVQSFPV 6925 2 1653 RGGAAGAAMEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRFJTALP EQGLDHIAFNILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMVRTDPLWKGLSERRGWDQVLFKRRPTGPPPNSFYRSLYPKI IQDIETIESNWRCGRINLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHEELVRCIRFDMKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRRTVEGHSGRVFRLQFDEFQIISSSHDDTILIWDFL	1 1			LDMGSTVARMSEDTEGUEDVINAS FOLGENST GENERALIS
1660 LGLFCILPIDTLCAVLERDTLSIRESRLFGAVVRWAEAECQRQQ LPVTFGNRQKVLGKALSLIRFPLMTI EEFAAGPAQSGILSDREV VNLFHFTVMPRVEYIDRPRCCLRGKECCINRFQQVESRWGY SGTSDRIRFTVNRRISIVGFGLYGSIHGPTDYQVNIQIIEYEKK QTLGQNDTGFSCDGTANTFRVMFKEPIEILPNVCYTACATLKGP DSHYGTKGLKKVVHETPAASKTVFFFFSSPGNNNGTSIEDGQIP EIIFYT PEERVICFVEYYLTAFHEGRKGALAKKPYNPIIGETFHCSWEVP KDRVKPRKTASRSPASCHEHPMADDPSKSYKLRFVAEQVSHHPP ISCFYCECEKRLCVNTHVWTKSKFMGMSVGVSMIGEGVLRLLE HGEEYVFTLPSAYARSILTIPWVELGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTAEVKHNPTNTIVCKAHGENNGTLEFTYNNG ETKVIDTTTLPVYPKKIRPLEKQGPMESRNLWREVTRYLRLGDI DAATEQKRHLEEKQRVEERKRENLRTPWKPKYFIQEGGSGILQ SPLESTLMGLEVQSFPV RGGAAGAAMEPDSVIEDKTIELMCSVPRSLWLGGANLVESMCAL SCLQSMPSVRCLQISNCTSSVIVGRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAENTLSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRRINLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVMDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAUNVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHEELVRCIRFDMKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR	1	}		VDAIKDWG.GKMOVE
LPVTFGNKOKVLGKALSLIRFPLMTIEFAAGPAQSGILSDREV VNLFLHFTVNPKPRVEYIDRPRCCLRGKECCINRFQCVESRWGY SGTSDRIRFTVNRRISIVGFGLYGS HGPTDYQVNIQIIEYEKK QTLGQNDTGFSCDGTANTFRWMFKEPIBILPNVCYTACATLKGP DSHYGTKGLKKVVHETPAASKTVFFFFSSPGNNNGTSIEDGQIP EIIFYT 6924 2210 1235 PEERVICFVEYYLTAFHEGRKGALAKKPYNPIIGETFHCSWEVP KDRVKPKTASRSPASCHEHPMADDPSKSYKLRFVAEQUSHHPP ISCFYCECEEKRLCVNTHVWTKSKFMGMSVGVSMIGECVLRLLE HGEEYVFTLPSAYARSILTIPWVBLGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTAEVKHNPTNTIVCKAHGEWNGTLEFTYNNG ETKVIDTTTLPVYPKKIRPLEKQGPMESRALWREVTRYLRLGDI DAATEQKRHLEEKQRVEERRRENLRTPWKPKYFIQEGDGSGILQ SPLESTLMGLEVQSFPV 6925 2 1653 RGGAAGAMEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHLAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPNNSFYRLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGYYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDDERVIVTGSSDS TVRVWDVNTGEVLNTLHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRWLVGGRAAVNVUVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLMDIEC GACLRVLEGHEELVRCTRFDNKRTVSGAYDGKIKWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTTYTISR	6923	2469	1660	
SGTSDRIRFTVNRRISIVGFGLYGSIHGPTDYQVNIGIIEYEKK QTLGQNDTGFSCDCTANTFRVMFKEPIEILPNVCYTACATLKGP DSHYGTKGLKKVVHETPAASKTVFFFFSSPGNNNGTSIEDGQIP EIIFYT 6924 2210 1235 PEERVICFVEYYLTAFHEGRKGALAKKPYNPIIGETFHCSWEVP KDRVKPKRTASRSPASCHEHPMADDPSKSYKLRFVAEQUSHHPP ISCFYCECEKRLCVNTHVWTKSKFMGMSVGVSMIGEGULRLLE HGEEYVFTLPSAYARSILTIPWVELGGKVSINCAKTGYSATVIF HIKKPFYGGKVHRVTAEVKHNPTNTIVCKAHGEWNGTLEFTYNNG ETKVIDTTTLPVYPKKIRPLEKQGPMESRALWREVTRYLRLGDI DAATEQRHLEEKQRVEERKRENLRTPWKPKYFIQEGDGSGILQ SPLESTLMGLEVQSFPV 6925 2 1653 RGGAAGAAMEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMVRTDFLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHBELVRCITFDNKRIVSGAYDGKIKWWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR		1	4000	LPVTFGNKOKVLGKALGLIBEDLMTLEBEAAGRAGGAVORWAEAECQRQQ
SGTSDRIRFTVNRRISIVGFGLYGSIHGPTDYQVNIQIIEYEKK QTLGQNDTGFSCDGTANTFRVMFKEPIBILPNVCYTACATLKGF DSHYGTKGLKKVVHETPAASKTVFFFFSSPGNNNGTSIEDGQIP BIIFYT PEERVICFVBYYLTAFHEGRKGALAKKPYNPIIGETFHCSWEVP KDRVKPKRTASRSPASCHEHPMADDPSKSYKLRFVAEQUSHHPP ISCFYCECEEKRLCVNTHVWTKSKFMGMSVGVSMIGEGVLRLLE HGEEYVFTLPSAYARSILTIPWVELGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTAEVKHNPTNTIVCKAHGEWNGTLEFTYNNG ETKVIDTTTLPVYPKKIRPLEKGGPMESRNLWREVTRYLRLGDI DAATEQKRHLEEKQRVEERKRENLRTPWKPKYFIQEGDGSGILQ SPLESTLMGLEVQSFPV 3 1653 RGGAAGAMEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVUCLQYDDEKVINGS TVRVWDDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVUDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTICLTRTVEHSGRVFFLQFDEFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR	1 1	}		WILELHETWING PROPERTY TO PROPERTY TO COMPANY
QTLGONDTGFSCDGTANTFRVMFKEPIEILPNVCYTACATLKGP DSHYGTKGLKKVVHETPAASKTVFFFFSSPGNNNGTSIEDGQIP EIIFYT PEERVICFVEYYLTAFHEGRKGALAKKPYNPIIGETFHCSWEVP KDRVKPKRTASRSPASCHEHPMADDPSKSYKLRFVAEQVSHHPP ISCFYCECEEKKLCVNTHVWTKSKFMGMSVGVSWIGEGVLRALE HGEEYVFTLPSAYARSILTIPWVELGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTAEVKHNPTNTIVCKAHGEWNGTLEFTYNNG ETKVIDTTTLPVYPKKIRPLEKQGPMESRNLWREVTRYLRLGDI DAATEQKRHLEEKQRVEERKRENLRTPWKPKYFIQEGDGSGILQ SPLESTLMGLEVQSFPV 3 RGGAAGAAMEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNCTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDDKXIVSASGDRTIKVW STSTCEFFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHBELVRCIRFDNKRIVSGAYDCKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR	ŀ	ì		SCTSDDIPETIMEDICINGEST VOCALISED TO SCHOOL S
DSHYGTKGLKKVVHETPAASKTVFFFFSSPGNNNGTSIEDGQIP EIIFYT PERVICFVEYYLTAFHEGRKGALAKKPYNPIIGETFHCSWEVP KDRVKPKRTASRSPASCHEHPMADDPSKSYKLRFVAEQVSHHPP ISCFYCECEEKRLCVNTHVWTKSKFMGMSVGVSMIGEGVIRLLE HGEEYVFTLPSAYARSILTIPWVELGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTAEVKHNPTNTIVCKAHGEWNGTLEFTYNNG ETKVIDTTTLPVYPKKIRPLEKQGPMESRNLWREVTRYLRIGDI DAATEQKRHLEEKQRVEERKRENLRTPWKPKYFIQEGDGSGILQ SPLESTLMGLEVQSFPV RGGAAGAAMEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFFVRTLNGHKRGIACLQYDRRLVVSGSSDNTIRLWDIEC GACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDBFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR] {	-		OTLGONDTGESCOCTANTEDIMENDED TO THE DAMAGE OF THE PROPERTY OF T
6924 2210 1235 PEERVICFVEYYLTAFHEGRKGALAKKPYNPIIGETFHCSWEVP KDRVKPKRTASRSPASCHEHPMADDPSKSYKLRFVAEQUSHHPP ISCFYCECEEKRLCVNTHVWTKSKFMGMSVGVSMIGEGVLRLLE HGEEYVFTLPSAYARSILTIEWVELGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTAEVKHNPTNTIVCKAHGEWNGTLEFTYNNG ETKVIDTTTLPVYPKKIRPLEKQGPMESRNLWREVTRYLRLGDI DAATEQKRHLEEKQRVEERKRENLRTPWKPKYFIQEGDGSGILQ SPLESTLMGLEVQSFPV 6925 2 1653 RGGAAGAAMEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPNSFYRSLYPKI IQDIETIESMWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKLWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGLACLQYRDRLVVSGSSDNTTRLWDIEC GACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR	1			DSHACLACTARACHEL BY Y CAMARDED COORDINATED TO THE
PEERVICFVEYYLTAFHEGRKGALAKKPYNPI IGETFHCSWEVP KDRVKPKRTASRSPASCHEHPMADDPSKSYKLRFVAEQVSHHPP ISCFYCECEEKRLCVNTHVWTKSKFMGMSVGVSMIGEGVLRLLE HGEEYVFTLPSAYARSILTIPWVELGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTAEVKHNPTNTIVCKAHGEWNGTLEFTYNNG ETKVIDTTTLPVYPKKIRPLEKQGPMESRNLWREVTRYLRLGDI DAATEQKRHLEEKQRVEERKRENLRTPWKPKYFIQEGDGSGILQ SPLESTLMGLEVQSFPV RGGAAGAAMBPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR	1	!		ETTEVT
KDRVKPKRTASRSPASCHEHPMADDPSKSYKLRFVAEQUSHHPPP ISCFYCECEEKRLCVNTHVWTKSKFMGMSVGVSNIGEGVIRLLE HGEEYVFTLPSAYARSILTIPWVELGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTAEVKHNPTNTIVCKAHGEMNGTLEFTYNNG ETKVIDTTTLPVYPKKIRPLEKGGPMESRNLWREVTRYLRLGDI DAATEQKRHLEEKQRVEERKRENLRTPWKPKYFIQEGDGSGILQ SPLESTLMGLEVQSFFV SPLESTLMGLEVQSFFV GGGAAGAAMBPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHBELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR	6924	2210	1235	
ISCFYCECEEKRLCVNTHVWTKSKFMGMSVGVSMIGEGVLRLLE HGEEYVFTLPSAYARSILTIPWVELGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTAEVKHNPTNTIVCKAHGEWMGTLEFTYNNG ETKVIDTTTLPVYPKKIRPLEKQGPMESRNLWREVTRYLRLGDI DAATEQKRHLEEKQRVEERKRENLRTPWKPKYFIQEGDGSGILQ SPLESTLMGLEVQSFPV 6925 2 1653 RGGAAGAAMEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHEELVRCIRFDNKRIVSGSYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR	į l	į		KDRVKPKRTASRSDASCUPUDMADDDGKGVVVI DDVA DOCTOR
HGEEYVFTLPSAYARSILTIPWVELGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTAEVKHNPTNTIVCKAHGEWNGTLEFTYNNG ETKVIDTTTLPVYPKKIRPLEKÇGPWESRNLWREVTRYLRLGDI DAATEQKRHLEEKQRVEERKRENLRTPWKPKYFIQEGDGSGILQ SPLESTLMGLEVQSFPV 6925 2 1653 RGGAAGAAMEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHEELVRCIRFDNKRIVSGSYDGKIKVWDLQAALDP RAPASTLCLRTIVEHSGRVFRLQFDEFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR		Ĭ		ISCFYCECERRICUMTHINITYEVENOMOTOTICATION
HTKPFYGGKVHRVTAEVKHNPTNTIVCKAHGEWNGTLEFTYNNG ETKVIDTTTLPVYPKKIRPLEKQGPMESRNLWREVTRYLRLGDI DAATEQKRHLEEKQRVEERKRENLRTPWKPKYFIQEGDGSGILQ SPLESTLMGLEVQSFPV RGGAAGAAMEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHEBLVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR		l		HGREVVETLDSAVARSTITT DAUGH COMMONS COMMON CO
ETKVIDTTLPVYPKKIRPLEKQGPMESRNLWREVTRYLRLGDI DAATEQKRHLEEKQRVEERKRENLRTPWKPKYFIQEGDGSGILQ SPLESTLMGLEVQSFPV RGGAAGAAMEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTGEVLNTLIHHNEAVI.HLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHEBLVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR	}	[HTKPFYCCKUHDUTAFUKUMDUMUTUCUANGRAMA
DAATEOKRHLEEKQRVEERKRENLRTPWKPKYFIQEGDGSGILQ SPLESTLMGLEVQSFPV RGGAAGAAMEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTGEVLNTLHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHEBLVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTIVEHSGRVFRLQFDEFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR				ETKVIDTTI.PVVPKKIPPI.FVCCDMECDMECDMECTLEFTYNNG
6925 2 1653 RGGAAGAMEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTIGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTIVEHSGRVFRLQFDEFQIISSSHDDTILIWDFL				DAATEOKRHIJEEKOPWEEPKDENI DEDWKOYWETABOOGGE
RGGAAGAMEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDGRVIVTGSSDS TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR				SPLESTIMGLEVOSERV
SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR	6925	2	1653	
DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR	[ľ		SCLOSMOSVECLOTSNOTES CUTTION TO DESCRIPTION TO STATE OF THE STATE OF TH
EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI ERMVRTDPLWKGGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR				DOWSESDOUFFURNI TEDMOUVONONTATATATATATATATATATATATATATATATATATA
ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHERLVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR				FOGLDUIAENTLEVIDABGI GARRI GORRI GAR
IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHEBLVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR	İ		1	ERMURTDDI.WKCI.GERDGWDOVI PROTESTOR DESCRIBENCE DE LA COMPTENDA DE LA COMPTEND
LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR	l		1	TODIETTESNING CORNER OF TOORS CHORNES CONTROL
TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVCHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR	1		l	LPDNSTYTHDYTSI FOLIVII TOURSENSKGVYCLQYDDEKIISG
WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR	1		i	TVD/MD/MTCEN APPLIANCE THE THE THE THE TENTON TO THE
STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC GACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR	1		. [WIDMA CATTLITUDE VINITALIAN AND THE STORY OF
GACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR		ł		WINASATDITLKKVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW
RAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDFL NVPPSAQNETRSPSRTYTYISR	ŧ	t		CACL BUT EGUERA AND CT TO THE COURT OF THE FOURTH AND CT TO THE FOURTH AND CT TO THE COURT OF TH
NVPPSAQNETRSPSRTYTYISR	1	į.		BADACH CLEGHELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP
	1	!		MAPAS TECHNICATIVE HSGRV FRLQFDEFQIISSSHDDTILIWDFL
SGRVAMDGLGDQFPEQGFPAGPPLLPPHMGGHYRDCQSLGAPPL	6926	1	727	
			/33	SOK VARIDGE GEORF PEOGRPAGPPLEPPHMGGHYRDCQSLGAPPL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
i i	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ŀ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ļ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ì	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
}	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
-	amino acid	sequence	Codon, /=possible nucleotide deletion,
İ	sequence		\=possible nucleotide insertion)
	·	 	DGYPLPTPDTSPLDGVDPDPAFFAAPMPGDCPAAGTYSYAQVSD
İ			YAGPPEPPAGPMHPRLGPEPAGPSIPGLLAPPSALHVYYGAMGS
1		İ	PGAGGGRGFQMQPQHQHQHQHQHPPGPGQPTPPPEALPCRDGT
-		Ī	DPSQPAELLGEVDRTEFEQYLHFVCKPEMGLPYQGHDSGVNLPD
	1	i .	SHGAISSVVSDASSAVYYCNYPDV
6927	2	1484	LTLCGDIQLMLAQNANNRAAHLEEFHYQTKEDQEILHSLHRESS
1	_	1404	CQGFAWATDLSTDLESQLSVSCKCYEAANEILQFRDLKSQNPEH
i	1		YVQVLKRMGNIRNEIGVFYMNQAAALQSERLVSKSVSAAEQQLW
1	ļ	1	VVCTCCEEVCIDIETCIDIATINALISERLVSKSVSAAEQQLW
	}		KKSFSCFEKGIHNFESIEDATNAALLLCNTGRLMRICAQAHCGA
1			GDELKREFSPEEGLYYNKAIDYYLKALRSLGTRDIHPAVWDSVN
ſ	(ĺ	WELSTTYFTMATLQQDYAPLSRKAQEQIEKEVSEAMMKSLKYCD
	1		VDSVSARQPLCQYRAATIHHRLASMYHSCLRNQVGDEHLRKQHR
j	1	}	VLADLHYSKAAKLFQLLKDAPCELLRVQLERVAFAEFQMTSQNS
	1	l	NVGKLKTLSGALDIMVRTEHAFQLIQKELIEEFGQPKSGDAAAA
ļ	1	•	ADASPSLNREEVMKLLSIFESRLSFLLLQSIKLLSSTKKKTSNN
1		į	IEDDTILKTNKHIYSQLLRATANKTATLLERINVIVHLLGQLAA GSAASSNAVQ
6928	1086	777	
1 3220	****	'''	EAIDLINNLLQVKMRKRYSVDKTLSHPWLQDYQTWLDLRELECK
		ĺ	IGERYITHESDDLRWEKYAGEQGLQYPTHLINPSASHSDTPETE ETEMKALGERVSIL
6929	1749	607	
""	1,43	807	RDQRGYRDDRSPAREPGDVSARTRSGGGGGRSATTAMPPPVPNG
		į	NLHQHDPQDLRHNGNVVVAGRPSCSRGPRRAIQKPQPAGGRRSG
			RGPAAGGLCLQPPDGGTCVPEEPPVPPMDWEALEKHLAGLQFRE
1	ł	1	QEVRNQGQARTNSTSAQKNERESIRQKLALGSFFDDGPGIYTSC
1			SKSGKPSLSSRLQSGMNLQICFVNDSGSDKDSDADDSKTETSLD
1 -	ĺ		TPLSPMSKQSSSYSDRDTTEEESESLDDMDFLTRQKKLQAEAKM
1			ALAMAKPMAKMQVEVEKQNRKKSPVADLLPHMPHISECLMKRSL
1			KPTDLRDMTIGQLQVIVNDLHSQIESLNEELVQLLLIRDELHTE
6930	131	545	QDAMLVDIEDLTRHAESQQKHMAEKMPAK
0,550	131	545	FKDTANVFVSLFQMRNNFRHYFIEPSQLKLFYDVITWIVTQVAI
			SYTVVPFVLLSIKPSLTFYSSWYYCLHILGILVLLLLPVKKTQR
1			RKNTHENIQLSQSKKFDEGENSLGQNSFSTTNNVCNQNQEIASR
6931		550	HSSLKQ
1 0331	2	659	FVERLPNRPACLLVASGAAEGVSAQSFLHCFTMASTAFNLQVAT
1			PGGKAMEFVDVTESNARWVQDFRLKAYASPAKLESIDGARYHAL
1			LIPSCPGALTDLASSGSLARILQHFHSESKPICAVGHGVAALCC
			ATNEDRSWVFDSYSLTGPSVCELVRAPGFARLPLVVEDFVKDSG
6932			ACFSASEPDAVHVVLDRHLVTGQNASSTVPAVQNLLFLCGSRK
0932	2	1131	FVDSPGQGEQAEEEEGGIQMNSRMRAHSPAEGASVESSSPGPKK
1			SDMCEGCRSLAAGHPGYISHDKETSIKYVSHQHPSHPQLFSIVR
1			QACVRSLSCEVCPGREGPIFFGDEQHGFVFSHTFFIKDSLARGF
1			QRWYSIITIMMDRIYLINSWPFLLGKVRGIIDELQGKALKVFEA
			EQFGCPQRAQRMNTAFTPFLHQRNGNAARSLTSLTSDDNLWACL
}			HTSFAWLLKACGSRLTEKLLEGAPTEDTLVQMEKLADLEEESES
	 		WDNSEAEEEEKAPVLPESTEGRELTQGPAESSSLSGCGSWQPRK
]		'	LPVFKSLRHMRQVGGRGTAHHELRRRANHGLCLPTRLASGPSTL
6022			KTLQEVTDSLLGGWLMAQGVGGII
6933	1431	890	SLNLHCTLPPPPHQYPAGYPSDKEGKKPKGQSKKQPSGTTKRPI
1			SDDDCPSASKVYKASDSAEAIEAFQLTPQQOHLIREDCONOKLW
[DEVLSHLVEGPNFLKKLEQSFMCVCCQELVYQPVTTECFHNVCK
] [DCLQRSFKAQVFSCPACRHDLGQNYIMIPNEILQTLLDLFFPGY
			SKGR
6934	3030	2588	DRDHSQCGGIRRVALARVSSVKLISKAKIRTVKMTFIIVLAFIV
1 1			CWTPFFFVQMWSVWDANAPKBASAFIIVMLLASLNSCCNPWIYM
]			LFTGHLFHELVQRFLCCSASYLKGRRLGETSASKKSNSSSFVLS
			HRSSSQRSCSQPSTA
		<u></u>	

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence		\=possible nucleotide insertion)
6935	886	543	NSALYVAGGNDGTSCLNSVERYSPKAGAWESVAPMNIRRSTHDL
	1		VAMDGWLYAVGGNDGSSSLNSIEKYNPRTNKWVAASCMFTRRSS
6036			VGVAVLELLNFPPPSSPTLSVSSTSL
6936	1347	567	RSHRRQFLSRALLEFFGKSHPPPHRLPRKSLNVGLHYSHIPFLT
1	1		TCLHFLRKRLQKGEVGLSVETSKPQVPVGGLSRKKVPQEPWATV
			MEKRLQEAQLYKEEGNQRYREGKYRDAVSRYHRALLQLRGLDPS
			LPSPLPNLGPQGPALTPEQENILHTTQTDCYNNLAACLLQMEPV
	ł		NYERVREYSQKVLERQPDNAKALYRAGVAFFHLQDYDQARHYLL AAVNRQPKDANVRRYLQLTQSELSSYHRKEKQLYLGMFG
6937	1	727	AVEFRCCPGRDPACFARGWRLDRVYGTCFCDQACRFTGDCCFDY
-	_	,	DRACPARPCFVGEWSPWSGCADQCKPTTRVRRRSVQQEPQNGGA
			PCPPLEERAGCLEYSTPQGQDCGHTYVPAFITTSAFNKERTRQA
			TSPHWSTHTEDAGYCMEFKTESLTPHCALENRPLTRWMQYLREG
1)		YTVCVDCQPPAMNSVSLRCSGDGLDSDGNQTLHWQAIGNPRCQG
			TWKKVRRVDQCSCPAVHSFIFI
6938	3	719	NSRKLELAERVOTDFMQLKKRRQSSEKENDSGTLDTVGAVVVDH
1			EGNVAAAVSSGGLALKHPGRVGQAALYGCGCWAENTGAHNPYST
1		•	AVSTSGCGEHLVRTILARECSHALQAEDAHQALLETMQNKFISS
l			PFLASEDGVLGGVIVLRSCRCSAEPDSSQNKQTLLVEFLWSHTT
1			ESMCVGYMSAQDGKAKTHISRLPPGAVAGQSVAIEGGVCRLGEP
6939	3	810	SELTLQAECEASQRHFRT KVTAPRRPQRYSSGHGSDNSSVLSGELPPAMGRTALFHHSGGSS
		010	GYESLRRDSEATGSASSAPDSMSESGAASPGARTRSLKSPKKRA
	ĺ		TGLQRRRLIPAPLPDTTALGRKPSLPGQWVDLPPPLAGSLKEPF
			EIKVYEIDDVERLQRPRPTPREAPTQGLACVSTRLRLAERRQQR
			LREVQAKHKHLCEELAETQGRLMLEPGRWLEQFEVDPELEPESA
			EYLAALERATAALEQCVNLCKAHVMMVTCFDISVAASAAIPGPQ
			EVDV
6940	1188	496	GKMAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEWDTQ
			VVKGSSPLGPAGLGAEEPAAGPQLPSWLQPERCAVFQCAQCHAV
İ	·		LADSVHLAWDLSRSLGAVVFSRVTNNVVLEAPFLVGIEGSLKGS
1			TYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKMVCYLL
			KTKAIVNASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILS EVTPDQSKPEN
6941	1	713	SLSRADSDPHGPHTCGHVLNVIIGSNVLALAEAQRQAEALGYQA
	_	, 4.5	VVLSAAMQGDVKSMAQFYGLLAHVARTRLTPSMAGASVEEDAQL
			HELAAELQIPDLQLEEALETMAWGRGPVCLLAGGEPTVQLQGSG
			RGGRNQELALRVGAELRRWPLGPIDVLFLSGGTDGQDGPTEAAG
			AWVTPELASQAAAEGLDIATFLAHNDSHTFFCCLQGGAHLLHTG
ļ			MTGTNVMDTHLLFLRPR
6942	1	246	GDYVERYDPKTDTWTMGAPLSMPTNAVGGCLLGDRLYADGGYDG
			QTYLNTMESYDPQTNEWTQMASLNIGRAGACVVVIKQP
6943	. 1	739	PMATGDGAKTLAIHVKALTADSIRITWKATLPASSFRLSWLRLG
			HSPAGGSITETLVQGDKTEYLLTALEPKPTYIICMVTMETTNAY
			VADETPVCAKAETADSYGPTTTLNQEQNAGPMASLPLAGIIGGA
			VALVFLFLVLGAICWYVHQAGELLTRERAYNRGSRKKDDYMESG
			TKKDNSILEIRGPGLQMLPINPYRAKEEYVVHTIFPSNGSSLCK
6944	960	156	ATHTIGYGTTRGYRDGGIPDIDYSYT VANILLNGVKYESELTGSSERAEQPLSVGRLCSTICNMPKALRT
]		7-10	LCVNHFLGWLSFEGMLLFYTDFMGEVVFQGDPKAPHTSEAYOKY
į (1		NSGVTMGCWGMCIYAFSAAFYSAILEKLEEFLSVRTLYFIAYLA
ļ J	1		FGLGTGLATLSRNLYVVLSLCITYGILFSTLCTLPYSLLCDYYO
	•		SKKFAGSSADGTRRGMGVDISLLSCQYFLAQILVSLVLGPLTSA
			VGSANGVMYFSSLVSFLGCLYSSLFVIYEIPPSDAADEEHRPLL
			LMV

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
j	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	Laleugine M Mathiani
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
i	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- 1	sequence	sequence	Codon, /=possible nucleotide deletion,
6945	2067	1	\=possible nucleotide insertion)
1 0343	2067	179	EGEDRGLPRTMGAALGTGTRLAPWPGRACGALPRWTPTAPAQGC
	1	1	HSKPGPARPVPLKKRGYDVTRNPHLNKGMAFTLEERLOLGTHGL
1	ł	}	IPPCFLSQDVQLLRIMRYYERQOSDLDKYIILMTI.ODRNEKI.FV
1			RVLTSDVEKFMPIVYTPTVGLACQHYGLTFRRPRGLFTTTHDKG
	1		HLATMLNSWPEDNIKAVVVTDGERILGLGDLGCYGMGTPYGKT.A
[1		LYTACGGVNPQQCLPVLLDVGTNNEELLRDPLYIGLKHORVHGK
- (1	î	AYDDLLDEFMQAVTDKFGINCLIOFEDFANANAFRIJNKYRNKY
			CMFNDDIQGTASVAVAGILAALRITKNKLSNHVFGFOGAGEAAM
			G\IAHLLVMALE\KEGVPKA\EATRKIW\MVDF\KGLTVOGPDU
		l	LNHEKEMFAQD\HPEVNSLEEVVRLVKPTAIIGVAAIAEA\FTE
ł			QILRDMASFHERP\IIFALSNPTSKAECTA\EKCYRVTEGPRGF
1	1	1	FAS\GSPF*GVLIWEMGKTFIPGGRGNNA*RVPRGWQLGVHSPG
1			GDPGHIP\DEIFLPDSRAKLPQEVSEQHLSQGRLYP\PLST\IR
}		j	NVFLRIAIKVFD*GYKHNLV\SYYPEPKD\KEAFCKIPGSYTPD
	<u></u>		YDSFYT/VDSYIWAQGKAMNVQTV
6946	133	2551	SCEYSGITVAPGDPCPGVAHLLAPSMASDTPESLMALCTDFCLR
1	1		NLDGTLGYLLDKETLRLHPDIFLPSEI\CDRLVNEYVELVNAAC
1	t I		NF\EPHE\SFFNPLFRDPRKQPASRRIHL\RED\LVQD\QD\LE
	1		AIRKQDL\VEL\YLTN\CEKLSAKSLQTLRSFSHTLGVP*AFFG
1	1		C\TNILLLRKENPGGL/CEDEYLFNPTCOVI.VKDFTFEGPGPI.P
1	j i		F\LKLGRMIDWVPVES\LLRPLNSLAALDLSGIOTSDAA\FLTO
j	[WKDSL\VSLVL\YNMDLSDDHIR\VIVOLHKLRHLDISRDRISS
}]		YYKFKLTREVLSLFVQKLGNLMSLDISG\HMILENCSISKIGKP
ļ			EAGQTSI\EPSK\SSIIPFRGFEGGPLOF\LGVF*GIFCGRLTH
			IPAYKVSGDKNEEQVLNAIEAYTEHRPEITSRAINLIFDTARTE
į			RCNQLLRALKLVITALKCHKYDRNIQVTGSAALFYLTNSEYRSE
	1		QSVKLRRQVIQVVLNGMESYOEVTVORNCCLTLCNFSTPFFLFF
			QYRRVNELLLSILNPTRQDESIQRIAVHLCNALVCOVDNDHKEA
			VGKMGFVVTMLKLTQKKLLDKTCDOVMEFSW\SALWNTTDETPD
1	1		NCEMFLNFNGMKLFLDCLNEFPEKOELHRNMLGLLGNVAEVKEL
	ļ .		RPQLMTSQFISVFSNLLESKADGIEVSYNACGVLSHIMFDGPEA
1	j j		WGVCEPQREEVEERMWAAIQSWDINSRRNINYRSFEPTI.RIJ.PO
1	1		GISPVSQHWATWALYNLVSVYPDKYCPLLIKEGGMPLLRDIIKM
6947			ATARQETKEMARKVIEHCSNFKEENMDTSR
094/	2	1682	TSVSTIPRGLASARPQSRSWRCCPVWRRSPGRARGRGLKMLNVP
1			SQSFPAPRSQQRVASGGRSKVPLKOGRSLMDWIRLTKSGKDLTG
	Ī		LKGRLIEVTEBELKKHNKKDDCWICIRGFVYNVSPYMEYHPGGE
	ı		DELMRAAGSDGTELFDQVHRWVNYESMLKECLVGRMAIKPAVLK
			DYREEEKKVLNGMLPKSQVTDTLAKEGPSYPSYDWFOTDST.VTT
	[1	/EHIY*TEGYQFRLNNS*SSE*FLYSRNNY*GLLISYTYW/R*A
	İ	·	MRFRKIFLCGL/CESVGKIEIVLQKKENTSWDFLGHPLKNHNSI.
	1	i	IPRKDTGLYYRKCQLISKEDVTHDTRLFCLMLPPSTHLOVPTGO
			HVYLKLPITGTEIVKPYTPVSGSLLSEFKEPVLPNNKYIYFIJK
			IYPTGLFTPELDRLQIGDFVSVSSPEGNFKISKFOELEDLFIJA
1 1			AGTGFTPMVKILNYALTDIPSLRKVKLMFFNKTEDDIIWRSOLE
1	j		KLAPKDKRLDVEFVLSAPISEWNGKQGHISPALLSEFLKRNLDK
1-000			SKVLVCICGPVPFTEQGVRLLHDLNFSKNEIHSFTA
6948	104	58	PDGAHSFFPDEYFTCSSLCLSCGVGCKKSMNHGKEGVPHEAKSP
1 1	1		CRYSHQYDNRVYTCKACYERGEEVSVVPKTSASTDSPWMGLAKV
1 I	1		AWSGYVIECPNCGVVYRSRQYWFGNQDPVDTVVRTEIVHVWPGT
1 1		ľ	DGFLKDNNNAAQRLLDGMNFMAQSVSELSLGPTKAVTSWLTDOI
1 1	1	į	APAYWRPNSQILSCNKCATSFKDNDTKHHCRACGEGFCDSCSSK
	1	{	TRPVPERGWGPAPVRVCDNCYEAR/TRPVSCYRGTSGR*RRRRT
1 600			QETVE
6949	152	4656	GLRLCLSRPLTRPGDDSVGGSAMASGAGGVGGGGGGKIRTRRCH
<u> </u>			QGPIKPYQQGRQQHQGILSRVTESVKNIVPGWLQRYFNKNEDVC

SEQ Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid residue of amino acid sequence sequenc
NO: nucleotide location corresponding to first amino acid residue of amino acid sequence sequ
location corresponding to first amino acid residue of amino acid sequence s
corresponding to first amino acid residue of amino acid residue of amino acid sequence L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, M=Tesidue of amino acid sequence Sequence Sequence L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, M=Tesidue of amino acid sequence Sequence Sequence Sequence SCSTDTSEVPRWPENKEDHLVYADEESSNITDGRITPEPAVSNT EEPSTTSTAST\YPDVLITRYSLYRSHLNFSMLESPALHCOPSTS SAFPIGSSGFSLYKEI KDSTSQHDDDNISTTGGFSSRSDKDIT VSKNTSLPPLMSPEAERSHIS.GOHTATSSKXPAJNLSAFGTLSP SLONSSILKTSQLGDSPYPGKTTYGGAAAVRQSKLRNTFYQA PVRRQMKAKQLSAQSYGVTSSTARRILQSLEKMSSPLADARRIP SIVSSPLNSSLDISTPSGBFSRTMSPLADARRIP SIVSSPLNSSPLDARREKVDGGYPPVGRIMTPKPV SIATNESVYKPSLTTPSGFFRKTNORIDKKCSTGYEKMTPGQN REGRESGFSYPNTSLPAANGLSSGVGGGGGKMRRERHAFVASKP LEEEEMEGPVLPKISLPITSSSLPTNFSSPEITTSSPSPINSS QALTIKKVQMTSFSSTGSSPMKFSSPIVKSTEANULPSSIGFTF SVPVAKTABLSGSSSTLEPIISSSAHVTTVNSTNCKKTPPEDC EGGFFRELIKEGSVLDILKSPGPASPKKTSANALPSSSTFTVYTGTSPVVY TRPAISSFSSSGIGFGESKKAGSSWCDTCLLQNKVTMKCIAC QAAKLSPRDTAKGTGTETPNKSGKTLLSAGTGFGDKFKPVIGT MPCDTCLVQNKPEAIKCVGKATLSAGSTGFGDKFKPVIGT MPCDTCLVQNKPEAIKCVGKTPRADILTVYSESAET MTASSSSCTVTTGTLGFGDKFKRPIGSBECSVCCVSNNAEDNKC VSCMSEKPGSSVFTSSSTSTSSSSSAASS SFKFGVSSSSSGPSTLTSTGNFKFGDQGGFKIGVSSDGGYINP MSGGF*FSKHIVGFKFGVSSSSAASS SFKFGVSSSSSGPSTLTSTGNFKFGDQGGFKIGVSSDGGYINP TKGGFSFGNVEFBASPLFASGFKGFTGTGVNNSTSLVFGGG KLIMKEPKC\QPVFFGGSSNFGTSSSNFTSSSTPATS AGGG\1FGSSTSSNPPVATFVFGQSSNFGSSS\AFGNTAESST VPANTYTGGSSPFGFGTGTKNNSSSSSTPATS AGGG\1FGSSTSSNPPVATFVFGGSSNFTTTTGGFFGFG KLIMKPKC\QPVFFGGSSNNTTTTGGFFGFG KLIMKPKC\QPVFFGGASSNNTTTTGGFFGFG KLIMKPKC\QPVFFGGASSNNTTTTGGFFGFG KLIMKPKC\QPVFFGGASSNNTTTTGGFFGFG KLIMKPKC\QPVFFGGASSNNTTTTGGFFGFG KLIMKPKC\QPVFFGGASSNNTTTTGGFFGFG KLIMKPKC\QPVFFGGASSNNTTTTGGFFGFG KLIMKPKC\QPVFFGGASSNNTTTTGGFFGFG KLIMKPKC\QPVFFGGASSNNTTTTGGFFGFG KLIMKPKC\QPVFFGGASSNNTTTTGGFFGFG KLIMKPKC\QPVFFGGASSNNTTTTGGFFGFGASSNNTTTTGGFFGFGASSNNTTTTGGFFGFGASSNTTTTGGFFGFGASSNTTTTGGFFGFGASSNTTTTGGFFGFGASSNTTTTGGFFGFGASSN
to first amino acid residue of amino acid sequence #P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Txyptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) ### SCSTDTBSPPRPEMEDHLVYADEESSNITDGRITPEPAVSNT EFPSTTSTAST\YPDVLTRVSLYRSHLNFSMLESPALHCQPSTS SAFPIGSSGFSLVKEIKDSTSQHDDNISTTSGFSSRASDKDIT VSKNTSLLPPLMSPPEARSHSLSQHTATSSKKPAFNLSAFGTLSP SLGNSSILKTSQLGDSPFYPGKTTYCGAAAAVQSKLRNTPYQA PVRRQMKAKQLSAGSYGVTSSTARRILQSLEKMSSPLADAKRIP SIATNRSVYFKPSLTPSGEFFRKTNORIDKKCSTGYEKNMTPGQN REQRESGFSYPNFSLPAANGLSSGVGGGGGKMRRERHAFVASKP LEEEEMEGPVLPKLSLPITSSSLPTMFSSPBITTSSPSPINS CALITNXQMTSPSSTGSFMFKFSSFIVXSTEANVLPPSSIGFTF SUPVAKTABLSGSSSTLEPIISSSAHVTITVNSTNCKKTPEDC EGPFRPAEILKEGSVLDILKSPGPASPKIDSVAAQPTATSPVVY TRPAISFSSSGIGFGESLKAGSSWQCDTCLLQNKVTDNKCIAC QAAKLSPRDTAKCTGIEFPNKSGKTTLSASGTGFGDKFKFVIGT WDCDTCLVQNKPEAIKCVACETPKRGTCVKRALTLTVVSESAET MTASSSSCTVTTTTLGFGDKFKFRIGSBECSUCCVSNNABDNKC VSCMSEKPGSSVPTSSSSTVPVSLPSGGSLGLEKFKKPEGIWDC ELCLUQNKADSTKCLACESAKPGTKSGFKGFTDSSSSSNSAASS SFKFGVSSSSGPSQTITTSTTGNFKFDDGGFKIGVSSDGGYINP MSEGF*FSKHIVGFKFCVSSESKPEEVKKDSKNDHFKFGLSFGL SNPVFLTFPGFGVSNLGQEEKKEELLKSSCAGFRFGTGVINSTR VPANTIVTSENKSSFNLGTIETKSVSVAPLKCQTSEAKKEEMPA AGGG\IFGSSTSSSNPVATFYFGGGSASNNTTTSGFGFG KLITMKEPKC\QPVFFSGEFGRAKPDLSYLNNSSSSSTPATS AGGG\IFGSSTSSSNPVATFYFGGGSASNNTTTSGFGFG ATTTSSSAGSSFYFGTGFSANSASSNASSNNTTTSGFGFG
residue of amino acid sequence Sequence
amino acid sequence Sequence
Sequence Sequence Sequence Sequence Sequence
SCSTDTSEUPRWENKEDHLVYADEESSNITDGRITPEPAVSNT BEPSTTSTAST\YPDVUTRVSLYRSHLNFSMLESPALHCOPSTS SAFPIGSSGFSLVKEIKDSTSQHDDDNISTTSGFSSRASDKDIT VSKNTSLPPLMSPEARSHSLSQHTATSSKKPAFRLSAFGTLSP SLGNSSILKTSQLGDSFFYPGKTTYGGAAAAVROSKLRNTPYQA PVRRQMKAKQLSAQSYGVTSSTARRILQSLEKMSSPLADAKRIP SIUSPLNSPLDRSGIDITDFQAKREKVDSQYPPVQRLMTPKFV SIATNRSVYFKPSLTPSGEFFRKTNORIDKKCSTGYEKMTPGQN REGRESGFSYPNFSLPAANGLSSGVGGGGGKMRRERHAFVASKP LEEEEMEGPVLPKISLPITSSSLPFFNFSSPEITTSSPSPINSS QALTNKVQMTSPSSTGSPMFKFSSPIVKSTEANLLPDSSIGFTF SVPVAKTABLSGSSSTLEPIISSSAHVTTVNSTNCKKTPPEDC EGPFRPAEILKEGSVLDILKSPGFASFKLDSVAAQFTATSPVVY TRPAISSFSSSGIGFGESLKAGSSSWQCDTCLLQNKVTUNKCIAC QAAKLSFRDTAKQTGIETPNKSGKTTLSASGTGFGKFKFVIGT WDCDTCLVQNKPEAIKCVACETPKFGTCVRRAITLTVVSESAET MTASSSCTVTTGTLGFGDKFKRPIGSWEGSVCCVSNAAEDNKC VSCMSEKPGSSVPTSSSTVPVSLPSGGSLGLEKFKKPEGIWDC USCMSEKPGSSVPTSSSTVPVSLPSGGSLGLEKFKKPEGIWDC ELCLVQNKADSTKCLACESAKPGTKSGFKGFDTSSSSNSAASS SFKFGVSSSSSGPSQTLTSTGNFKPGQCGGFKIGVSSDSGYINP MSEGF*FSKHIVGFKFGVSSESKPEVKKDSKNDNFKFGLSFGL SNPVFLTPFQFGVSNLGTIETKSVVAPLKCQTSESAKKEEMPA TKGGFSFGNVEPASLPSASVFVLGRTEEKQOEPVTSTSLVFGEG KLTMKEPKC\QPVFSFGEFQRQTKDENSSKSTFSFSMTKPSEKE SEQPAKATFAFGAOTNTTADGGAKRPDLSYLNNSSSSSSTPATS AGGG IFGSSTSSNPVATFVFGQSSNPGSSS\AFGNTAESST SQSLLFSQDSKLATTSSTGTAVTPFVFGGASSNNTTTSGFGFG
SCSTDTSEVPRWERKEDHLVYADEESSNITDGRITFEPAVSNT EEPSTTSTAST\YPDVLTRVSLYRSHLNFSMHLESPALHCQPSTS SAFFIGSSGFSLVKEIKDSTSQHDDDNISTTSGFSSRASDKDIT VSKNTSLPPLWSPEAERSHSLSQHTATSSKKPAFNLSAFGTLSP SLGNSSILKTSQLGDSFFYPGKTTYGGAAAVRQSKLRNTPYQA PVRRQMKAKQLSAGSYGVTSSTARRILQSLEKMSSPLADAKRIP SIVSSPLNSPLDRSGIDITDFQAKREKVDSQYPPVQRLMTPKPV SIATNRSVYFKPSLTPSGEFRKTNORIDKKCSTGYEKNMTPGQN REORESGFSYPFSLPAANGLSSGVGGGGKMRERHAFVASKP LEEEEMEGPVLPKISLPITSSSLPTFNFSSPEITTSSPSPINSS QALTINKUQMTSPSSTGSPMFKFSSPIVKSTEANVLPPSSIGFTF SVPVAKTABLSGSSSTLEPIISSSAHVTTVNSTNCKKTPPEDC EGPFRPAEILKEGSVLDILKSPGPASFKIDSVAAQPTATSPVVY TRPAISSFSSGIGFGESLKAGSSWQCDTCLLQNKVTDNKCIAC QAAKLSPRDTAKQTGIETPNKSGKTTLSASGTGFGDKFKPVIGT WDCDTCLVQNKPEAIKCVACETPKPGTCVKRALTLTVVSESAET MTASSSCTVTTGTLGFGDKFKRPIGSWECSVCCVSNNAEDINKC VSCMSEKPGSSVPTSSSTVPVSLPSGGSLGLEKFKKPEGIWDC ELCLVQNKADSTKCLACESAKPGTKSGFKGFDTSSSSNAASS SFKFGVSSSSSGPSQTLTSTGNFKFGDQGGFKIGVSSDSGYINP MSEGFFFSKHIVGFKFGVSSEKPEVKKDSKNDNFKFGLSFGL SNPVFLTPFPGFGVSNLQGEKKEELLKSSCAGFRFGTGVINSTR VPANTIVTSENKSSFNLGTIETKSVSVAPLKCQTSEAKKEEMPA TKGGFSFGNVEPASLPSASVFVLGRTEEKQOEPVTSTSLVFGGG KLTMKEPKC\QPVFFSFGEFQRQTKDENSKSTFFSTMKFSEKE SEQPAKATFARGAQTNTTADQGAAKPDLSVLNNSSSSSSTPATS AGGG\IFGSSTSSSNPVATFVFGQSSNPGSSS\AFGNTAESST SQSLLFSQDSKLATTSSTGTAVTFFVFGQASSNNTTTSGFGFG ATTTSSSAGSSFVFGTGPSSASSPAGNNTTTTSGFGFG
SAFPIGSSGFSLYBLIKDSTSQHDDNISTTSGFSRASDKDIT VSKNTSLPPLWSPEARSHSLSQHTATSSKKPAFMLSAFGTLSP SLGMSSILKTSQLGDSPFYPGKTTYGGAAAAVRQSKLRNTPYQA PVRRQMKAKQLSAQSYGVTSSTARRILQSLEKMSSPLADAKRIP SILSPLMSPLDRSGIDITDFQAKREKVDSQYPPVQRLMTPKPV SIATNRSVYFKPSLTPSGEFRKTNQRIDKKCSTGYEKMNTPGQN REQRESGFSYPNFSLPAANGLSSGVGGGGKMRRERHAFVASKP LEEEEMEGPVLPKISLPITSSSLPTFNFSSPEITTSSPSPINSS QALTNKVQMTSPSSTGSPMFKFSSPIVKSTEANVLPPSSIGFTF SVPVAKTABLSGSSSTLEPIISSSAHVTTVNSTNCKKTPPEDC EOPFRPABILKEGSVLDILKSPGPASPKIDSVAAQPTATSPVVY TRPAISSFSSGIGFGESLKAGSSWQCDTCLLQNKVTDNKCIAC QAAKLSFRDTAKQTGIETPNKSGKTTLSASGTGFGDKFKPVIGT WDCDTCLVQNKPBAIKCVACETPKPGTCVKRALTLTVVSESAET MTASSSCTVTTGTLGFDKFKFRPIGSWECSVCCVSNNAEDNKC VSCMSEKPGSSVPTSSSSTVPVSLPSGGSLGLEKFKKPEGIWDC USCMSEKPGSSVFTSSSTVPVSLPSGGSLGLEKFKKPEGIWDC ELCLVQNKADSTKCLACESAKPGTKSGFKGFDTSSSSSNSAASS SFKFGVSSSSSGPSQTLTSTGMFKFGDQGGFKIGVSSDSGYINP MSEGF*FSKHIVGFKFGVSSEKKPEELKKSCAGFFFGTGVINSTR VPANTIVTSENKSSFNLGTIETKSVSVAPLKCQTSEAKKEENPA TKGGFFSGVBFBASLFSAVFVLGRTEEKQOEPVTSTSLVFGGG KLITMKSPKC\QPVFSFGEFQRQTKDENSKSTFSFSMKPSEKE SEQPAKATFAFGAQTINTTADGGAAKPDLSYLNNSSSSSSTPATS AGGG IFGSSTSSSNPVATFVFGQSSNSSSTSTATS AGGG IFGSSTSSSNPVATFVFGQSSNSNTTTSGFGFG SQSLLFSQDSKLATTSSTGTAVTFVFFGCSSNNTTTSGFGFG
VSKNTSLPPLMSPEAERSHSJENTATSKKPAFNLSAFGTLSS SLGNSSILKTSQLGDSPFYPGKTTYGGAAAAVRQSKLRNTPYQA PVRRQMKAKQLSQSYGVTSSTARRILQSLEKMSSPLADAKRIP SIVSSPLNSPLDRSGIDITDFQAKREKVDSQYPPVORIMTPKPV SIATNRSVYFKPSLTPSGEFRKTNQRIDKKCSTGYEKNMTPGQN REQRESGFSYPNFSLPAANGLSSGVGGGGKMRRERHAFVASKP LEEEEMEGPVLPKISLPITSSSLPTENFSSPEITTSSPSPINSS QALTNKVQMTSPSSTGSPMFKFSSPIVKSTEANVLPPSSIGFTF SVPVAKTAELSGSSSTLEPIISSSAHHVTTVNSTNCKKTPPEDC EGFFRPAEILKEGSVLDILKSPGPASPKIDSVAAQPTATSPVVY TRPAISSFSSSGIFFGESLKAGSSWQCDTCLLQNKVTDNKCIAC QAAKLSPRDTAKQTGIETENKSGKTTLSASGTGFGDKFKPVIGT WDCDTCLVQNKPEAIKCVACETPKRGTCVKRALTLTVVSESAET MTASSSSCTVTTGTLGFGNFKRPIGSWECSVCCVSNNAEDNKC VSCMSEKPGSSVPTSSSSTVPVSLPSGGSLGLEKFKKPEGIWDC ELCLVQNKADSTKCLACESAKPGTKSGFKGFDTSSSSNNSAAS SFKFGVSSSSSGPSQTLTSTGNFKFGDQGGFKIGVSSDSGYINP MSEGF*FSKHIVGFKFGVSSESKPEVKKNSKNDMFKFGLSFGL SNPVFLTPFOFGGVSNLGGBEKKEELLKSSCAGFFFGTGVINSTR VPANTIVTSENKSSFNLGTIETKSVVAPLKCQTSEAKKEEMPA TKGGFSFGNVEFASLPSASVFVLGRTEEKQOEPVTSTSLVFGGG KLITMKEPKC\QPVFSFGEFQRQTKDENSSKSTFSFSMTKPSEKE SEQPAKATFAFGAQTNTTADQGAAKPDLSYLNNSSSSSTPATS AGGG\fFGSSTSSNPPVATFVFQQSSNPGSSS\AFGNTAESST SQSLLFSQDSKLATTSSTGTAVTFFVFGGASSNNTTTSGFFGF
SLGNSSILKTSQLGDSPFYPGKTTYGGAAAAVRQSKLRNTPYQA PVRRQMKAKQLSAQSYGVTSSTARRILQSLEKMSSPLADAKRIP SIUSSPLNSPLDRSGIDITDFQAKREKVDSQYPPVORLMTPKPVV SIATNRSVYFKPSLTPSGEFRKTNQRIDKKCSTGYEKNMTPGQN RECRESGFSYPNFSLPAANGLSSGVGGGGKMRREHHAFVASKP LEEEMEGPVLPKISLPITSSSLPTFNFSSPEITTSSPPINSS QALTNKVQMTSPSSTGSPMFKFSSPIVKSTEANVLPPSSIGFTF SVPVAKTAELISGSSSTLEPIISSSAHHVTTVNSTNCKKTPPEDC EGFFRPAEILKEGSVLDILKSPGPASPKIDSVAAQPTATSPVVY TRPAISSFSSGIGFGESLKAGSSWQCDTCLLQNKVTDNKCIAC QAAKLSPRDTAKQTGIETPNKSGKTTLSASGTGFGDKFKPVIGT WDCDTCLVQNKPEAIKCVACETPKPGTCVKRALTLTVVSESAET MTASSSSCTYTTGTLGFGDKFKRPIGSWECSVCCVSNNAEDNKC VSCMSEKPGSSVPTSSSSTVPVSLPSGGSLGLEKFKKPEGIWDC ELCLVQNKADSTKCLACESAKPGTKSGFKGFDTSSSSNSAASS SFKFGVSSSSGPSQTLTSTGNFKFGDQGFKIGVSSDSGYINP MSEGF*FSKHIVGFKFGVSSEKPEEVKKDSKNDNFKFGLSFGL SNPVFLTPFQFGVSNLGQEEKKEELLKSSCAGFFFFGTGVINSTR VPANTIVTSENKSSFNLGTIETKSVSVAPLKCQTSEAKKEEMPA TKGGFSFGNVEPASLPSASVFVLGRTEEKQOEPVTSTSLVFGGG KLITMKEPKC\QPVFSFGEFGRQTKDENSKSTFSFSMTKPSEKE SEQPAKATFAFGAQTNTTADQGAAKPDLSYLNNSSSSSSTPATS AGGG\IFGSSTSSSNPPVATFVFQQSSNPGSSS\AFGNTAESST SQSLLFSQDSKLATTSSTGTAVTPFVFGGFASSNNTTTSGFGFFG
PVRRQMKAKQLSAQSYGVTSTARRILQSLEKMSSPLADAKRIP PVRRQMKAKQLSAQSYGVTSTARRILQSLEKMSSPLADAKRIP SIVSPLNSPLNSGIDITDFQAKREKVDSQYPPVORLMTPKPV SIATNRSVYFKPSLTPSGEFRKTNQRIDKKCSTGYEKNMTPGQN REQRESGFSYPNFSLPAANGLSSGVGGGGKMRRERHAFVASKP LEEEEMEGPVLPKISLPITSSLPTFNFSSPEITTSSPSPINSS QALTNKVQMTSPSTGSPMFKFSSPIVKSTEANVLPPSSIGFTF SVPVAKTABLSGSSSTLEPIISSSAHHVTTVNSTNCKKTPPEDC EGPFRPAEILKEGSVLDILKSPGPASPKIDSVAAQPTATSPVVY TRPAISSFSSSGIGFGESLKAGSSWQCDTCLLQNKVTDNKCIAC QAAKLSPRDTAKQTGIETPNKSGKTTLSASGTGFGDKFKPVIGT WDCDTCLVQNKPEAIKCVACETPKPGTCVKRALTLTVVSESAET MTASSSCTVTTGTLGFGDKFKRPIGSWECSVCCVSNNAEDNKC VSCMSEKPGSSVPTSSSSTVPVSLPSGGSLGLEKFKKPEGIWDC ELCLVQNKADSTKCLACESAKPGTKSGFKGFDTSSSSNSAASS SFKFGVSSSSSGPSQTITSTGNFKFGDQGGFKIGVSSDSGYINP MSEGF*FSKHIVGFKFGVSSESKPEVKKDSKNDNFKFGLSFGL SNPVFLTPFQFGVSNLGQEEKKEELLKSSCAGFRFGTGVINSTR VPANTIVTSENKSSFNLGTIETKSVSVAPLKCQTSEAKKEEMPA TKGGFSFGNVEPASLPSASVFVLGRTEEKQQEPVTSTSLVFGEG KLTMKEPKC\QPVFSFGEFQRQTKDENSSKSTFSFSMTKPSEKE SEQPAKATFAFGAQTINTADQGAAKPDLSYLNNSSSSSSTPATS AGGG\IFGSSTSSSRPPVATFVFGQSSNPGSSS\AFGNTAESST SQSLLFSQDSKLATTSSTGTAVTPFVFGPASSNNTTTSGFGFG ATTTSSSAGSSFVFGTGPSAPSASPAFGANNTTTTGGFGFG
SIVSSPLMSQLEKMSSPLADAKRIP SIVSSPLMSQLDITDFQAKREKVDSQYPPVQRIMTPKPV SIATMRSVYFKPSLTPSGEFRKTNQRIDKKCSTGYEKMMTPGQN REQRESGFSYPNFSLPAAMGLSSGVGGGGKMRERHAFVASKP LEEEEMEGPVLPKISLPITSSLPTFNFSSPEITTSSPSPINSS QALTINKVQMTSPSSTGSPMFKFSSPIVKSTEANVLPPSSIGFTF SVPVAKTABLSGSSSTLEPIISSSAHVTTVNSTNCKKTPPEDC EGPFRPAEILKEGSVLDILKSPGPASPKIDSVAAQPTATSPVVY TRPAISSFSSSGIGFGESLKAGSSWQCDTCLLQNKVTDNKCIAC QAAKLSPRDTAKQTGIETPNKSGKTTLSASGTGFGDKFKPVIGT WDCDTCLVQNKPEAIKCVACETPKPGTCVKRALTLTVVSESAET MTASSSSCTVTTGTLGFGDKFKRPIGSWECSVCCVSNNAEDMKC VSCMSEKPGSSVPTSSSTVPVSLPSGGSLGLEKFKKPEGIWDC ELCLVQNKADSTKCLACESAKPGTKSGFKGFDTSSSSNSAASS SFKFGVSSSSSGPSQTLTSTGNFKFGDQGGFKIGVSSDSGVINP MSEGF*FSKHIVGFKFCVSSESKPEEVKKDSKNDNFKFGLSFGL SNPVFLTPFOFGVSNLGQEEKKEELLKSSCAGFRFGTGVINSTR VPANTIVTSENKSSFNLGTIETKSVSVAPLKCQTSEAKKEEMPA TKGGFSFGNVEPASLPSASVFVLGRTEEKQOEPVTSTSLVFGEG KLTMKEPKC\QPVFSFGEFQRQTKDENSSKSTFSFSMTKPSEKE SEQPAKATFAFGAQTNTTADQGAAKPDLSYLNNSSSSSSTPATS AGGG\IFGSSTSSSNPPVATFVFGGSSNPGSS\AFGNTAESST QSSLLFSQDSKLATTSSTGTAVTPFVFGPGASSNNTTTSGFFGF
SIVSSPLNSPLDRSGIDITDFQAKREKVDSQYPPVQRLMTPKPV SIATNRSVYFKPSLTPSGEFRKTNQRIDKKCSTGYEKNMTPGQN REQRESGFSYPNFSLPAANGLSSGVGGGGGKMRRERHAFVASKP LEEEEMEGPVLPKLSLPITSSSLPTFNFSSPEITTSSPSPINSS QALTNKVQMTSPSSTGSPMFKFSSPIVKSTEANVLPPSSIGFTF SVPVAKTABLSGSSSTLEPIISSSAHHVTTVNSTNCKKTPPEDC EGPFRPAEILKEGSVLDILKSPGFASPKIDSVAAQPTATSPVVY TRPAISSFSSGIGFGESLKAGSSWQCDTCLLQNKVTDNKCIAC QAAKLSPRDTAKQTGIETPNKSGKTTLSASGTGFGDKFKPVIGT WDCDTCLVQNKPEAIKCVACETPKPGTCVKRALTLTVVSESAET MTASSSSCTVTTGTLGFGDKFKRPIGSWECSVCCVSNNAEDNKC VSCMSEKPGSSVPTSSSSTVPVSLPSGGSLGLEKFKKPEGIWDC ELCLVQNKADSTKCLACESAKPGTKSGFKGFDTSSSSSNSAASS SFKFGVSSSSSGPSQTLTSTGNFKFGDQGGFKIGVSSDSGYINP MSEGF*FSKHIVGFKFGVSSESKPEEVKKDSKNDNFKFGLSFGL SNPVFLTPFOFGVSNLGQEEKKEELLKSSCAGFRFGTGVINSTR VPANTIVTSENKSSFNLGTIETKSVSVAPLKCQTSEAKKEEMPA TKGGFSFGNVEPASLPSASVFVLGRTEEKQOEPVTSTSLVFGEG KLTMKEPKC\QPVFSFGEFQRQTKDENSSKSTFSFSMTKPSEKE SEQPAKATFAFGAQTNTTADQGAAKPDLSYLNNSSSSSSTPATS AGGG\IFGSSTSSSNPPVATFVFGQSSNNSTTSGFGFG SQSLLFSQDSKLATTSSTGTAVTPFVGGPASSNNTTTSGFGFG ATTTSSSAGSSFVFGTGPSAPSASPAFGANOTPTFFGGSOMSOR
SIATMKSVYFKPSLTPSGEFRKTNORIDKKCSTGYEKNMTPGQN REQRESGFSYPNFSLPAANGLSSGVGGGGKMRRERHAFVASKP LEEEEMEGPVLPKISLPITSSSLPTFNFSSPITTSSPSPINSS QALTNKVQMTSPSSTGSPMFKFSSPIVKSTEANVLPPSSIGFTF SVPVAKTAELSGSSSTLEPIISSSAHHVTTVNSTNCKKTPPEDC EGPFRPAEIIKEGSVLDILKSPGPASPKIDSVAAQPTATSPVVY TRPAISSFSSSGIGFGESLKAGSSWQCDTCLLQNKVTDNKCIAC QAAKLSPRDTAKQTGIETPNKSGKTTLSASGTGFGDKFKPVIGT WDCDTCLVQNKPEAIKCVACETPKPGTCVKRALTLTVVSESAET MTASSSSCTVTTGTLGFGDKFKRPIGSWECSVCCVSNNAEDNKC VSCMSEKPGSSVPTSSSSTVPVSLPSGGSIGLEKFKKPEGIWDC ELCLVQNKADSTKCLACESAKPGTKSGFKGFDTSSSSNSAASS SFKFGVSSSSSGPSQTLTSTGNFKFGDQGGFKIGVSSDSGYINP MSEGF*FSKHIVGFKFGVSSESKPEEVKKDSKNDNFKFGLSFGL SNPVFLTPFQFGVSNLGQEEKKEELLKSSCAGFRFGTGVINSTR VPANTIVTSENKSSFNLGTIETKSVSVAPLKCQTSEAKKEEMPA TKGFSFFGNVEPASLPSASVFVLGRTEEKQOEPVTSTSLVFGEG KLTMKEPKC\QPVFSFGEFQRQTKDENSSKSTFSFSMTKPSEKE SEQPAKATFAFGAQTNTTADQGAAKPDLSYLNNSSSSSSTPATS AGGG\IFGSSTSSSNPPVATFVFGQSSNPGSSS\AFGNTAESST SQSLLFSQDSKLATTSSTGTAVTPFVFGPASSNNTTTSGFFGFG
DEEEMGPVLPKISLPITSSSLPTFNFSSPEITTSSPSPINSS QALTNKVQMTSPSSTGSPMFKFSSPIVKSTEANVLPPSSIGFTF SVPVAKTAELSGSSTLEPIISSSAHVTTVNSTNCKKTPPEDC EGFPRAEILKEGSVLDILKSPGPASPKIDSVAAQPTATSPVVY TRPAISSFSSSGIGFGESLKAGSSWQCDTCLLQNKVTDNKCIAC QAAKLSPRDTAKQTGIETPNKSGKTTLSASGTGFGDKFKPVIGT WDCDTCLVQNKPEAIKCVACETPKPGTCVKRALTLTVVSESAET MTASSSSCTVTTGTLGFGDKFKRPIGSWECSVCCVSNNAEDNKC VSCMSEKPGSSVPTSSSSTVPVSLPSGGSLGLEKFKKPEGIWDC ELCLVQNKADSTKCLACESAKPGTKSGFKGFDTSSSSSNSAASS SFKGVSSSSSGPSQTLTSTGNPKFGDQGGFKIGVSSDSGYINP MSEGF*FSKHIVGFKFGVSSESKPEVVKDSKNDNFKFGLSFGL SNPVFLTPFQFGVSNLGQEEKKEELLKSSCAGFRFGTGVINSTR VPANTIVTSENKSSFNLGTIETKSVSVAPLKCQTSEAKKEEMPA TKGGFSFGNVEPASLPSASVFVLGRTEEKQQEPVTSTSLVFGEG KLTMKEPKC\QPVFSFGEFQRQTKDENSSKSTFSFSMTKPSEKE SEQPAKATFAFGAQTNTTADQGAAKPDLSYLNNSSSSSSTPATS AGGG\IFGSSTSSSNPPVATFVFGQSSNPGSSS\AFGNTAESST SQSLLFSQDSKLATTSSTGTAVTPFVFGPGASSNNTTTSGFGFG ATTTSSSAGSSFVFGTGFSAPSASPAFGANOTPTEGOSOGASOR
QALTINKVQMTSPSSTGSPMFKFSSPIVKSTEANVLPPSSIGFTF SVPVAKTABLSGSSSTLEPIISSSAHHVTTVNSTNCKKTPPEDC EGPFRPAEILKEGSVLDILKSPGPASPKIDSVAAQPTATSPVVY TRPAISSFSSGIGFGESLKAGSSWQCDTCLLQNKVTDNKCIAC QAAKLSPRDTAKQTGIETPNKSGKTTLSASGTGFGDKFKPVIGT WDCDTCLVQNKPEAIKCVACETPKPGTCVKRALTLTVVSESAET MTASSSCTVTTGTLGFGDKFKRPIGSWECSVCCVSNNAEDNKC VSCMSEKPGSSVPTSSSSTVPVSLPSGGSLGLEKFKKPEGIWDC ELCLVQNKADSTKCLACESAKPGTKSGFKGFDTSSSSSNSAASS SFKGVSSSSSGPSQTLTSTGNPKPGDQGGFKIGVSSDSGYINP MSEGF*FSKHIVGFKFGVSSESKPEEVKKDSKNDNFKFGLSFGL SNPVFLTPFQFGVSNLGQEEKKEELLKSSCAGFRFGTGVINSTR VPANTIVTSENKSSFNLGTIETKSVSVAPLKCQTSEAKKEEMPA TKGGFSFGNVEPASLPSASVFVLGRTEEKQQEPVTSTSLVFGEG KLTMKEPKC\QPVFSFGEFQRQTKDENSSKSTFSFSMTKPSEKE SEQPAKATFAFGAQTNTTADQGAAKPDLSYLNNSSSSSSTPATS AGGG\IFGSSTSSSNPPVATFVFGQSSNPGSSS\AFGNTAESST SQSLLFSQDSKLATTSSTGTAVTPFVFGPGASSNNTTTSGFGFG ATTTSSSAGSSFVFGTGFSAPSASPAFGANOTPTFGOSOGASOR
SVVAKTABLISGSSTLEPIISSSAHHVTTVNSTNCKKTPPEDC EGPFRPAEIIKEGSVLDIIKSPGPASPKIBSVAAQPTATSPVVY TRPAISSFSSGIGFGESLKAGSSWQCDTCLLQNKVTDNKCIAC QAAKLSPRDTAKQTGIETPNKSGKTTLSASGTGFGDKFKPVIGT WDCDTCLVQNKPEAIKCVACETPKPGTCVKRALTLTVVSESAET MTASSSCTVTTGTLGFGDKFKRPIGSWECSVCCVSNNAEDNKC VSCMSEKPGSSVPTSSSSTVPVSLPSGGSLGLEKFKKPEGIWDC ELCLVQNKADSTKCLACESAKPGTKSGFKGFDTSSSSSNSAASS SFKFGVSSSSSGPSQTLTSTGNFKFGDQGGFKIGVSSDSGYINP MSEGF*FSKHIVGFKFGVSSESKPEEVKKDSKNDNFKFGLSFGL SNPVFLTPFQFGVSNLGQEEKKEELLKSSCAGFRFGTGVINSTR VPANTIVTSENKSSFNLGTIETKSVSVAPLKCQTSEAKKEEMPA TKGGFSFGNVEPASLPSASVFVLGRTEEKQOEPVTSTSLVFGEG KLITMKEPKC\QPVFSFGEFQRQTKDENSSKSTFSFSMTKPSEKE SEQPAKATFAFGAQTNTTADQGAAKPDLSYLNNSSSSSSTPATS AGGG\IFGSSTSSSNPPVATFVFGQSSNPGSSS\AFGNTAESST SQSLLFSQDSKLATTSSTGTAVTPFVFGPGASSNNTTTSGFGFG ATTTSSSAGSSFVFGTGFSAPSASPAFGANOTPTFGOSOGASOR
TRPAISFSSSGIFGESLKAGSSWQCDTCLLQNKVTDNKCIAC QAAKLSPRDTAKQTGIETPNKSGKTTLSASGTGFGDKFKRVIGT WDCDTCLVQNKPEAIKCVACETPKPGTCVKRALTLTVVSESAET MTASSSSCTVTTGTLGFGDKFKRPIGSWECSVCCVSNNAEDNKC VSCMSEKPGSSVPTSSSSTVPVSLPSGGSLGLEKFKKPEGIWDC ELCLVQNKADSTKCLACESAKPGTKSGFKGFDTSSSSSNSAASS SFKFGVSSSSSGPSQTLTSTGNFKFGDQGGFKIGVSSDSGYINP MSEGF*FSKHIVGFKFGVSSESKPEEVKKDSKNDNFKFGLSFGL SNPVFLTPFQFGVSNLGQEEKKEELLKSSCAGFRFGTGVINSTR VPANTIVTSENKSSFNLGTIETKSVSVAPLKCQTSEAKKEEMPA TKGGFSFGNVEPASLPSASVFVLGRTEEKQQEPVTSTSLVFGEG KLTMKEPKC\QPVFSFGEFQRQTKDENSSKSTFSFSMTKPSEKE SEQPAKATFAFGAQTNTTADQGAAKPDLSYLNNSSSSSSTPATS AGGG\IFGSSTSSSNPPVATFVFGQSSNPGSSS\AFGNTAESST SQSLLFSQDSKLATTSSTGTAVTPFVFGPGASSNNTTTSGFGFG ATTTSSSAGSSFVFGTGFSAPSASPAFGANOTPTFGOSOGASOR
TRFATSSFSSGIGFGESLKAGSSWQCDTCLLQNKVTDNKCIAC QAAKLSPRDTAKQTGIETPNKSGKTLSASGTGFGDKFKPVIGT WDCDTCLVQNKPEAIKCVACETPKPGTCVKRALTLITVYSESAET MTASSSSCTVTTGTLGFGDKFKKPIGSWECSVCCVSNNAEDNKC VSCMSEKPGSSVPTSSSSTVPVSLPSGGSLGLEKFKKPEGIWDC ELCLVQNKADSTKCLACESAKPGTKSGFKGFDTSSSSNSAASS SFKFGVSSSSSGPSQTLTSTGNFKFGDQGGFKIGVSSDSGYINP MSEGF*FSKHIVGFKFGVSSESKPEEVKKDSKNDNFKFGLSFGL SNPVFLTPFQFGVSNLGQEEKKEELLKSSCAGFRFGTGVINSTR VPANTIVTSENKSSFNLGTIETKSVSVAPLKCQTSEAKKEEMPA TKGGFSFGNVEPASLPSASVFVLGRTEEKQOEPVTSTSLVFGEG KLTMKEPKC\QPVFSFGEFQRQTKDENSSKSTFSFSMTKPSEKE SEQPAKATFAFGAQTNTTADQGAAKPDLSYLNNSSSSSSTPATS AGGG\IFGSSTSSSNPPVATFVFGQSSNPGSSS\AFGNTAESST SQSLLFSQDSKLATTSSTGTAVTPFVFGPGASSNNTTTSGFGFG ATTTSSSAGSSFVFGTGFSAPSASPAFGANOTPTFGOSOGASOR
QAAKLSPRDTAKQTGIETPNKSGKTTLSASGTGFGDKFKPVIGT WDCDTCLVQNKPEAIKCVACETPKPGTCVKRALTLITVVSESAET MTASSSSCTVTTGTLGFGDKFKRPIGSWECSVCCVSNNAEDNKC VSCMSEKPGSSVPTSSSSTVPVSLPSGGSLGLEKFKKPEGIWDC ELCLVQNKADSTKCLACESAKPGTKSGFKGFDTSSSSNSAASS SFKFGVSSSSSGPSQTLTSTGNFKFGDQGGFKIGVSSDSGYINP MSEGF*FSKHIVGFKFGVSSESKPEEVKKDSKNDNFKFGLSFGL SNPVFLTPFQFGVSNLGQEEKKEELLKSSCAGFRFGTGVINSTR VPANTIVTSENKSSFNLGTIETKSVSVAPLKCQTSEAKKEEMPA TKGGFSFGNVEPASLPSASVFVLGRTEEKQOEPVTSTSLVFGEG KLTMKEPKC\QPVFSFGEFQRQTKDENSSKSTFSFSMTKPSEKE SEQPAKATFAFGAQTNTTADQGAAKPDLSYLNNSSSSSSTPATS AGGG\IFGSSTSSSNPPVATFVFGQSSNPGSSS\AFGNTAESST SQSLLFSQDSKLATTSSTGTAVTPFVFGPGASSNNTTTSGFGFG ATTTSSSAGSSFVFGTGFSAPSASPAFGANOTPTFGOSOGASOR
MICDTCLVQNKPEAIKCVACETPKPGTCVKRALTLTVVSESAET MTASSSSCTVTTGTLGFGDKFKRPIGSWECSVCCVSNNAEDNKC VSCMSEKPGSSVPTSSSSTVPVSLPSGGSLGLEKFKKPEGIWDC ELCLVQNKADSTKCLACESAKPGTKSGFKGFDTSSSSSNSAASS SFKFGVSSSSGPSQTLTSTGNFKFGDQGGFKIGVSSDSGYINP MSEGF*FSKHIVGFKFGVSSESKPEEVKKDSKNDNFKFGLSFGL SNPVFLTPFQFGVSNLGQEEKKEELLKSSCAGFFFGTGVINSTR VPANTIVTSENKSSFNLGTIETKSVSVAPLKCQTSEAKKEEMPA TKGGFSFGNVEPASLPSASVFVLGRTEEKQQEPVTSTSLVFGEG KLTMKEPKC\QPVFSFGEFQRGTKDENSSKSTFSFSMTKPSEKE SEQPAKATFAFGAQTNTTADQGAAKPDLSYLNNSSSSSSTPATS AGGG\IFGSSTSSSNPPVATFVFGQSSNPGSSS\AFGNTAESST SQSLLFSQDSKLATTSSTGTAVTPFVFGPGASSNNTTTSGFGFG ATTTSSSAGSSFVFGTGFSAPSASPAFGANOTPTEGOSOGASOR
MTASSSCTVTTGTLGFGDKFKRPIGSWECSVCCVSNNAEDNKC VSCMSEKPGSSVPTSSSSTVPVSLPSGGSLGLEKFKKPEGIWDC ELCLVQNKADSTKCLACESAKPGTKSGFKGFDTSSSSSNSAASS SFKFGVSSSSSGPSQTLTTSTGNFKFGDQGGFKIGVSSDSGYINP MSEGF*FSKHIVGFKFGVSSESKPEEVKKDSKNDNFKFGLSFGL SNPVFLTPFQFGVSNLGQEEKKEELLKSSCAGFRFGTGVINSTR VPANTIVTSENKSSFNLGTIETKSVSVAPLKCQTSEAKKEEMPA TKGGFSFGNVEPASLPSASVFVLGRTEEKQQEPVTSTSLVFGEG KLTMKEPKC\QPVFSFGEFQRQTKDENSSKSTFSFSMTKPSEKE SEQPAKATFAFGAQTNTTADQGAAKPDLSYLNNSSSSSSTPATS AGGG\IFGSSTSSSNPPVATFVFGQSSNPGSSS\AFGNTAESST SQSLLFSQDSKLATTSSTGTAVTPFVFGPGASSNNTTTSGFGFG ATTTSSSAGSSFVFGTGFSAPSASPAFGANOTPTEGOSOGASOR
VSCMSEKPGSSVPTSSSTVPVSLPSGGSLGLEKFKKPEGIWDC ELCLVQNKADSTKCLACESAKPGTKSGFKGFDTSSSSSNSAASS SFKGVSSSSSGPSQTLTSTGNFKFGDQGGFKLGVSSDSGYINP MSEGF*FSKHIVGFKFGVSSESKPEEVKKDSKNDNFKFGLSFGL SNPVFLTPFQFGVSNLGQEEKKEELLKSSCAGFRFGTGVINSTR VPANTIVTSENKSSFNLGTIETKSVSVAPLKCQTSEAKKEEMPA TKGGFSFGNVEPASLPSASVFVLGRTEEKQQEPVTSTSLVFGEG KLTMKEPKC\QPVFSFGEFQRQTKDENSSKSTFSFSMTKPSEKE SEQPAKATFAFGAQTNTTADQGAAKPDLSYLNNSSSSSSTPATS AGGG\IFGSSTSSSNPPVATFVFGQSSNPGSSS\AFGNTAESST SQSLLFSQDSKLATTSSTGTAVTPFVFGPGASSNNTTTSGFGFG ATTTSSSAGSSFVFGTGFSAPSASPAFGANOTPTEGOSOGASOR
SFKFGVSSSSGPSQTLTSTGNFKFGDQGGFKIGVSSDSGYINP MSEGF*FSKHIVGFKFGVSSESKPEEVKKDSKNDNFKFGLSFGL SNPVFLTPFQFGVSNLGQEEKKEELLKSSCAGFRFGTGVINSTR VPANTIVTSENKSSFNLGTIETKSVSVAPLKCQTSEAKKEEMPA TKGGFSFGNVEPASLPSASVFVLGRTEEKQQEPVTSTSLVFGEG KLITMKEPKC\QPVFSFGEFQRQTKDENSSKSTFSFSMTKPSEKE SEQPAKATFAFGAQTNTTADQGAAKPDLSYLNNSSSSSSTPATS AGGG\IFGSSTSSSNPPVATFVFGQSSNPGSSS\AFGNTAESST SQSLLFSQDSKLATTSSTGTAVTPFVFGPGASSNNTTTSGFGFG ATTTSSSAGSSFVFGTGFSAPSASPAFGANOTPTEGOSOGASOR
SFREGVSSSSGBQTLTSTGNFKFGDQGGFKIGVSSDSGYINP MSEGF*FSKHIVGFKFGVSSESKPEEVKKDSKNDNFKFGLSFGL SNPVFLTPFQFGVSNLGQEEKKEELLKSSCAGFRFGTGVINSTR VPANTIVTSENKSSFNLGTIETKSVSVAPLKCQTSEAKKEEMPA TKGGFSFGNVEPASLPSASVFVLGRTEEKQOEPVTSTSLVFGEG KLITMKEPKC\QPVFSFGEFQRQTKDENSSKSTFSFSMTKPSEKE SEQPAKATFAFGAQTNTTADQGAAKPDLSYLNNSSSSSSTPATS AGGG\IFGSSTSSSNPPVATFVFGQSSNPGSSS\AFGNTAESST SQSLLFSQDSKLATTSSTGTAVTPFVFGPGASSNNTTTSGFGFG ATTTSSSAGSSFVFGTGFSAPSASPAFGANOTPTFGOSOGASOR
MSEGF*FSKHIVGFKFGVSSESKPEEVKKDSKNDNFKFGLSFGL SNPVFLTPFQFGVSNLGQEEKKEELLKSSCAGFRFGTGVINSTR VPANTIVTSENKSSFNLGTIETKSVSVAPLKCQTSEAKKEEMPA TKGGFSFGNVEPASLPSASVFVLGRTEEKQQEPVTSTSLVFGEG KLTMKEPKC\QPVFSFGEFQRQTKDENSSKSTFSFSMTKPSEKE SEQPAKATFAFGAQTNTTADQGAAKPDLSYLNNSSSSSTPATS AGGG\IFGSSTSSSNPPVATFVFGQSSNPGSSS\AFGNTAESST SQSLLFSQDSKLATTSSTGTAVTPFVFGPGASSNNTTTSGFGFG ATTTSSSAGSSFVFGTGPSAPSASPAFGANOTPTEGOSOGASOR
SNPVFLTPFQFGVSNLGQEEKKEELLKSSCAGFRFGTGVINSTR VPANTIVTSENKSSFNLGTIETKSVSVAPLKCQTSEAKKEEMPA TKGGFSFGNVEPASLPSASVFVLGRTEEKQOEPVTSTSLVFGEG KLTMKEPKC\QPVFSFGEFQRQTKDENSSKSTFSFSMTKPSEKE SEQPAKATFAFGAQTNTTADQGAAKPDLSYLNNSSSSSTPATS AGGG\IFGSSTSSSNPPVATFVFGQSSNPGSSS\AFGNTAESST SQSLLFSQDSKLATTSSTGTAVTPFVFGPGASSNNTTTSGFGFG ATTTSSSAGSSFVFGTGPSAPSASPAFGANOTPTEGOSOGASOR
TKGGFSFGNVEPASLPSASVFVLGRTEEKQQEPVTSTSLVFGEG KLTMKEPKC\QPVFSFGEFQRQTKDENSSKSTFSFSMTKPSEKE SEQPAKATFAFGAQTNTTADQGAAKPDLSYLNNSSSSSTPATS AGGG\IFGSSTSSSNPPVATFVFGQSSNPGSSS\AFGNTAESST SQSLLFSQDSKLATTSSTGTAVTPFVFGPGASSNNTTTSGFGFG ATTTSSSAGSSFVFGTGPSAPSASPAFGANOTPTEGOSOGASOR
KLIMKEPKC\QPVFSFGEFQRQTKDENSSKSTFSFSMTKPSEKE SEQPAKATFAFGAQTNTTADQGAAKPDLSYLINISSSSSTPATS AGGG\IFGSSTSSSNPPVATFVFGQSSNPGSSS\AFGNTAESST SQSLLFSQDSKLATTSSTGTAVTPFVFGPGASSNNTTTTSGFGFG ATTTSSSAGSSFVFGTGFSAPSASPAFGANOTPTFGOSOGASOR
SEQPARATFAFGAQTNTTADQGAAKPDLSYLNNSSSSSSTPATS AGGG I FGGSTSSSNPPVATFVFGQSSNPGSSS \AFGNTAESST SQSLLFSQDSKLATTSSTGTAVTPFVFGPGASSNNTTTSGFGFG ATTTSSSAGSSFVFGTGFSAPSASPAFGANOTPTFGOSOGASOR
AGGG IFGSSTSSSNPPVATFVFGQSSNPGSSS AFGNTAESST SQSLLFSQDSKLATTSSTGTAVTPFVFGPGASSNNTTTSGFGFG ATTTSSSAGSSFVFGTGPSAPSASPAFGANOTPTFGOSOGASOR
SQSLLFSQDSKLATTSSTGTAVTPFVFGPGASSNNTTTSGFGFG ATTTSSSAGSSFVFGTGPSAPSASPAFGANOTPTFGOSOGASOR
ATTISSSAGSSFVFGTGPSAPSASPAFGANOTPTFGOSOGASOR
NDDCECCICOCENT TOTAL CANCIPTE GOSQGASQP
NFFUFUSIONALIFPIGSOPADDTEGTUGGGGGGDDTTDGGGDG
SAFGSGTTPNSSSAFQFGSSTTNFNFTNNSPSGVFTFGANSSTP
AASAQPSGSGGPPFNQSPAAFTVGSNGKNVFSSSGTSFSGRKIK
TAVRRK
PRPGSRSGLCRRAGERGAVRAGGLSRRTRAE*IMDFLHVODTDG
DVPEQRDSKCKVKWTHEEDEOLRALVROFGOODWKFLAGUEDND
TDQQCQYRWLRVLNPDLVKGPWTKEEDOKVIELVKKYGTKOWTL
TAKHLKGRLGKQCRERWHNHLNPEVKKSCWTEEEDPTICEAUVX
LGNRWAEIAKMLPGRTDNAVKNHWNSTIKRKVDTGGFLSESKDC
KPPVYLLLELEDKDGLQSAQPTEGQGSLLTNWPSVPPTIKEEEN
SEEELAAATTSKEQEPIGTDLDAVRTPEPLEEFPKREDQEGSPP
ETSLPYKWVVEAANLLIPAVGSSLSEALDLIESDPDAWCDLSKF
DLPEEPSAEDSINNSLVQLQASHQQQVLPPRQPSA\LVPSVTEY RLDGHTISDLSRSSRGELIPISPSTEVGGSGIGTPPSVLKRQRK
RRVALSPVTENSTSLSFLDSCNSLTPKSTPVKTLPFSPSQFLNF
WNKQDTLELESPSLTSTPVCSQKVVVTTPLHRDKTPLHQKHAAF
VTPDQKYSMDNTPHTPTPFKNALEKYGPLKPLPQTPHLEEDLKE
VLRSEAGIELIIEDDIRPEKQKRKPGLRRSPIKKVRKSLALDIV
DEDMKLMMSTLPKSLSLPTTAPSNSSSLTLSGIKEDNSLLNQGF
LQAKPEKAAVAQKPRSHFTTPAPMSSAWKTVACGGTRDOLFMOR
KARQLLGRLKPSHTSRTLILS
AGPDDTMKRSLQALYCOLLSFLLILALTEALAFATOFFGSDFGT
QVLPSGTPPGTMVTAPHSSTRHTSVVMLTPNPDGPPSOAAADMA
TPTPRAEGHPPT\TPSPPSLRO*PPPILKAP/SSTGPADAMAT
TSSKPEGRPRGQAAPTILLTKPPGATSRPTTAPPRTTTPPPDDD
PGSSRKGAGNSSRPVPPAPGGHSRSKEGORGRNPSSTPLGOKPR
LGKIFQIYKGNFTGSVEPEPSTLTPRTPLWGYSSSPQPQTVAAT

SEO	Drod/ -b - 3		
ID	Predicted beginning	Predicted end	
NO:	nucleotide	nucleotide	I WATER GRADUE, CELVSTRIDE DENGRALIE NEED I -
	location	location	Crucamic Acid, Febbery alaning C.C.
	corresponding	corresponding	M-Miscluing, imisclencing V-tyroing
	to first	to first amino acid	Debeucine, Mamerhionine Nagramatica
1	amino acid	residue of	F=FLOLING, O=GLUtamina D=N
	residue of		S=Serine, T=Threonine V-Valine
1	amino acid	amino acid sequence	W=Tryptophan, Y=Turosine V-Unknown
1	sequence	sequence	COUCH, /=DOSSIDIE mucleotido dolen-
	1 4-01102		\=Possible nucleotide insertion\
ŀ	1		TVPSNTSWAPTTTSLGPAKDKPGLRRAAGGGGGTETTGGGGGTTS
			I TARGUAP V SP/ PSCPSAFSAPPPR* PTGWPOD++T T NYGYEN GW
[1		1 SAFIGISSGVFTAATGPTPAAFDTGVGADGOCTDOGAGTTGGAG
			1 ***FORVOESTISGAKEETVA\ PSD*DTCCDIG CDOUWDOD
			I DIAMSEEGSLGOOGTS PMWDDCTWDCTCDDCX + N DWT
]		T TESACESPE LUCPADGV LHEREREDDODORODD STORTS TO THE
	İ	1	1 Serie (ROMAPOEL PVPLKPLRTOLSEPRSDANCOVDOCATE
6952	658	204	
	المحت	304	PESEGESGEMTDRYTIHSQLEHLQSKYIGT\ATPTPPSGSG\CE
- 1			FIFKUVULUNGPLKPSOLLRHCGE*FOGAGDIOT DOWN ANT
6953	1512	340	1 ADRUARGE LIKECTTTAVRCTSDSVSDVCASS
		349	NWGKTRALASGKHVPFGKOTNPNKS /VHCDS+C++DDHMMS
	[TOPRERGAMGGVV \ KLEKETENTEODUGGNEG + EURITMONT
			T THE DOUBLE PLOUDING SERVICE AND A TRANSPORTED TO THE PROPERTY OF THE PROPERT
			OCCUPATION OF THE PROPERTY OF
	į į		T D V LINIO SUP I V RNEGPSSAEGENTARCODEVO DA CTT T MOURTON N
1 1			TAXABLEAUTPSVKKWALRRONEDI, FUDI OUT ED DOWN VICTORIA
]			I EIFEREVRRIKUREAKRI ORMOETDEODARDI ODDADANES
1 1			I WAR TERVENARY TREATMENT AND THE TRANSPORTER
6954	819	1	1 STREET CUPYSGVELDSOLLGKMA PPPONECET **
		-	PPPPFIIPSHPREAGT*AG*KRSGDSECSDBVEO************************************
			"FYA" RWIEGNSPOASAVATPGOGASDAADDCUD+DGDDUDT D
1 1	1		I FUNKERAG AAPAPIKPWI AGPAGADADGAADT GAAAAA
1 1	}		CASAMARGRERRURS PREPERFORCE SWEET DEPOSITION OF CHAPTER
	ŀ		DAG AGGR GORORPS TGR * DDGVCGAGDCUDDDGGT DGV
1			1 12 12 13 15 15 PART POP / REWGL*EPOGEEMSGPGGPGGPGA PDMATTGR
6955	1968	782	41.51.101.01
1	Į	702	PPGRRQVRAQVAGAPVGHWGTRARQVKTGGRRRARRTMPFLGQD
1 1	i		MOLONSWILLIEDGWKRCESCSOKI.FDFMMICNITCHCTTT. NOOD
1 1	}		ODITING COLUMN TARGET ASKKKKKDH FRNOTNIT OCH TO DEVELT WITH THE COLUMN TARGET ASKKKKKDH FRNOTNIT OCH TO DEVELT WITH THE COLUMN TARGET ASKKKKK DH FRNOTNIT OCH TO DEVELT WITH THE COLUMN TARGET ASKKKKK DH FRNOTNIT OCH TO DEVELT WITH THE COLUMN TARGET ASKKKKKK DH FRNOTNIT OCH TO DEVELT WITH THE COLUMN TARGET ASKKKKK DH FRNOTNIT OCH TO DEVELT WITH THE COLUMN TARGET ASKKKKK DH FRNOTNIT OCH TO DEVELT WITH THE COLUMN TARGET ASKKKK DH FRNOTNIT OCH TO DEVELT WITH THE COLUMN TARGET ASKKKK DH FRNOTNIT OCH TO DEVELT WITH THE COLUMN TARGET ASKKK DH FRNOTNIT OCH TO DEVELT WITH THE COLUMN TARGET ASKKK DH FRNOTNIT OCH TO DEVELT WITH THE COLUMN TARGET ASKK DH FRNOTNIT OCH TO DEVELT WITH THE COLUMN TARGET ASKK DH FRNOTNIT OCH TO DEVELT WITH THE COLUMN TARGET ASK
1 1	1		DOIGICILGEAFNRLDFSSATONTDDDDTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
	ł		DOG ANGIGUE ENTTRINT ACKAIN UNITED TANK TO THE TANK TO
1 1	ļ		/ WINDREVELOGREDIED I PROVEDI A TOTAL CONDENS OF A COLUMN TOTAL COLUMN TOTAL CONDENS OF A COLUMN TOTAL CONDENS OF A COLUMN TOTAL COLUMN
	1		THE PERSON OF TH
1 1	}	ļ	AND WITH ABROYCE HLILSEKGHTENVI MV BAT OVIVER TO THE TOTAL OF THE PROPERTY OF
		1	GDTLHFCRHCSILFWKDSGHPCTAADPDSCFTPVSPQHFIDLFK F
6956	8605	3839	
	j		QTSTS1FASPTSPPVLGESVLQDNSFDLNNGSDAEQEEMETQSS
1	1	1	DFPPSLTQPAPDQSSTIQLHPATSPAVSPTTSPAVSLVVSPAAS PEISPFVCPAASTIVSPAVECHUSPA
]			PEISPEVCPAASTVVSPAVFSVVSPASSAVLPAVSLEVPLTASV TSPKASPVTSPA A PETA SPAVENCE
1 1	j		
]]	1		ASGSGDVMRRRIATPEEVRLPLQHGWRREVRIKKGSHRWQGETW
1 1	1	j.	1 TO CORRER OF PEVIKYLSRNVVHSVPPPHESESPPMENON
		i	DESCRIPTION OF STREET AND ALL
1		1	PKVKRGRGRPPKVKITELLNKTDNRPLKKLEAQETLNEEDKAKI
]]			ANDANNIRUKVURGECOTTIOGOARNKRKOFTKGIKOKENKKK
1	i	1	WARRENGY I KORYPKEK AKKEKAKMKEKEEDIMAA ADAGASA
1		1 .	**************************************
1 1		['	ODIDEGGAE SUCLITIVE FLHSFCKVI GEDDA KUUDGI GER ODGE
] [1 '	PCZGDGLGEVQDLLVKLLKAALHDDGEDGVCOGI VII CEVICET
	1	1.	*DIADN VSEIDKUFDMAYGVEPALCDDLDTODEOAODDOOM
1	ļ	1 .	MAI DVACLINGSTLLINEIDKTLESMSSVDVMVMTIMODI DD
		1	VIDICAL GROUP VENEGIEE PEEC CORPRESED THE TIME CAMERINA
j j	ļ	1 4	AV FORRGRRUGEVDATASSTPFI.FPOTEVI.CVDOT FED VICE 1
1	ĺ	1 5	SOUTH AND DOUDKYKKKYWVT.PVT.ACTEURGREGANT TIPESTER I
·			KETDSLKVAAHASLNPALFSMKMELAGSNTTASSPARARGRPRK
			The state of the s

SEO	Predicted	I Described and a second	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
ì	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
(amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acid	sequence	Codon, /=possible nucleotide deletion,
1 :	sequence	•	\=possible nucleotide insertion)
			TKPGSMQPRHLKSPVRGQDSEQPQAQLQPEAQLHAPAQPQPQLQ
	,		LQLQSHKGFLEQEGSPLSLGQSQHDLSQSAFLSWLSQTQSHSSL
[LSSSVLTPDSSPGKLDPAPSQPPEEPEPDEAESSPDPQALWFNI
	**		SAQMPCNAAPTPPPAVSEDQPTPSPQQLASSKPMNRPSAANPCS
j			PVQFSSTPLAGLAPKRRAGDPGEMPQSPTGLGQPKRRGRPPSKF
			FKQMEQRYLTQLTAQPVPPEMCSGWWWIRDPEMLDAMLKALHPR
1 !			GIREKALHKHLNKHRDFLQEVCLRPSADPIFEPRQLPAFQEGIM
			SWSPKEKTYETDLAVLQWVEELEORVIMSDLOIRGWTCPSPDST
			REDLAYCEHLSDSQEDITWRGRGREGLAPORKTTNPLDLAVMPL
			AALEONVERRYLREPLWPTHEVVLEKALLSTPNGAPEGTTTFIC
1 1			YEITPRIRVWRQTLERCRSAAOVCLCLGOLERSTAWEKSUNKUT
			CLVCRKGDNDEFLLLCDGCDRGCHIYCHRPKMEAVPEGDWECTV
1			CLAQQVEGEFTQKPGFPKRGQKRKSGYSLNFSEGDGRRRRVILLR
1 1	1		GRESPAAGPRYSEEGLSPSKRRRLSMRNHHSDLTFCEITIMEME
1	ļ		SHDAAWPFLEPVNPRLVSGYRRIIKNPMDFSTMRERLLRGGYTS
1 1			SEEFAADALLVFDNCQTFNEDDSEVGKAGHIMRRFFE\SRWEEF
1 1			YQGKQGQSVRQGRWGVTLWHLPPTFQTKTCHFHLLMLPWVQTQV
6957	82	3514	RYNPDF
1 1		2214	HLIVAMPEPTKKEENEVPAPAPPPEEPSKEKEAGTTPAKDWTLV
1 [1		ETPPGEEQAKQNANSQLSILFIEKPQGGTVKVGEDITFIAKVKA EDLSEKPTINGSRKWMDLASKAGKHLQLKETFERHSRVYTFEMQ
1			IIKAKDNFAGNYRCEVTYKDKFDSCSFDLEVHESTGTTPNIDIR
]]	1		SAFKRSGEGQEDAGELDFSGLLKRREVKQQEEEPQVDVWELLKN
	į.		TKPSEYEKIAFQYESPTCSGMLKRLKRSIREEKKSAAFAKILDP
	ł		VYQVDKGGRVRFVVELADPKLEVKWNKNGQELRPSTKYIFEDTR
1 1	1		CQSILNIDNCQMTDDSEYYVTAGDEKCSTELLVREPPIMVTKOL
			EDTTDYCGERVELECEVSEDDAQVKWFKNGEEIILVOTRYRTRV
1			EGKKHILIIEGATKADAADYSVMTTGGOSSAKLSVDLKPLKTLT
1 1	i		PLTDQTVNLGKEICLKCEISENIPGKWTKNGLPVOESDRIKTARU
1 1	1		KGRIHKLVIDHALTEDEGDYVFAPDAYNVTLPAKVHVIDPPKII
			LDGLDADNTVTVIAGNKLRLEIPISGEPPPKAMWSRGDKAIMEG
1			SGRIRTESYPDSSTLVIDIAERDDSGVYHINLKNEAGEAHASIK
] [į		VKVVDFPDPPVAPTVTEVGDDWCIMNWEPPAYDGGSPILGYFIE
1 1	1		RKKKQSSRWMRLNFDLCKETTFEPKKMIEGVAYEVRIFAVNA\I
1	1		GISKPSMPSRPFVPLAVTSPPTLLTVDSVTDTTVTMRWRPPDHI
[]	İ		GAAGLDGYVLEYCFEGSTSAKQSDENGEAAYDLPAEDWIVANKD LIDKTKFTITGLPTDAKIFVRVKAVNAAGASEPKYYSQPILVKE
]			IIEPPKIHSPKHLKQTYIRRVGDRVILVIPFQGKPRPELTWKKD
! [ĺ		GAEIDKNQINIRNSETDTIIFIRKAERSHSGKYDLQVKVDKFVE
] [TASIDIRIIDRPGPPQIVKIEDVWGRNVALTWTPPKDDGNAAIT
!	1		GYTIQKADKKSMEWLRVIEHIIEPVPHTELVIGNEYYFRVFSEN
[. [MCGLSEDATMTKESAVIARDGKIYKNPVYEDFDFSEAPMFTQPL
	1	1	VNRLCHSGYMATLNCSVRGNPKPKITWMKNKVAIVDDPRYRMFS
			NQGVCTLEIRKPSPYDGGTYCCKAVNDLGTVEIECKLEVKVIAO
6958	274	1663	PRTSRVKTEGSQGSSAMDFSVKVDIEKEVTCPICLELLTEPLSI
	ļ	i	DCGHSFCQACITAKIKESVIISRGESSCPVCOTRFOPGNLR PND
		į	HLANIVERVKEVKMSPOEGOKRDVCEHHGKKLOIFCKEDGKVIC
		ļ	WVCELSQEHQGHQTFRINEVVKECQEKLOVALORLIKENORAEK
		1	LEDDIRQERTAWKNYIQIERQKILKGFNEMRVILDNEEORELOK
		,	LEEGEVNVLDNLAAATDOLVOORODASTLISDLORRIRGSSVEM
ļ		1	LQDVIDVMKRSESWTLKKPKSVSKKLKSVFRVPDLSGMLOVTKE
		i i	LTDVQYYWVDVMLNPGSATSNVAISVDOROVKTVRTCTFKNSNP (
1	1	1	CDFSAFGVFGCQYFSSGKYYWEVDVSGKIAWILGVHSKISSLNK
			RKSSGFAFDPSVNYSKVYSRYRPQYGYWVIGLQNTCEYNAFEDS
6959		1469	SSSDPKVLTLFMAV\LPVVLGFS
			SLVHVVEFGRGIEDFPYLFFQLTHCQQRICSVTQAGVQWCDHSS

数 >

Deginning nucleotide location corresponding to first amino acid residue of amino acid residue of amino acid sequence Proline, O-Quittamine, R-Arginine, S-Serine, N-Asparagine, P-Proline, O-Quittamine, R-Arginine, Corresponding to first amino acid residue of amino acid sequence Proline, O-Quittamine, R-Arginine, S-Serine, T-Threonine, V-Valine, W-Tryptophan, Y-Tyrosine, X-Unknown, *-Stop Codon, /-possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide insertion) Provine, O-Quittamine, R-Arginine, S-Serine, T-Threonine, V-Valine, W-Tryptophan, Y-Tyrosine, X-Unknown, *-Stop Codon, /-possible nucleotide deletion, \p	SEQ	Predicted	Predicted end	Amino acid segment containing signal montile
No: nucleotide location corresponding to first amino acid residue of amino acid residue of amino acid sequence				Amino acid segment containing signal peptide
Corresponding to first amino acid residue of amino acid residue of amino acid sequence L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine,	NO:		ľ	Glutamic Acid. F=Phenylelenine C-Clu-i-
L=Leucine, M=Methionine, N=Asparagine, amino acid residue of amino acid sequence P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, w=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, _=possible nucleotide deletion, _=possible nucleotide deletion, _=possible nucleotide insertion	İ			H=Histidine T=Tsolengine V=Lygine
amino acid residue of amino acid sequence sequen		corresponding		LeLeucine, Memerhionine Nederland
amino acid residue of amino acid sequence Seserine, T=Threonine, V=Valine, m=Txyptophan, V=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible n				Paproline OaGlutamine Palrainine
residue of amino acid sequence Codon, /=possible nucleotide deletion, -possible nucleotide deletion, -possible nucleotide insertion LQPQTPGLNQSSHLSLLSSEDYRMLSSNEWFMQDRFWLPPNV-WTELEDRDGRVYPHPQDLLAALPLALVLLAMRLAFERFIGLPL-WTELEDRDGRVYPHPQDLLAALPLALVLLAMRLAFERFIGLPL-WTELEDRDGRVYPHPQDLTKKFCEASWRFLFYLSSFVGGLST-LYHESWLMAPDVMCWDRYPNQLTLSCPAADSEA\SLYWWILLELGTURF LYHESWLMAPDVMCWDRYPNQLTLSCPAADSEA\SLYWWILLELGTURFYSANLLRIGSLVLLLHNSSDYLLBACKMVNYM-YQQVCDALFLIFSFYVTRIVLFPTQILYTTYYESISNRGPFI-GYYFFNGLLMLLQLLHVFWSCLILRMLYSFMKKGQMEKDLTSD-GYYFFNGLLMLLQLLHVFWSCLILRMLYSFMKKGQMEKDLTSD-GYYFFNGLLMLLQLLHVFWSCLILRMLYSFMKKGQMEKDLTSD-GYYFFNGLLMLLQLLHVFWSCLILRMLYSFMKKGQMEKDLTSD-EESDSSEBAAAQEPLQLKNGTAGGPRPAPTDGPRSRVAGRLT-TATA AKWAREKEMQEF\TRSFF\RGRPDLSTLTHSIVRRRYLAHSGRS-HLEPERKGPLAKRAVESEPLKWQVDEAASREDKLDLTKKGKRPFI-PCSDPERKFFFNSESGSGEASSPDYFGPPAKNGVASSRHTH-KEENPRRA\SKAVEESSDEERGASSPDYFGPPAKNGVASSRHTH-KEENPRRA\SKAVEESSDEERGASSPTYGPPAKNGVASSRHTH-KEENPRRA\SKAVEESSDEERGRDHPAVARKVEGA-KGTKSKKSGARGRGBHPAVARKVEGA-KGTKSKKSEGESEEELLAQKKEGGEEVEEEEKEDEEKGDEW-PRTRSNGRKSAREERSCKGKSQAKRLIGDSDSEECKEAASSG-DEDGGRGEPTY-KGSKKAKALGSTSGEESDLEDREVSDSEAGGGPGGERKNRSSKKS-SRKGRTRSSSSSSSSSSSSBEDESGKGEPTY-AMHRIKRYIT-ACGBINKKKLIGSCSKEPLS-LAGKGTPSSGKGEPT-LYRRTLSDEERFPRAPPDWSHMRGIISSDGESN-LYRRTLSDEERFPRAPPDWSHMRGIISSDGESN-LYRRTLSDEERFPRAPPDWSHMRGIISSDGESN-LYRRTLSDEERFPRAPPDWSHMRGIISSDGESN-LYRRTLSDEEFFRRAPPDWSHMRGIISSDGESN-LYRRTLSDEEFFRRAPPDWSHMRGIISSDGESN-LYRRTLSDEEFFRRAPPDWSHMRGIISSDGESN-LYRRTLDSDEERFPRAPPDWSHMRGIISSDGESN-LYRRTLSDEEFFRRAPPDWSHMRGIISSDGESN-LYRRTLDSDEERFPRAPPDWSHMRGIISSDGESN-LYRRTLSDEEFFRAPPDWSHMRGIISSDGESN-LYRRTLSDEEFFRAPPDWSHMRGIISSDGESN-LYRRTLSDEEFFRAPPDWSHMRGIISSDGESN-LYRRTLSDEEFFRAPPDWSHMRGIISSDGESN-LYRRTLSDEEFFRAPPDWSHMRGIISSDGESN-LYRRTLSDEEFFRAPPDWSHMRGIISSDGESN-LYRRTLSDEEFFRAPPDWSHMRGIISSDGESN-LYRRTLSDEEFFRAPPDWSHMRGIISSDGESN-LYRRTLSDEEFFRAPPDWSHMRGIISSDGESN-LYRRTLSDEEFFRAPPDWSHMRGIISSDGESN-LYRRTLSDEEFFRAPPDWSHMRGIISSDGESN-LYRRTLSDEFFRAPPDWSHARGIISSCKSFTI-LYRRTLSDEFFRAPPDWSHARGIISSCKSFTI-LYRTLSDEFFRAPPDWSHARGIISSCKSFTI-LYRTLSDEFFR	1	amino acid		S=Serine. T=Threonine V-Valine
Sequence Codon, /=possible nucleotide deletion, -possible nucleotide insertion -possible nucleotide insertion		residue of		W=Tryptophan V-Tyrosine V-Unknown to Share
Sequence \ \ \ \ \ \ \ \ \ \ \ \ \		amino acid		Codon /=nossible nucleotide deletion
LOPOTPGLNQSSHUSLUSSRDYRMLSSFNEWFWQDRFWLPPNVWTELEDRDGRVYPHPQDLLAALPLALVLLANRLAFERFIGLPLIARWIGGREDGREWYPHPQDLLAALPLAAQCG RWLGVRDOTRRQVKPNATLEKHFLTEGHPPKEPQLSLLAAQCG TLQCTQRWFRRRRNQDRPQLTKKFCEASWRFLFYLSSFVCGLST LYHESWLWAPVMCWBRYPQLTLSCPAADSEA\SLYWWYLLELK FYLSLLIRLPFDVKRKGGGPSSIKPPHYDPPSTA\DFKEQVIJ HFVAVILMTFSYSANLLRIGSLVLLLHDSSDYLLEACKMVNYMM YQQVCDALFLIFSFVFFYTRLVLFPTQILYTTYYESISNRGPFI GYYFFNGLIMLLQLHVWWSCLILKMLYSFMKKGOMEKDIRSDY EESDSSEBAAAQEPLQLKNGTAGGPRPAPTDGPRSRVAGRLTT RHTTAT AKWAREKEMQEF\TRSFF\RGRPDLSTLTHSIVRRRYLAHSGRE HLEPEEKQALKRLVEBEPLKMQVDEAASREDKLDLTKKGKRPPP PCSDPERKRFRNSESSGSEASSPDYFGPPAKNGVASRSHTHI KEEMPRRA\SKAVEESSDEERQRDLPAQRGEESSEEEEKGYKGI TRKKFVVKKQAPGKASVSRKQAREESEESEAEPVQRTAKKVUEGI KGTKSLKESEQESEEILAGKKEQREEVEEEEKEEDEEKGDWIJ PRTRSNGRRKSAREERSCKQKSQAKRLLGDSDSEEEQKEAASSG GKGTKSLKSSEGESEBLLAGKKEQREEVEEEKEEDEEKGDWIJ PRTRSNGRRKSAREERSCKQKSQAKRLLGDSDSEEEQKEAASSG SRKGRTRSSSSSSDSPPAKGGKAGSGRRGEDHPAVMRLKRYII ACGAHRNYKKLLGSCCSHKERLSILRAELEALGMKGTPSLGKCF ALKEQREEAAEVASLDVANIISGSGRPRRTTAMNPLGEAAPPGF LYRRTLDSDEERRPRPPPDWSHMRGIISSDGESN ALKEQREEAAEVASLDVANIIGSGGRPRRTTAMNPLGEAAPPGF NORSPDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSC LCVFSKHPIQELTQHIYTLNGYPYMIHGGWFSGKAVGLLVLHI SGMVLNAYVTHLHAEYNRQKDIYLAKRAGAWELAQFIHTSKK ADUVLLCGBLMMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEGC NTMVPKNCYVSQOELKPFPFFGVRIDYLYRAVSGFYISCKSFFII TTGFDPHRGTPLSDHEALMATLIYVRHSPPQONPSSTHEGP\AERS	i	1		\=nossible nucleotide incertion\
WTELEDRDGRVYPHPODLLAALPLALVLLAMRLAFERFIGLPLE RWLGVRDOTRRQVKPNATLEKHFLTEGHRPKEPQLSLLAAQCG TLQQTQRWFRRRRNQDRPQLTKKFCEASWRFLFYLSFVGGLSY LYHESWLWAPVMCWDRYPNQLTLSCPAADSEA\SLYWWYLLELG FYLSLLIRLPFDVKRKKGGESSIKPRPHYDPPSTA\DFKEQVII HPVAVILMTFSYSANLLRIGSLVLLLHDSSDYLLEACKMVNYMG YQQVCDALFLIFSFVFFYTRLVLFFTQILYTTYYESISNRGPFI GYYFFNGLMULQLHVFWSCLILRMLYSFMKKGQMEKDIRSDY EESDSSEEAAAAQEPLQLKNGTAGGPRPAPTDGPRSRVAGRLTI RHTTAT AKWAREKEMQEF\TRSFF\RGRPDLSTLTHSIVRRRYLAHSGRI HLEPEEKQALKRLVBEEPLKMQVDEAASREDKLDLITKKGKRPFI PCSSDFERKRFFRNSESESGSEASSPDYFGPPAKNGVASRSHTHI KEENPRA\SKAVEESSDEERQRDLPAORGEESSEEEEKGYKGI TRKKPUVKKQAPGKASVSRKQAREESEESEAEPUQRTAKKUEGI KGTKSLKESEQESEEILAQKKEQREEEVEEEEKEEDEEKGYKGI PRTRSNGRRKSAREERSCKQKSQAKRLLGDSDSEEGCKBASSG DDSGRDRBPPVQRKSEDRTQLKGGKRLSGSSEDEEDSGKGEPTI KGSRKMARLGSTSGEESDLEREVSDSEAGGGPGERKNRSSKK SRKGRTRSSSSSSDSPBAKGGKAGSGRRGEDHPAVMRLKRYIT ACGAIRNYKKLLGSCCSHKERLSILRAELEALGMKGTPSLGKCF ALKEQREBAAEVASLDVANIISGSGEPRRRTAMPLGBAPPGG LYKRTLDSDEERPRPAPPDWSHMRGIISSGGES ALKEQREBAAEVASLDVANIISGSGEPRRRTAMPLGBAPPGG LYKRTLDSDEERPRPAPPDWSHMRGISSGGEN NGESPDLALLEEVMSEQDFQYLRCKLSPTYPAAHHFRSGIIGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHI SGMVLNAVTHHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEGG NTMVPKNCYVSQQELKPFPFGVRIDTVUYLKAVSGFYISCKSFFI TTGFDPHRSTPLSDHEALMATLFVRHSPPQQNPSSTHGF\AEKS		-		LOPOTROL MOSSUL ST. LESED VRM CORNEWS CORNEWS
RWLGVRDOTRRQVKPNATLEKHFLTEGHRPKEPQLSLLAAQCG TLQQTQRWFRRRRRQDRPQLTKKFCEASWRFLFYLSSFVQGLST LYHESWLWAPVWCWDRYPNQLTLSCPAADSEA\SLYWWYLLELK FYLSLLIRLPFDVKRKGGGPSSIKPRPHYDPPSTA\DFKEQVII HFVAVILMTFSYSANLLRIGSLVLLLHDSSDYLLEACKWYNYM YQQVCDALFLIFSFYFFYTRLVLFPTQILYTTYYESISNRGPFI GYYFFNGLLMLLQLLHVFWSCLILRMLYSFMKKGGMEKDIRSDD EESDSSEEAAAAQEPLQLKNGTAGGPRPAPTDGPRSRVAGRLTI RHTTAT 6960 387 2068 AKWAREKEMQEF\TRSFF\RGRPDLSTLTHSIVRRRYLAHSGRS HLEPBEKQALKRLVBEEPLKMQVDEAASREDKLDLTKKGKRPPT PCSDPERKRFRFNSESESGSEASSPDYFGPPAKNGVASRHTHI KEEMPRRA\SKAVEESSDEERQRDLPAQRGEESSEEEKGYKGI TRKKPVVKKQAPGKASVSRKQAREESEEEEKGYKGI KGTKSLKESEQESEEEILAQKKEGREEVVEEEKEEDEKGDWI PRTRSNGRRKSAREERSCKQKSQAKRLLGDSDSEEQKEAASSC DDSGRDRPPVQRKSEDTTQLKGGKRLGSGSPGECKEASSC GKGSRKMARLGSTSGEESDLEREVSDSEAGGGPQGERKNRSSKK SRKGRTRSSSSSDSPEAKGGKAGSGRRGEDHPAVMRLKRYIF ACGAIRNYKKLLGSCCSHKERLSILRAELEALGMKGTPSLGKCF ALKEQREEAAEVASLDVANIISGGSPRRRTAMPLGEAAPPGG LYKRTLDSDEERRPAPPDWSHMRGIISSDGESN ACGAIRNYKKLLGSCCSHKERLSILRAELEALGMKGTPSLGKCF ALKEQREEAAEVASLDVANIISGGSPRRRTAMPLGEAAPPGG LYKRTLDSDEERRPAPPDWSHMRGIISSDGESN NGESPDLALLEEVWSEODFOYLRCKLSTTYPAAHHFRSGIIGSC LCVFSKHPIQELTQHIYTLNGYPYMIHGDWFSGKAVGLLVLHI SGMVLNAVVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEGC NTMVPKNCYVSQQELKPFPFGVRIUVUKYASGFYISCKSFEI TTGFDPHRGTPLSDHEALMATLFVRHSPPQONPSSTHGF\AEKS				WTFI-FODDCDIVOUDODITANI DI NI ILI NADI NEWI-WODKIWDPPNVT
TLQOTQRWFRRRRNQDRPQLTKKFCEASWRFLFYLSSFVGGLST LYHESWLWAPVMCWDRYPNQLTLSCPAADSEA\SLYWWILLELL LYHESWLWAPVMCWDRYPNQLTLSCPAADSEA\SLYWWILLELL FYLSLLIRLPFDVKRKGGGPSSIKPRPHYDPPSTA\DFKEQVII HFVAVILMTFSYSANLLRIGSLVLLLHDSSDYLLEACKWNYNM YQQVCDALFLIFSFVFTTRLVLIFPTQILYTTYYESISMRGPFI GYYFFNGLMLLQLLHVFWSCLILRMLYSFMKKGQMEKDIRSDY EESDSSEEAAAAQEPLQLKNGTAGGPRPAPTDGPRSRVAGRLTT RHTTAT AKWAREKEMQEF\TRSFF\RGRPDLSTLTHSIVRRRYLAHSGRS HLEPEKQALKRLVBEEPLKMQVDEAASREDKLDLTKKGKRPPT PCSDPERKRFRNSESESGSEASSPDYFGPPAKNGVASRSHTHI KEEMPRRA\SKAVESSDEERGRDLPAQRGEESSEEEEKGYKGI TRKKPVVKKQAPGKASVSRKQAREESEESEAEPVQRTAKKVEGG KGTKSLKESSQESEEILAQKKEQREESEAEEPVQRTAKKVEGG PRTRSNGRRKSAREERSCKQKSQAKRLLGDSDSEEEQKEAASSC DDSGRDEPPVQRKSEDRTCLKGGKRLSGSSEDEEDGGGEPTU KGSRKMARLGSTSGEESDLEREVSDSEAGGGPQGERKNRSKKS SRKGRTRSSSSSSDSPEAKGGKAGSGRRGEDHPAVMRLKRYIT ACGAHIRNYKKLLGSCCSHKERLSILRAELEALGMKGTPSLGKCF ALKEQREEAAEVASLDVANIISGSGRPRRTAWNPLGEAAPPGE LYRRTLDSDEERPRRPAPPDMSHMRGIISSDGESN 6961 340 1646 RPWSSPTMKPNFSLRRIFINLNCWGIPYLSKHRADRMRRLGDFI NQESFDLALLEEVWSBCDFGYLRQKLSFTYPAAHHFRSGIIGSG SGMVLNAYVTHLHAEYNRQKDIYLAKRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRIPFKGSEGG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFFTI TTGFDPHRGTPLSDHEALMATLFVRHSPPQONPSSTHGP\AEKS	1			PWI.GUPDOTPROVYDNATE EVOLET TEGUP PURPOT OF THE PROVINCE TO TH
LYHESMLWAPVMCWBRYPNQLTLSCPAADSEA\SLYWWYLLELG FYLSLLIRLPFDVKRKGGGPSSIKPRPHYDPSTA\DFKEQVII HFVAVILMTFSYSANLLRIGSLVLLLHDSSDYLLBACKMVNYM YQQVCDALFLIFSFVFFYTRLVLFPTQTLYTTYYESISMRGPFI GYYFFNGLLMLLQLHVFWSCLILRMLYSFMKKGQMEKDIRSD EESDSSEAAAAQEPLQLKNGTAGGPRPAPTDGPRSRVAGRLTT RHTTAT 6960 387 2068 AKWAREKEMQEF\TRSFF\RGRPDLSTLTHSIVRRRYLAHSGRS HLEPBEKQALKRLVBEEPLKMQVDEAASREDKLDLTKKGKRPPT PCSPDERKRFRFNSBESGSEASSPDVYGPPAKNGVASRSHTHI KEEMPRA\SKAVEESSDEERQRDLPAORGEESSEEEKGYKGI TRKKPVVKKQAPGKASVSRKQAREESSEESEAPPVQRTAKKVEGS KGTKSLKESRQESEEILAQKKEQREEEVEEEKEEDEKGDWI PRTRSNGRRKSAREERSCKQKSQAKRLLGBDSEEEQKEAASSC UDGGRDREPPVQRKSEDRTQLKGGKRLGGSSEDEEDSGKGEPTI KGSRKMARLGSTSGEESDLEREVSDSEAGGGPQERKNRSSKKS SRKGRTRSSSSSDGSPEAKGGKAGSGRRGEDHPAVMRLKRYIH ACGAIRNYKKLLGSCCSHKERLSILRAELEALGMKGTPSLGKCF ALKEQREEAAEVASLDVANIISGSGPPRRTAMPLGEAAPPGG LYRRTLDSDEERPRPAPPDWSHMRGILSSDGESN 6961 340 1646 RPWSSPTMKPNFSLRLRIFINLNCWGIPYLSKRRADRMRRLGDFI NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIGGG LCVFSKHPIQELTCHIYTLNGYPYMIHHGDWFSGKAVGLUVLHI SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKR ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRIPFKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFETI TTGFDPHRGTPLSDHEALMATLFVRHSPPQONPSSTHGP\AERS	1	1		TI OOTODWEDDDDDDDD OX WINTEDD GIRDY THE CO
FYLSLLIRLPFDVKRKGGGFSSIKPRPHYDPPSTA\DFKEQVII HFVAVILMTFSYSANLRIIGSLVLLLHDSDYLLEACKMYNYM YQQVCDALFLIFSFVFFTRLVLFPTQILYTTYYESISNRGPFI GYYFPNGLLMLLQLLHVFWSCLILRMLYSFMKKGQMEKDIRSDY EESDSSEEAAAAQEPLQLKNGTAGGPRPAPTDGPRSRVAGRLTI RHTTAT AKWAREKEMQEF\TRSFF\RGRPDLSTLTHSIVRRRYLAHSGRS HLEPEEKQALKRLVEEEPLKMQVDEAASREDKLDLTKKGKRPPI PCSDPERKRFFRNSESESGSEASSPDYFGPPAKNGVASRSHTHI KEENPRA\SKAVESSDEERQRDLPAQRGEESSEEEEKGYKGI TRKKPVVKKQAPGKASVSRKQAREESEESEAEPVQFTAKKVEG KGTKSLKESEQESEEILAQKKEQREEVEEEKEEDEEKGDWI PRTRSNGRRKSALERSCKQKSQAKRLLGDSDSEEEQKEAASSC DDSGRDREPPVQRKSEDRTQLKGGKRLSGSSEDEEDSGKGEPTI KGSRKMARLGSTSGEESDLEREVSDSEAGGGPQGERKNRSSKK SRKGRTRSSSSSDGSPEAKGGKAGSGRRGEDHPAVMRLKRYIR ACGAIRNYKKLLGSCCSHKERLSILRAELEALGMKGTPSLGKCI SALKEQREEAAEVASLDVANIISGSGRPRRTAMNPLGBAPPGE LYRRTLDSDEERPRPAPPDWSHMGIISSDCESN 6961 340 1646 RPWSSPTMKPNFSLIKIFNLNCWGIPYLSKHRADRMRRLGDFI NQESPSDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGGC LCVPSKHPIQELTOHIYTLNGYPYMIHHGDWFSGKAVGLUVLHI SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKR ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFFI TTGFDPHRGTPLSDHEALMATLEVRHSPPQQNPSSTHGP\AERS	į.			LVHECHI HA DUMCHDDUDAY OF GGDAAD GAAA
HFVAVILMTFSYSANLLRIGSLVLLLHDSSDYLLEACKMVNYMG YQQVCDALFLIFSVFFYTRLVLFPTQILYTTYYESISNRGPFI GYYFFNGLLMLLQLLHVFWSCLILRMLYSFMKKGQMEKDIRSDN EESDSSEEAAAAQEPLQLKNGTAGGPRPAPTDGPRSRVAGRLTT RHTTAT 6960 387 2068 AKWAREKEMQEF\TRSFF\RGRPDLSTLTHSIVRRRYLAHSGRS HLEPEKQALKRLVEEEPLKMQVDEAASREDKLDLTKKKGKRPFI PCSDPERKFFFNSESESGSEASSPDYFGPPAKNGVASRSHTHI KEENPRRA\SKAVEESSDEERQRDLPAQRGEESSEEEKGYKGI TRKKPVVKKQAPGKASVSRKQAREESEESEAEPVQRTAKKVEGN KGTKSLKESEQESEEILAQKKEQREEEVEEEKEDDEKGDWI PRTRSNGRRKSAREERSCKQKSQAKRLLGDSDSEEEGKEAASC GOBGRDREPPVQRKSEDRTQLKGGKRLSGSSEDEEDSGKGEPPI KGSRKMARLGSTSGEESDLEREVSDSEAGGGPQGERKNRSSKKS SRKGRTRSSSSSDGSPEAKGGKAGSGRRGEDHPAVMRLKRYIF ACGAIRNYKKLLGSCCSHKERLSILRAELEALGMKGTPSLGKCF ALKEQREEAAEVASLDVANIISGSGRPRRRTAWNPLGEAAPPGG LYRRTLDSDEERPRPAPPDWSHMRGIISSDGESN 6961 340 1646 RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFI NQESPDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHI SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKF ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEGG NTMYPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSSPQQNPSSTHGP\AERS TTGFDPHRGTPLSDHEALMATLFVRHSSPQQNPSSTHGP\AERS	l .	İ		BIRESWEWAPVMCWDRIPNQLTESCPAADSEA\SLYWWYLLELG
YQQVCDALFLIFSFVFFYTRLVLFPTQILYTTYYESISNRGPFI GYYFFNGLLMLLQLLHVFWSCLILRMLYSFMKKGQMEKDIRSD EESDSSEAAAAQEPLQLKNGTAGGPRPAPTDGPRSRVAGRLTI RHTTAT 387 2068 AKWAREKEMQEF\TRSFF\RGRPDLSTLTHSIVRRRYLAHSGRS HLEPEEKQALKRLVEEEPLKMQVDEBASREDKLDLTKKGKRPFI PCSDPERKRFRFNSESESGSEASSPDYFGPPAKNGVASRSHTHI KEENPRRA\SKAVEESSDEERQRDLPAQRGEESSEEEEKGYKGI TRKKPVVKKQAPGKASVSRKQAREESEESEAEPVQRTAKKVEGN PRTRSNGRKSAREERSCKQKSQAKRLLGDSDSEEEKGDWI PRTRSNGRKSAREERSCKQKSQAKRLLGDSDSEEEGKEDWI PRTRSNGRKSAREERSCKQKSQAKRLLGDSDSEEGKEDWI KGSRKMARLGSTSGEESDLEREVSDSEAGGGPQGERKNRSSKKS SRKGTTRSSSSSSDSPFAKGGKAGSGRRGEDHPAVMRLKRYII ACGAIRNYKKLLGSCCSHKERLSILRAELEALGMKGTPSLGKCF ALKEQREEAAEVASLDVANIISGSGRPRRTAMNPLGEAAPPGE LYRRTLDSDEERPRPAPPDWSHMRGIISSDGESN 6961 340 1646 RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFI NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSC LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLUVLHI SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKR ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETTDFKGSEEG NTMVPKNCVYSQQELKPFFFGVRIDYVLYKAVSGFYISCKSFEI TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNESSTHGP\ABRE	}			HENNYL MEEGYCANI I BEGGES I KPRPHYDPPSTA DFKEQVIH
GYYFFNGLMLLQLLHVFWSCLILRMLYSFMKKGQMEKDIRSDN EESDSSEEAAAAQEPLQLKNGTAGGPRPAPTDGPRSRVAGRLTT RHTTAT AKWAREKEMQEF\TRSFF\RGRPDLSTLTHSIVRRRYLAHSGRS HLEPEEKQALKRLVEEEPLKMQVDEAASREDKLDLTKKGKRPPP PCSDPERKRFRFNSESESGSEASSPDYFGPPAKNGVASRSHTHI KEENPRRA\SKAVEESSDEERQRDLPAQRGEESSEEEEKGYKGI TRKKPVVKKQAPGKASVSRKQAREESSEESEEEKGYKGI KGTKSLKESEQESEEILAQKKEQREEEVEEEEKEEDEEKGDWI PRTRSNGRRKSAREERSCKQKSQAKRLLGDSDSEEEQKEAASSG DDSGRDREPPVQRKSEDRTQLKGGKRLSGSSEDEEDSGKGEPTI KGSRKMARLGSTSGEESDLEREVSDSEAGGGPQGERKNRSSKKG SRKGRTKSSSSSDSSPEAKGGKAGSGRRGEDHPAVMRLKRYIK ACGAHRNYKKLLGSCCSHKERLSILRAELEALGMKGTPSLGKCI ALKEQREEAAEVASLDVANIISGSGRPRRTAWNPLGEAAPPGE LYRRTLDSDEERPRPAPPDWSHMRGIISSDGESN 6961 340 1646 RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFI NQESFPLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSC LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHH SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMYPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFEI TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNESSTHGP\ABRS	ļ.	1		THE VAN LEWITS ISANGERIGS BY LEGACKMYNYMQ
EESDSSEEAAAAQEPLQLKNGTAGGPRPAPTDGPRSRVAGRLTT RHTTAT AKWAREKEMQEF\TRSFF\RGRPDLSTLTHSIVRRYLAHSGRS HLEPEEKQALKRLVEEEPLKMQVDEAASREDKLDLTKKGKRPPT PCSDPERKRFRPNSESEGSEASSPDYFGPPAKNGVASRSHTHI KEENPRRA\SKAVEESSDEERQRDLPAQRGEESSEEEKGYKGI TRKKPVVKKQAPGKASVSRKQAREESEESEAEPVQRTAKKVEGN KGTKSLKESEQESEEILAQKKEQREEEVEEEKEEDEEKGDWI PRTRSNGRRKSAREERSCKQKSQAKRLLGDSDSEEQKEAASSD DDSGRDREPPVQRKSEDRTQLKGGKRLSGSSEDEEDSGKGEPTI KGSRKMARLGSTSGEESDLEREVSDSEAGGGPQGERKNRSSKKS SRKGRTRSSSSSSDGSPEAKGGKAGSGRRGEDHPAVMRLKRYIF ACGAHRNYKKLLGSCCSHKERLSILRAELEALGMKGTPSLGKCF ALKEQREEAAEVASLDVANIISGSGRPRRTAWNPLGEAAPPGF LYRRTLDSDEERPRPAPPDWSHMRGIISSDGESN 6961 340 1646 RPWSSPTMKPNFSLRIFINLNCWGIPYLSKHRADRMRRLGDFI NQESPDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHI SGMVLNAYVTHLHAEVNRQKDIYLAHRVAQAWELAQFIHHTSKR ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMYPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS				1QQVCDALFLIFSFVFFYTRLVLFPTQILYTTYYESISNRGPFF
RHTTAT 6960 387 2068 AKWAREKEMQEF\TRSFF\RGRPDLSTLTHSIVRRRYLAHSGRS HLEPEEKQALKRLVEEEPLKMQVDEAASREDKLDLTKKGKRPPT PCSDPERKFFRPNSESESGSEASSPDYFGPPAKNGVASRSHTHI KEENPRRA\SKAVEESSDEERQRDLPAQRGEESSEEEEKGYKGI TRKKPVVKKQAPGKASVSRKQAREESEESEAEPVQRTAKKVEGN KGTKSLKESEQESEEEILAQKKEQREEEVEEEEKEEDEEKGDWI PRTRSNGRRKSAREERSCKQKSQAKRLLGDSDSEEEQKEAASSG DDSGRDREPPVQRKSEDRTQLKGGKRLSGSSEDEEDSGKGEPTI KGSRKMARLGSTSGEESDLEREVSDSEAGGGPQGERKNRSSKKS SRKGRTRSSSSSSDGSPEAKGGKAGSGRRGEDHPAVMRLKRYIF ACGAHRNYKKLLGSCCSHKERLSILRAELEALGMKGTPSLGKCF ALKEQREEAAEVASLDVANIISGSGRPRRTAWNPLGEAAPPGF LYRRTLDSDEERPPAPPDWSHMRGIISSDGESN 6961 340 1646 RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFI NQESPDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHI SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKR ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS	ł			GYYFFNGLLMLLQLLHVFWSCLILRMLYSFMKKGQMEKDIRSDV
AKWAREKEMQEF\TRSFF\RGRPDLSTLITHSIVRRRYLAHSGRE HLEPEEKQALKRLVEEEPLKMQVDEAASREDKLDLTKKGKRPPT PCSDPERKRFRPNSESESGSEASSPDYFGPPAKNGVASRSHTHI KEENPRRA\SKAVEESSDEERQRDLPAQRGEESSEEEEKGYKGI TRKKPVVKKQAPGKASVSRKQAREESEESEAEPVQRTAKKVEGN KGTKSLKESEQESEEILLAQKKEQREEEVEEEEKEEDEEKGDWH PRTRSNGRRKSAREERSCKQKSQAKRLLGDSDSEEEQKEAASSC DDSGRDREPPVQRKSEDRTQLKGGKRLSGSSEDEEDSGKGEPTM KGSRKMARLGSTSGEESDLEREVSDSEAGGGPQGERKNRSSKKS SRKGRTRSSSSSDGSPEAKGGKAGSGRRGEDHPAVMRLKRYIFF ACGAHRNYKKLLGSCCSHKERLSILRAELEALGMKGTPSLCKCFF ALKEQREEAAEVASLDVANIISGSGRPRRTAWNPLGEAAPPGFF LYRRTLDSDEERPRPAPPDWSHMRGIISSDGESN 6961 340 1646 RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFI NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSC LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHI SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKFF ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCTVYSQQELKFFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGF\AERS				EESDSSEEAAAAQEPLQLKNGTAGGPRPAPTDGPRSRVAGRLTN
HLEPEEKQALKRLVBEEPLKMQVDEAASREDKLDLTKKGKRPPT PCSDPERKRFRPNSESESGEASSPDYFGPPAKNGVASRSHTHI KEENPRRA\SKAVEESSDEERQRDLPAQRGEESSEEEEKGYKGI TRKKPVVKKQAPGKASVSRKQAREESEESEAEPVQRTAKKVEGN KGTKSLKESEQESEEEILAQKKEQREEEVEEEKEEDEEKGDWI PRTRSNGRRKSAREERSCKQKSQAKRLLGDSDSEEGQKEAASSO DDSGRDREPPVQRKSEDRTQLKGGKRLSGSSEDEEDSGKGEPTM KGSRKMARLGSTSGEESDLEREVSDSEAGGGPQGERKNRSSKKS SRKGRTRSSSSSSDGSPEAKGGKAGSGRRGEDHPAVMRLKRYIFF ACGAHIRNYKKLLGSCCSHKERLSILRAELEALGMKGTPSLGKCFF ALKEQREEAAEVASLDVANIISGSGRPRRRTAWNPLGEAAPPGEF LYRRTLDSDEERPRPAPPDWSHMRGIISSDGESN RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFI NQESPDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHI SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKM ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFEI TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGF\AERS	6960	397	2000	
PCSDPERKRFRPNSESESGSEASSPDYFGPPAKNGVASRSHTHI KEENPRRA\SKAVEESDEERQRDLPAQRGEESSEEEKGYKGI TRKKPVVKKQAPGKASVSRKQAREESEESESEEPVQRTAKKVEGI KGTKSLKESEQESEEILLAQKKEQREEEVEEEEKEEDEEKGDWI PRTRSNGRRKSAREERSCKQKSQAKRLLGDSDSEEEQKEAASSC DDSGRDREPPVQRKSEDRTQLKGGKRLSGSSEDEEDSGKGEPTI KGSRKMARLGSTSGEESDLEREVSDSEAGGGPQGERKNRSSKKS SRKGRTRSSSSSDGSPEAKGGKAGSGRRGEDHPAVMRLKRYIF ACGAHRNYKKLLGSCCSHKERLSILRAELEALGMKGTPSLCKCF ALKEQREEAAEVASLDVANIISGSGRPRRTAWNPLGEAAPPGF LYRRTLDSDEERPRPAPPDWSHMRGIISSDGESN 6961 340 1646 RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFI NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSC LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHI SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKF ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGF\AERS	1 3380	100	∠∪68	AKWAKEKEMQEF\TRSFF\RGRPDLSTLTHSIVRRRYLAHSGRS
KEENPRRA\SKAVEESSDEERQRDLPAQRGEESSEEEEKGYKGI TRKKPVVKKQAPGKASVSRKQAREESEESEAEPVQRTAKKVEGR KGTKSLKESEQESEEILAQKKEQREEEVEEEEKEEDEEKGDWI PRTRSNGRRKSAREERSCKQKSQAKRLLGDSDSEEQKEAASSG DDSGRDREPPVQRKSEDRTQLKGGKRLSGSSEDEEDSGKGEPTI KGSRKMARLGSTSGEESDLEREVSDSEAGGGPQGERKNRSSKKS SRKGRTRSSSSSSDGSPEAKGGKAGSGRRGEDHPAVMRLKRYIF ACGAHIRNYKKLLGSCCSHKERLSILRAELEALGMKGTPSLGKCF ALKEQREEAAEVASLDVANIISGSGRPRRTAWNPLGEAAPPGE LYRRTLDSDEERPRPAPPDWSHMRGIISSDGESN NQESPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFI NQESPDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHI SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKF ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFETI TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGF\AERS	1	ĺ	Ì	HLEFELKQALKRIVEEEPLKMQVDEAASREDKLDLTKKGKRPPT
TRKKPVVKKQAPGKASVSRKQAREESEESEAEPVQRTAKKVEGN KGTKSLKESEQESEEILAQKKEQREEVEEEEKEEDEEKGDWI PRTRSNGRRKSAREERSCKQKSQAKRLIGDSDSEEQKEAASSC DDSGRDREPPVQRKSEDRTQLKGGKLSGSSEDEEDSGKGEPTI KGSRKMARLGSTSGEESDLEREVSDSEAGGGPQGERKNRSSKKS SRKGRTRSSSSSSDSPEAKGGKAGSGRRGEDHPAVMRLKRYIF ACGAHRNYKKLLGSCCSHKERLISILRAELEALGMKGTPSLGKCF ALKEQREEAAEVASLDVANIISGSGRPRRTAWNPLGEAAPPGH LYRRTLDSDEERPRPAPPDWSHMRGIISSDGESN 6961 340 1646 RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFI NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSC LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHI SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKH ADDVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKFFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGF\AERS	ł			PCSDPERKRFRFNSESESGSEASSPDYFGPPAKNGVASRSHTHP
KGTKSLKESEQESEEEILAQKKEQREEEVEEEEKEEDEEKGDWI PRTRSNGRRKSAREERSCKQKSQAKRLLGDSDSEEEQKEAASSC DDSGRDREPPVQRKSEDRTQLKGGKRLSGSSEDEEDSGKGEPTY KGSRKMARLGSTSGEESDLEREVSDSEAGGGPQGERKNRSSKKS SRKGRTRSSSSSSDSPEAKGGKAGSGRRGEDHPAVMRLKRYIF ACGAHRNYKKLLGSCCSHKERLSILRAELEALGMKGTPSLGKCF ALKEQREEAAEVASLDVANIISGSGRPRRRTAWNPLGEAAPPGH LYRRTLDSDEERPRPAPPDWSHMRGIISSDGESN 6961 340 1646 RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFI NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSC LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHI SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKH ADDVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKFFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGF\AERS	1			KEENPRRA\SKAVEESSDEERQRDLPAQRGEESSEEEEKGYKGK
PRTRSNGRRKSAREERSCKQKSQAKRLLGDSDSEEEQKEAASSC DDSGRDREPPVQRKSEDRTQLKGGKRLSGSSEDEEDSKGEPTI KGSRKMARLGSTSGEESDLEREVSDSEAGGGPQGERKNRSSKKS SRKGRTRSSSSSDGSPEAKGGKAGSGRRGEDHPAVMRLKRYIF ACGAHRNYKKLLGSCCSHKERLSILRAELEALGMKGTPSLGKCF ALKEQREEAAEVASLDVANIISGSGRPRRTAWNPLGEAAPPGF LYRRTLDSDEERPRPAPPDWSHMRGIISSDGESN 6961 340 1646 RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFI NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSC LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHI SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKF ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKFFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGF\AERS	ł	J		TRKKPVVKKQAPGKASVSRKQAREESEESEAEPVQRTAKKVEGN
DDSGRDREPPVQRKSEDRTQLKGGKRLSGSSEDEEDSGKGEPTA KGSRKMARLGSTSGEESDLEREVSDSEAGGPQGERKNRSSKKS SRKGRTRSSSSSSDSPEAKGGKAGSGRRGEDHPAVMRIKRYIF ACGAHRNYKKLLGSCCSHKERLSILRAELEALGMKGTPSLGKCF ALKEQREEAAEVASLDVANIISGSGRPRRRTAWNPLGEAAPPGF LYRRTLDSDEERPRPAPPDWSHMRGIISSDGESN 6961 340 1646 RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFI NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHI SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKF ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKFFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGF\AERS				KGTKSLKESEQESEEILAQKKEQREEEVEEEEKEEDEEKGDWK
KGSRKMARLGSTSGEESDLEREVSDSEAGGGPQGERKNRSSKKS SRKGRTRSSSSSDGSPEAKGGKAGSGRRGEDHPAVMRLKRYIF ACGAHRNYKKLLGSCCSHKERLSILRAELEALGMKGTPSLCKCF ALKEQREEAAEVASLDVANIISGSGRPRRTAWNPLGEAAPPGF LYRRTLDSDEERPRPAPPDWSHMRGIISSDGESN 6961 340 1646 RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFI NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHI SGMVLNAVYTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKF ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGF\AERS	1			PRIRSNGRRKSAREERSCKQKSQAKRLLGDSDSEEEQKEAASSG
SRKGRTRSSSSSDGSPEAKGGKAGSGRRGEDHPAVMRLKRYIE ACGAHRNYKKLLGSCCSHKERLSILRAELEALGMKGTPSLGKCF ALKEQREEAAEVASLDVANIISGSGRPRRTAWNPLGEAAPPGE LYRRTLDSDEERPRPAPPDWSHMRGIISSDGESN 6961 340 1646 RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFI NQESPDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHI SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKE ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGF\AERS				DDSGRDREPPVQRKSEDRTQLKGGKRLSGSSEDEEDSGKGEPTA
ACGAHRNYKKLLGSCCSHKERLSILRAELEALGMKGTPSLGKCF ALKEQREEAAEVASLDVANIISGSGRPRRRTAWNPLGEAAPPGE LYRRTLDSDEERPRAPPDWSHMRGIISSDGESN 6961 340 1646 RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFI NQESPDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLDVLHI SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKH ADVVLLCGDLMMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGF\AERS	1			KGSKKMARLGSTSGEESDLEREVSDSEAGGGPQGERKNRSSKKS
ALKEQREEAAEVASLDVANIISGSGRPRRRTAWNPLGEAAPPGE LYRRTLDSDEERPRAPPDWSHMRGIISSDGESN 6961 340 1646 RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFI NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLDVLHI SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKH ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGF\AERS				SKKGKTRSSSSSSDGSPEAKGGKAGSGRRGEDHPAVMRLKRYIR
LYRRTLDSDEERPRPAPPDWSHMRGIISSDGESN 6961 340 1646 RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFI NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSC LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHI SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGF\AERS				ACGAIRNYKKLLGSCCSHKERLSILRAELEALGMKGTPSLGKCR
6961 340 1646 RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFI NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHI SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGF\AERS	į l			
NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHI SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGF\AERS	6961	340	1606	
LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHI SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS	0,01	OFC	1040	RPWSSPIMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFL
SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS				NOESFOLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG
ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS				ECVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL
NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS	1	i i		ADVALL CODE NAMEDED COOL TANDERS TO BE SEEN THE SERVICE OF THE SER
TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS		i		NTMVPKNCYVSOOFI KDEDEGUCTEREWIGLHDAYLETRDFKGSEEG
PL/MCVCLKEALDGSLGLGMA\OARWWA\TFA\QVIITGIGI\TT	1			TTGEDDUCTDI CDUENT MARI TERRICORDONNO CONTROLLO
	1	ļ		PI. /MCVCI KEAL DOCT CLOWA CARWAA MEAA CHILL
LALLOW ANGERACEA II I MEDIUM II MANGELAL	1 1	1		LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG
LVD AO DET ALUM CEN DEPART VALLE VAL				LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ
6962 340 1646 RPWSSPTMKPNFSLRLRIFNLNCWGTPVLSKHDADDMDDT CDBT	6962	340	1646	RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFL
MI WOOF INNEAR SURLIK I FALMCWGI PILLSKAKADKWKKLGDFI			T040	MORSEDIALI. EPUNICEODEOVI DOVI COMUNA SANCE
I_CVECTUDIOET WASQUICT LKQKLSTTYPARHIFRSGIGSG				NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL
SCHWIND VURHILD EVENDOVDIVE INTHROUGH VINING				SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK
DDWY LINGT V TIBITAD INKOLD I LAHKVAQAWELAQF I HHTSKK	, ,			ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG
NTWO DECOMMENDED COLLEGE OF THE PROPERTY OF TH	, ,			NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET
	i l			TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS
DI. MOUNT WELL DOOR OF DOOR DOOR DOOR OF THE PROPERTY OF THE P	į į	<u> </u>		PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL
LAILOULARGEAGDATTI WARMALTRASYUGLGLILL				LALLCYLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG
I.VDAOPI.O.HUI CHARPADO CONDO VALVA CA	j l	ł		I'ABYOFEI UHAI CEPENUDI CIDEDOT ATTA A COMMACALA TELLA CENTRA CANT
6963 374 2618 RVTPLILKLLKKPKTAENOKASEENETTOPGGSSAKPGLECINE	6963	374	2619	LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ
TITE TO THE PROPERTY OF THE	[~0TO	FAVE CODDAL THOUSE OF THE LANGUAGE CONTROL OF THE C
LUNESPORALIGSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN	į	1		EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN
LHNFSNSVLETINEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS	1	ļ		DEFORM I I CARDINEDOMINIO STATEMENT TO STATE
FFEDALLLIGISDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA	, 1	İ		PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA
LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG	, ·			TRECOMCOCORDERGON OF THE CONTROL OF
TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE	, I	1	ſ	PRESCRIPTION OF THE STATE OF TH
RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL	i l	1	ľ	RSF 13GAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL
STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ	l			SITYLTTHCKKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ
ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV	l	į		THERMESELUTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV
EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE	l		ł	EQUIFORGARUSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE
RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR		1		KSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR
QTETLTSNLRMPLTLTSNTQVIGTAGNTYLPALFTTQPAGSGPK				QTETLTSNLRMPLTLTSNTQVIGTAGNTYLPALFTTQPAGSGPK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	U-Wight dies T. Tlaw in Geglycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid		P=Proline, Q=Glutamine, R=Arginine,
l .	residue of	residue of	S=Serine, T=Threonine, V=Valine,
		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
1			PFLFSLPQPLAGQQTQFVTVSQPGLSTFTAOLPAPOPLASSAGH
			STASGQGEKKPYECTLCNKTFTAKQNYVKHMFVHTGEKPHQCSI
	İ		CWRSFSLKDYLIK\HMVTHTGVRAYQCSICNKRFTQKSSLNVHM
		ſ	RLHRGEKSYECYICKKKFSHKTLLERHVALHSASNGTPPAGTPP
	}		GARAGPPGVVACTEGTTYVCSVCPAKFDQIEQFNDHMRMHVSDG
6964	1	178	SGRPFFFFFSNTDVYFIKKVTNRWTAGSSYKMTRMKSIGKILLL
ļ			QIFIG\NCSMFVLVI
6965	757	208	MARIED LOSSMANDS
1	1 .3.	208	NVFIEPRIQGFMKTSAHPGQKHPDFSMGLLFPLLAALEVCSCGS
	1		SGSLGYNLPQNH\GLLGRNTLVLLGQMRRISPFLCLKDRSDFRF
1	1		PQEKVEVSQLQKA\QAMSFLYDVLQQVFNFSHKALL\CCMEHDL
			PGPTPHFTSSAAGTPGDLLGAGDGRRRSWGQWVIEGSTLALRRY
1			FQESISTLE
6966	820	1867	IITALGVRGMPGCPCPGCGMAGPRLLFLTALALELLGRAGGSQP
ı	{		ALRSRGTATACRLDNKESESWGALLSGERLDTWICSLLGSLMVG
í	1		LSGVFPLLVIPLEMGTMLRSEAGAWRLKQLLSFALGGLLGNVFL
	1		HLLPEAWAYTCSASPGGEGQSLQQQQQLGLWVIAGILTFLALEK
)			/HVPGQQGGDQPGPQQRPHCCCRRAQWRPLSGPAGCRARPRCR
1	{ ·		GP\DIKVSGYLNLLANTIDNFTHGLAVAASFLVSKKIGLLTTMA
		•	ILLHEIPHEVGDFAILLRAGFDRWSAAKLQLSTALGGLLGAGFA
			ICTQSPKGVEETAAWVLPFTSGGFLYIALVNVLPDLLEEEDPW
6967	162	633	CRIDERAMIT DI CA COMMENDATIONALI AGNICATIONALI
1	202	033	GFLPFKYWILDLSASSRMETDCNPMELSSMSGFEEGSELNGFEG
		-	TDMKDMRLEAEAVVNDVLFAVNNMFVSKSLRCADDVAYINVETK
1	ſ		ERNRYCLELTEAGLKVVGYAFDQVDDHLQTPYHETVYSLLDTL\
6968	1	2005	SPAYREAFGKR\LLQRLEALKRDGQS
1 0300	-	2265	RGGGGGRGGPGARERERPGEPERTMEAAAGGRGCFQPHPGLQKT
1			LEQFHLSSMSSLGGPAAFSARWAQEAYKKESAKEAGAAAVPAPV
1	1		PAATEPPPVLHLPAIQPPPPVLPGPFFMPSDRSTERCETVLEGE
1	ļ		TISCFVVGGEKRLCLPQILNSVLRDFSLQQINAVCDELHIYCSR
			CTADQLEILKVMGILPFSAPSCGLITKTDAERLCNALLYGGAYP
			PPCKKELAASLALGLELSERSVRVYHE\CFGKCKGL\LVPELYS
			SPSAACIQCLD\CRLMYPPHKFVVHSHKALENRTCHWGF\DSA\
]	ľ		NWRAYILLSQDYTGKEEQARLGR\CLDDVKEKFDYGNKYKRRVP
ľ			RVSSEPPASIRPKTDDTSSQSPAPSEKDKPSSWLRTLAGSSNKS
			LGCVHPRQRLSAFRPWSPAVSASEKELSPHLPALIRDSFYSYKS
			FETAVAPNVALAPPAQQKVVSSPPCAAAVSRAPEPLATCTQPRK
	l		RKLTVDTPGAPETLAPVAAPEEDKDSEAEVEVESREEFTSSLSS
1			LSSPSFTSSSSAKDLGSPGARALPSAVPDAAAPADAPSGLEAEL
i l			FULDON FOOL DOVEN VEW OF THE THE PROPERTY OF THE POPULATION OF THE
j			EHLRQALEGGLDTKEAKEKFLHEVVKMRVKQEEKLSAALQAKRS
			LHQELEFLRVAKKEKLREATEAKRNLRKEIERLRAENEKKMKEA
1 1			NESRLRLKRELEQARQARVCDKGCEAGRLRAKYSAQIEDLQVKL
1	 		QHAEADREQLRADLLREREAREHLEK\VVK\ELQEQLWPRARPE
h			AAGSEG\AAELEP
6969	1855	118	AGTMHGRLKVKTSEEQAEAKRLEREQKLKLYQSATQAVFQKRQA
1	Į.		GELDESVLELTSQILGANPDFATLWNCRREVLQQLETQKSPEEL
1			AALVKAELGFLESCLRVNPKSYGTWHHRCWLLGRLPEPNWTREL
1	1		ELCARFLEVDERNFHCWDYRRFVATQAAVPPAEELAFTDSLITR
]	}		NFSNYSSWHYRSCLLPQLHPQPDSGPQGRLPEDVLLKELELVQN
1	1		AFFTDPNDQSAWFYHRWLLGRADPQDALRCLHVSRDEACLTVSF
1	• 1		SPOLINGEDMETI I I MUDDODI TURNIDADADE
1 1	1		SRPLLVGSRMEILLLMVDDSPLIVEWRTPDGRNRPSHVWLCDLP
1	ļ		AASLNDQLPQHTFRVIWTAGDVQKECVLLKGRQEGWCRDSTTDE
1	İ		QLFRCELSVEKSTVLQSELESCKELQELEPENKWCL\LTIILLM
}			RALDPLLYEKETLQYFQTLK\AWDPKRATY\LDDLRSKFLLENS
į į	1		VLKMEYAEVRVLHLAHKDLTVLCHLEQLLLVTHLDLSHNRLRTL
]	į		PPALAALRCLEDPPPRT\VLQASDNAIESLDGVTNLPRLOELLL
j i	I		CNNRLQQPAVLQPLASCPRLVLLNLQGNPLCQAVGILEQLAELL
			PSVSSVLT

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6970	3	1528	SFPPLLSSPSAVGEGKVAVAAPCPGRSECARAKMAYIOLEPLNE
"		2000	GFLSRISGLLLCRWTCRHCCQKCYESSCCQSSEDEVEILGPFPA
			QTPPWLMASRSSDKDGDSVHTASEVPLTPRTNSPDGRRSSSDTS
	}		KSTYSLTRRISSLESRRPSSPLIDIKPIEFGVLSAKKEPIOPSV
1	J.		LRRTYNPDDYFRKFEPHLYSLDSNSDDVDSLTDEEILSKYOLGM
			LHFSTQYDLLHNHLTVRVIEARDLPPPISHDGSRQDMAHSNPYV
	1		KICLLPDQKNSKQTGVKRKTQKPVFEERYTFEIPFLEAQRRTLL
			LTVVDFDKFSRHCVIGKVSVPLCEVDLVKGGHWWKALIPSSQNE
j	1		VELGELLLSLNYLPSAGRLNVDVIRAKQLLQTDVSQGSDPFVKI
1			QLVHGLKLVKTKKTSFLRGTIDPFYNESFSFKVPQEELENASLV
i	Ì		FTVFGHNMKSSNDFIGRIVIG\QYSSGP\SEPNHWRRMLNTHRT
	1		AVEOWHSLRSRAECDRVSPASLEVT
6971	37	3702	ACFYVPGSRSFKLIPRHGLVNMGRSGKLPSGVSAKLKRWKKGHS
	-		SDSNPAICRHRQAARSRFFSRPSGRSDLTVDAVKLHNELQSGSL
1	i		RLGKSEAPETPMEEEAELVLTEKSSGTFLSGLSDCTNVTFSKVO
	İ		RFWESNSAAHKEICAVLAAVTEVIRSQGGKETETEYFAALIRKA
1			AQHGVCSVLKGSEFMFEKAPAHHPAAISTAKFCIQEIEKSGGSK
į			EATTTLHMLTLLKDLLPCFPEGLVKSCSETLLRVMTLSHVLVTA
			CAMQAFHSLFHARPGLSTLSAELNAQIITALYDYVPSENDLOPL
ſ	[LAWLKVMEKAHINLVRLQWDLGLGHLPRFFGTAVTCLLSPHSOV
İ			LTAATQSLKEILKECVAPHMADIGSVTSSASGPAQSVAKMFRAV
			EEGLTYKFHAAWSSVLQLLCVFFEACGRQAHPVMRKCLQSLCDL
			RLSPHFPHTAALDQAVGAAVTSMGPEVVLQAVPLEIDGSEETLD
	f		FPRSWLLPVIRDHVQETRLGFFTTYFLPLANTLKSKAMDLAOAG
			STVESKIYDTLQWQMWTLLPGFCTRPTDVAISPKGLARTLGMAI
			SERPDLRVTVCQALRTLITKGCQAEADRAEVSRFAKNFLPILFN
1]		LYGQPVAAGDTPAPRRAVLETIRTYLTITDTQLVNSLLEKASEK
	ļ		VLDPASSDFTRLSVLDLVVALAPCADEAAISKLYSTIRPYLESK
	i	,	AHGVQKKAYRVLEEVCASPQGPGALFVQSHLEDLKKTLLDSLRS
1	}		TSSPAKRPRLKCLLHIVRKLSAEHKEFITALIPEVILCTKEVSV
Ì			GARKNAFALLVEMGHAFLRFGSNQEEALQCYLVLIYPGLVGAVT
			MVSCSILALTHLLFEFKGLMGTSTVEQLLENVCLLLASRTRDVV
1			KSALGFIKVAVTVMDVAHLAKHVQLVMEAIGKLSDDMRRHFRMK
1			LRNLFT\KFIPK\FGILTWGKKAVGPKEYHRVLVNIRKAEARAK
ı			RHRALSQAAVEEEEEEEEEEEPAQGKGDSIEEILADSEDEEDNE
1			EEERSRGKEQRKLARQRSRAWLKEGGGDEPLNFLDPKVAQRVLA
1	S		TQPGPGRGRKKDHSFKVSADGRLIIREEADGNKMEEEEGAKGED
		ii	EEMADPMEDVIIRNKKHQKLKHQKEAEEEELEIPPQYQAGGSGI
1			HRPVAKKAMPGAEYKAKKAKGDVKKKGRPDPYAYIPLNRSKLNR
L		L	RKKMKLQGQFKGLVKAAQRGSQVGHKNRRKDRRP
6972	2179	973	PGGAILLPLWRRTRPREATVPRGAAQRGRARSAEGRIPSSQSPS
1			PAEAGGATRSPPPRPPRPARPPGPSAPPLLRSDAGPGATVSAAA
1			AAATERARRGATMGAQLSTLGHMVLFPVWFLYSLLMKLFQRSTP
l	j l		AITLESPDIKYPLRLIDREIISHDTRRFRFALPSPQHILGLPVG
			QHIYLSARIDGNLVVRPYTPISSDDDKGFVDLVIKVYFKDTHPK
1			FPAGGKMSQYLESMQIGDTIEFRGPSGLLVYQGKGKFAIRPDKK
			SNPIIRTVKSVGMIAGGTGITPMLQVIRAIMKDPDDHTVCHLLF
1]		ANOTEKDILLRPELEELRNKHSARFKLWYTLDRAFEAWDYGOG\
1			FVNEEMIRDHLPPPE\EEPLVLMCGPPPMIQYACLPNL\DHVGH
1			PTERCFVF
6973	1	1964	LQPRCAHRGLRAQKCGRPAPGVDAMVLCPVIGKLLHKRVVLASA
1			SPRRQEILSNAGLRFEVVPSKFKEKLDKASFATPYGYAMETAKQ
1	[KALEVANRLYQKDLRAPDVVIGADTIVTVGGLILEKPVDKQDAY
}			RMLSRFE/SGREHSVFTGVAIVHCSSKDHQLDTRVSEFYEETKV
1	[KFSELSEELLWEYVHSGEPMDKAGGYGIQALGGMLVESVHGDFL
1			NVVGFPLNHFCKOLVKLYYPPRPEDLRRSVKHDSIPAADTFEDL
	L	·····	TOTAL ENGINEERING VARIOUS FRADIFIED

SEO Predicted in uncleotide location (action in uncleotide location (corresponding to first almo acid amino acid amino acid amino acid amino acid amino acid amino acid sequence sequen				
Degranding Courseponding	SEQ	10	Predicted end	Amino acid segment containing signal pentide
Cotation Corresponding Corresponding Corresponding Corresponding Coffice Corresponding Coffice Cof	1		nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
Corresponding to first anino acid tresidue of maino acid residue of anino acid sequence anino acid sequence seq	NO:	3	location	Glutamic Acid, F=Phenylalanine, G=Glycine
to first amino acid residue of residue of residue of residue of amino acid residue of amino acid sequence ##Proline, Q-Gultamine, %-Arginine, \$-Serine, T-Threonine, w-Valline, ##Proline, Q-Gultamine, X-Unknown, *-Stop Codon, /-possible nucleotide deletion, -> **Proline, Q-Gultamine, K-Unknown, *-Stop Codon, /-possible nucleotide deletion, -> **Proline, Q-Gultamine, K-Unknown, *-Stop PPPTRIBLIE [GENERAL Nature PPPTRIBLIE [GENERAL Nature PPPTRIBLIE [GENERAL Nature PPPTRIBLIE [GENERAL Nature PPPTRIBLIE [GENERAL Nature PPPTRIBLIE [GENERAL Nature PPPTRIBLIE [GENERAL Nature PPPTRIBLIE [GENERAL Nature PPPTRIBLIE [GENERAL Nature PPPTRIBLIE [GENERAL Nature PPPTRIBLIE [GENERAL Nature PPPTRIBLIE [GENERAL Nature PPPTRIBLIE [GENERAL Nature PPPTRIBLIE [GENERAL Nature PPPTRIBLIE [GENERAL Nature PPPTRIBLIE [GENERAL Nature PPPTRIBLIE [GENERAL Nature PPPTRIBLIE [GENERAL Nature PPPTRIBLIE PPPTRIBLIE [GENERAL Nature PPPTRIBLIE [GENERAL Nature PPTRIBLIE PPTRIBLIE [GENERAL Nature PPTRIBLIE PPTRIBLIE [GENERAL Nature PPTRIBLIE PPTRIBLIE [GENERAL Nature PPTRIBLIE PPTRIBLIE [GENERAL Nature PPTRIBLIE PPTRIBLIE [GENERAL Nature PPTRIBLIE	İ			H=Histidine, I=Isoleucine, K=Lvsine.
amino acid residue of amino acid residue of amino acid	1			L=Leucine, M=Methionine, N=Asparagine,
residue of amino acid sequence sequ	-]		amino acid	P=Proline, Q=Glutamine, R=Arginine,
### ### ### ### ### ### ### ### ### ##			residue of	S=Serine, T=Threonine, V=Valine,
sequence Codon, /-possible nucleotide deletion		i	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
SPUNGGESPTOPRIORASSREAMAGEAGATAGARACHTEFTLP PPPTRLIELIESPHLSKGLLTACKKKVPDLIKDEAPQKADIAS KVOASACCHERLDICAMAGLEKTEQGYSTHATVILASDE YSLHGTHMINDLIWLIFYLEARREGTKOHHRALGKKAEDLF ODAYYGSPETRIRMAHHGILKKTEQGYSTHANVILASDE YSLHGTHMINDLIWLIFYLEARREGTKOHHRALGKKAEDLF ODAYYGSPETRIRMAHHGIKKTKATQVATANSFRSSACUV HEFAAGDFERPDLESAELTYLCKIHLDWEDRIKSPRSSACUV HEFAAGDFERPDLESAELTYLCKIHLDWENKLISKVRSSC KPGAGLLLVETLLDEEKKVAGRALMGSLINHLVQTEGKERSLEY CCLLEHLERFONDUSVILGULAIL \ PREMISTRICTACY CALLEHLERFONDUSVILGULAIL \ \text{PREMISTRICTACY CALLEHLERFONDUSVILGULAIL \ \text{PREMISTRICTACY CALLEHLERFONDUSVILGULAIL \ \text{PREMISTRICTACY CALLEHLER \ \text{PREMISTRICTACY CALLEHLER \ \text{PREMISTRICTACY CALLEHLER \ \text{PREMISTRICTACY CALLEHLER \ \text{PREMISTRICTACY CALLEHLER \ \text{PREMISTRICTACY CALLEHLER \ \text{PREMISTRICTACY CALLEHLER \ \text{PREMISTRICTACY CALLEHLER \ \text{PREMISTRICTACY CALLEHLER \ \text{PREMISTRICTACY CALLEHLER \ \text{PREMISTRICTACY CALLEHLER \ \text{PREMISTRICTACY CALLEHLER \ \text{PREMISTRICTACY CALLEHLER \ \ \text{PREMISTRICTACY CALLEHLER \ \ \text{PREMISTRICTACY CALLEHLER \ \ \text{PREMISTRICTACY CALLEHLER \ \ \text{PREMISTRICTACY CALLEHLER \ \ \text{PREMISTRICTACY CALLEHLER \ \ \text{PREMISTRICTACY CALLEHLER \ \ \text{PREMISTRICTACY \ \text{PREMISTRICTACY \ \ \text{PREMISTRICT	})	sequence	Codon, /=possible nucleotide deletion.
SDVEGGGSEPTORDASSRDERARGEGGGTARABCHRITETION PPEPTRILLEI ISPHLIKGUITACKLKVPULKORAPOKADATAS KVDASAGCMERILDI ICAMGGLEKTEOGYSNTETANVYLASDGE YSLIGPIMINDILUMILPTILE FARRESTORAPICKARDLIV ODAYYGSPETELREMRAHIGHTKLTACQVATAFNISHSSACUV GGCTGALARELREYPROVVPUPDDI ILEHARDIGKRABLIV HFAAGDFFRDEPSBELVVLCRILHDPDDKVHRLISHSSACUV GGCTGALARELREYPROVVPUPDDI ILEHAPPOPGORAVO HFAAGDFFRDEPSBELVVLCRILHDPDDKVHRLISHSSACUV GCLLELHGEHOVOVVHLIGVUDAILA PPKMPPBCADACGI. 6974 3082 2172 RSCAAFASFSAFPLELEAPPGHREYPSGAVTERGCALSUK LIAARPGLGTKYQATMVKTT.PALCILTAGHRVQSLETBAPLGV SLPPNIVPPTTIVTSSGPONDATASSPONTENVIPVTATASP TSLLIFNISHSTUTSOPTORAPTAPESPTISHS TSLLIFNISHSTUTSOPTORAPTAPESPTISHS TSLLIFNISHSTUTSOPTORAPTAPESPTISHS TSLIFNISHSTUTSOPTORAPTAPESPTISHSSSSINT PTSRATABEVPQCKTPPTTVASGAPPTILE PRESSISHS STSPPEVPSASVTTNISSTVTSOPTORAPTAPESPTISHSSISSIS STSPPEVPSASVTTNISSTVTSOPTORAPTAPESPTISHSSISSIS STSPPEVPSASVTTNISSTVTSOPTORAPTAPESPTISHSSISSIS STSPPEVPSASVTTNISSTVTSOPTORAPTAPESPTISHSSSSSINT PSHATABEVPQCKTPPTTVASGAPPTILHTPRESSISSIST PSHATABEVPGCKTPTTAMPERTISHTSPHATESPTORAPTAPESPTISHSSISSIST SLEPANOPOPPTV-LASAVEPTILHTPRESSISSIST SLEPANOPOPPTV-LASAVEPTILHTPRESSISSIST SLEPANOPOPPTV-LASAVEPTILHTPRESSISSIST SLEPANOPOPPTV-LASAVEPTILHTPRESSISSIST SLEPANOPOPPTV-LASAVEPTILHTPRESSISSIST SLEPANOPOPPTV-LASAVEPTILHTPRESSISTEM RELOTELSGELOVELING ANTACKTORAPTAPESPTISHSSSSSIST SLEPANOPOPPTV-LASAVEPTILHTPRESSISTIST SLEPANOPOPPTV-LASAVEPTILHTPRESSISTIST SLEPANOPOPPTV-LASAVEPTILHTPRESSISTIST SLEPANOPOPPTV-LASAVEPTILHTPRESSISTIST SLEPANOPOPPTV-LASAVEPTILHTPRESSISTIST SLEPANOPOPPTV-LASAVEPTILHTPRESSISTIST SLEPANOPOPPTV-LASAVEPTILHTPRESSISTIST SLEPANOPOPPTV-LASAVEPTILHTPRESSISTIST SLEPANOPOPPTV-LASAVEPTILHTPRESSISTIST SLEPANOPOPPTV-LASAVEPTILHTPRESSISTIST SLEPANOPOPPTV-LASAVEROPPT-LASAVEROP	L	sequence	,	\=possible nucleotide insertion)
FPFTRLELIESPHLSKGILTACKKUVPOLIKUSEAPOKABOTAS KVDASACGMERLDICAMGLEKKTEGGYSTHATVYLLASOE YSLHIGTHIMINDLTWILFTYLERATREGTMOHHRALGKKAEDLF ODAYYOSPETELRYMANIGHTKILTACQVATRISAFSSACUV GGCTGALARELAREYPRMQVTVPDLDDIIELAAHROPPEGDAVO HEFAADDFROPLDESAELTVLCKIHLDWDRDKISAFSSACUV CHEHAGHOVOVHLIGGVLCKIHLDWDRALGKKAEDLF OCALBLHGFHOVOVHLIGGVLCKIHLDWDRAGACSLI KYGAGLLLVETLLDESKRVAORALMOSLMHUVTTGGERSKIGEY CCLLEHLGFHOVOVHLIGGVLDAILV PKWPAGACSLI RSCAAFASFASFFPLELFAPPGSHRSPGSGVATTSACCALSURK LLAARGGLTKYQATMVYKTLACLLITACMAUVGLETSAPLSV SLPTNIVPPTTIWTSSFONTDADTASFSNOTHINNSVLYTASAP TSLLPHNISI ESKREELTSPGSWREOTHTDPSGSTSTGGVH LITTLEBHSLGTPEAGVAATLSQAABEPFILISPOAFASSPSL STSPEWFSASVTINNSSTVTSTOPTOAPTASFSTESSSHFT FTSHATABPVPQEKTPPTTVSGKVMCELIMBT\PPPTAFASFSSSL STSPEWFSASVTINNSSTVTSTOPTOAPTASFTESSSSHFT PTSHATABPVPQEKTPPTTVSGKVMCELIMBT\PPPTAFASPSSL SLPPAOOPPPTVL-LSAVPFFILINVPHANGSGGDKYKLJSKGEL KELLQTELSGFLDVKELML*ATEALKTFEBA*KSBFIQCSSSRS SLPPAOOPPPTVL-LSAVPFFILINPPHALBEGODKYKLJSKGEL KELLQTELSGFLDVKELML*ATEALKTFEBA*KSBFIQCSSSRS SLPPAOOPPPTVL-LSAVPFFILINPPHALBEGODKYKLJSKGEL KELLQTELSGFLDVKELML*ATEALKTFEBA*KSBFIQCSSSRS SLPPAOOPPPTVL-LSAVPFFIHIPPLPLEPPGAQNADVADKWM BLDENDGGUPGGFXTUGNSKOMITIGGGGHTALEDFPHTH PKVQEVQVUGVKDDRNGETCACIFLKNOGETTVEBAUDDGKW WYNTODVATIMEGGFCKTUGNSKOMITIGGGGHTALEDFPHTH PKVQEVQVUGVKDDRNGETCACIFLKNOGETTVEBAUTDGKK SIFFKTPRXT UFVTNPTJTTSGKJCKKFKLERGMERHINL**LKQ ACCGLIA 6977 1298 588 SLEINTNLLANGTRKTSFGMCSEPISDNTEDGKGKKLKTPDFA*R ANKKSKHWNSNTVEPPFFFOTOMAVFGSKCFWGABRGHWULKG VYSTOWFFAGGTYSNPTTKSVCSKEKTGHAEVVRUVQDEHMSFF ELLKVWENNHDPTQGMRGGGDHGTQYRSAITYTSAKQMEBALSS KENYQKULSEINGGFGTTSTOFTTATATATATATATATATATATATATATATATATATA				SDVEGGGSEPTQRDAGSRDEKAEAGEAGOATAFAECHRTRETLD
SVELGET MENNDLTMENT_TLEFATERGYSTETANYTLASTORS YSLIGGT MENNDLTMENT_TLEFATERGYSTETANYTLASTORS GGCTGALABELARETERMAMIGHTKLITACQVATAFILLSEFSSACUV GGCTGALABELARETERMAMIGHTKLITACQVATAFILLSEFSSACUV GGCTGALABELARETERMAQDALMOSLMINUOTEKERSIGEY KPGAGLILVETTLIDEEKRAQORALMOSLMINUOTEKERSIGEY OCLLEHIGFHOVOVVHIGGAUDALIA PERMPPRAQAACSI SKARAFASPASPEPELEFSPOSENSPEGATSACCLSUFK LIAARPGIGTKYQATMYTTIPALCILTAGURVOSLUSTAPLSV LIAARPGIGTKYQATMYTTIPALCILTAGURVOSLUSTAPLSV LIAARPGIGTKYQATMYTTIPALCILTAGURVOSLUSTAPLSV LIAARPGIGTKYQATMYTTIPALCILTAGURVOSLUSTAPLSV LIAARPGIGTKYQATMYTTIPASPESPSTESSSTSGOVH LITTLESERSLISPESGENDEGTNTDPSPSGSFSSTGGOVH LITTLESERSLISPESGENDEGTNTDPSPSGSFSSTGGOVH LITTLESERSLISPESGENDEGTNTDPSPGSFSSTGGOVH LITTLESERSLISPESGENDEGTNTDSAMPGTNTDPSPSGSFSSLS STSPPRUFSASVITINISSTVTSTDPTGAPTAPEPSTSSSSSTS STSPRUFSASVITINISSTVTSTDPTGAPTAPEPSTSSSSSTS STSPRUFSASVITINISSTVTSTDPTGAPTAPEPSTSSSSSTSGOVH LITTLESERSLISPEQAGNATICSGARAPT APPEPTINISPEGATISCALES MEDITICAGURV LITTLESERSLISPEQAGNATICSGARAPT APPEPTINISPEGATISCALES MEDITICAGURV LITTLESERSLISPEQAGNATICAGURV SELDENGGGEVPOPEYVVIDAGURVORAUS MEDITICAGURV SELDENGGGEVPOPEYVVIDAALTVACHNISPEGATER MEDITICAGURV WITCHAULANTEGGECILOGRACUM APPERPORTERATODORM WITCHAULANTEGGECILOGRACUM APPERPORTERATODORM WITCHAULANTEGGECILOGRACUM APPERPORTERATODORM WITCHAULANTEGGECILOGRACUM APPERPORTERATODORM WITCHAULANTEGGECILOGRACUM APPERPORTERATODORM WITCHAULANTEGGECILOGRACUM APPERPORTERATODORM WITCHAULANTEGGECILOGRACUM APPERPORTERATORMENT APPERPORTERATOR			J	PFPTRLLELIEGFMLSKGLLTACKLKVFDLLKDEAPOKAADTAS
VSLLEGIMENDLITMINITIANIFITIESTICHHALDKKAEDLE ODAYYOS PETRLETMENMENMENTACOVATHALISESSACOV GGCTGALARELARETPEMOVIVIFILIPII ELAAHFOP PGGDAVO HHAAGDF FROP DE PSASLVIVLERILHUNDKIKLISENVARSC KPGAGLILVETLIDEEKRVAQRALMOSLMILVOTEKKEISLGEY OCLLELHGFHOVOVVHLIGAUDAIL A PROPRAÇAACSI. ESCAPAS PASE PIELFAPESERISEFKROVATSACALSVIK KPGAGLILVETLIDEEKRVAQRALMOSLAMILVOTEKKEISLGEY OCLLELHGFHOVOVVHLIGAUDAIL A VINTENDERPROQACSI. ESCAPAS PASE PIELFAPESERISEFKROVATSACALSVIK KPGAGLILVETLIDEEKRVAQRAVITLERICLITANIVOSLETSAPLSV SLPTINIVPPTTIWTSEFONDETTIVROVSLETSAPLSV SLPTINIVPPTTIWTSEFONDETTIVROPP PGOFS STOGOVH LITTLEEHSLGTPERGVAATILEGAAEPTILISPOAPASSESSI. SLPTAKATAEVVPOEKTPPTIVASKWEGLIDMET, PPFPG TSHLATAEVVPOEKTPPTIVASKWEGLIDMET, PPFPG FTSHLATAEVVPOEKTPPTIVASKWEGLIDMET, PPFPG KELLOTTELSGELDVKEHME.*ATREALSTREEA*KEPTILGESSSRS SLPPARQIPPTIL*ISAVPPPTHLEHLIPPOAGROVATUKKKEEL ELEMENDGEVOPOEVVLIVAALITVACHMENFENS 6976 1216 970 GCQL*VAYGTTENSFVTFAHFPEDTVECKAESVGRIMPHTEART MINEASTLIAKLNITGEGLICTGYCVMIGHOKTERAVDOKK WITGOVATHNEGGEKIVORSKUMILRGGENIYPAELDEFHTH PKVOEVQVVGKDERMGESICACIRLKOGENTEVELELDFFHTH PKVOEVQVVGKDERMGESICACIRLKOGENTEVELELDFFHTH PKVOEVQVVGKDERMGESICACIRLKOGENTEVELIKAFTDEFAK ANKKSHHHVONNTVEPFPECTOMAVFGMGFMAENKFWLIK VYSTOVGFAGGYTINTYKEVCSSKTGHAEVVRVVOOPEHMSFE ELIKVPERMHPTOGRAGONHOTOYRSALVINOOPEHMSFE ELIKVPERMHPTOGRAGONHOTOYRSALVINOOPEHMSFE ELIKVPERMHPTOGRAGONHOTOYRSALVINOOPEHMSFE ELIKVPERMHPTOGRAGONHOTOYRSALVINOOPEHMSFE ELIKVPERMHPTOGRAGONHOTOYRSALVINOOPEHMSFE ELIKVPERMHPTOGRAGONHOTOYRSALVINOOPEHMSFE ELIKVPERMHPTOGRAGONHOTOYRSALVINOOPEHMSFE ELIKVPERMHPTOGRAGONHOTOYRSALVINOOPEHMSFE ELIKVPERMHPTOGRAGONHOTOYRSALVINOOPEHMSFE ELIKVPERMHPTOGRAGONHOTOYRSALVINOOPEHMSFE ELIKVPERMHPTOGRAGONHOTOYRSALVINOOPEHMSFE ELIKVPERMHPTOGRAGONHOTOYRSALVINOOPEHMSFE ELIKVPERMHPTOGRAGONHOTOYRSALVINOOPEHMSFE ELIKVPERMHPTOGRAGONHOTOYRSALVINOOPEHMSFE ELIKVPERMHPTOGRAGONHOTOYROOPHOTOYLICUM ORGONATAESSALVINOOPHOTOTICLIMG GGGGAPTICALVINOOPHOTOTICLIMG GGGGAPTICALVINOOPHOTOTICLIMG ORGONATATICALVINOOPHOTOTICLIMG GGGGAPTICALVINOOPHOTOTICLIMGAARSOOPHOTOTICLIMGAARASIG VR	ļ		1	KVDASACGMERLLDICAAMGLLEKTEOGYSNTETANUVLAGDGE
GGCTGALAGELAREPTEMQVTYFILDTIELAHFOPOFGAVO HFRAGDFFRDPLESABLYVLCRILHDWPDNKVIKLLSRVABSC KPGAGLLIVETTLIDEEKRVAQRAMMOSLMYOTGKERSIGEY QCLLELHGFHOVOVVHLGGVLDAIL\PPKWPPPRQAACSL 86974 3082 2172 RSCAAFASFASFPLELFEAPDFSHERBEGSWTASAGCALSVKK LLAARPGLGTKYQATMVYKTLFALCILTAGWRQSLPTSAFLSV SLEPNIVPTTHTSFSONTDATAGESGRTHNSVLTYTASAP TSLLPNIVBTTHTSSONTDATAGESGRTHNSVLTYTASAP TSLLPNIVBTTHTSSONTDATAGESGRTHNSVLTYTASAP TSLLPNIVBTTHTSSONTDATAGESGRTHNSVLTYTASAP TSLLPNIVBTAGESTSONTDATAGESGRTHNSVLTYTASAP TSLLPNIVBTAGESSONTDATAGESGRTHNSVLTYTAGAP TSLLPNIVBTAGESGRTHNSVLTYTAGAPAGESSSST STSPRVFSASVTTNSSTVTTGYTGATAFESPTEESSSOHT FTSHATAFVPQEKTPTTVSGKWGELIDMET\PPFPG 6975 2 500 RFRFTVHCKWALKLETAGETLINVFRAHFSESGEGDKYKLSKKEL KELLQTELSGFLDVKELML*ATEALKTFSEA*KSFTIQCSSSNS SLPPAROTPTVL*SAVPTPHLIPLELLGAGCDKYKLSKKEL KELLQTELSGFLDVKELML*ATEALKTFSEA*KSFTIQCSSSNS SLPPAROTPTVL*SAVPTPHLIPLELLGAGCKDDKYKLSKKEL KELLQTELSGFLDVKELML*ATEALKTFSEA*KSFTIGCSSSNS SLPPAROTPTVL*SAVPTPHLIPLELGAGCKDDKYKLSKKEL KELLQTELSGFLDVKELML*ATEALKTFSEA*KSFTIGCSSSNSTHFTTERRI MNMEASTLAKLNTYSGLCTRGYCVMLGYWGEPOKTERATOG MNMEASTLAKLNTYSGLCTRGYCVMLGYWGEPOKTERATOG MNMEASTLAKLNTYSGLCTRGYCVMLGYWGEPOKTERATOG MNSGATHANDEGGCKIVGNSENDHITGGENTYDAELDFFHTT PKVQEVQVVGVKDDRMSEEICACTIRLKDGEFTTVBEIKAFCKGK VYGTOGFAGGGTSNDTYNEGSENTYNEKARDOKKKKTPDFA*R ANKSKHHVNGNRTVSPFECTOMAVCGCCFWGABRKFWULK VYSTOVGFAGGTSNDTYNEVCYSKTGHAEVWRVVVGEHMSFE ELLKYWENHIDPTOGMRQONDHOTOYRSAITPTSAKQMEAALSS KENYOKUSBEGGFTTTDIREGGTFYVAEDYHQVLSKNNOK VYSTOVGFAGGTSNDTYNEVCSKTGHAEVWRVVVGEHMSFE ELLKYWENHIDPTOGMRQONDHOTOYRSAITPTSAKQMEAALSS KENYOKUSBEGGFTTTDIREGGTFYVAEDYHQVLSKNNOK VGGGGTABAPGTSURGARAMVTRISKERAFQLOOLFKGSG 6979 3917 1146 DEARWGRAVABALLERCEHMSGFPFFFFSSPFDKKLRGTFEDW AGGGGGATAGARMVTRISKERAFQLOOLFKGS LEGGGGYNGCHAMNOKTRIGKRARTVLLOTTGGLKTSLLAG RQAPPSGLOPABPGCGYSPFFTGHAMDHITKGSSLDSCTOL GGEFFSYGYGGTKKKSTNSRFENYGDKARDDVIGGTSLOTTGLKTSLLAG RNAFFFBGFGRKALTVICTTEGEKDVPHAVGLKGR NYAGRWCLEMKWGIAFFICHELGGERAFTVLDCTWYGSARA RNAFFBGFGRYNSGGGGFFRYSTGGGFPTSTTORGSNAFAYS PPEKKFDNORGGGFFRRGGGGGGTORTKRRGCPGARGGFORGG GGGGGMYKGNORGOSFORGTONDNNNNNNGSYNAA POQOP	i			YSLHGFIMHNNDLTWNLFTYLEFAIREGTNOHHRALGKKAEDLE
GGCTGALARELARETYRMOVTYFOLPDITELAAHFOPGGGAVO HHAPAGDFFPDPLESALVUCRIHMUNVIKLISKVARSC KYGAGLILVETLLDEKRVAQRALMOSLMMLVOTEGKERSLGEY OCLLEHGFFOVOVVHIGGUDAIL\PPPEAQACSI. 6974 3082 2172 RSCAAFASFASEPPLEIFAPGSRRSFFGRGVATSAGCALSVRK KYGAGLILVETLLDEKRVAQRAVITLEALCILLARVOSLDTSAGLSVRK SLPTNIVFPTTWTSFONTDATTAGFSRCTHNISVLYPTASAP TSLLFNNISIESREEBITSGSNCHTHNISVLYPTASAP TSLLFNNISIESREEBITSGSNCHTHNISVLYPTASAP TSLLFNNISIESREEBITSGSNCHTHNISVLYPTASAP TSLLFNNISIESREEBITSGSNCHTHNISVLYPTASAP TSLLFNNISIESREEBITSFGSNCHTHNISVLYPTASAP TSLLFNNISIESREEBITSFGSNCHTHNISVLYPTASAP TSLLFNNISIESREEBITSFGSNCHTHNISVLYPTASAP TSLFPNISIESREEBITSFGSNCHTHNISVLYPTASAP TSHATAEVYDOKTPTTVSGKVACKLITMET\PPPPPGG TSTSPFBVTSASVTTHNISTVTTSTOTTCHTEPPTESTSSSCHT FTSHATAEVYDOKTPTTVSGKVACKLITMET\PPPPPG TSTSPFBVTSASVTTHNISTVTTSTOTTCHTEPPTTESTSSCHTYRKEE FTSHATAEVYDOKTPTTVSGKVACKLITMET\PPPPPG TSTSPFBVTSASVTTHNISTVTTSTTTGTCHTTSFTTSTSTTTSTT TSSPFBVTSASVTTHNISTVTSTTTSTCHTTSFTTSTSTTTTSTT TSSPFBVTSASVTTHNISTSTOTTCHTTSTT PKVQEVOVVGKDRMGGETGVALSVGRENGTHTTAGTNITHTERAT PKVQEVOVVGKDRMGGETCACTLRKGGETTVEEIKAPFCKG ISHFKIPKITYFTYNTYFITISGKJOKFKLREOMERILAN-IKQQ TSSFFTSTYTKEVCSSKTGHAEVYRVVJCPHNFFE ELLKYVEKRHUPTGGRGCOKHHGTGYTSAITYTSAKQMEAALSS KRHYQGKVLSEHGFGYTTTIEBGGTTYAEDYTIQOVLSKNIPNG CGGGTGVGCYVGIKK 6978 3242 SPFPRDSRCGCCKGGSLRHTAVAMVEKKBAKQRLOLFKGSG ELKKYVEKRHUPTGGRGCONHHGTGYTSAITYTSAKQMEAALSS KRHYQGKVLSEHGFGPTTTTIEBGGTTYAEDYTIQOVLSKNIPNG CGGGTGVGCYVGIKK GGGGGTARPFTSTUTTIEBGGTTYLSLIMG PARMYTELTYTITICKAGAPPOMPEPTYLSLIMG PARMYTELTYTITICHTICHTAGARAPOMPETYLSLIMG PARMYTELTYTITICHTICHTAGARAPOMPETYLSLIMG RGGGGTAFRAMDURGKKKNINGERGPPFPFPSPFREAGLET AQPPPGLOPHAEPGGYSGPGGAPMOMPTYLSLIMG RGGGGTAFRAMDURGKKKNINGERGPPFPFPSPFREAGLET RGGRATTAGARAMOVRIKKNINGERGPPFPFPSPSPDKCLGCTCHAAPTOGARAPTOGARAPT RGGGGGTTAGARAMOVRIKKNINGERGPPFPFPSPSPDKRCLGCTCHAAPTOGARAPT GRAPPTCHAAPTOGARAMOVRIKHINGETSTOTTSKAGARASTG VRGGRVCTEMINETSTVALIDIARRIKKNINGERGPPFPSPCGARGGCGGGGGTGTTAGARAPTURGGRAAPT GGRAPPTCAGARAMOVRIKHINGETSTAATATAGARAPTURGGRAAPT GGRAPPTCAGARAMOVRIKGGGGGGGGGTGTTAGARAPTURGGRAAPT POOQPPPQCOPPPPQOPPPPQOPPPPGSSRGGGF	}	ļ	1	QDAYYQSPETRLRFMRAMHGMTKLTACOVATAFNLSRFSSACDV
HFRAGDFFRDELPSAELYVLICHDMPDDKYKKLISKEVAGE (PGAGLILVETLIDESKRVAQRAKMSIMMLVOTEKKERSIGEY (PGAGLILVETLIDESKRVAQRAKMSIMMLVOTEKKERSIGEY (PCAGLILVETLIDESKRVAQRAKMSIMMLVOTEKKERSIGEY (PCAGLILVETLIDESKRVAQRAKMSIMMLVOTEKKERSIGEY (PCAGLILVETLIDESLEPPEGSHRBGRVATSAQCALSUFK LLAARPGLGTKVQATMVYKTI.FALCILTACKRVQSLPTEAPLSV SLPYNIVIPTITWTSEPERPEGSHRBGTHNNSUL PYTAAPA TSLLPKNISIESREETISPOSHBGTHNNSUL PYTAAPA TSLLPKNISIESREETISPOSHBGTHNNSUL PYTAAPA TSLLPKNISIESREETISPOSHBGTHNNSUL PYTAAPA TSLLPKNISIESREETISPOSHBGTHTDSPEPGFSSTSGVH LTTTLEEBLGTPERGVAATLSQCAAEPPTILISPQAAFASSESSHT PTSHATAEPVPOKTPFTTVSKCVMCBLIDMET\PPPPPGFSSSSHST FTSHATAEPVPOKTPFTTVSKCVMCBLIDMET\PPPPPGFSSSSHST RELIQTELSGFLDVKELML*ATTAELKTEER*KEFIQCSSKRS SLPPARCIPPPYL*LSGKLDVKELML*ATTAELKTEER*KEFIQCSSKRS SLPPARCIPPPYL*LSGKLDVKELML*ATTAELKTEER*KEFIQCSSKRS SLPPARCIPPPYL*LSGKLDVKELML*ATTAELKTEER*KEFIQCSSKRS SLPPARCIPPPYL*LSGKLOVKELML*ATTAELKTEER*KEFIQCSSKRS SLPPARCIPPPYL*LSGKLOVKELML*ATTAELKTEER*KEFIQCSSKRS SLPPARCIPPPYL*LSGKLOVKENDHITTEKKEFIQCKOKDUKWKM BLDENGDGKVDPGEVVLVAAALTVACNNFKWEBYGKIMPHTEART MNMEAGTILAKLNTPGELCIRGVCVMLGVWGEPQKTERAVDDKW WITGDVAATTNEQGFCKLVGRKDMTIRGKEGVTYBABEHQDDKW WITGDVAATTNEQGFCKLVGRKDMTIRGKGKKKTERAVDDKW WITGDVAATTNEQGFCKLVGRKDMTIRGWGRIKKTERAR MNMEAGTILAKLNTPGELCIRGVCVMLGVWGEPQKTERAVDDKW WITGDVAATTNEQGFCKLVGRKDMTIRGWGRIVAGEPGKTERAVDDKW SISHKYLFKLVJVGVTNYFLTISGKGJCKFKERAVDDCKKKTERAVD ACPGRLA SPIFTINILISNOIRKTSFGWCSEPISONTEDGKGKIKTFDBA*R ANKKSKHHVNGNRTVBFPPEGTOMAVFGMCCPMGRBRKFWULKC VYSTOVGFAGGYTSTTDTRRGGTFYYABCHUGQYLSKWNNGV CGLGGTGVSCPWGIKK SPFFROSRCGCCKGSSLRHTAVAMVKLSKEAKORLOQHISFSG FAIRMGFIPLOTHOTGMRQCMDHGTCYRSAIYPTSAKQMAALSS KRYQKVLSHEHGPGDTTTDTRRGGTFTYABCHUGQYLSKWNNGV CGLGGTGVSCPWGIKK 6979 3917 1146 DERRVGGBAVAAALLSRCCHMSGPPPFFSFPBFRGLGKTGFTFWG ACPPPFGCKGCCKGSSLRHTAVAMVKLSKEAKORLOQHISFG ACPPSGACGCCKGSSCRRYFTHRENERSPCOPAEBEBDDD DTLVAIDTYNCDLHFKVAADRSSGYPLTEGFALWSGARASVG VRRGRVCCHMINESTITRONOPYTOVIKGE NSSGYBRRYEDKRGGFFGFGGFGFGFTGNSGGVFGFGFGGGGGGFGFGGFGGGGGGGGGGGGGGGGG		1		GGCTGALARELAREYPRMQVTVFDLPDIIELAAHFOPPGPOAVO
RPGGGLLVETLIDEERRVAQRAIMSIMMUVTICKERESIGEY		1	l	IHFAAGDFFRDPLPSAELYVLCRILHDWPDDKVHKLLSRVAESC
6974 3082 2172 RSCAAFASPASRPELEAPPGSHRSQNACSLEVRK LLAARPGLGTKYQATMVYKTLELALTAGRGVATSAQCALSVRK LLAARPGLGTKYQATMVYKTLELALTAGRGVQSLPTAAPLSV SLPTNIVPFTITMTSSPONTDATAGSENGTHINDSVLPVTASAP TSLLPKNISIESREETISPGSHWEGTNIPDS-PSGSSTSGGVH LTTILEEHSLGTPEAGVAATLSGNABEPTILISPGAPASSYSL STSPEWFSASVITHSSTVTSOPTGAPTAPESYTESSSCHT FYSHATLARPVPQEKTPPTTVAGKWCELIDMPY,PPPPF FSHATLARPVPQEKTPPTTVAGKWCELIDMPY,PPPPF FSHATLARPVPQEKTPPTTVAGKWCELIDMPY,PPPPF FSHATLARPVPQEKTPPTTVAGKWCELIDMPY,PPPPF GCGD.*VAYGTTENSFYVFAHFSETVESGKREKERIVGSSKREKERPPTLISPGAPAGKOUDAVDKWM KELDENEGGEVOPQEVVLVAALTVACNNFFWENS GCGD.*VAYGTTENSFYTFAHFFEDTVECKAESVGRIMHTEART MNNEAGTLAKLNTRGELCIRGYCVWIGWGEPAGKOUDAVDKWM WYGTOUATNNEGGFGKYGNGSHUFAHEROGRETVUEIKAFCKGK VWYGTOUATNNEGGFGKYGNGSHUFAHEROGRETVEEIKAFCKGK SISHFXIPKYIVVVTNYPLTISKGKIGKEEMSWERTHARAT PKVQEVQVVGVVGVKDDRMGEELCALTRIKGGENTYPAELDFHTT PKVQEVQVVGVVGVKDDRMGEELCALTRIKGGENTYPAELDFHTT PKVQEVQVVGVVGVKDDRMGEELCALTRIKGGENTYPAELDFHTT PKVQEVQVVGVVGVKDDRMGEELCALTRIKGGENTYPAELDFHTT PKVQEVQVVGVVGVKDRMGEELCALTRIKGGENTYPAELDFHTT PKVQEVQVVGVVGVKDRMGEELCALTRIKGGENTYPAELGPHTT PKVQEVQVVGVVGVKDRMGEELCALTRIKGGENTYPAELGPHTT PKVQEVQVVGVVGVKDRMGEELCALTRIKGGENTYPAELGPHTT PKVQEVQVVGVVGVKDRMGEELCALTRIKGGENTYPAELGPHTT PKVQEVQVVGVVGVKDRMGEELCALTRIKGGENTYPAELGPHTT PKVQEVQVVGVVGVKDRMGEELCALTRIKGGENTYPAELGPHTT PKVQEVQVVGVVGVKDRMGEELCALTRIKGGENTYPAELGPHTT PKVQEVQVVGVVGVKDRMGEELCALTRIKGGENTYPAELGPHTT PKVQEVQVGVGVTGNTATTGGGTTTT PKVGEVGVTGVTGTTTTTTTTTTTTTTTTTTTTTTTTTTTT	1	J	}	KPGAGLLLVETLLDEEKRVAORALMOSLNMLVOTEGKERSLGEV
### B994 ### BITTS ### BIT		L	ł	QCLLELHGFHQVQVVHLGGVLDAIL\PPKWPPEAOAACSI.
LLARREGLERKYQATMYKKTJALCILITAGMRQGLFTSALISV SLPTNINIPPTILITSPRONTDADTAS PRONTINDRUSTPYTASASP TSLLPKNIS I ESREEITSPGSNMEGINTPDSPSGFSSTSGGVH LTTILLEHSLGTFEAVAATLISGATATPDSPSGFSSTSGGVH FTSHATAEPVPQEKTAVATLISGATPTLSPASPSFSTSGGVH FTSHATAEPVPQEKTAVATLISGATPTLSPASPSFSTSGGVH FTSHATAEPVPQEKTPPTTVSGKVMCELUMT\PPPFPE SSSDHT FTSHATAEPVPQEKTPPTTVSGKVMCELUMT\PPPFPE SSSDHT FTSHATAEPVPQEKTPPTTVSGKVMCELUMT\PPPFPE KELLQTELSGFLDVKELML-TATEALKTFEEA-KSPI IQCSSSRS SLPPATQPPPYI-LSAVPFPTHLPEHPQAQKDVDAVDKVM ELDENGGGEVDFQEYVVLVAALTVACNNFTPENS 6976 1216 970 GCQL-VAYGTTENS-BYTFAHPEDTVEOKAESVGRIMPHTEARI MNMEAGTLAKLATPGELCIRGYCVMLGYMGEPQKTERAVDDGKW YNTGDUAVTNMEGGFCKIVGRSKUMTIGGENIYPAELDDFPHTH PKVQEVQVVQVVGNDDMGEEICACIRLKDGEFTTVEEIKAFCKGK LISHFKTPKYIVFVTNYPLTISGKIQKFKLREQMERHLML-IKQQ ACPGRLA 6977 1298 588 SLPINTNLLSNQIRKTSFGMCSEPISDNTEDQKGKKLKTPDFA-R ANKSKHNUGMRTVEPPFBECTOMAVFGMGCFWGGREKFWULKS VYSTOVGFAGGTSSPTYKEVCSEKTGHAEVVRVVQVGEHMSFE ELLKVFMEHNDET/GGMRGGNDHGT/SAITPTSAKGMEALASS KENYQKULSEHGFGPITTDIREGGTFYYAEDYHQQYLSKNPNGY CGLGGGVSVCPVGIK 6978 3 242 SPPFRDSRRGGCKGGSLRHTAVAMVKLKEAKQRLQOLFKGSQ FALWGRHENDEVTGGGVSGGVSGVARIPTSAKGMEALASS KENYGKULSEHGFGPITTGHEAGHTPFPFPFSPFDRKGLRGTEPWE AGGGSGATFGARAMDVRLKVNBLRSELQRRGLDTRGLKTELLE RQAALEAEPDDDEREHLDADDEEGRHINEVETTEGSSLEGT AQPPPGLQPHAEPGGYSGFDGHYAMDNITGROFYDTOVIKGE NESGYBRPLEMEQOAYAPEMITKKQGAFTSLLPFBASQLKW DRQGFGSRRPPLEMEQOAYAPEMTKKQGAFTSLLPFBASQLKW DRGGFGRRPLEMEGOAYAPEMTKKQGAFTSLLPFBASQLKW DRGGFGRRPLEMEGOAYAPEMTKKQGAFTSLLPFBASQLKW GGEPFSTYGGTGKKSTNSRFRYGDKFARRODVIGCFADFECON DVELSFTRNGKMMISETRICKGROALYHVLVKNCAVENNF GGRAPPYCS-UPGFTFTQHHDLSERIRGTGRGPQARGG NYAGRWOULIQOATQCLNRLIGINARMWGLRRGG NYAGRWOULIQOATQCLNRLIGINARMWGLRRGGR NYAGRWOULIGOATQCLNRLIGINARMSMRGLRRGG NYAGRWOULIGOATQCLNRLIGINARMSMRGLRRGG NYAGRWOULIGOATQCLNRLIGINARMSMRGLRRGG NYAGRWOULIGOATQCLNRLIGINARMSMRGLRRGG NYAGRWOULIGOATQCLNRLIGINARMSMRGLRRGG NYAGRWOULIGOATQCLNRLIGINARMSMRGLRRGG NYAGRWOULIGOATQCLNRLIGINARMSMRGLRRGG NYAGRWOULIGOATQCLNRLIGGRAGGGGGGGGGTORYHOLNRCGRRGG GGGGGGGGGGGGGGGGTORYHOLNRGGRGRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	6974	3082	2172	RSCAAFASFASRPPLELFAPPGSHRSPPGRGVATSAOCALSVRK
SLPNNIVPPTIMTSSPONTDDTASPSNOTTHNISSULPYTASAP TSLIPKNISISERSEEDITPGSNNEGTNTDPSPSSFSSTSGOWL LTTTLEEHSLGTPEAGVAATLIGSAAPPTLISPOAPASSPSSL STSPPEVFSASVITNISSTVISTOTTCAPTAPSPSTEESSBTH PTSHATAEPVPQEKTPPTVSGKWCELIDMET\PPPPPG RPFVHCCKWALKLETMAETLINVFHAHSGEGDKYKLSKKEL KELLQYTELSGFLDVKELML*ATEALKTFEEA*KSPIIQCSSRS SLPPATQTPPYL*LSAVPFPHLPLPLPLPQAGKDVDAVDKVMK ELDENGGBUPGGEVYUVAALTAKTFEEA*KSPIIQCSSRS SLPPATQTPPYL*LSAVPFPHLPLPLPLPQAGKDVDAVDKVMK ELDENGGBUPGGEVYVUVAALTAKNFFWENS 6976 1216 970 GCQL*VAYGTTENSFVTFAHFEEDTVEOKAES VGRIMPHTEART MNMEAGTLAKLATPGELCIRG VUNGVKHSWEPOKTEBAVDQDKW YWTGDVAATNMEQGFCKIVGRSKDMIIRGGENIYPAELEDFFHTH PKVQEVQVVGVKDDRMGEEICACTRIKCGEETTVEEIKAFCKGK LISHFKIPKVIVEVTHYPLTISIGKOFKKERGMERHLUL*TKQQ ACPGRLA 586 SLFINTNLLSNQIRKTSFGMCSEFISDNTEDGKGKLKTPDFA*R ANKKSKHHVNGRRTUPFPEGTOMAVFGMCCWGAERKFWVLKG VYSTOVSFAGGTISMPTYKEVCSEKABEVVRUVQOPEHMSFE ELLKVFWENHOPTQGMRGGNHGTQYRSAIYPTSAKGMEAALSS KENYQKVLSEHGFGPITTUTREQGTFYVAEDYHQQYLSKKPNGY CCLGGTGVSCPVGIKK 6978 3 242 SFPFRDSRRGGCKGSSLRITAVAMVKLSKEAKQRLQOLFKGSQ FAIRMFFILVIYLGFKRGADDEMPPTVLSLLMS 6979 3917 1146 DEARVRGEAVAAAILSRCHMSGPPFPDSPPDBKGLEGTEPPE AGGSGATFGAARMVRRLKVMIELEQRGLDTRGLKTELAR RLQAALEAEEPDDERELDADDEPGRPBPTNGDFYTQVIKGE NESGYBRRPLEMEQQQAYRPEMKTEKQGAFTSFLIPFASQLKP DRQQFQSKRRPYEENRGRGYFEHREDRRGRSPPPAEDEDDFD DRTVAAIDTYNCDLHFKVARDRSSGYPLTIEGFAPLWSGARASYG VRRGRVCFEMKINESISVKHLPSTEPDPHVVRIGWSLDSCSTOL GEBPFSYGYGGTGKKSTISSFENGKGPAPECON DVELSFTKNGKWMGIAPRIQKEAREDDVIGCFAPPECON DVELSFTKNGKWMGIAPRIQKEAREDDVIGCFAPPECON DVELSFTKNGKWMGIAPRIQKEAREDDVIGCFAPPECON DVELSFTKNGKWMGIAPRIQKEAREDDVIGCFAPPECON NYAGRWOULIQOATQCLNRLIGITAARMNRMWGLRRGR NYAGRWOULIQOATQCLNRLIGITAARMORMWGLRRGR NYAGRWOULIQOATQCLNRLIGITAARMORMWGLRRGR GGGGGGNYRGGFNRSGGGGGGGGGGRYFRORFBFGGRGGGGGGGROPPEGPPPESYSPROPPESYSPROPPTYNGGGSG GGGGGGTYRGGFRSGGGGGGGGGRYFRORFBFRORSTYNKMSNI PEKKPDNGGGGFFRSGGGGGGGGGFYRFRORFPSTYCHGGFSYGGGGGGGGGGGGFPNRGGFPRSGGGGGGGGGFPNRGGFPNRGGGGGGGGGGGGFPNRGGFPNRGGFPNRGGGGGGGGGG	1	}	J	LLAARPGLGTKYQATMVYKTLFALCILTAGWRVOSI,PTSAPI,SV
TSLLPKNISIESREEITSPGSNNEGTNTDPSSCGVENTSGVH LTTLLEBHSLGTFERAVANTUSGAPPTLISPOAPASSESSL STSPEVFSASVITNISSTVISTOPTCAPTAPESPTEESSSCHT PTSHATAEPVPOEKTRALKIPTMEGLINDET\PPPPPG 6975 2 500 RPRFTVICKKRALKIETMEFLINVFHAHSGKEGDKYKLSKKEL KELLOTELSGFLDVKEIML*ATEALKITEEA* KSEIIQCSSSRS SLPPARQPPPYL*LEXAPFPIHLPHLPPQAQKDVADVEKWR ELDENGGGEVDFQEYVULVAALTVACNNIFMENS 6976 1216 970 GCQL*VAYGTTENSEVTFAHPEDIPTEOKAESVGRIMPHTEAKI MNMEAGTLAKLNIFGELCIRGYCWHLGYMGEPGKTERAVDQDKW YNTGDUATNNEGGFGKIVGRSKUMI INGGENI YPAELDPFHTHI PKVQEVQLVVGVKNDDRMGEEICACIRLKDGEFTIVEEIKAPCKGK 1SIFKIPKIVFTNYDITISGKIQKFKLREQMERHLNI*IKQQ ACPGRLA 6977 1298 588 SLFINTNLLSNQIRKTSFGMCSEPISDNTEDQKGKLKTPDFA*R ANKKSHHVNGRNTVEPFPEGTOMAVFGMGCFWGAERKFWULKG VYSTOVGFAGGTISMPTYKEVCSEKTGHAEVVRVVYQDEIMSFE ELLKVWENHDPTGOMRGONDHGTYSAIPTSAKGMEAALSS KENYQKULSEHGFGFITTDIREGGTFYVAEDTVQVLSKNPNGY CGLGGGVSSCPVGIKK 6978 3 242 SPPREDBREGGCKGGSLRHTAVAMVKLKERKQELQOLFKGSQ FAIRWGFIELVILVFKGADPGMPEDTVLSLING 6978 3 242 SPPREDBREGGCKGGSLRHTAVAMVKLKERKQELQOLFKGSQ FAIRWGFIELVILVFKGADPGMPEDTVLSLING 6979 3917 1146 DEARVRGEAVAAAILSRCRHWGFPFFFFFSPFDKRGGRGTEPWE AGGGSGATFGRAMDVRLKVNELREELQRRGLDTRGLKTELLE RIQAALEAEEPDDEREDLADDEEGGFHINEEVETEGSSLEGT AQPPPGLQPHAEPGGYSGFDGHYAMDNITKRQOFYDTQVIKQE NESYSERPLEMEQGQAYFERMENGOFPPFFPSPDDPD DRQAFGSRRPPLEMEQGYSGFDGHYAMDNITKRQOFYDTQVIKQE NESGYSERPLEMEQGAYFERREDRRGSSPPAEEDEDDPD DTIVATDTYNCLHKVANDRSSGYTERREDRRGSRPPAEEDEDDPD DTIVATDTYNCLHKVANDRSSGYTERREDRRGSRPPAEEDEDDPD DTIVATDTYNCCHKVANDRSSGYTERREDRRGSRPPAEEDEDDPD DTIVATDTYNCCHKVANDRSSGYTERREDRRGSRPPAEEDEDDPD DTIVATDTYNCCHKVANDRSSGYTERREDRRGSRPPAEEDEDDPD DTIVATDTYNCCHKVANDRSSGYTERREDRRGSRPPAEEDEDDPD DTIVATDTYNCCHKVANDRSSGYTERREDRRGSRPPAEEDEDDPD DTIVATDTYNCCHKVANDRSSGYTERREDRRGSRPPAEEDEDDPD DTIVATDTYNCCKHKTURGTBARDVRKWGLRRGR NYAGRWOULIQOATQCLNRLIGTARMOKRMVGLRRGR NYAGRWOULIQOATQCLNRLIGTARMOKRMVGLRRGR NYAGRWOULIQOATQCLNRLIGTARMOKRMVGLRRGR RNRPPFEFFGFRKATVICPTDEDLKOPKSKAECEILMMV GEPAASKTTWAIKMAN LIGTNAMMOKRGLRRGR PPEKKFDDWGGGGFFGRGGGGGGGGTORY*ENGPPGGNGGGROGGNRGG GGGGGGGGGGGGGGGGGGGGGGGGG		[SLPTNIVPPTTIWTSSPONTDADTASPSNGTHNNSVLPVTASAP
LITTLEBRISGTPEAGVARILSGAARPTILSPOAPASSPSSIGHT STSPEVFSASVTMINISTVITSTOPTGAPTAPESPTEESSSDHT PTSHATAEPVPQEKTPPTTVSGKVMCELIDMET\PPPPPG APPPTVHCKCKALKLETAMETLINVFHAHSGKEGDKYKLSKKEL KELLQTELSGLDVKELMI-ATEALKTTERA-KSPIIQCSSSRS SLPPARQPPPYL-LSANPFPIHLPPLLPPQAQKOVDAVDKVMK ELDEBROGBUDPGEVYULVAALTONNFFHENS 6976 1216 970 GCQL*VAYGTIENSPVTFAHFPEDTVEQKESVGRIMPHTEAR MNEMEGILARLINTPGELCTRG YCVMLGWGEPQKTERAVQDCM YWTGDVATMMEQGFCKIVGRSKDMIIRGGEMIYPAELEDFFHTH PKVQCVVVGVAVDAVDMGEEICACIRLKOGEETTVEIKARCKGK LSHFKIPKYIVFVTWYPLTISGKICKFKLREQMERHLNL-IKQQ ACPGRLA 6977 1298 588 SLFININLISNQIRKTSFGMCSEPISDNTEDQKGKLKTPDFA*R ANKKSKHHVMGNRTVSPFEGTOMAVPGMGFWGABEKFWULKS KENYQKVLSEHGEPQTTTDIREGGMGFWGABEKFWULKS KENYQKVLSEHGEPQTTTDIREGGTFYYAEDVYQDEHMSFE ELLKVFWENNDPTQGNRQGNDDGTQYRSAIYPTSAKQMEAALSS KENYQKVLSEHGEPQTTTDIREGGTFYYAEDVYQDEHMSFE ELLKVFWENNDPTQGNRQGNDDGTQYRSAIYPTSAKQMEAALSS KENYQKVLSEHGEPQTTTDIREGGTFYYAEDYHQQVEKKNPMY CGLGGTGVSCPVGIKK 6979 3917 1146 DEARVRGEAVAAALLSECHMSGPPFPFSSFDRKGLRGTEPPE AGGSGATFCARAMDVRLKKUREELQRRGLDTRGLKTELAE RLQAALEAEPDDERSLDADDEPGRPGHINEEVETEGGSELEGT AQPPPPCLOPHAEPGGYSGPDCHYAMNITRQNGPYDTOVIKQE DEGGTSYGGGTGKKSTNSRFREEELQRRGLDTGCLKTELAE RLQAALEAEPDDERSLDADDEPGRPGPHINEEVETEGGSELEGT AQPPPPCLOPHAEPGGYSGPDCHYAMNITRQNGPYDTOVIKQE DEGGFFSYGGGGTGKKSTNSRFREEELQRRGSPQPPAEEDEDPD DTLVAIDTNINCLHFKVARDRSSGPPLTISGFAFYLMSGARASYG VRRGRVCFFMKINEEISVKHLPSTEPPHVVRIGMSLDSCSTOL GEBFFSYGGGGTKKSTNSRFREEGLORGSPQPPAEEDEDPD DTLVAIDTNINCLHFKVARDRSSGPPLTISGFAFYLMSGARASYG VRRGRVCFFMKINEEISVKHLPSTEPPHVVRIGWSLDSCSTOL GEBPFSYGGGGTKKSTNSRFREDGRFROPGPPROKEGMGFONGGG VRRGRWDVLIQATCLMRLIOLAARKRWILDOTNVVGSAQR NYAGRWDVLIQATCLMRLIOLAARKRWILDOTNVVGSAQR RMRTPFGFGFRATUICTDEDLKDRTIKRTDEEGGVPDHAVL EMKANFTLPDVGDFLDEVLIFELGREADLVRQYMEGRRGGPONRGG GGGGGNYRGGFNRSGCGGYSONRWGNNNRDNNNNNNRGSYNRA PQQQPPPQQPPPPQPPPPPSYSPANPPGASTYNKNSNI PPEKKFPDNRGGGGFRGGGGGGFGRGGGGGONRGGFONRGG GGGGGNYRGGFNRSGCGGYSONRWGNNNRDNNNNNNNNNNRGSYNRA PQQQPPPQQPPPPQPPPPSYSPANPPGASTYNPPPPTTAQTYPQPSY GTTAPPPPPPPPAYNNGSYGGYNDAGYTYPPPPTTAQTYPQPSY		į	ŀ	TSLLPKNISIESREEEITSPGSNWEGTNTDPSPSGESSTSGGW
STSPPEVFSASVTTNISSTVTSTOPTGAPTAPESFTEESSSDHT FTSHATAEPVPGCKPALTMETT.INVFHAHSGKEGDKYKLSKKEL 6975 2 500 RPRPTVBCCKPALKLETAMET.INVFHAHSGKEGDKYKLSKKEL KELLOTELSGFLDVKELMI-ATEALKTFEA-KEFIIQCSSESS SLPPACQPPPYL-LSAVPPFHHPLPLEPPGARGKOVDAVDKVMK ELDENGDGEVDFGEYVVLVAALTVACNIFFENS 6976 1216 970 GCQL-VAYGTTENSTYFTAHFPEDTVEGKAESVGRIMPHTEARI MNMEAGILAKLNTPGELCTGYCVMLGWEDPQKTEERAVDDDKW YWTGDVATMMEGGFCKIVGRSKDMIIRGGENIYPABLEDFFHTH PKVQEVQVVGVKDDRMGEEICACIRLKDGEETTVEEIKARCKCK ISHFKIPKYIVFVTNYPLITISCKIQKFKLREQMERHLINI-IKQQ ACPGRIA 6977 1298 588 SLFINITALLSNQIRKTSFGMCSEPISDNTEDGKKLKTPDFA-R ANKKSKHHVMGNATVSPFPEGTOMAVPGMCFMCAERKFWLKV VYSTOVGFAGGYTSNPTYKEVCSEKTGHAEVVRVVQPEHMSFE ELLKVFWENHDPTOGMRQCNDHGTQYRSAIPYTSAKQMEAALSS KENYQKVLSEHGFGPITTDIREGGFYYYAEDYHQQVISKNPNGY CGLGGTGVSCPVGIKK 6978 3 242 SFFFRBSRRGGCKGSSLEHTAVAMVKLSKEAKQRLQOLFKGSQ FAIRWGFIPLVIYLGFKGADDGMPEPTVLSLIMG 6979 ASPIT 1146 DEARWGSAVAAAILSRCRHWSGPPFFFFSPPDFKFGLGCTEPWE AGPGSGATFGARAMDVRLKVNELREELQRRGLDTRGLKTELAE RLQAALEAEPDDERELDADDEPGRPGHINEEVETEGGSELGGT AQPPPPCLQPHAPEGGYSCPDAUMNITRGMCFDTQVIKQE NESGYBRRPLEMEQQQAVRPEMKTEMKQGAAPTS FLPPEASQLKP DRQQFGSRRFYESPERNGRGCFENGKFAEDDIFDD DTLVAIDTYNCDLHFKVARDRSGYPLTIEGFAYLMSGARASYG VARGRVCFFMKINEEISVKHLPSTEPDPHVVRIGMSLDSCSTQL GEBPFSYGGGGGKKSTINSRENBGRGFBORGPBOPPDD DTLVAIDTYNCDLHFKVARDRSGYPLTIEGFAYLMVGGAABYG VARGRVCFFMKINEEISVKHLPSTEPDPHVVRIGMSLDSCSTQL GEBPFSYGGGGGKKSTINSRENBGRGFBORGFBORGGFONGG GGRAPYCSVLPGFTFIOHLBLSRIRGTGFGFSKAECSILMMV GLPAAGKTWAAIKHAASNPSKKYNILGTNAIMDKMRVMCLKRQR NYAGRWDVLIQQATQCLMRLIQIAARKRWILDGTNAVGGRAQR RNMRPFEGFGRKAIVICTDEBLIKRTITEDGEGDVPDHAVL EMKANFTLPDVGDFLDEVLIFLLQREEADLVRQYMEGGRAGP PPEKKFPDNRGGGFGRGGGGGFGRGGGGFONRGG GGGGGGNYRGGFNRSGGGGSYSQNRWGMNDNINNNNNRGSYNRA PQQQPPPPQQPPPPPPPPPAYNNGSYGGYNRAGPRGGFNRGG GGGGGGNYRGGFNRSGGGGSYSQNRWGMNDNINNNNNRGSYNRA PQQQPPPQQPPPPPQPPPPQPPPPTAQTYPPPPTTAQTYPPPPTTAQTYPPPPTTAQTYPPPPTTAQTYPPPPTTAQTYPPPPTTAGTYPPPPTTAGTYPPPPTTAGTYPPPPTTAGTYPPPPTTAGTYPPPPTTAGTYPPPPTTAGTYPPPTTAGTYPPPTTAGTYPPPTTAGTYPQPSY		j	j	LTTTLEEHSLGTPEAGVAATLSOSAAEPPTIJSPOAPASSDSST
6975 2 500 RPRPTVJGCKMELIJNETLINVEHAHSGKEGELYKLSKKEL KELLOTELSGFLDVKELML*ATEALKTPEEA*KSPIIQCSSSRS SLPPAPQPPPYL*LSANPFPIHLPLLPPQAQKDVDAVDKVMK ELDENGGGEVPGEYVVLVAALTANNFFHENS 6976 1216 970 GCQL*VAYGTENSFVTFAHFPEDTVCMGKEPGKESVGRIMPHTEARI MNMEAGTLARLINTPGELCTRGVMGWGREPQKTEBAVDDKM YWTGDVATMMEQGFCKIVGRSKDMIIRGGENIYPAELEDFFHTH PKVQEVQVVGVKDDRGBEICACIRLKNGGETTVEEIKAPCKGK 1SHFKTPKYIVFVTNYPLTISCKIKKFKLREDMERHLNL*IKQQ ACPGRLA 6977 1298 588 SLFITINILLSNQIRKTSFGMCSEPISDNTEDQKGKLKTPDFA*R ANKKSKHHVMGNRTVSPFPECTOMAVFGMGCFWGAERKFWULKG VYSTQVGFAGGYTSNFTYKEVCSEKTGHABVRKVVQCPEMMSFE ELLKVFWENHDPTQGMRQCNDMGTQYRSATYPTSAKQMEAALS KENYQKULSEHGFGPITTDIRRQQTFYXAEDYHQQYLSKNPNGY CGLGGTWSCPVGIKK 6978 3 242 SPPFRDSRRGGCCKGSSLRHTAVANVKLSKEAKQRLQQLFKGSQ FAIRWGFIPLVIYLGFKRGADPGMPEPTYSLLMG 6979 3917 1146 DERRVKGEAVAAAILSRCCHWSGPFPFPSPPDFRKGLRGTEPWE AGGGSGATFGARAMDVRRLKVMELREELQRGLDTKGLKTELAE RLQAALEAEEPDDEREDADDEPGHINEEVETEGGSELEGT AQPPPPGLQPHAEPGGYSGPDGHYAMDNITRQNOFYDTQVIKQE NESGYERRPLEMEQQQAYRPEMKTEMKQGATFFLPFEASQLKF DRQQFGSRRPYEBNRGGVFEHEDRRGRSPQPPAEEDEDDFD DTLVAALDTVNCDLHFKVARDRSSGYPLTIEGFAYLMSGARASYG VRRGRVCFEMKINEEISVKHLZSRCHWSGANTSFLPFEASQLKF GGRAEPYCSVLDEFFIGHLESRIRGTUFFKKACEILMMV GLPAAGKTTWAIKHAASMPSKKYNILGTNAIMDKMEVMGLRRQR NYAGRMDVLIQQATCCLMRLIJARKRNYILDQTNVYGSAQR RKMRPFEFFDNRGGGFGRGGGGFORNGG GGRGGNYKAGFFRNGGGFGRGGGGFORNGG GGRGGNYKAGFFRNGGGFGRGGGGFORNGG GGRGGNYKAGFFRNGGGFGRGGGGFORNGG GGRGGNYKAGFPDRSSGGGYSONNEGNNGNFNNSNNRGYWRA POQOPPQAPPPPDPPPPPPPTAQTYPPPPTAQTYPQFSY GGRANTSTPTVSSYSPPQSFGFFFSTFORSYGPPTNNSNI PGSSANTSTPTVSSYSPPQSFGFFFSTFORSTGOPTNNSNI PGSSANTSTPTVSSYSPPQSFGFFFSTFORSTGOPTSTO	1	•		STSPPEVFSASVTTNHSSTVTSTOPTGAPTAPESPTERSSDUT
6976 6976 1216 970 GCQL*VAYGTTENSPVIFALKTPEER*KSPI1QCSSSRS SLPPADQPPYL*LSAVEFP1HLPLPLPLPQAQKDVDAVDKVMK ELDENGDGEVDFQEYVVLWAALTVACKNFFWENS GCQL*VAYGTTENSPVIFALKTPEER*KSPI1QTANI MNMEAGILAKLNTPGELCIRGYCVMLGYWEDPQKTEAVDDLKM YWTGDVATMMEGGEKIVGRSKDMIIRGGENIYPABLEDFHTH PKVQEVQUVGVKDDRMGEEICACTRLKDGEETTVEEIKAFCKGK LSHFKIPKYIVFVTNYPLTISKKIQKETTVEEIKAFCKGK ACPGRLA 6977 1298 588 SLFINTHLENQIRKTSFGMCSEPISDNTEDQKGKLKTPDFA*R ANKKSHHWGNRTVEFPERTOMAVFGMCCFWGARRKFWLKG VYSTOVGFAGGYTSNPTYKEVCSEKTCHAEVVRUVVQDEHMSFE ELLKVFWENEDDPTQGMRCGMTGTYRSAIYPTSAKQMEAALS KENYQKVLSEHGFGFITTDIREGQTFYYAEDTHQVLSKNPNGY CGLGGTGVSCPVCIIKK 6978 3 242 SFPFRDSRRGCCKGSSLRHTAVAMVKLSKEAKQRLQQLFKGSQ FAIRWGFIPLVIYLGFKGADPGMPEPTVISLLMG 6979 3917 1146 DEARNGGEVANAALIERCRINGPPFPPSPPDRKGLRGTEPWE AGPGSGATPGARAMDVRRLKVNELREELQRRGLDTRGLKTELAE RLQAALEAEPDDERELDADDEGGREHINEEVETEGGSELEGT AOPPPSCLQPHAEPGGYSGPDGHYAMDNITRGNFYDTQVIKQE NESGYBRRPLEMBQQQAYRPEMETHENGGAFTSFLPPEASQLKP DRQGFGSKRPYESNENGGYPFENDPROPPAEDEDDFD DTLVAIDTYNCDLHFKVARDRSSGYPLTIEGFAYLWSGARASYG VRRGRVCFFMKINGEISVKHLESTEPDHVVRIGWSLDSCSTQL GEEPFSYGNGGTKKSTNSFENYGKFAENDVIGCFADFEGN DVELSFTKNSKWMGIAFRIQKEALGGALYFHVLVKNCAVEFNF GGRAPPYCSULPGFFTIGHLBGERIRGRYSKAGEEILIMMV GLPAAGKTTWAI KHAASNPSKKYNILGTAIMDKMRVMGLRRQR NYAGRMDVLIQQATQCLNRLIQIAARKKNILDGTNVYGSAQR RRMRPFEGFGRRAIVICETDEDLKDRTIKRTDEEGKDVPDHAVL EMKANFTLEDVGDFLDEVLFIELGEERGKKSTNSFEGGRGRGFORKGG GRGGGGNYRGGFRRSGGGFGRYENRGFPGRGRGFGRNGG GRGGGGGTRGGGGGFRRYENGGFGRRGFGRNGG GSGGGGNYRGGFNRSGGGFGRYENRGFPGRGRGFORRGF GGGGGGGFRRSGGGFFRYENGGFGRRGFORRGF GFRENDNINGGGFFRGRGGGFGRYENRGFPGRGRGFORRGG GSGGGGNYRGGFRRSGGGFFRFTFDFTYDFSYSOPPYNGGGFSOQ GYTAPPPPPPPPPPAMYNGSYGGYNPGYNNYDGSYSONTOGGTTON OVGUTAQDWNYCYNYNGGYPPYYNNYDFSYSONTOGGTSO				PTSHATAEPVPQEKTPPTTVSGKVMCELIDMET\ PPPFPG
KELLOTELSGFLDWLELM-*ATEALKTFERA*KSPIIQCSSSRS SLPPAPORPPYL*LSAVPFHLPPLLPPQAQKUDAVDKVMK ELDENGGGEVDFQEYVLVAALTVACNNFFWENS GCQL*VAYGTTENSFVTFAHFFEDTVEXKAESVGRIMPHTEARI MNMEAGTLAKLNTTGGECIRGYCVMLGYWGEPQKTERAVDQDKW YWTGDVATNMEQGFCKIVGRSKDMIIGGENIYPAELEDFFHTH PKVQEVQVUGVKDRMGETCACTIRLKOGETTVEEIKAFCKGK ISHFKIPKYIVFVTNYPLTISGKIQKFKLEQMERRILNI*IKQQ ACPGRLA SLFINTMLLSNQIRKTSFGMCSEPISDNTEDQKGKLKTPDFA*R ANKKSKHWNGNRTVEPFPEGTOMAVVEWGMCFWGREKFWULKG VYSTOVGFAGGYTSNPTYKSEVSEKTCHAEVVEWVVQPEHMSFP ELLKVFWENHDPTOGMRQGNDHGTQYRSAIYPTSAKQMEAALSS KRMYQKULSEHGGGPITTDIREGQTFYYAEDVHQQVLSKNPNGY CGLGGTGVSCPVGIKK 6978 3 242 SPPFNDSRRGGCCKGSSLRHTAVAMVKLSKEAKQRLQQLFKGSQ FAIRWGFIPLVIYLGFKRGADMPEPTVISLLMG 6979 3917 1146 DEARVRGEAVAAAILSRCRHWGGPPFPPSPDRKGLRGTEPWE AGGGSGATPGARAMDVRRLKVNELRELQRGLDTRGLKTELME RLQAALEAEEPDDERELDADDEPGRCHINDEVTFGGSELGT AQPPPDCLQPHASPGGYSGPDGHYAMDNITRQNGFYDTQVIKQE MESGYBRRPLEMEQQQAYRPEMKTEMKQAPTSFIPPERSQLKP DRQQPGSRKRPYSENRGRGYFFERBRRGRGFQPPAEEDEDDFD DRQQPGSRKRPYSENRGRGFYFERBRRGRGFQPPAEEDEDDFD DTLVAIDTINCDLHFKVARDRSSGYPLTIEGFAYLWSGARASYG VRRGVCFFEMKIMEEISVKHLIPSTEPDHVVKIGSNLDGSSTQL GEEPFSYGGGTGKKSTNSFENYGDKFAENDVIGCFADFECGN DVELSFTKNGKWMGIAFRIQKEALGQALYPHLVLWCAVEFNF GGRAPYCSVLPGFTFIQHLPLSERIRGTVGPKSKAECEILMMV GLPAAGKTTWAIKHASNPSKKYNILIOTANVKGSAQR RKMPPEGFQRKAIVICPTDEDLKDRTIKRTDEGKDVPDIAVL EMKANFTLEDVGDFLDGVFI ELQREEBADKLVRQYNGGGRGG GGGGGTNRGGFRRSGGGGFGRYENGGGFGRRGGGGFRRGGG PPEKKFDNRGGGGFFRSGGGGFGRYENGGFGRRGFGRRGG GGGGGTNRGGFRRSGGGGFGRYENGGFGRRGFGRRGG GGGGGGTNRGGFRRSGGGGFGRYENGFGRGRGFGRRGG GGGGGGTNRGGFRRSGGGGFGRYENGFGRGRGFGRRGG GGGGGGTNAGGFRRSGGGGFGRYENGFGRGRGFGRRGG GGGGGGTNAGGFRRSGGGGFGRYENGFGRGFGRRGFGRGG GGGGGGTNAGGFRRSGGGGFGRYENGFGRGFGRRGGGFGR	6975	2	500	RPRPTVHCCKWALKLETAMETLINVFHAHSGKEGDKYKLSKKET
SLPPAPGPPPYL*LSAVPPIHLPPLLPPQAQKDVDAVDKVMK ELDENGGGGVDFQEYVLVAALTVACMIPFWENS GCQL*VAYGTTENSFVTFAHPFEDTVEQKAESVGRIMPHTEARI MNMEAGTLAKLMITBEGELTRGYCVGWLGYWGEPQKTEEADVDQDKW YWTGDVATMINEQGFCKIVGRSKDMIIGGGGENIYPAELEDFFHTH PKVQEVQVVGVKDDRMGEEICACIRLKDGEFTTVEEIKAFCKGK ISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLANL*IKQ ACPGRLA SLPINTALLSNQIRKTSFGMCSEPISDNTEDQKGKLKTPDFA*R ANKKSKHHVNGNRTVEPPFEGTOMAVFGMCGFWGAERKFWYLKG VYSTOVGFAGGYTSNPTYKEVCSEKTGHAEVVRVVYQPEHMSFE ELLKVFWENHDPTQGMRGGNDHGTYGRSAIYPTSAKQMEAALSS KENYQKVLSEHGFGPITTDIREGQTFYYAEDYHQQYLSKNPNGY CGLGGTGVSCPVGIKK 6978 3 242 SPPFDSBRGGCKGSSLRHTAVANVKLSKEAKQRLQQLFKGSQ FAIRWGFIPLVIYLGFKRGAPPGMPEPTVLSLLWG AGPGSGATFGCARMDVRKUMELREELGRGGLTGGELDTG AGPGPGGATFGARAMDVRKUMELREELGRGGLTGGLTTGLKETLAE RLQAALEAEEPDDERELDADDEPGRPGHINEEVETEGGSELEGT AQPPPBGLQPHABPGGVSGPDGHVAMDMITRQNQFYDTQVIKQE NESGYERRPLEMEQQQAYPEMKTEMKGGAPTSFLPPERSQKKP DRQQFGGRKRPYEENRGGVFEHREDRGRSPQPPAEEDEDDFD DTUVAIDTVMCDLHFKVARDRSGGYPFITEGFAYLWSGARASYG VRRGRVCFEMKINEEISVKHLPSTEPDPHVVRIGWSLDSCSTQL GEEPFSYGYGGTGKKSTINSRFENYGDKFAENDVIGCFADFECGN DVELSFTKINGKWMGIAFRIQKEALGGALYPHULVKACAVFNF GGRAEPYCSVLPGFFTIQHLPLSERIRGTVGFKSKAECEILMMV GLPAAGKTWAIKHASNPSKYNILGTNAIMDKRWMGLRRCQR NYAGRMOVLJQATQCLMRIJQIAARKKNYILDOTNAYWGSAQR RKMPPFEGFGRKAIVICPTDEDLKDRTIKRTDEEGKDVPDHAVL EMKANFTLPDVGDFLDEVLFIELQREEAKNYILDGTNAYWGSAGR RKMPPFEGFGRKAIVICPTDEDLKDRTIKRTDEEGKDVPDHAVL EMKANFTLPDVGDFLDEVLFIELQREEACKLVRQYNEGERKAGP PPEKRFDNRGGGFRGRGGGGFGRYENGGFGGNRGGFORNGG GSGGGGNYRGGFRNSGGGGGGGGRCYENRGPFGGNRGGFORNGG GSGGGGNYRGGFRNSGGGGGGGRYRENRGPFGGNRGGFORNGG GSGGGGNYRGGFRNSGGGGGGGGCGTCYENRGPFGGNRGGFORNGG GSGGGGNYRGGFRNSGGGGGGGGCGTSANRPPTADPTSTYNGNSNI PGSSANTSTPTVSSYSPPQSFGFFPSTFOPSYSQPPVNQGYSQ GYTAPPPPPPPPPPAATYTOSYSGTGTTDOSTSOT				KELLQTELSGFLDVKELML*ATEALKTFEEA*KSPIJOCSSSRS
ELDENGGEVPJCGVVLVAALTVACNNFFWENS GCQL*VAVGTTENSPYTHAPPEDTVEQKAESVGRIMPHTEARI MNMEAGTLAKLNTPGELCIRGYCVMLGYWGEPQKTEEAVDQDKW YWTGDVATMNEQGFCKIVGRSKDMIRGGENTYPAELEDFFHTH PKVQEVQVVQVKDDRMGEEICACIRLKDGGETTVEEIKAPCKGK LSHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL*IKQQ ACPGRLA 6977 1298 588 SLFINTNLLSNQIRKTSFGMCSEPISDNTEDQKGKLKTPDFA*R ANKKSKHHVNGNRTVEPFPEGTOMAVFGMGCFWGAERKFWVLKG VYSTQVGFAGGYTSNPTVKEVCSEKTGHAEVVRVVVPQPEHMSFE ELLKVFWENHDPTQGMRGGNHGTJYRSAIYPTSAKQMEAALSS KERNQKVLSEHGFGPITTDIREGQTFYYAEDYPQQYLEKNPMGY CGLGGTGVSCPVGIKK 6978 3 242 SFPFRDSRCGCCKGSSLRHTAVAMVKLSKEAKQRLQOLFKGSQ FAIRWGFIPLVIVLGFKGADPGMPEPTVLSLLWG FAIRWGFIPLVIVLGFKGADPGMPEPTVLSLLWG AGPGSGATPGARAMDVRLKVNELRELQRGGLDTRGLKTELAE RLQAALEAEFPDERELDADDEPGRPGHINEEVTETGGSELKGT AQPPPPGLQPHAEPGGYSGPDCHVAMDMITRQNQPYDTQVIKOE NESGYBRRPLEMEQQQAYPEMKTEMKGGAPTSFLPPEASQLKP DRQQFQSRKRPYEENRGRGYFEHEDRRGRSPQPPAEDEDDFDD DTLVAIDTTWCDLHFKAADRNSGYPLTIEGFAVLWSCARASYG VRRGRVCFFKKINEEISVKHLPSTEPDPHVVRIGWSLDSCSTOL GEEPFSYGYGGTGKKSINSRFENYGDKFAENDVIGCFADFECGN DVELISFTKNGKWMGIAFRIQKEALGGALYPHVLVKNCAVEFNF GCRAEPYCSVLPGFFTIQHDLDEERIRGTUPKSKAECEILMMV GLPAAGKTTWAIKHAASNPSKKYNILGTNATMDKRVWGLRRQR NYAGRMOVLFUQATOCLNICIOARKKRNYILDOTNYVGSAQR RKMPPFEGFORKAIVIQCATOCLNICIOARKKRNYILDOTNYVGSAQR RKMPPFEGFORKAIVIQCATOCLNICIOARKKRNYILDOTNYVGSAQR RKMPPFEGFORKAIVIQCATOCLNICIOARKKRNYILDOTNYVGSAQR RKMPPFGGFORKAIVIQCATOCLNICIOARKKRNYILDOTNYVGSAQR RKMPPFGGFORKAGOPPPOPPPPPGPFGNNGGSTONRA PQOQPPPQDPPDPPPPPPPPSYSPARNPPGASTYNKNSNI PGSSANTSTPTVSSYSPPQSFGFFPSTFQPSYSGPPNNGGSYNRA PQOQPPPQDPPPDPPPPPPSYSPARNPPGASTYNKNSNI PGSSANTSTPTVSSYSPPQSFGFFPSTFOPSYSGPPNNGGSTSTO WQQYQYAQQMONYYONGQMPPYYGNDYGSYSGNTOGGTSTO				SLPPAPQPPPYL*LSAVPFPIHLPLPLLPPOAOKDVDAVDKVMK
GCQL*VAYGTTENSPYTFAHFPEDTVECKAESVGRIMPHTEARI MNMRAGTLAKINTPGELCIRGYCVMLGYWGEPQKTERAVDQDKW YWTGDVATMNEQGFCK IVGRSKDMIIRGGENIYPAELEDFFHTH PKVQEVQVVQVKDDDMGEEICACIRLKDGETTVEEIKAFCKGK ISHFKIPKYIPVITVPITITISKIQKFKKREQMERHLNL*IKQQ ACPGRLA 588 SLFINTNLLSNQIRKTSFGMCSEPISDNTEDQKGKLKTPDFA*R ANKKSKHHVNGNRTVEPFPEGTOMAVFGMGCFWGAERKFWULKG VYSTOVGFAGGYTSNPTYKEVCSBKTGHAEVVRVUYQPEHMSFE ELLKFFKENHDPTQCMRGDDWGTQYRSAIYPTSAKQMEAALSS KENYQKULSEHGFGPITTDIREGGTFYYAEDYHQQYLSKNPNGY CGLGGTGVSCPVGIKK 6978 3 242 SPPFNDSRGGCKGSSLRHTAVAMVKLSKEAKQRLQQLFKGSQ FAIRWGFIPLVIYLGFKRGADPGMPEPTVLSLLWG 6979 3917 1146 DEARVRGEAVAAALISRCHHWSGPPFFFSFPDKRGLKGTEPWE AGPGSGATFGARAMDVRKLVMELREELQRGGLDTGKLYELAE RLQAALEAEEPDDERELDADDEPGRPGFHINEEVETEGGSELEGT AQPPPPGLQPHAEPGGYSGPDGHYAMDNITKQNOFYDTQVIKQE NESGYBRRPLEMEQQQAYRPEMKTEMKGGAFTSTLPPEASQLKP DRQQFGSRKRPYEENRGGGYFEHEBDRGSGPPPEASQLEGD DTUVAIDTYMCDLHFKVANDSGSGYPLTEGFAYLWSGARASYG VRRGRVCFEMKINEEISVKHLPSTEPPPHVVRIGWSLDSCSTQL GEEPFSYGYGGTGKKSTNSRFENYGDKFALGGOALYHVLVKACAVEFNF CGRAEPYCSVLPGFFFJQHLDLSERIRGTVGPKSKAECEILMMV GLPAAGKTTWAIKHANSNPSKYRNILGTNAIMMOKRVWGLRRQR NYAGRMDVLIQQATQCLMRIJQIAARKRNYILDOTNVYGSAQR RKMFPFEGFGRKAIVICPTDEDLKDRTIKRTDEEGKDVPDHAVL EMKANFTLPDVGPFLDEVLFIELQREEABCLVRQYNEEGRKAGP PPEKRFDNRGGGGFRGRGGGGFGRYENGFGFGRRGGFPRRGG GSGGGGNYRGGFMRGGGGGGGGGGGFGRNEGGFGRRGG GSGGGGNYRGGFMRGGGGGGGGGGGGGGGFGRNEGGFGRRGG GSGGGGNYRGGFMRGGGGGGGGGGGGGGFGRNEGGFGRRGG GSGGGGNYRGGFMRGGGGGGGGGGFTFPSTFQPSYSQPPVNQGGYSQ GYTAPPPPPPPPPPPAANYGSYGGTSTO				ELDENGDGEVDFQEYVVLVAALTVACNNFFWENS
MMMEAGTLAKLNTPGELCIRGYCVMLGYWGEPQKTERADDORM YWTGUDAYMNEGGFGT, UGRSKMMI IRGGENI YPAELEDFFTTH PKVQEVQVVGVKDDRMGEEICACIRKDGETTVEEIKAFCKGK ISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL*IKQQ ACCGRLA ACCGRLA SLFINTNLLSNQIRKTSFGMCSEPISDNTEDQKGKLKTPDFA*R ANKKSKHHVNGMRTVEPFPEGTOMAVFGMGGFWGAERKFWULKG VYSTQVGFAGGYTISNFTYKEVCSSKTGHAEVVRUVYOPEHMSFE ELLKVFWENHDPTQGMRQGNDHGTQYRSAIYPTSAKQMEAALSS KENYQKVLSEHGFGPITTDIRBQGTFYYABDYHQQYLSKNPMGY CGLGGTGVSCPVGIKK SPPFRDSRRCGGCKGSSLRHTAVAMVKLSKEAKQRLQQLFKGSQ FAIRWGFIPLVIYLGFKRGADPGMPEPTVLSLWG 6978 3 242 SPPFRDSRRCGGCKGSSLRHTAVAMVKLSKEAKQRLQQLFKGSQ FAIRWGFIPLVIYLGFKRGADPGMPEPTVLSLWG AGPGSGATFGRARMDVRLKVNELREELQRRGLDTRGLKTELAE RLQAALEAEEPDDERELADDDEPGRPBFHINEEVETEGGSELEGT AQPPPBGLQPHAEPGGYSGPDCHYAMDNITRQNQFYDTQVIKQE NESGYBERPLEMEQQQAYRPEMKTEMKQGAPTSFLPPEASQLKP DRQQFQSRKPYEENRGQVFFHREDRRGSPQPPAEEDEDDFD DTLVAIDTYNCDLHFKVARDRSSGYLITIGGFAYLWSGARASYG VRRGRVCFFMKINGEISVKHLPSTEPDPHVVRIGWSLDSCSTQL GEEPFSYGYGGTGKKSTRSFENYGDKFAENDVIGCFADFECGN DVELSFTKNGKWMGIAFRIQKEALGQQALYPHVLVKNCAVEFNF GGRAEPYCSVLPGFFFIGHDLFLSRIRGTVGPKSKABCEILMMV GIPPAGKTTWAIKHABSKKYNILDQTNVYGSAQR RKMRPFEGFORKAIVICTDEDLKDRTIKRTDEEGKDVPDHAVL EMKANFTLIPDVOGFLIEDELKDRTIKRTDEEGKDVPDHAVL EMKANFTLIPDVOGFLIEDELKDRTIKRTDEEGKDVPDHAVL EMKANFTLIPDVOGFLIEDELKDRTIKRTDEEGKDVPDHAVL EMKANFTLIPDVOGFLIEDELKDRTIKRTDEEGKDVPREGRRAGP PPEKRFDNRGGGGFRRGGGGGFORYENRGPRGGGFORRGG GSGGGGNYRGGFRRSGGGGFORNKGMNNRDNNSNNRRGSYNRA PQQQPPPQQPPPPQPPPPPPSPPTAQTTYQPSY NQYQQYAQQWNQYYYQNGQWPPYYGNYDPSYSGRTYNKSNI PGSSANTSTPTVSSYSPPQSFGFFPSTFQPSYSQPPYNGGYSQ GYTAPPPPPPPPANYNGSYGNPAPYTPPPPTAQTTYQPSY NQYQQYAQQWNQYYYQNGQWPPYYGNYDPSSYSGNTG	6976	1216	970	GCQL*VAYGTTENSPVTFAHPPEDTVEOKAESVGRIMPHTEART
YWTGDVATMNEGGFCXIVGRSKMIIRGEBIIYPAELEDFFHTH PKYQEVQUVQKUDMGEEICACIRLKDGEETTVEEIKAFCKGK ISHFXIPKYIVFVTNYPLTISGKIQKFKLERQMEEHLALL*IKQQ ACCGRLA SLFINTNILISNQIRKTSFGMCSEPISDNTEDQKGKLKTPDFA*R ANKKSKHHVNGRRTVBPPPEGTOMAVFGMGCFWGAERKFWULKG VYSTQVGFAGGYTSNPTYKEVCSEKTGHAEVVRVVYQPEHMSFE ELLKVFWENHDPTQGMRQCNDHGTQYRSAIYPTSAKQMEAALSS KENYQKULSEHGFGPITTDIREGGTFYYAEDYHQQYLSKNPNGY CGLGGTGVSCPVGIKK SFPFRDSRRCGCCKGSSLRHTAVAMVKLSKEAKQRLQQLFKGSQ FAIRWGFIPLVIYLGFKRGADPGMPEPTVLSLLMG 6979 3917 1146 DEARVRGGAVAAAILSRCKHWSGPPPFPSPPDRKGLRGTEPWE AGPGSGATPGARAMDVRRLKVNELREELQRRGLDTRGLKTELAE RLQAALEAEEPDDERELDADDEGRECHINEEVETEGGSELEGT AQPPPBLOPHAEPGGYSGPDCHYAMDNITRQNGPYDTQVIKQE NESGYERRPLEMEQQQAYRPEMKTEMKQGAPTSFLPPEASGLKP DRQCFGSRKRPYEENRGRGYFEHREDRRGRSPPPFPBASGLKP DRQCFGSRKRPYEENRGRGYFEHREDRRGRSPPPFPBASGLKP VRRGRVCFEMKINESISVKHLPSTEPDPHVVRIGWSLDSCSTQL GEEPFSYGYGGTGKKSTNSFFENYGDKFAENDVIGCFADFECGN DVELSFTKNGKWMGIAFFIQKEALGQQALYPHULVKNCAVEFNF GGRAEPYCSVLPGFFFIGHLDLSRTIRGTVGPKSKABCEILMMV GLPAAGKTTWAIKHAASNPSKKYNILGTNAIMDKMRVMGLRRQR NYAGRMDVLIQQATQCLMRLIQIAARKKNYILDQTNVYGSAQR RKMRPFEGFGRKATVICTTDEDLKDRTIKRTDEGKDVPDHAVL EMKANFTLEPDVOGPFLDGVLFPTIRGPGGNRGGFONRGG GSGGGGNYRGGFNRGGGGGGGFORYENGPPGGRRGGFONRGG GSGGGGNYRGGFNRGGGGGGGFORYENGPPGGRRGGFONRGG GSGGGGNYRGGFNRGGGGGGGGFORYENGPPGGRSGFNRGG GSGGGGNYRGGFNRGGGGGGGGFORYENGPPGSTYNKNSNI PGSSANTSTPTVSSYSPPQSFGFFPSTFQPSYSQPPYNGGGYSQ GYTAPPPPPPPPPPPPPPANYGSYGGYNPAPYTPPPPPTPATQTTYQPSY NQYQQYAQQMNQYYQNGQQWPPYYGNPGYSSGTTO				MNMEAGTLAKLNTPGELCIRGYCVMLGYWGEPOKTERAVDODKW
PKYQEVQVVGVKDDRMGEEICACIRIKDGEETTYJEE IKAFCKGK ISHFKIPKYIVFVTNYPJTISGKIQKFKLREQMERHLNL*IKQQ ACPGRLA 588 SLFINTNLISNQIRKTSFGMCSEPISDNTEDQKGKLKTPDFA*R ANKKSKHYMGNRTVEPFPEGODMAVFGMGCFWGAERKFWVLKG VYSTQVGFAGGYTSNPTYKEVCSEKTGHAEVVRVVYQDEHMSFE ELLKVFWENHDPTQGMRQGNDHGTQYRSAIYPTSAKQMEAALSS KENYQKVUSEHGFGPITTDIREGQTFYYAEDYNQQYLSKNPNGY CGLGGTGVSCPVGIKK 5978 3 242 SFPFRDSRRCGCKGSSLRHTAVAMVKLSKEAKQRLQQLFKGSQ FAIRWGFIPLVIYIGFKRGADPGMPEPTVLSLLWG 6979 3917 1146 DEARVRGEAVAAAILSRCRHWSGPPFFPSPPDRKGLRGTEPWE AGPGSGATPGARAMDVRRLKVNELREELQRRGLDTRGLKTELAE RLQAALEAEEPDDERBLANDDEDGERGHINEEVTEGGSELEGT AQPPPDGLQPHAEPGGYSGPDGHYAMDNITRQNQFYDTQVIKQE NESGYERRPLEMEQQQAYRPEMKTEMKQGAPTSFLPPEASQLKP DRQQFQSGKRPYEEMBRGGYFEHREDRGRSPOPPAEEDEDFD DTLVAIDTYNCDLHFKVARDRSGYPHTEGFAYLWSGARASYG VRRGVCFEMKINEEISVRHLBSTEPDPHVVIGGFADFECGN DVELSFYKNGKMMGIAFRIQKEALGGQALYPHVLVKNCAVEFNF GQRAEPYCSVLPGFTFIQHLBJEERIRGTVGPKSKAECEILMMV GLPAAGKTTWAIKHAASNPSKKYNILGTNAIMDKMEVMGLRRQR NYAGRMDVLIQQATQCLNRLIQIAARKKNYILDQTNVYGSAQR RKMRPFEGFQRKAIVICPTDEDLKDRTIKRTDEEGGDVPDHAVL EMKANFILPDVGGFIDDEVLFIELQREEADKLVPQTNEEGRKAGP PPEKRFDNRGGGGFRGRGGGGGGRGVYENRGPPGGNRGG GSGGGGNYRGGFNRSGGGFRGRGGGGGRGVYENRGPPRRGRAP PPEKRFDNRGGGGFRRSGGGGFRGRYENRGPPGGNRGGFQNRGG GSGGGGNYRGGFNRSGGGFFPSTFQPSYSQPPVNQGGYSQ GYTAPPPPPPPPAYNYGSYGGNPAPYTPPPPPTAQTYPQPSY NYQQQYAQQMNQYYQNQGWPPYYGNDYGSYGGTOGTSTO	1			YWTGDVATMNEQGFCKIVGRSKDMIIRGGENIYPAELEDFFHTH
ISHPKTPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL*IKQQ ACCGRIA SLFINTNLLSNQIRKTSFGMCSEPISDNTEDQKGKLKTPDFA*R ANKKSKHHVNGNRTVEPFPEGTOMAVFGMGCFMGAERKFWVLKG VYSTOVGFAGGYTSNPTYKEVCSEKTGHAEVVRVVQDEHMSFE ELLKVFMENHDPTQGMRQGNDHGTQYRSAIYPTSAKQMEAALSS KENYQKVLSEHGFGPITTDIREGQTFYYAEDYHQQYLSKNPNGY CGLGGTGVSCPVGIKK 6978 3 242 SFPFRDSRRCGCCKGSSLRHTAVAMVKLSKEAKQRLQOLFKGSQ FAIRWGFIPLVIYLGFKRGADPGMPEPTVLSLLWG AGPGSGATFGARAMDVRLKVNELREELQRRGLRGTEPWE AGPGSGATFGARAMDVRLKVNELREELQRRGLDTRGLKTELAE RLQAALEAEEPDDERELDADDEPGRPGHINEEVETEGGSELEGT AQPPPPLQPHAEPGGYSGFDGHVAMDNITRQNQFYDTQVIKQE DRQQFQSKRPYEENRGRGYFEHREDRRGSPQPPAEEDEDDFD DTLVAIDTYNCDLHFKVARDRSSGYPLTIEGFAYLWSGARASYG VRRGRVCFFMKINEEISVKHLPSTEPDPHVVRLGWSLDSCSTQL GBEPFSYGYGGTGKKSTNSRFENYGDKFAENDVIGGFADFECGN DVELSFTKNGKMMGIAFRIQKEALGGQALYFHVLVKNCAVEFNF GGRAEPYCSVLPGFFTIQHLPLSERIRGTVGPKSKAECEILMMV GLPAAGKTTWAIKHAASNPSKKVNILGTNAMDKMEVMGLRRQR NYAGRMOVLIQQATQCLNRLIQIAARKKRNYILDQTNVYGSAQR RRMNPFEBFGQRKAIVCPTDEDLKDRTIKRTDEEGKDVPDHAVL EMKANFTLPDVGDFLDEVLFIELQREEADKLVRQYNEEGRRAGP PPEKRFDNRGGGGFFRGRGGGGFGRYENRGPFGGNRGG GSGGGGNYRGGFNRSGGGFSORYENRGPFGGNRGGFONRGG GSGGGGNYRGGFNRSGGGFSORYENRGPFGGNRGGFONRGG GSGGGGNYRGGFNRSGGGFSORYENRGPFGGNRGGFONRGG GSGGGGNYRGGFNRSGGGFSTSTONNNNNNNRGSYNRA PQQQPPPQOPPPQPPPPPPPSYSSARNPPGASTYVNNSNI PGSSANTSTPTVSSYSPPQSFGFFPSTTOPSYSQPPVNQGGYSQ GYTAPPPPPPPPPAYNYGSYGGNPAPYTPPPPPTAGTTOP				PKVQEVQVVGVKDDRMGEEICACIRLKDGEETTVEEIKAFCKGK
6977 1298 588 SLETITNILLSNQIRKTSFGMCSEPISDNTEDQKGKLKTPDFA*R ANKKSKHHVNGNRTVEPFPEGTOMAVFGMGGFWGAERKFWVLKG VYSTQVGFAGGYTSNPTTVEVCSEKTGHAEVVRVVQDEHMSFE ELLKVFWENHDPTGMRQGNDHGTQYRSAIYPTSAKQMEAALSS KENYQKVLSEHGFGPITTDIREQGTFYYAEDYHQQVLSKNPNGY CGLGGTGYSCPVGIKK SPPFRDSRRGGCCKGSSLRHTAVAMVKLSKEAKQRLQQLFKGSQ FAIRWGFIPLVIYLGFKRGADPGMPEFTVLSLLWG FAIRWGFIPLVIYLGFKRGADPGMPEFTVLSLLWG AGPGSGATPGARAMILSRCHWSGPPPFPPSPDRKGLRGTEPWE AGPGSGATPGARAMOVRLKVNELREELQRRGLDTRGLKTELAE RLQAALEAEEPDDERELDADDEPGRPCHINEEVETEGGSELEGT AQPPPDGLQPHAEPGGYSGPDCHYAMDNITRQNQFYDTQVIKQE NESGYERRPLEMEQQQAYRPEMKTEMKQGAPTSFLPPEASQLKP DRQQFQSRKRPYTEENRGRGYFFHREDRRGRSPQPPAEEDEDDFD DTLVAIDTYNCDLHFKVARDRSSGYPLTIEGFAYLWSGARASYG VRRGRVCFEMKINEEISVKHLPSTEPDPHVVRIGWSLDSCSTQL GEEPFSYGYGGTGKKSINSRFENYGDKFAENDVIGCFADFECGN DVELSFTKNGKMGIAFRIQKEALGGQALYPHVLUKNCAVEFNF GGRAEPYCSVLPGFTFIQHLPLSERIRGTVGPKSKAECEILMMV GLPAAGKTTWAIKHAASNPSKKYNILGTNAIMDKMRVMGLIRRQR NYAGRWDVLIQQATQCLNRLIQIAARKKRNYILDOTNVYGSAQR RKMRPFEGFQRKAIVICPTDEDLKDRTIKRTDEBGKDVPDHAVL EMKANFTLPDVGDFLDEVLFIELQREEADKLVRQYNEEGRKAGP PPEKRFDNRGGGGFRGRGGGGFQRYENRGPPGGNRGG GSGGGNYRGGFNRSGGGGYSQNRWGNNNRDNNNSNNRGSYNRA PGGSGGRYRGGFNRSGGGGSFORYENRGPPGGNRGGFQNRGG GSGGGNYRGGFNRSGGGGSFORYENRGPNRGNNRDNNNSNNRGSYNRA PGQQPPPQQPPPPPPPPYSSYSPPDFPSSYSPARNPPGASTTWNNSNI PGSSANTSTPTVSSYSPPQSFGFFPSTFQPSYSQPPYNQGGYSQ GYTAPPPPPPPPPPAYNGGYGGYBFYYGPYPPPPTAQTYPQPSY NQYQQYAQQMNQYYQNQGGPSYGGNYRGGNSTSTO				ISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL*IKOO
ANKKSKHHURGNRTUEPFPEGTOMAUFGMGFHGABERKFWULKG VYSTQUGFAGGYTSNPTYKEVCSEKTGHAEVURVVYQPEHMSFE ELLKVFWENHDPTQGMRQGNDHGTQYRSATYPTSAKQMEAALSS KENYQKULSEHGFGPITTDIREGQTFYYAEDYHQQYLSKNPNGY CGLGGTGVSCPVGIKK 6978 3 242 SFPFRDSRRCGCCKGSSERHTAVAMVKLSKEAKQRLQOLFKGSQ FAIRWGFIPLUTYLGFKRGADPGMPEPTVLSLLWG 6979 3917 1146 DEARVRGEAVAAAILSRCRHWSGPPFPFSPPDRKGLRGTEPWE AGPGSGATPGARAMDVRRLKVNELREELQRRGLDTRGLKTELAE RLQAALEAEPDDERELDADDEPGRPGHINEVETEGGSELEGT AQPPPGLQPHAEPGGYSGFDGHVAMDNITRQNOFYDTQVIKQE NESGYERRPLEMEQQQAYRPEMKTEMKQGAPTSFLPPEASQLKP DRQQFQSRKRPYEENRGRGYFEHREDRGRSPQPPAEEDEDDFD DTLVAIDTYNCDHFKVAADRSGYPLTIEGFAYLWSGARASYG VRRGRVCFEMKINEEISVKHLPSTEPDPHVVRIGWSLDSCSTQL GEEPFSYGYGGTGKKSTNSRFENYGGKFAENDVIGCFADFECGN DVELSFTKNGKWMGIAFRIQKEALGGQALYPHVLVKNCAVEFNF GGRAEPYCSVLPGFTFIQHLPLEERIRGTVGPKSKAECEILMMV GLPAAGKTTWAIKHAASNPSKKYNILGTNAIMDKMRVMGLRRQR NYAGRWDVLIQQATQCLNRLIQIAARKKRNYILDQTNVYGSAQR RKMRPFEGFQRKAIVICTTDEDLKDRTIKRTDEEGKDVPDHAVL EMKANFTLPDVGDFLDEVLFIELQREEADKLVRQYNEEGRKAGP PPEKRFDNRGGGGFRRSGGGGFGRYENRGPFGGNRGG GGGGGGGRYGGFRRSGGGGFGRYENRGPFGGNRGGFONRGG GGGGGGGRYRGGFRRSGGGGFGRYENRGPFGNRGGFGNRGG GGGGGGGRYGGFRRSGGGGFGRYENRGPFGNRGGFGNRGG GGGGGGGRYRGGFRRSGGGGFGRYENRGPFGNRGGFGNRGG GGGGGGGRYGGFRRSGGGGFGRYENRPPGASTYNKNSNI PGSSANTSTPTVSSYSPPQSFGFFPSTFQPSYSQPPYNQGGYSQ GYTAPPPPPPPPANYNGGYGGYGNPGNNPANTNPDSTSTO				ACPGRLA
ANKKSKHHVNGNRTVEPFEGTOMAVFGMGCFWGAERKFWULKG VYSTOVGFAGGYTSNPTYKEVCSEKTGHAEVVRVVYQPEHMSFE ELLKVFWENHDPTQGMRQGNDHGTQYRSATYPTSAKQMEAALSS KENYQKVLSEHGFGPITTDIREGQTFYYAEDYHQQYLSKNPNGY CGLGGTGVSCPVGIKK SPPFRDSRRGGCCKGSSLRHTAVAMVKLSKEAKQRLQQLFKGSQ FAIRWGFIPLVIYLGFKRGADPGMPEPTVLSLLWG 6979 3917 1146 DEARVRGEAVAAAILSRCRHWSGPPPFPSPPDRKGLRGTEPWE AGPGSGATPGARAMDVRRLKVNBELREELQRRGLDTRGLKTELAE RQAALEAEEPDERELDADDEPGRPGHINBEVETEGGSELBGT AQPPPPGLQPHAEPGGYSGPDGHYAMDNITRQNQFYDTQVIKQE NESGYERRPLEMEQQQAYRPEMKTEMKQCAPTSFLPPEASQLKP DRQOFQSRKRPYSENRGRGYFEHREDRGRGPQPPAEEDBDDFD DTLVAIDTYNCDLHFKVARDRSSGYPLTIEGFAYLWSGARASYG VRRGRVCFEMKINEEISVKHLPSTEPDPHVVRIGWSLDSCSTQL GBEPFSYGYGGTGKKSTNSRFENYGDKFAENDVIGCFADFECGN DVELSFTKNGKWMGIAFRIQKEALGGQALYPHVLVKNCAVEFNF GORAEPYCSVLPGFTFIQHLPLSERIRGTVGPKSKAECEILMMV GLPAAGKTTWAIHHAASNPSKKYNILGTNAIMMKMVMGLRQR NYAGRMDVLIQQATQCLNRLIQIAARKKRNYILDQTNVYGSAQR RKMRPFEGFQRKAIVICTDEDLKDRTIKRTDEEGKDVPDHAVL EMKANFTLPDVGDFLDEVLFIELQREEADKLVRQYNEEGRKAGP PPEKRFDNRGGGGFRRSGGGGGGFORYENRGPFGNRGGFQNRGG GSGGGGNYRGGFNRSGGGGGGGFORYENRGPFGNRGGFQNRGG GSGGGGNYRGFNRSGGGGGGGGFORYENRGPFORRGG GSGGGGNYRGFNRSGGGGGGGFORYENRDPGASTYNKNSNI PGSSANTSTPTVSSYSPQSFGFFPSTFQPSYSQPPYNQGGYSQ GYTAPPPPPPPPPANYYGSYGYNPAMNTNNSNNRGSYNRA PQQQPPPQPPPPPPPANYYGSYGYNPAMNTNNSNTGSTTO	69//	1298	588	SLFINTNLLSNQIRKTSFGMCSEPISDNTEDQKGKLKTPDFA*R
VYSTQUEFAGGYTSNPTYKEVCSEKTGHABVVRVUYQPEHMSFE ELLKVFWENHDPTQGMRQGNDHGTQYRSAIYPTSAKQMEAALSS KENYQKULSEHGFGPTTTDIRRGQTFYYAEDYHQQYLSKNPNGY CGLGGTGVSCPVGIKK 5978 3 242 SPPFRDSRRCGCCKGSSLRHTAVAMVKLSKEAKQRLQQLFKGSQ FAIRWGFIPLVIYLGFKRGADPGMPEPTVLSLLWG 6979 3917 1146 DEARVRGEAVAAAILSRCRHWSGPPPFPSPPDRKGLRGTEPWE AGPGSGATFGARAMDVRLKVNELREELQRRGLDTRGLKTELAE RLQALEAEEPDDERELDADDEPGRPGHINEEVETEGGSELEGT AQPPPGLQPHAEPGGYSGPDCHYAMDNITRQNQFYDTQVIKQE NESGYERRPLEMEQQQAYRPEMKTEMKQGAPTSFLPPEASQLKP DRQQFQSRKRPYEENRGRGYFEHREDRRGRSPQPPAEEDEDDFDF DTLVAIDTVNCDLHFKVARDRSSGYPLTIEGFAYLWSGARASYG VRRGRVCFEMKINEEISVKHLPSTEPDPHVVRIGWSLDSCSTQL GEEPFSYGYGGTGKKSTNSRFENYGDKFAENDVIGCFADFECGN DVELSFTKNSKWMGIAFRIQKEALGGQALYPHVLVKNCAVEFNF GQRAEPYCSVLPGFTFIQHLPLSERIRGTVOPKSKAECEILMMV GLPAAGKTTWAIKHAASNPSKKYNILGTNAIMDKMRVWGLRRQR NYAGRWDVLIQQATQCLNRLIQIAARKKRNYLDDTNVYGSAQR RKMRPFEGFGRKAIVICPTDEDLKDRTIKRTDEEGKDVPDHAVL EMKANFTLPDVGDFLDEVLFIELQREEADKLVRQYNEEGRKAGP PPEKRFDNRGGGFRRSGGGGGFGRYENRGPPGGNRGGFQNRGG GSGGGMYRGGGGFRNSGGGGSFORYENRGPPGGNRGGFQNRGG GSGGGGGYRGGGGFRNSGGGGSFORYENRGPPGGNRGGFORGG GSGGGGGYRGGGGFRNSGGGGSFORYENRGPPGASTYNKNSNI PGSSANTSTPTVSSYSPPQSFGFFPSTFQPSYSQPPYNQGGYSQ GYTAPPPPPPPPPANYGSYGGYNPAPYTPPPPPTTAQTYPQPSY NQYQQYAQQWNQYYQNGGWPPYYGNYDYGSSYGGTTGGTSTO				ANKKSKHHVNGNRTVEPFPEGTQMAVFGMGCFWGAERKFWVLKG
KENYQKVLSEHGFGPITTDIREGQTFYYAEDYHQQYLSKNPNGY CGLGGTGVSCPVGIKK SPPFRDSRCGCCKGSSLRHTAVAMVKLSKEAKQRLQQLFKGSQ FAIRWGFIPLVIYLGFKRGADPGMPEPTVLSLLWG 6979 3917 1146 DEARVRGEAVAAAILGRCRHWSGPPPFPSPPDRKGLRGTEPWE AGPGSGATPGARAMDVRLKVNELREELQRRGLDTRGLKTELAE RLQAALEAEDDDERELDADDEPGRPGHINEEVETEGGSELEGT AQPPPPGLQPHAEPGGYSGPDGHYAMDNITRQNQFYDTQVIKQE NESGYERRPLEMEQQQAYRPEMKTEMKQGAPTSFLPPEASQLKP DRQQFQSRKRPYEENRGRGYFEHREDRRGRSPQPPAEDEDDDFD DTLVAIDTYNCDLHFKVARDRSSGYPLTIEGFAYLWSGARASYG VRRGRVCFEMKINEEISVKHLPSTEPPDHVVRIGWSLDSCSTQL GEEPFSYGYGGTGKKSTNSRFENYGDKFAENDVIGCFADFECGN DVELSFTKNGKWMGIAFRIQKEALGGQALYPHVLVKNCAVEFNF GQRAEPYCSVLPGFFTPIQHLPLSERIRGTVGPKSKAECEILMMV GLPAAGKTTWAIKHAASNPSKKNILGTNAIMDKMRVMGLRRQR NYAGRWDVLIQQATQCLNRLIQIAARKKRNYILDQTNVYGSAQR RKMRPFEGFQRKAIVICPTDEDLKDRTIKRTDEEGKDVPDHAVL EMKANFTLPDVGDFLDEVLFIELQREEADKLVRQYNEEGRKAGF PPEKRFDNRGGGFFRRSGGGGFFGRYENRGPPGGNRGGFQNRGG GSGGGGNYRGGFNRSGGGGFSCNRWGNNNRDNNNSNNRGSYNRA PQQQPPQQPPPQPPPPPPSYSPARNPPGASTYNKNSNI PGSSANTSTPTVSSTSPPQSFGFFPSTFGPSYSQPPYNQGGYSQ GYTAPPPPPPPPPAYNYGSYGGYNPAPYTPPPPTAQTYPQPSY NQYQQYAQQWNQYYQNQGQWPPYYGNYDYGSYSGNTOGGTSTO	1			VYSTQVGFAGGYTSNPTYKEVCSEKTGHAEVVRVVYOPEHMSFE
KENYQKVLSEHGFGPITTDIREGQTFYYAEDYHQQYLSKNPNGY CGLGGTGVSCPVGIKK SPPFRDSRCGCCKGSSLRHTAVAMVKLSKEAKQRLQQLFKGSQ FAIRWGFIPLVIYLGFKRGADPGMPEPTVLSLLWG 6979 3917 1146 DEARVRGEAVAAAILGRCRHWSGPPPFPSPPDRKGLRGTEPWE AGPGSGATPGARAMDVRLKVNELREELQRRGLDTRGLKTELAE RLQAALEAEDDDERELDADDEPGRPGHINEEVETEGGSELEGT AQPPPPGLQPHAEPGGYSGPDGHYAMDNITRQNQFYDTQVIKQE NESGYERRPLEMEQQQAYRPEMKTEMKQGAPTSFLPPEASQLKP DRQQFQSRKRPYEENRGRGYFEHREDRRGRSPQPPAEDEDDDFD DTLVAIDTYNCDLHFKVARDRSSGYPLTIEGFAYLWSGARASYG VRRGRVCFEMKINEEISVKHLPSTEPPDHVVRIGWSLDSCSTQL GEEPFSYGYGGTGKKSTNSRFENYGDKFAENDVIGCFADFECGN DVELSFTKNGKWMGIAFRIQKEALGGQALYPHVLVKNCAVEFNF GQRAEPYCSVLPGFFTPIQHLPLSERIRGTVGPKSKAECEILMMV GLPAAGKTTWAIKHAASNPSKKNILGTNAIMDKMRVMGLRRQR NYAGRWDVLIQQATQCLNRLIQIAARKKRNYILDQTNVYGSAQR RKMRPFEGFQRKAIVICPTDEDLKDRTIKRTDEEGKDVPDHAVL EMKANFTLPDVGDFLDEVLFIELQREEADKLVRQYNEEGRKAGF PPEKRFDNRGGGFFRRSGGGGFFGRYENRGPPGGNRGGFQNRGG GSGGGGNYRGGFNRSGGGGFSCNRWGNNNRDNNNSNNRGSYNRA PQQQPPQQPPPQPPPPPPSYSPARNPPGASTYNKNSNI PGSSANTSTPTVSSTSPPQSFGFFPSTFGPSYSQPPYNQGGYSQ GYTAPPPPPPPPPAYNYGSYGGYNPAPYTPPPPTAQTYPQPSY NQYQQYAQQWNQYYQNQGQWPPYYGNYDYGSYSGNTOGGTSTO				ELLKVFWENHDPTQGMRQGNDHGTQYRSAIYPTSAKQMEAALSS
GGLGGTGVSCPVGIKK SFPFRDSRRCGCCKGSSLRHTAVAMVKLSKEAKQRLQQLFKGSQ FAIRWGF 1PLV1VLGFKRGADPGMPEPTVLSLLWG 6979 3917 1146 DEARVRGEAVAAAILSRCRHWSGPPPFPSPPDRKGLRGTEPWE AGPGSGATPGARAMDVRLKUNELREELQRRGLDTRGLKTELAE RLQAALEAEEPDDERELDADDEPGRPGHINEEVETEGGSELEGT AQPPPGLOPHAEPGGYSGPDCHYAMDNITRQNQFYDTQVIKQE NESGYERRPLEMEQQQAYRPEMKTEMKQGAPTSFLPPEASQLKP DRQQFQSRKRPYEENRGRGYFEHREDRRGRSPQPPAEEDEDDFD DTLVAIDTYNCDLHFKVARDRSSGYPLTIEGFAYLWSGARASYG VRRGRVCFFMKINEE ISVKHLPSTEPDPHVVRIGWSLDSCSTQL GEEPFSYGYGGTGKKSTNSRFENYGDKFAENDVIGCFADFECGN DVELSFTKNGKWMGIAFRIQKEALGGQALYPHVLVKNCAVEFNF GORAEPYCSVLPGFTFIQHLPLSERIRGTVGPKSKAECE ILMMV GLPAAGKTTWAIKHAASNPSKKYNILGTNAIMDKMRVMGLRRQR NYAGRWDVLIQQATQCLNRLIQIAARKKRNYILDQTNVYGSAQR RKMRPFEGFQRKAIVICPTDEDLKDRTIKRTDEEGKDVPDHAVL EMKANFTLPDVGDFLDEVLFIELQREEADKLVRQYNEEGRKAGP PPEKR FDNRGGGGFRRGGGGGGFQYYENRGPPGGNRGG GSGGGMYRGGFNRSGGGGYSQNRWGMNNNSNNRNGSYNRA PQQQPPPQQPPPPQPPPPQPPPPSYSPARNPPGASTYNKNSNI PGSSANTSTPTVSSYSPPQSFGFFFSTFQPSYSQPPYNQGGYSQ GYTAPPPPPPPPPANYNGGYGGYNPAPYTPPPPPTAQTYPQPSY NQYQQYAQQWNQYYQNGCQWPPYYGNYDYGSYSGNTOGGTSTO	[KENYQKVLSEHGFGPITTDIREGQTFYYAEDYHQQYLSKNPNGY
FAIRWGFIPLVIYLGKRGADPGMPEPTVLSLLWG 6979 3917 1146 DEARVRGEAVARAILSRCHWSGPPFPPSPPDRKGLRGTEPWE AGPGSGATPGARAMDVRLKVNELREELQRRGLDTRGLKTELAE RLQAALEAEEPDDERELDADDEPGRPGHINEEVETEGGSELEGT AQPPPPGLQPHAEPGGYSGPDGHYAMDNITRGNQFYDTQVIKQE NESGYERRPLEMEQQQAYRPEMKTEMKQGAPTSFLPPEASQLKP DRQQFQSRKRPYEENRGRGYFEHREDRRGRSPQPPAEEDEDDFD DTLVAIDTYNCDLHFKVARDRSSGYPLTIEGFAYLWSGARASYG VRRGRVCFEMKINEEISVKHLPSTEPDPHVVRIGWSLDSCSTQL GEEPFSYGYGGTGKKSTNSRFENYGDKFAENDVIGCFADFECGN DVELSFTKNGKWMGIAFRIQKEALGGQALYPHVLVKNCAVEFNF GQRAEPYCSVLPGFTFIQHLPLSERIRGTVGPKSKAECEILMMV GLPAAGKTTWAIKHAASNPSKKYNILGTNAIMDKMRVMGLRRQR NYAGRWDVLIQQATQCLNRLIQTAARKKRNYILDQTNVYGSAQR RKMRPFEGFQRKAIVICPTDEDLKDRTIKRTDEEGKDVPDHAVL EMKANFTLPDVGDFLDEVLFIELQREEADKLVRQYNEEGRKAGP PPEKRFDNRGGGGFRGRGGGGGFQRYENGPPGGNRGG GSGGGGNYRGGFNRSGGGGYSQNRWGMNNRDNNNSNNRGSYNRA PQQQPPPQQPPPPQPPPPPSYSPARNPPGASTYNKNSNI PGSSANTSTPTVSSYSPPQSFGFPSTFQPSYSQPPYNKNGSNI PGSSANTSTPTVSSYSPPQSFGFPSTFQPSYSQPPYNCGGYSQ GYTAPPPPPPPPPPAYNYGSYGGYNPAPYTPPPPPTAQTYPQPSY NQYQQYAQQWNQYYQNQGQWPPYYGNYDYGSYSGNTOGGTSTO	6070		-	CGLGGTGVSCPVGIKK
DEARVRGEAVAAAILSRCRHWSGPPPFPPSPPDRKGLRGTEPWE AGPGSGATPGARAMDVRRLKVNELREELQRGLDTRGLKTELAE RLQAALEAEEPDDERELDADDEPGRPGHINEEVETEGGSELEGT AQPPPPPGLQPHAEPGGYSGPDGHYAMDNITRQNQFYDTQVIKQE NESGYERRPLEMEQQQAYRPEMKTEMKQGAPTSFLPPEASQLKP DRQQFQSRKRPYEENRGRGYFEHREDRRGRSPQPPAEEDEDDFD DTLVAIDTYNCDLHFKVARDRSSGYPLTIEGFAYLWSGARASYG VRRGRVCFEMKINEEISVKHLPSTEPDPHVVRIGWSLDSCSTQL GEEPFSYGYGGTGKKSTNSRFENYGDKFAENDVIGCFADFECGN DVELSFTKNGKWMGIAFRIQKEALGGQALYPHVLVKNCAVEFNF GQRAEPYCSVLPGFTFIQHLPLSERIRGTVGPKSKAECEILMMV GLPAAGKTTWAIKHAASNPSKKYNILGTNAIMDKMRVMGLRRQR NYAGRWDVLIQQATQCLURLIQIAARKKRNYILDQTNVYGSAQR RKMRPFEGFQRKAIVICPTDEDLKDRTIKRTDEEGKDVPDHAVU EMKANFTLPDVGDFLDEVLFIELQREEADKLVRQYNEEGRKAGP PPEKRFDNRGGGGFFRRGGGGGFQRYENRGPPGGNRGGFQNRGG GSGGGGNYRGGFNRSGGGGYSQNRWGNNRDNNNSNNRGSYNRA PQQQPPQQPPPPQPPPPQPPPPSYSPARNPPGASTYNKNSNI PGSSANTSTPTVSSYSPPQSFGFFPSTFQPSYSQPPVNQGGYSQ GYTAPPPPPPPPANYNGSYGGYNPAPYTPPPPPTAQTYPQPSY NQYQQYAQQWNQYYQNQGWPPYYGNYDYGSYSGNTOGGTSTO	95/8	3 .	242	SFPFRDSRRCGCCKGSSLRHTAVAMVKLSKEAKQRLQQLFKGSQ
AGPGSATPGARAMDVRLKVNELREELQRRGLDTRGLKTELAE RLQAALEAEEPDDERELDADDEPGRPGHINEEVETEGGSELEGT AQPPPPGLQPHAEPGGYSGPDGHYAMDNITRQNQFYDTQVIKQE NESGYERRPLEMEQQQAYRPEMKTEMKQGAPTSFLPPEASQLKP DRQQFQSRKRPYEENRGRGYFEHREDRRGRSPQPPAEEDEDDFD DTLVAIDTYNCDLHFKVARDRSSGYPLTIEGFAYLWSGARASYG VRRGRVCFEMKINEEISVKHLPSTEPDPHVVRIGWSLDSCSTQL GEEPFSYGYGGTGKKSTNSRFENYGDKFAENDVIGCFADFECGN DVELSFTKNGKWMGIAFRIQKEALGGQALYPHVLVKNCAVEFNF GORAEPYCSVLPGFTFIQHLPLSERIRGTVGPKSKAECEILMMV GLPAAGKTTWAIKHAASNPSKKYNILGTNAIMDKNRVMGLRRQR NYAGRWDVLIQQATQCLNRLIQIAARKKRNYILDQTNVYGSAQR RKMRPFEGFQRKAIVICPTDEDLKDRTIKRTDEEGKDVPDHAVL EMKANFTLPDVGDFLDEVLFIELQREEADKLVRQYNEEGRKAGP PPEKRFDNRGGGGFRRGGGGGFORYENRGPPGGNRGGFQNRGG GSGGGGNYRGGFNRSGGGGYSQNRWGNNNRDNNNSNNRGSYNRA PQQQPPQQPPPQPPPPQPPPPSYSPARNPPGASTYNKNSNI PGSSANTSTPTVSSYSPPQSFGFFPSTFQPSYSQPYNQGYSQ GYTAPPPPPPPPAYNYGSYGGYNPAPYTPPPPTAQTYPQPSY NQYQQYAQQWNQYYQNGGWPPYYGNYDYGSYSGNTOGGTSTO	6070	2010		FAIRWGFIPLVIYLGFKRGADPGMPEPTVLSLLWG
RLQAALEAEEPDDERELDADDEPGRPGHINEEVETEGGSELEGT AQPPPPGLQPHAEPGGYSGPDGHYAMDNITRQNQFYDTQVIKQE NESGYERRPLEMEQQQAYRPEMKTEMKQGAPTSFLPPEASQLKP DRQQFQSRKRPYEENRGRGYFEHREDRRGRSPQPPAEEDEDDFD DTLVAIDTYNCDLHFKVARDRSSGYPLTIEGFAYLWSGARASYG VRRGRVCFEMKINEEISVKHLPSTEPDPHVVRIGWSLDSCSTQL GEEPFSYGYGGTGKKSTNSRFENYGDKFAENDVIGCFADFECGN DVELSFTKNGKWMGIAFRIQKEALGGQALYPHVLVKNCAVEFNF GQRAEPYCSVLPGFTFIQHLPLSERIRGTVGPKSKAECEILMMV GLPAAGKTTWAIKHAASNPSKKYNILGTNAIMDKMRVWGLRRQR NYAGRWDVLIQQATQCLNRLIQIAARKKRNYILDQTNVYGSAQR RKMRPFEGFQRKAIVICPTDEDLKDRTIKRTDEEGKDVPDHAVL EMKANFTLPDVGDFLDEVLFIELQREEADKLVRQYNEEGRKAGP PPEKRFDNRGGGGFRRSGGGGGFQRYENRGPFGGNRGGFQNRGG GSGGGGNYRGGFNRSGGGGYSQNRWGNNNRDNNNSNNRGSYNRA PQQQPPPQQPPPPQPPPPPSYSPARNPPGASTYNKNSNI PGSSANTSTPTVSSYSPPQSFGFFPSTFQPSYSQPYNQGGYSQ GYTAPPPPPPPPPPAYNYGSYGGYNPAPYTPPPPPTAQTYPQPSY NQYQQYAQQWNQYYQNQGWPPYYGNYDYGSYSGNTOGGTSTO	1 65/5	391/	1146	DEARVRGEAVAAAILSRCRHWSGPPPFPPSPPDRKGLRGTEPWE
AQPPPGLQPHAEPGGYSGPDGHYAMDNITRQNQFYDTQVIKQE NESGYERRPLEMEQQQAYRPEMKTEMKQGAPTSFLPPEASQLKP DRQQFQSKKRPYEENRGRGYFEHREDRGRSPQPFAEEDEDDFD DTLVAIDTYNCDLHFKVARDRSSGYPLTIEGFAYLWSGARASYG VRRGRVCFEMKINEE ISVKHLPSTEPDPHVVRIGWSLDSCSTQL GEEPFSYGYGGTGKKSTNSRFENYGDKFAENDVIGCFADFECGN DVELSFTKNGKWMGIAFRIQKEALGGQALYPHVLVKNCAVEFNF GQRAEPYCSVLPGFTFIQHLPLSERIRGTVGPKSKAECE ILMMV GLPAAGKTTWAIKHAASNPSKKYNILGTNAIMDKMRVMGLRRQR NYAGRWDVLIQQATQCLNRLIQIAARKKRNYILDQTNVYGSAQR RKMRPFEGFQRKAIVICPTDEDLKDRTIKRTDEEGKDVPDHAVL EMKANFTLPDVGDFLDEVLFIELQREEADKLVRQYNEEGRKAGP PPEKRFDNRGGGGFRGRGGGGGFQRYENRGPPGGNRGGFQNRGG GSGGGGNYRGGFNRSGGGGYSQNRWGNNNRDNNNSNNRGSYNRA PQQQPPPQQPPPQQPPPPPSYSPARNPPGASTYNKNSNI PGSSANTSTPTVSSYSPPQSFGFFPSTFQPSYSQPPYNQGGYSQ GYTAPPPPPPPPPAYNYGSYGGYNPAPYTPPPPPTAQTYPQPSY NQYQQYAQQWNQYYQNQGWPPYYGNYDYGSYSGNTOGGTSTO				AGPGSGATPGARAMDVRRLKVNELREELQRRGLDTRGLKTELAE
NESGYERRPLEMEQQQAYRPEMKTEMKQGAPTS FLPPEASQLKP DRQQFQSRKRPYEENRGRGYFEHREDRGRSPQPPAEEDEDDFD DTLVAIDTYNCDLHFKVARDRSSGYPLTIEGFAYLWSGARASYG VRRGRVCFEMKINEE ISVKHLPSTEPDPHVVRIGWSLDSCSTQL GBEPFSYGYGGTGKKSTNSRFENYGDKFAENDVIGCFADFECGN DVELS FTKNGKWMGIAFRIQKEALGGQALYPHVLVKNCAVEFNF GQRAEPYCSVLPGFTFIQHLPLSERIRGTVGPKSKAECE ILMMV GLPAAGKTTWAIKHAASNPSKKYNILGTNAIMDKMRVMGLRRQR NYAGRWDVLIQQATQCLNRLIQIAARKKRNYILDQTNVYGSAQR RKMRPFEGFQRKAIVICPTDEDLKDRTIKRTDEEGKDVPDHAVL EMKANFTLPDVGDFLDEVLFIELQREEADKLVRQYNEEGRKAGP PPEKRFDNRGGGGFFRRGGGGGGFQRYENRGPPGGNRGG GSGGGGNYRGGFNRSGGGGYSQNRWGNNNRDNNNSNNRGSYNRA PQQQPPPQQPPPPQPPPPQSYSPARNPPGASTYNKNSNI PGSSANTSTPTVSSYSPPQSFGFFPSTFQPSYSQPPYNQGGYSQ GYTAPPPPPPPPPAYNYGSYGGYNPAPYTPPPPTAQTYPQPSY NQYQQYAQQWNQYYQNQGWPPYYGNYDGSYSGNTOGGTSTO	1			RLQAALEAEEPDDERELDADDEPGRPGHINEEVETEGGSELEGT
DRQQFQSRKRPYEENRGRGYFEHREDRRGRSPQPPAEEDEDDFD DTLVAIDTYNCDLHFKVARDRSGYPLTIEGFAYLWSGARASYG VRRGRVCFEMKINEEISVKHLPSTEPDPHVVRIGWSLDSCSTQL GEEPFSYGYGGTGKKSTNSRFENYGDKFAENDVIGCFADFECGN DVELSFTKNGKWMGIAFRIQKEALGGQALYPHVLVKNCAVEFNF GQRAEPYCSVLPGFTFIQHLPLSERIRGTVGPKSKAECEILMMV GLPAAGKTTWAIKHAASNPSKKYNILGTMAIMDKMRVMGLRRQR NYAGRWDVLIQQATQCLNRLIQIAARKKRNYILDQTNVYGSAQR RKMRPFEGFQRKAIVICPTDEDLKDRTIKRTDEEGKDVPDHAVL EMKANFTLPDVGDFLDEVLFIELQREEADKLVRQYNEEGRKAGP PPEKRFDNRGGGGFRRGGGGGGFQRYENRGPPGGNRGG GSGGGGNYRGGFNRSGGGGYSQNRWGNNNRDNNNRNGSYNRA PQQQPPPQQPPPPQQPPPPDSYSPARNPPGASTYNKNSNI PGSSANTSTPTVSSYSPPQSFGFFPSTFQPSYSQPPNQGGYSQ GYTAPPPPPPPPPAYNYGSYGGYNPAPYTPPPPTAQTYPQPSY NQYQQYAQQWNQYYQNQGQWPPYYGNYDYGSYSGNTOGGTSTO	1			AQPPPPGLQPHAEPGGYSGPDGHYAMDNITRQNQFYDTQVIKQE
DTLVAIDTYNCDLHFKVARDRSSGYPLTIEGFAYLWSGARASYG VRRGRVCFEMKINEEISVKHLPSTEPDPHVVRIGWSLDSCSTQL GEEPFSYGYGGTGKKSTNSFENYGDKFAENDVIGCFADFECGN DVELSFTKNGKWMGIAFRIQKEALGGQALYPHVLVKNCAVEFNF GQRAEPYCSVLPGFTFIQHLPLSERIRGTVGPKSKAECEILMMV GLPAAGKTTWAIKHAASNPSKKYNILGTMAIMDKMRVMGLRRQR NYAGRWDVLIQQATQCLNRLIQIAARKKRNYILDQTNVYGSAQR RKMRPFEGFQRKAIVICPTDEDLKDRTIKRTDEEGKDVPDHAVL EMKANFTLPDVGDFLDEVLFIELQREEADKLVRQYNEEGRKAGP PPEKRFDNRGGGGFRGRGGGGGFQRYENRGPPGGNRGG GSGGGGNYRGGFNRSGGGGYSQNRWGNNNRDNNNRNGSYNRA PQQQPPPQQPPPPQPPPPQYPPPSYSPARNPPGASTYNKNSNI PGSSANTSTPTVSSYSPPQSFGFFPSTFQPSYSQPPYNQGGYSQ GYTAPPPPPPPPPAYNYGSYGGYNPAPYTPPPPTAQTYPQPSY NQYQQYAQQWNQYYQNQGQWPPYYGNYDYGSYSGNTOGGTSTO	[NESG I EKKPLEMEQQQAYRPEMKTEMKQGAPTSFLPPEASQLKP
DTLVAIDTYNCDLHFKVARDRSSGYPLTIEGFAYLWSGARASYG VRRGRVCFEMKINEEISVKHLPSTEPDPHVVRIGWSLDSCSTQL GEEPFSYGYGGTGKKSTNSFENYGDKFAENDVIGCFADFECGN DVELSFTKNGKWMGIAFRIQKEALGGQALYPHVLVKNCAVEFNF GQRAEPYCSVLPGFTFIQHLPLSERIRGTVGPKSKAECEILMMV GLPAAGKTTWAIKHAASNPSKKYNILGTMAIMDKMRVMGLRRQR NYAGRWDVLIQQATQCLNRLIQIAARKKRNYILDQTNVYGSAQR RKMRPFEGFQRKAIVICPTDEDLKDRTIKRTDEEGKDVPDHAVL EMKANFTLPDVGDFLDEVLFIELQREEADKLVRQYNEEGRKAGP PPEKRFDNRGGGGFRGRGGGGGFQRYENRGPPGGNRGG GSGGGGNYRGGFNRSGGGGYSQNRWGNNNRDNNNRNGSYNRA PQQQPPPQQPPPPQPPPPQYPPPSYSPARNPPGASTYNKNSNI PGSSANTSTPTVSSYSPPQSFGFFPSTFQPSYSQPPYNQGGYSQ GYTAPPPPPPPPPAYNYGSYGGYNPAPYTPPPPTAQTYPQPSY NQYQQYAQQWNQYYQNQGQWPPYYGNYDYGSYSGNTOGGTSTO	1 1			DKQQFQSKKKPYEENRGRGYFEHREDRRGRSPQPPAEEDEDDFD
GEEPFSYGYGGTGKKSTNSRFENYGDKFAENDVIGCFADFECGN DVELS FTKNGKWMGIAFRIQKEALGGQALYPHVLVKNCAVEFNF GQRAEPYCSVLPGFTFIQHLPLSERIRGTVGPKSKAECEILMMV GLPAAGKTTWAIKHAASNPSKKYNILGTNAIMDKMRVMGLRRQR NYAGRWDVLIQQATQCLNRLIQIAARKKRNYILDQTNVYGSAQR RKMRPFEGFQRKAIVICPTDEDLKDRTIKRTDEEGKDVPDHAVL EMKANFTLPDVGDFLDEVLFIELQREEADKLVRQYNEEGRKAGP PPEKRFDNRGGGGFRGRGGGGGFQRYENRGPFGGNRGGFQNRGG GSGGGGNYRGGFNRSGGGGYSQNRWGNNNRDNNNSNNRGSYNRA PQQQPPPQQPPPPQQPPPPPSYSPARNPPGASTYNKNSNI PGSSANTSTPTVSSYSPPQSFGFFPSTFQPSYSQPYNQGGYSQ GYTAPPPPPPPPPAYNYGSYGGYNPAPYTPPPPPTAQTYPQPSY NQYQQYAQQWNQYYQNQGQWPPYYGNYDYGSYSGNTOGGTSTO	[i		DTLVAIDTYNCDLHFKVARDRSSGYPLTIEGFAYLWSGARASYG
DVELS FTKNGKWMGIAFRIQKEALGGQALYPHVLVKNCAVEFNF GQRAEPYCSVLPGFTFIQHLPLSERIRGTVGPKS KAECE ILMMV GLPAAGKTTWAI KHAASNPS KKYNILGTNAIMDKMRVMGLRRQR NYAGRWDVLIQQATQCLNRLIQIAARKKRNYILDQTNVYGSAQR RKMRPFEGFQRKAIVICPTDEDLKDRTIKRTDEEGKDVPDHAVL EMKANFTLPDVGDFLDEVLFIELQREEADKLVRQYNEEGRKAGP PPEKRFDNRGGGGFRGRGGGGGFQRYENRGPPGGNRGGFQNRGG GSGGGGNYRGGFNRSGGGGSGFQRYENRGPPGGNRGGFQNRG GSGGGGNYRGGFNRSGGGGYSQNRWGNNNRDNNNSNNRGSYNRA PQQQPPPQQPPPQPPPDPSYSPANPPGASTYNKNSNI PGSSANTSTPTVSSYSPPQSFGFFPSTFQPSYSQPYNQGGYSQ GYTAPPPPPPPPPAYNYGSYGGYNPAPYTPPPPPTAQTYPQPSY NQYQQYAQQWNQYYQNQGWPPYYGNYDYGSYSGNTOGGTSTO		ļ		VKKGKVCFEMKINEEISVKHLPSTEPDPHVVRIGWSLDSCSTQL
GQRAEPYCSVLPGFTFIQHLPLSERIRGTVGPKSKAECEILMMV GLPAAGKTTWAIKHAASNPSKKYNILGTNAIMDKMRVMGLRRQR NYAGRWDVLIQQATQCLNRLIQIAARKKRNYILDQTNVYGSAQR RKMRPFEGFQRKAIVICPTDEDLKDRTIKRTDEEGKDVPDHAVL EMKANFTLPDVGDFLDEVLFIELQREEADKLVRQYNEEGRKAGP PPEKRFDNRGGGGFRGRGGGGGFQRYENRGPPGGNRGGFQNRGG GSGGGNYRGGFNRSGGGGYSQNRWGNNNRDNNNSNNRGSYNRA PQQQPPPQQPPPQQPPPPSYSPARNPPGASTYNKNSNI PGSSANTSTPTVSSYSPPQSFGFFPSTFQPSYSQPPYNQGGYSQ GYTAPPPPPPPPAYNYGSYGGYNPAPYTPPPPTAQTYPQPSY NQYQQYAQQWNQYYQNQGQWPPYYGNYDYGSYSGNTOGGTSTO		[GEEPFSYGYGGTGKKSTNSRFENYGDKFAENDVIGCFADFECGN
GLPAAGKTTWAIKHAASNPSKKYNILGTNAIMDKMRVMGLRRQR NYAGRWDVLIQQATQCLNRLIQIAARKKRNYILDQTNVYGSAQR RKMRPFEGFQRKAIVICPTDEDLKDRTIKRTDEEGKDVPDHAVL EMKANFTLPDVGDFLDEVLFIELQREEADKLVRQYNEEGRKAGP PPEKRFDNRGGGGFRGRGGGGGFQRYENRGPPGGNRGGFQNRGG GSGGGNYRGGFNRSGGGGYSQNRWGNNNRDNNNSNNRGSYNRA PQQQPPPQQPPPPQQPPPPSYSPARNPPGASTYNKNSNI PGSSANTSTPTVSSYSPPQSFGFFPSTFQPSYSQPPYNQGGYSQ GYTAPPPPPPPPAYNYGSYGGYNPAPYTPPPPTAQTYPQPSY NQYQQYAQQWNQYYQNQGWPPYYGNYDYGSYSGNTOGGTSTO	1	1	j	DVELSFIKNGKWMGIAFRIQKEALGGQALYPHVLVKNCAVEFNF
NYAGRWDVLIQQATQCLNRLIQIAARKKRNYILDQTNVYGSAQR RKMRPFEGFQRKAIVICPTDEDLKDRTIKRTDEEGKDVPDHAVL EMKANFTLPDVGDFLDEVLFIELQREEADKLVRQYNEEGRKAGP PPEKRFDNRGGGGFRGRGGGGFQRYENRGPPGGNRGGFQNRGG GSGGGGYRRGGFRRSGGGGYSQNRWGNNNRDNNRGSYNRA PQQQPPPQQPPPPQPPPPSYSPARNPPGASTYNKNSNI PGSSANTSTPTVSSYSPPQSFGFFPSTFQPSYSQPPYNQGGYSQ GYTAPPPPPPPPAYNYGSYGGYNPAPYTPPPPTAQTYPQPSY NQYQQYAQQWNQYYQNQGWPPYYGNYDYGSYSGNTOGGTSTO	<u> </u>	İ		GURAEPYCSVLPGFTFIQHLPLSERIRGTVGPKSKAECEILMMV
RKMRPFEGFQRKAIVICPTDEDLKDRTIKRTDEEGKDVPDHAVL EMKANFTLPDVGDFLDEVLFIELQREEADKLVRQYNEEGRKAGP PPEKRFDNRGGGGFRGRGGGGGFQRYENGGPPGGNRGGFQNRGG GSGGGGYRGGFNRSGGGGSQNRWGNNNRDNNNRSYNRA PQQQPPPPQPPPPQPPPPSYSPARNPPGASTYNKNSNI PGSSANTSTPTVSSYSPPQSFGFFPSTFQPSYSQPPYNQGGYSQ GYTAPPPPPPPPAYNYGSYGGYNPAPYTPPPPPTAQTYPQPSY NQYQQYAQQWNQYYQNQGQWPPYYGNYDYGSYSGNTOGGTSTO		ì	Ì	GLPAAGKTTWAIKHAASNPSKKYNILGTNAIMDKMRVMGLRRQR
EMKANFTLPDVGDFLDEVLFIELQREEADKLVRQYNEEGRKAGP PPEKRFDNRGGGGFRGRGGGGGFQRYENRGPFGGNRGG GSGGGGYRGGFNRSGGGGYSQNRWGMNNRDNNNRSYNRA PQQQPPPQQPPPPQQPPPPSYSPARNPPGASTYNKNSNI PGSSANTSTPTVSSYSPPQSFGFFPSTFQPSYSQPPYNQGGYSQ GYTAPPPPPPPPAYNYGSYGGYNPAPYTPPPPTAQTYPQPSY NQYQQYAQQWNQYYQNQGQWPPYYGNYDYGSYSGNTOGGTSTO	[İ	i	NYAGRWDVLIQQATQCLNRLIQIAARKKRNYILDQTNVYGSAQR
PPEKRFDNRGGGGFQRYENRGPFGGNRGGFQNRGG GSGGGGYYRGGFNRSGGGYSQNRWGMNNRDNNNSNNRGSYNRA PQQQPPPPQQPPPPQSPPPPSYSPARNPPGASTYNKNSNI PGSSANTSTPTVSSYSPPQSFGFFPSTFQPSYSQPYNQGGYSQ GYTAPPPPPPPPAYNYGSYGGYNPAPYTPPPPPTAQTYPQPSY NQYQQYAQQWNQYYQNQGQWPPYYGNYDYGSYSGNTOGGTSTO	ļ			RKMRPFEGFQRKAIVICPTDEDLKDRTIKRTDEEGKDVPDHAVL
GSGGGGNYRGGFNRSGGGYSQNRWGNNNRDNNNRGSYNRA PQQQPPPQQPPPPQPPPPSYSPARNPPGASTYNKNSNI PGSSANTSTPTVSSYSPPQSFGFFPSTFQPSYSQPPYNQGGYSQ GYTAPPPPPPPAYNYGSYGGYNPAPYTPPPPPTAQTYPQPSY NQYQQYAQQWNQYYQNQGQWPPYYGNYDYGSYSGNTOGGTSTO] [į		EMKANFTLPDVGDFLDEVLFIELQREEADKLVRQYNEEGRKAGP
PQQQPPPQQPPPPQPPPPSYSPARNPPGASTYNKNSNI PGSSANTSTPTVSSYSPPQSFGFFPSTFQPSYSQPPYNQGGYSQ GYTAPPPPPPPAYNYGSYGGYNPAPYTPPPPPTAQTYPQPSY NQYQQYAQQWNQYYQNQGQWPPYYGNYDYGSYSGNTOGGTSTO	[[PPEKKFDNRGGGGFRGRGGGGGGFQRYENRGPPGGNRGGFQNRGG
PGSSANTSTPTVSSYSPPQSFGFFPSTFQPSYSQPPYNQGGYSQ GYTAPPPPPPPPAYNYGSYGGYNPAPYTPPPPPTAQTYPQPSY NQYQQYAQQWNQYYQNQGQWPPYYGNYDYGSYSGNTOGGTSTO	l			GSGGGGNYRGGFNRSGGGGYSQNRWGNNNRDNNNSNNRGSYNRA
GYTAPPPPPPPPAYNYGSYGGYNPAPYTPPPPPTAQTYPQPSY NQYQQYAQQWNQYYQNQGQWPPYYGNYDYGSYSGNTOGGTSTO]			PQQQPPPPQPPPQQPPPPSYSPARNPPGASTYNKNSNI
NQYQQYAQQWNQYYQNQGQWPPYYGNYDYGSYSGNTOGGTSTO				PGSSANTSTPTVSSYSPPQSFGFFPSTFQPSYSQPPYNQGGYSQ
6980 1 420 GTRGRKTGRVAAPSTRRTGNMQKLQTRSPAMSLSDPGLGYHPT			1	GYTAPPPPPPPPAYNYGSYGGYNPAPYTPPPPPTAQTYPQPSY
GTRGRKTGRVAAPSTRRTGNMQKLQTRSPAMSLSDPGLGYHPT	6980		420	NQYQQYAQQWNQYYQNQGQWPPYYGNYDYGSYSGNTQGGTSTQ
			740	GIRGRAIGHVAAPSTRRKTGNMQKLQTRSPAMSLSDPGLGYHPT

SEQ	Predicted	Predicted end	Amino agid gomest
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Ì	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	Watrontophan V. Transier V. T.
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
1	sequence	1	\=possible nucleotide insertion)
		 	CWTLRWPPLCSLHALHVFHCLFSSRLGTPVSPRLAMDPNCSCEA
i		1	GGSCACAGSCKCKKCKCKCKCKCGGGGGGGGA
1	İ	į	GGSCACAGSCKCKKCKCTSCKKSCCSCCPLGCAKCAQGCICKGA SEKCSCCA
6981	10	1054	
1	ł		PGRGFRRASLRPAFAARGVFQGGLGQAKQARTRACAALPTPHPS
			APRILEPOGVFSLFPPPPGPWPNMILTKAQYDEIAQCLVSVPPT
1	[ROSLRKLKORFPSQSQATLLSIFSQEYQKHIKRTHAKHHTSEAI
1			ESYYQRYLNGVVKNGAAPVLLDLANEVDYAPSLMARLILERFLQ
			EHEETPPSKSIINSMLRDPSQIPDGVLANQVYQCIVNDCCYGPL
1			VDCIKHAIGHEHEVLLRDLLLEKNLSFLDEDQLRAKGYDKTPDF
Į			ILQVPVAVEGHIIHWIESKASFGDECSHHAYLHDQFWSYWNRFG
6982	153	1285	PGLVIYWYGFIQELDCNRERGILLKACFPTNIVTLCHSIA
1		1200	FPQQDCSAPAAPGLAGSEPRRLRAYRRRQRARGLKRVAWLAPP
1			PSLLQGLQGWAQAPVDGTLGPEDSRASSPMIQNSRPSLLQPQDV
			GDTVETLMLHPVIKAFLCGSISGTCSTLLFQPLDLLKTRLQTLQ
1	1		PSDHGSRRVGMLAVLLKVVRTESLLGLWKGMSPSIVRCVPGVGI
1	1		YFGTLYSLKQYFLRGHPPTALESVMLGVGSRSVAGVCMSPITVI
1	•		KTRYESGKYGYESIYAALRSIYHSEGHRGLFSGLTATLLRDAPF
	Į i		SGIYLMFYNQTKNIVPHDQVDATLIPITNFSCGIFAGILASLVT
-		•	QPADVIKTHMQLYPLKFQWIGQAVTLIFKDYGLRGFFQGGIPRA LRRTLMAAMAWTVYEEMMAKMGLKS
6983	82	773	EMCEL ODDCE TIMOMIC TO THE TOTAL L TOTAL
]		EMSFLQDPSFFTMGMWSIGAGALGAAALALLLANTDVFLSKPQK
1			AALEYLEDIDLKTLEKEPRTFKAKELWEKNGAVIMAVRRPGCFL
}	{		CREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDFQPYFKGE
}	[]		IFLDEKKKFYGPQRRKMMFMGFIRLGVWYNFFRAWNGGFSGNLE
			GEGFILGGVFVVGSGKQGILLEHREKEFGDKVNLLSVLEAAKMI KPQTLASEKK
6984	1845	1282	
1 .	-	1202	GGRSAYSLPAGSLPRVPATAAAKMASGVQVADEVCRIFYDMKVR
			KCSTPEEIKKRKKAVIFCLSADKKCIIVEEGKEILVGDVGVTIT
1			DPFKHFVGMLPEKDCRYALYDASFETKESRKEELMFFLWAPELA
1			PLKSKMIYASSKDAIKKKFQGIKHECQANGPEDLNRACIAEKLG GSLIVAFEGCPV
6985	1887	1324	
1 1			RRTAGIYPCFPKPGRTRHALCSVVLLLLTGQLAFDDFQESCAMM
1	: <u>1</u>		WQKYAGSRRSMPLGARILFHGVFYAGGFAIVYYLIQKFHSRALY
1 1			YKLAVEQLQSHPEAQEALGPPLNIHYLKLIDRENFVDIVDAKLK
1 1	1		IPVSGSKSEGLLYVHSSRGGPFQRWHLDEVFLELKDGQQIPVFK LSGENGDEVKKE
6986	642	1350	
1	ł		YHLYFKMGDPNSRKKQALNRLRAQLRKKKESLADQFDFKMYIAF
	ł		VFKEKKKKSALFEVSEVIPVMTNNYEENILKGVRDSSYSLESSL
			ELLQKDVVQLHAPRYQSMRRDVIGCTQEMDFILWPRNDIEKIVC LLFSRWKESDEPFRPVQAKFEFHHGDYEKQFLHVLSRKDKTGIV
	j	ĺ	VNNPNOSVELEIDBOHLOTDVNVATETTV COTO
, 1	1	j	VNNPNQSVFLFIDROHLQTPKNKATIFKLCSICLYLPQEQLTHW AVGTIEDHLRPYMPE
6987	1623	341	
			LEAAEKASRAFKESQRQTDSKNYETENWSPQKSQRRYDMYNTAC
	j		FLGEIEVGLYTIQILQLTPFFHKENELSKKHMVQFLSGKWTIPP
	1		DPRNECYLALSKFTSHLKNLQSDLKRCFDFFIDYMVLLKMRYTQ
	1		KEIAEIMLSKKVSRCFRKYTELFCHLDPCLLQSKESQLLQBENC
j			RKKLEALRADRFAGLLEYLNPNYKDATTMESIVNEYAFLLQQNS
ĺ		1	KKPMTNEKQNSILANIILSCLKPNSKLIQPLTTLKKQLREVLQF
	1		VGLSHQYPGPYFLACLLFWPENQELDQDSKLIEKYVSSLNRSFR
	1	}	GQYKRMCRSKQASTLFYLGKRKGLNSIVHKAKIEOYFDKAONTN
	Í	1	SLWHSGDVWKKNEVKDLLRRLTGQAEGKLISVEYGTEEKIKIPV
6988	3		ISVYSGPLRSGRNIERVSFYLGFSIEGPPGL
	د	689	TQLLRRPAVFVGSAASGIRSGLWSASSGHWCAPAAGRAHAPVPR
]	İ		LVRGLGAASTAAPQDAQTGPQPMPRADCIMRHI,PYFCRGQADG
i j	}	1	FGRGSKQLGIPTANFPEQVVDNLPADISTGIYYGWASYGSGDYU
			KMVVSIGWNPYYKNTKKSMETHIMHTFKEDFYGEILNVAIVGYL

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
			RPEKNFDSLESLISAIQGDIBEAKKRLELPEHLKIKEDNFFQVS
			KSKIMNGH
6989	2	1118	LMPSDRPLSPSTHASAGSHCHAPPTTARRAFPIPFGSKSNMATL
ľ			KDQLIYNLLKEEQTPQNKITVVGVGAVGMACAISTIMKDLADEL
1			ALVDVIEDKLKGEMMDLQHGSLFLRTPKIVSGKDYNVTANSKIV
1	1		11TAGARQQEGESRLNLVQRNVNIFKFIIPNVVKYSPNCKTJTV
1	ì		SNPVDILTYVAWKISGFPKNRVIGSGCNLDSARFRYLMGERLGV
1			HPLSCHGWVLGEHGDSSVPVWSGMNVAGVSLKTLHPDLGTDKDK
1			EQWKEVHKQVVESAYEVIKLKGYTSWAIGLSVADLAESIMKNLR
[[RVHPVSTMIKGLYGIKDDVFLSVPCILGQNGISDLVKVTLTSEE
6990	719	258	EARLKKSADTLWGIQKELQF
	'"	250	THASGMASVVLALRTRTAVTSLLSPTPATALAVRYASKKSGGSS
1	{		KNLGGKSSGRRQGIKKMEGHYVHAGNIIATQRHFRWHPGAHVGV
			GKNKCLYALEEGIVRYTKEVYVPHPRNTEAVDLITRLPKGAVLY KTFVHVVPAKPEGTFKLVAML
6991	169	451	
		132	RRSSDFHNPGFLSRPVSLRENIHHQVICSTKNKRRNPKKIAYLL
1			SSLLMTNLNPNESTENQPVDAYWAFTLDQEFLTYACVEGTGCLF
6992	944	510	RQAPGCSSLALRQVRQVYCGLVRAPQVQTRPLSSRFVERRGALY
l I			RSPMNQENPPPYPGPGPTAPYPPYPPQPMGPGPYPPPQGY
1			PYQGYPQYGWQGGPQEPPKTTVYVVEDQRRDELGPSTCLTACWT
			ALCCCCLWDMLT
6993	1	374	QWCVTCPQHNARQGPAVPPGIQAYGAAPFEDLQVDFTEMSKCRG
i l			DRVWIKNWNVASLCPLWKGPOTVVLSPPTAVKVEGIPAWIHHEH
6994			VKPAARETWEARPSPDNPFRVTLKKTTSPAPVTPGS
6994	346	1100	QWPEKDPVMAASSISSPWGKHVFKAILMVLVALILLHSALAQSR
î i		•	RDFAPPGQQKREAPVDVLTQIGRSVRGTLDAWIGPETMHLVSES
l	,		SSQVLWAISSAISVAFFALSGIAAOLLNALGIAGDYLAOGLKIS
			PGQVQTFLLWGAGALVVYWLLSLLLGLVLALLGRILWGLKLVIF
i !			LAGFVALMRSVPDPSTRALLLLALLILYALLSRLTGSRASGAQL
6995	144	1346	EAKVRGLERQVEELRWRQRRAAKGARSVEEE
1 1		1310	GSVAVGLSGIMAAQKDLWDAIVIGAGIQGCFTAYHLAKHRKRIL
1			LLEQFFLPHSRGSSHGQSRIIRKAYLEDFYTRMMHECYQIWAQL
1 1	- 1		EHEAGTQLHRQTGLLLLGMKENQELKTIQANLSRQRVEHQCLSS EELKQRFPNIRLPRGEVGLLDNSGGVIYAYKALRALQDAIRQLG
ľ	i		GIVRDGEKVVEINPGLLVTVKTTSRSYQAKSLVITAGPWTNQLL
1	į		RPLGIEMPLQTLRINVCYWREMVPGSYGVSQAFPCFLWLGLCPH
	i i		HIYGLPTGEYPGLMKVSYHHGNHADPEERDCPTARTDIGDVQIL
1	}		SSFVRDHLPDLKPEPAVIESCMYTNTPDEQFILDRHPKYDNIVI
			GAGFSGHGFKLAPVVGKILYELSMKLTPSYDLAPFRISRFPSLG
			KAHL
6996	543	1942	ETANAEAAARKSAMDWKEVLRRRLATPNTCPNKKKSEQELKDEE
		1	MDLFTKYYSEWKGGRKNTNEFYKTIPRFYYRLPAENEVIJOKID
		j	EESRAVFLQRKSRELLDNEELQNLWFLLDKHOTPPMIGERAMIN
		ļ	YENFLKVGEKAGAKCKQFFTAKVFAKLLHTDSYGRISIMOFFNV
1	1		VMRKVWLHQTRIGLSLYDVAGQGYLRESDLENYILEI,TPTLDOI
	1		DGLEKSFYSFYVCTAVRKFFFFLDPLRTGKIKIODILACSFLDD
	1	ľ	LLELRDEELSKESQETNWFSAPSALRVYGOYLNLDKDHNGMLSK
1			EELSRYGTATMTNVFLDRVFQECLTYDGEMDYKTYLDFVLALEN
1	1		RKEPAALQYIFKLLDIENKGYLNVFSLNYFFRAIOELMKTHGOD
i	į	•	PVSFQDVKDEIFDMVKPKDPLKISLQDLINSNOGDTVTTII.TDI.
6997	370	- 1103	NGFWTYENREALVANDSENSADLDDT
	3,3	1104	AMELTIFILRLAIYILTFPLYLLNFLGLWSWICKKWFPYFLVRF
		1	TVIYNEQMASKKRELFSNLQEFAGPSGKLSLLEVGCGTGANFKF
			YPPGCRVTCIDPNPNFEKFLIKSIAENRHLQFERFVVAAGENMH

SEO	Predicted	Drodicted and	
ID	beginning	Predicted end	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	1		QVADGSVDVVVCTLVLCSVKNQERILREVCRVLRPGGAFYFMEH
1	1	İ	VAAECSTWNYFWQQVLDPAWHLLFDGCNLTRESWKALERASFSK
1	1	Į.	LKLQHIQAPLSWELVRPHIYGYAVK
6998	2	616	FVSRALLRVRSRRHPAEERAAPGRPEDAPIECPGATNCPEPLWC
[ſ		SHLPVPYAPPTMESRGKSASSPKPDTKVPQVTTEAKVPPAADGK
1		ĺ	APLTKPSKKEAPAEKQQPPAAPTTAPAKKTSAKADPALLNNHSN
	1		LKPAPTVPSSPDATPEPKGPGDGAEEDEAASGGPGGRGPWSCEN
1	1		FNPLLVAGGVAVAAIALILGVAFLVRKK
6999	14	1591	GRAGACSRRDTAMSIEIESSDVIRLIMQYLKENSLHRALATLOE
]		ETTVSLNTVDSIESFVADINSGHWDTVLQAIQSLKLPDKTLIDL
1	J		YEQVVLELIELRELGAARSLLRQTDPMIMLKQTQPERYIHLENL
			LARSYFDPREAYPDGSSKEKRRAAIAQALAGEVSVVPPSRLMAL
1	}	l	LGQALKWQQHQGLLPPGMTIDLFRGKAAVKDVEEEKFPTQLSRH
1	1	1	IKFGQKSHVECARFSPDGQYLVTGSVDGFIEVWNFTTGKIRKDL
	1		KYQAQDNFMMMDDAVLCMCFSRDTEMLATGAQDGKIKVWKIQSG
			QCLRRFERAHSKGVTCLSFSKDSSQILSASFDQTIRIHGLKSGK
}		ŀ	TLKEFRGHSSFVNEATFTQDGHYIISASSDGTVKIWNMKTTECS
		<u> </u>	1
İ]		NTFKSLGSTAGTDITVNSVILLPKNPEHFVVCNRSNTVVIMNMQ
	1		GQIVRSFSSGKREGGDFVCCALSPRGEWIYCVGEDFVLYCFSTV
7000	2	827	TGKLERTLTVHEKDVIGIAHHPHQNLIATYSEDGLLKLWKP
7000	\	827	GPGVVFLELMESEGPPESERSEFFSQREEENEEEEAQEPEETGP
	Ì		KNPLLQPALTGDVEGLQKIFEDPENPHHEQAMQLLLEEDIVGRN
		i	LLYAACMAGQSDVIRALAKYGVNLNEKTTRGYTLLHCAAAWGRL
j	j .	J	ETLKALVELDVDI EALNFREERARDVAARYSQTECVEFLDWADA
			RLTLKKYIAKVSLAVTDTEKGSGKLLKEDKNTILSACRAKNEWL
		į	ETHTEASINELFEQRQQLEDIVTPIFTKMTTPCQVKSAKSVTSH
			DQKRSQDDTSN
7001	2056	844	RRCLIIAFLKGCFIFIYFIFIFETEFLSCCPGWSAVAQSRLIAN
	1		FASQVQAIFILPKDSQVGPDVKSEAAPKRALYESVFGSGEICGP
			TSPKRLCIRPSEPVDAVVVVSVKHDPLPLLPEANGHRSTNSPTI
į.	1	ļ	VSPAIVSPTQDSRPNMSRPLITRSPASPLNNQGIPTPAQLTKSN
			APVHIDVGGHMYTSSLATLTKYPESRIGRLFDGTEPIVLDSLKQ
1]		HYFIDRDGQMFRYILNFLRTSKLLIPDDFKDYTLLYEEAKYFQL
1	1		QPMLLEMERWKQDRETGRFSRPCECLVVRVAPDLGERITLSGDK
1	1	ļ	SLIEEVFPEIGDVMCNSVNAGWNHDSTHVIRFPLNGYCHLNSVQ
1			VLERLQQRGFEIVGSCGGGVDSSQFSEYVLRRELRRTPRVPSVI
L			RIKQEPLD
7002	1043	498	PMPSSTRWTTS*TYTDTSSAWACRPTTGTCT*TAAPGPTVRWWP
I			TPCSRHQSRRRLTCWCSTSRPCGR*GGLCVRTAPTRPTTSASSS
1	į		SWTSAGTSWPAGRRTGTATSGTATTTSVWPGCGTRMWSTQWSSV
1			PRSRSCCSRPATTPPSKPGAPHAPCASSRHLAHGLAPSSPGLPA
1	1		RGAEVC
7003	818	61	QGRFRAFCWQRDFLQPPGMRLSALLALASKVTLPPHYRYGMSPP
1			GSVADKRKNPPWIRRRPVVVEPISDEDWYLFCGDTVEILEGKDA
1	l		GKQGKVVQVIRQRNWVVVGGLNTHYRYIGKTMDYRGTMIPSEAP
1			LLHRQVKLVDPMDRKPTEIEWRFTEAGERVRVSTRSGRIIPKPE
Į			FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLOEEVMEAM
1			GIKETR\NTRRSIGIEPGAEQLLPNFCPSLEG
7004	121	2285	FLLPVLTSRSLROPAVPHARLGGVEPAAMKSARAKTPRKPTVKK
1	1	2203	G\PKRTLKTQLG/YYCRVRPLGFPDQECCIEVINNTTVOLHTPE
1	1		GYRLNRNGDYKETQYSFKQVFGTHTTQKELFDVVANPLVNDLIH
			GKNGLLFTYGVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGSF
			QAKRYVFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQ
1	1		VDPEFADMITVQBFCKAEEVDEDSVYGVFVSYIEIYNNYIYDLL
1	Į.		EEVPFDPINPNLHNLNCFVKIKNHNMYVAGCTEVEVKSTEEAFE
	l .	i	VFWRGQKKRRIANTHLNRESSRSHSVFNIKLVQAPLDADGDNVL

SEQ	Predicted	Predicted end	7mino
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ļ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence		\=possible nucleotide insertion)
			QEKEQITISQLSLVDLAGSERTNRTRAEGNRLREAGNINQSLMT
			LRTCMDVLRENQMYGTNKMVPYRDSKLTHLFKNYFDGEGKVRMI
1		1	VCVNPKAEDYEENLQVMRFAEVTQEVEVARPVDKAICGLTPGRR
			YRNQPRGP\IGNEPLVTDVVLQSFPPLPSCEILDINDEQTLPRL IEALEKRHNLRQMMIDEFNKQSNAFKALLQEFDNAVLSKENHMQ
1			GKLNEKEKMISGQKLEIERLEKKNKTLEYKIEILEKTTTIYEED
			KRNLQQELETQNQKLQRQFSDKRRLEARLQGMVTETTMKWEKEC
	{		ERRVAAKQLEMONKLWVKDEKLKOLKAIVTEPKTEKPERPSRER
			DREKVTQRSVSPSPVPVSYL
7005	63	876	RNMALYQRWRCLRLQGLQACRLHTAVVSTPPRWLAERLGLFEEL
		j	WAAQVKRLASMAQKEPRTIKISLPGGQKIDAVAWNTTPYOLARO
	(ISSTLADTAVAAQVNGEPYDLERPLETDSDLRFLTFDSPEGKAV
			FWHSSTHVLGAAAEQFLGAVLCRGPSTEYGFYHDFFLGKERTIR
			GSELPVLERICQELTAAARPFRRLEASRDQLRQLFKDNPFKLHL
1		ē	IEEKVTGPTATVYGCGTLVDLCQGPHLRHTGQIGGLKLLSNSSS LWRSSG
7006	22	898	NAFGRHSTAVKMAAAAWLQVLPVILLLLGAHPSPLSFFSAGPAT
1			VAAADRSKWHIPIPSGKNYFSFGKILFRNTTIFLKFDGEPCDLS
			LNITWYLKSADCYNEIYNFKAEEVELYLEKLKEKRGLSGKYQTS
1			SKLFQNCSELFKTQTFSGDFMHRLPLLGEKQEAKENGTNLTFIG
-			DKTAMHEPLQTWQDAPYIFIVHIGISSSKESSKENSLSNLFTMT
i			VEVKGPYEYLTLEDYPLMIFFMVMCIVYVLFGVLWLAWSACYWR
7007	ļ <u>-</u>	3.004	DLLRIQFWIGAVIFLGMLEKAVFYAGFQ
/00/	2	1001	AMTVSGPGTPEPRPATPGASSVEQLRKEGNELFKCGDYGGALAA
1			YTQALGLDATPQDQAVLHRNRAACHLKLEDYDKAETEASKAIEK
			DGGDVKALYRRSQALEKLGRLDQAVLDLQRCVSLEPKNKVFQEA LRNIGGQIQEKVRYMSSTDAKVEQMFQILLDPEEKGTEKKQKAS
			QNLVVLAREDAGAEKIFRSNGVQLLQRLLDMGETDLMLAALRTL
			VGICSEHQSRTVATLSILGTRRVVSILGVESQAVSLAACHLLQV
i I			MFDALKEGVKKGFRGKEGAIIVGEWKQVWGLLDVTVMEGMGLSQ
7000			PGQFFGDQTCSCRLFGIRFGDIILL
7008	70	1478	CRSALGHERPPPAHLPAGGRRLQTCPRSCRWLGRPPSGLPPGPR
			SPPPLAGPGQKMVQKKPAELQGFHRSFKGQNPFELAFSLDQPDH
1			GDSDFGLQCSARPDMPASQPIDIPDAKKRGKKKKRGRATDSFSG
i			RFEDVYQLQEDVLGEGAHARVQTCINLITSQEYAVKIIEKQPGH
			IRSRVFREVEMLYQCQGHRNVLELIEFFEEEDRFYLVFEKMRGG SILSHIHKRRHFNELEASVVVQDVASALDFLHNKGIAHRDLKPE
			NILCEHPNQVSPVKICDFDLGSGIKLNGDCSPISTPELLTPCGS
1	}		AEYMAPEVVEAFSEEASIYDKRCDLWSLGVILYILLSGYPPFVG
[RCGSDCGWDRGEACPACQNMLFESIOEGKYEFPDKDWAHISCAA
			KDLISKLLVRDAKQRLSAAQVLQHPWVQGCAPENTLPTPMVLOR
· 7009	1		WDSHFLLPPHPCRIHVRPGGLVRTVTVNE
,005	1	626	ARQLRNSWVDDFVAAPLIPLSQQIPTGNSLYESYYKQVDPAYTG
			RVGASEAALFLKKSGLSDIILGKIWDLADPEGKGFLDKQGFYVA
1	1		LRLVACAQSGHEVTLSNLNLSMPPPKFHDTSSPLMVTPPSAEAH WAVRVEEKAKFDGIFESLLPINGLLSGDKVKPVLMNSKLPLDVL
			GRVWDLSDIDKDGHLVRDEFAVAMHLVYRALE
7010	79	571	SHTRRAVVPETLLSPLCPLLGGGTAMSGGEQKPERYYVGVDVGT
			GSVRAALVDQSGVLLAFADQPIKNWEPQFNHHEQSSEDIWAACC
	1		VVTKKVVQGIDLNQIRGLGFDATCSLVVLDKQFHPLPVNQEGDS
<u> </u>			HRNVIMWLDHRAVSQVNRINETKHSVLQYVGG
7011	3	994	RIQTLPNQNQSQTQPLLKTPPAVLQPIAPQTTFGVQTQPQPQSL
			LQAQISAASITPLLQTQPQPLLQQPQQKAGLLQPPVRIVSQPQP
			ARRLDPPSRFSGRNDRGDQVPNRKDDRSRERERERRRSRERSPQ
	į		RKRSRERSPRRERERSPRRVRRVVPRYTVQFSKFSLDCPSCDMM
			ELRRRYQNLYIPSDFFDAQFTWVDAFPLSRPFQLGNYCNFYVMH

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
}	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	334	\=possible nucleotide insertion)
	1		REVESLEKNMAILDPPDADHLYSAKVMLMASPSMEDLYHKSCAL
	İ	j	AEDDOEL BECEOUPERLAND AND ASSESSMENT ASSESSMENT AND ASSESSMENT ASSESSMENT ASSESSMENT AND ASSESSMENT ASSESSME
1	1 .		AEDPQELRDGFQHPARLVKFLVGMKGKDEAMAIGGHWSPSLDGP
7012	1 1	2661	DPEKDPSVLIKT\AIRCCKALTG
/012	1	2001	RRAGSVKRGEARLFGPTERQSERPLRPSAARRPEMLSGKKAAAA
1			AAAAAAATGTEAGPGTAGGSENGSEVAAQPAGLSGPAEVGPGA
}	J.		VGERTPRKKEPPRASPPGGLAEPPGSAGPQAGPTVVPGSATPME
1	•	ĺ	TGIAETPEG\RRTSRRKRAKVEYREMDESLANLSEDEYYSEEER
1	i		NAKAEKEKKLPPPPPPQAPPEEENESEPEEPSGVEGAAFQSRLPH
	1	}	DRMTSQEAACFPDIISGPQQTQKVFLFIRNRTLQLWLDNPKIQL
1	•	1	TFEATLQQLEAPYNSDTVLVHRVHSYLERHGLINFGIYKRIKPL
	1	1	PTKKTGKVIIIGSGVSGLAAARQLQSFGMDVTLLEARDRVGGRV
			ATFRKGNYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKQKCP
			LYEANGQAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP
	[VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLNKMV
			NLKEKIKELHQQYKEASEVKPPRDITAEFLVKSKHRDLTALCKE
1	i		YDELAETQGKLEEKLQELEANPPSDVYLSSRDRQILDWHFANLE
	<u> </u>		FANATPLSTLSLKHWDQDDDFEFTGSHLTVRNGYSCVPVALAEG
1	Ī		LDIKLNTAVRQVRYTASGCEVIAVNTRSTSQTFIYKCDAVLCTL
	ĺ		PLGVLKQQPPAVQFVPPLPEWKTSAVQRMGFGNLNKVVLCFDRV
			FWDPSVNLFGHVGSTTASRGELFLFWNLYKAPILLALVAGEAAG
1			IMENISDDVIVGRCLAILKGIFGSSAVPQPKETVVSRWRADPWA
i .	1		RGSYSYVAAGSSGNDYDLMAQPITPGPSIPGAPQPIPRLFFAGE
			HTIRNYPATVHGALLSGLREAGRIADQFLGAMYTLPRQATPGVP
7022			AQQSPSM
7013	. 1	2661	RRAGSVKRGEARLFGPTERQSERPLRPSAARRPEMLSGKKAAAA
1			AAAAAAATGTEAGPGTAGGSENGSEVAAQPAGLSGPAEVGPGA
1	·		VGERTPRKKEPPRASPPGGLAEPPGSAGPQAGPTVVPGSATPME
j			TGIAETPEG\RRTSRRKRAKVEYREMDESLANLSEDEYYSEEER
	İ		NAKAEKEKKLPPPPPQAPPEEENESEPEEPSGVEGAAFQSRLPH
]			DRMTSQEAACFPDIISGPQQTQKVFLFIRNRTLQLWLDNPKIQL
			TFEATLQQLEAPYNSDTVLVHRVHSYLERHGLINFGIYKRIKPL
1			PTKKTGKVIIIGSGVSGLAAARQLQSFGMDVTLLEARDRVGGRV
1			ATFRKGNYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKQKCP
!			LYEANGQAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP
	}		VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLNKMV
			NLKEKIKELHQQYKEASEVKPPRDITAEFLVKSKHRDLTALCKE
1	1		YDELAETQGKLEEKLQELEANPPSDVYLSSRDRQILDWHFANLE
{			FANATPLSTLSLKHWDQDDDFEFTGSHLTVRNGYSCVPVALAEG
			LDIKLNTAVRQVRYTASGCEVIAVNTRSTSQTFIYKCDAVLCTL
į l			PLGVLKQQPPAVQFVPPLPEWKTSAVQRMGFGNLNKVVLCFDRV
		•	FWDPSVNLFGHVGSTTASRGELFLFWNLYKAPILLALVAGEAAG
1 1			IMENISDDVIVGRCLAILKGIFGSSAVPQPKETVVSRWRADPWA
Į l	l		RGSYSYVAAGSSGNDYDLMAQPITPGPSIPGAPQPIPRLFFAGE
1			HTIRNYPATVHGALLSGLREAGRIADQFLGAMYTLPRQATPGVP
1 7014			AQQSPSM
7014	3	3950	DFEVGDKIRILATLEDGWLEGSLKGRTGIFPYRFVKLCPDTRVE
i			ETMALPQEGSLARIPETSLDCLENTLGVEEQRHETSDHEAEEPD
1			CIISEAPTSPLGHLTSEYDTDRNSYQDEDTAGGPPRSPGVEWEM
1 1		ĺ	PLATDSPTSDPTEVVNGISSQPQVPFHPNLQKSQYYSTVGGSHP
			HSEQYPDLLPLEARTRDYASLPPKRMYSQLKTLQKPVLPLYRGS
1 1		İ	SVSASRVVKPRQSSPQLHNLASYTKKHHTSSVYSISERLEMKPG
	i	ſ	PQAQGLVMEAATHSQGDGSTDLDSKLTQQLIEFEKSLAGPGTEP
	Į.	1	The state of the s
			DKILRHFSIMDFNSEKDIVRGSSKLITEQELPERRKALRPPPPR
			DKILRHFSIMDFNSEKDIVRGSSKLITEQELPERRKALRPPPPR PCTPVSTSPHLLVDQNLKPAPPLVVRPSRPAPLPPSAQORTNAV
			DKILRHFSIMDFNSEKDIVRGSSKLITEQELPERRKALRPPPPR PCTPVSTSPHLLVDQNLKPAPPLVVRPSRPAPLPPSAQQRTNAV SPKLLSRHRPTCETLEKEGPGHMGRSLDQTSPCPLVLVRIEEME
			DKILRHFSIMDFNSEKDIVRGSSKLITEQELPERRKALRPPPPR

050	I Breadd ab - S	L Door 32 art = 3 1 1 2	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide		Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first		P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
]	MELQQLREMTLLSSQSSSLVAPSGSVSAENPEQRMLEKRAKVIE
	[ELLQTERDYIRDLEMCIERIMVPMQQAQVPNIDFEGLFGNMQMV
			IKVSKQLLAALEISDAVGPVFLGHRDELEGTYKIYCQNHDEAIA
]		LLEIYEKDEKIQKHLQDSLADLKSLYNEWGCTNYINLGSFLIKP
	į		VQRVMRYPLLLMELLNSTPESHPDKVPLTNAVLAVKEINVNINE
	j	1	YKRRKDLVLKYRKGDEDSLMEKISKLNIHSIIKKSNRVSSHLKH
	ļ		LTGFAPQIKDEVFEETEKNFRMQERLIKSFIRDLSLYLQHIRES
	1		ACVKVVAAVSMWDVCMERGHRDLEQFERVHRYISDQLFTNFKER
	ł	1	TERLVISPLNQLLSMFTGPHKLVQKRFDKLLDFYNCTERAEKLK
		İ	DKKTLEELQSARNNYBALNAQLLDELPKFHQYAQGLFTNCVHGY
			AEAHCDFVHQALEQLKPLLSLLKVAGREGNLIAIFHEEHSRVLQ
		j	QLQVFTFFPESLPATKKPFERKTIDRQSARKPLLGLPSYMLQSE
		I	ELRASLLARYPPEKLFQAERNFNAAQDLDVSLLEGDLVGVIKKK
	[1	DPMGSQNRWLIDNGVTKGFVYSSFLKPYNPRRSHSDASVGSHSS
	J	}	TESEHGSSSPRFPRQNSGSTLTFNPN\S\MAVSFTSGSCQKQPQ
		1	DASPPPKEWDQGTLSASLNPSNSESSPSRCPSDPDSTSQPRSGD
			SADVARDVKQPTATPRSYRNFRHPEIVGYSVPGRNGQSQDLVKG
			CARTAQAPEDRSTEPDGSEAEGNQVYFAVYTFKARNPNELSVSA
			NQKLKILEFKOVTGNTEWWLAEVNGKKGYVPSNYIRKTEYT
7015	1842	513	RQAWHE\VAAPSWRGARLVQSVLRVWQVGPHVARERVIPFSSLL
	1		GFQRRCVSCVAGSAFSGPRLASASRSNGQGSALDHFLGFSQPDS
	Í	1	SVTPCVPAVSMNRDEQDVLLVHHPDMPENSRVLRVVLLGAPNAG
	ł	!	KSTLSNQLLGRKVFPVSRKVHTTRCQALGVITEKETQVILLDTP
]	GIISPGKQKRHHLELSLLEDPWKSMESADLVVVLVDVSDKWTRN
	ł	1	QLSPQLLRCLTKYSQIPSVLVMNKVDCLKQKSVLLELTAALTEG
			VVNGKKLKMRQAFHSHPGTHCPSPAVKDPNTQSVGNPQRIGWPH
		1	FKEIFMLSALSQEDVKTLKQYLLTQAQPGPWEYHSAVLTSQTPE
	i.	i	EICANIIREKLLEHLPQEVPYNVQQKTAVWEEGPGGELVIQQKL
			LVPKESYVKLLIGPKGHVISQIAQEAGHDLMDIFLCDVDIRLSV
			KLTK
7016	167	2513	ILNAPKPPPPRDSVEAVAAKRDTGGGSWGTGMDVSGQETDWRST
		1	AFRQKLVSQIEDAMRKAGVAHSKSSKDMESHVFLKAKTRDEYLS
	[LVARLIIHFRDIHNKKSQASVSDPMNALQSLTGGPAAGAAGIGM
	ĺ	1	PPRGPGQSLGGMGSLGAMGQPMSLSGQPPPGTSGMAPHSMAVVS
		1	TATPQTQLQLQQVAAAAAATARSSSSSRRRYSSSSSSNSKQ
		[FQAQQSAMQQ\QFQA\VVQQQQQL\QQQQQQQQHLIKLHHQNQQ
			QIQQQQQLQRIAQLQLQQQQQQQQQQQQQQQQQALQAQPPIQQP
	ļ		PMQQPQPPPSQALPQQLQQMHHTQHHQPPPQPQQPPVAQNQPSQ
	Í	1	LPPQSQTQPLVSQAQALPGQMLYTQPPLKFVRAPMVVQQPPVQP
		1	QVQQQQTAVQTAQAAQMVAPGVQVSQSSLPMLSSPSPGQQVQTP
			QSMPPPPQPSQQPSQPNSNVSSGPAPSPSSFLPSPSPQPF
	1	İ	\QSPVTARTPQNFSVPSPGPLNTPVNPSSVMSPAGSSQAEEQQY
		ł	LDKLKQLSKYIEPLRRMINKIDKNEDRKKDLSKMKSLLDILTDP
		1	SKRCPLKTLQKCBIALEKLKNDMAVPTPPPPPVPPTKQQYLCQP
	ļ		1
		1	LLDAVLANIRSPVFNHSLYRTFVPAMTAIHGPPITAPVVCTRKR
			LLDAVLANIRSPVFNHSLYRTFVPAMTAIHGPPITAPVVCTRKR RLEDDERQSIPSVLQGEVARLDPKFLVNLDPSHCSNNGTVHLIC
			LLDAVLANIRSPVFNHSLYRTFVPAMTAIHGPPITAPVVCTRKR RLEDDERQSIPSVLQGEVARLDPKFLVNLDPSHCSNNGTVHLIC KLDDKDLPSVPPLELSVPADYPAQSPLWIDRQWQYDANPFLQSV
			LLDAVLANIRSPVFNHSLYRTFVPAMTAIHGPPITAPVVCTRKR RLEDDERQSIPSVLQGEVARLDPKFLVNLDPSHCSNNGTVHLIC KLDDKDLPSVPPLELSVPADYPAQSPLWIDRQWQYDANPFLQSV HRCMTSRLLQLPDKHSVTALLNTWAQSVHQACLSAA
7017	1	1785	LLDAVLANIRSPVFNHSLYRTFVPAMTAIHGPPITAPVVCTRKR RLEDDERQSIPSVLQGEVARLDPKFLVNLDPSHCSNNGTVHLIC KLDDKDLPSVPPLELSVPADYPAQSPLWIDRQWQYDANPFLQSV HRCMTSRLLQLPDKHSVTALLNTWAQSVHQACLSAA INLGNTCYMNSVI*ALFMATDFRRQVLSLNLNGCNSLMKKLQHL
7017	1	1785	LLDAVLANIRSPVFNHSLYRTFVPAMTAIHGPPITAPVVCTRKR RLEDDERQSIPSVLQGEVARLDPKFLVNLDPSHCSNNGTVHLIC KLDDKDLPSVPPLELSVPADYPAQSPLWIDRQWQYDANPFLQSV HRCMTSRLLQLPDKHSVTALLNTWAQSVHQACLSAA INLGNTCYMNSVI*ALFMATDFRRQVLSLNLNGCNSLMKKLQHL FAFLAHTQREAYAPRIFFEASRPPWFTPRSQQDCSEYLRFLLDR
7017	1	1785	LLDAVLANIRSPVFNHSLYRTFVPAMTAIHGPPITAPVVCTRKR RLEDDERQSIPSVLQGEVARLDPKFLVNLDPSHCSNNGTVHLIC KLDDKDLPSVPPLELSVPADYPAQSPLWIDRQWQYDANPFLQSV HRCMTSRLLQLPDKHSVTALLNTWAQSVHQACLSAA INLGNTCYMNSVI*ALFMATDFRRQVLSLNLNGCNSLMKKLQHL
7017	1	1785	LLDAVLANIRSPVFNHSLYRTFVPAMTAIHGPPITAPVVCTRKR RLEDDERQSIPSVLQGEVARLDPKFLVNLDPSHCSNNGTVHLIC KLDDKDLPSVPPLELSVPADYPAQSPLWIDRQWQYDANPFLQSV HRCMTSRLLQLPDKHSVTALLNTWAQSVHQACLSAA INLGNTCYMNSVI*ALFMATDFRRQVLSLNLNGCNSLMKKLQHL FAFLAHTQREAYAPRIFFEASRPPWFTPRSQQDCSEYLRFLLDR
7017	1	1785	LLDAVLANIRSPVFNHSLYRTFVPAMTAIHGPPITAPVVCTRKR RLEDDERQSIPSVLQGEVARLDPKFLVNLDPSHCSNNGTVHLIC KLDDKDLPSVPPLELSVPADYPAQSPLWIDRQWQYDANPFLQSV HRCMTSRLLQLPDKHSVTALLNTWAQSVHQACLSAA INLGNTCYMNSVI*ALFMATDFRRQVLSLNLNGCNSLMKKLQHL FAFLAHTQREAYAPRIFFEASRPPWFTPRSQQDCSEYLRFLLDR LHEEEKILKVQASHKPSEILECSETSLQEVASKAAVLTETPRTS
7017	1	1785	LLDAVLANIRSPVFNHSLYRTFVPAMTAIHGPPITAPVVCTRKR RLEDDERQSIPSVLQGEVARLDPKFLVNLDPSHCSNNGTVHLIC KLDDKDLPSVPPLELSVPADYPAQSPLWIDRQWQYDANPFLQSV HRCMTSRLLQLPDKHSVTALLNTWAQSVHQACLSAA INLGNTCYMNSVI*ALFMATDFRRQVLSLNLNGCNSLMKKLQHL FAFLAHTQREAYAPRIFFEASRPPWFTPRSQQDCSEYLRFLLDR LHEEEKILKVQASHKPSEILECSETSLQEVASKAAVLTETPRTS DGEKTLIEKMFGGKLRTHIRCLNCRSTSQKAEAFTDLSLAFWPS
7017	1	1785	LLDAVLANIRSPVFNHSLYRTFVPAMTAIHGPPITAPVVCTRKR RLEDDERQSIPSVLQGEVARLDPKFLVNLDPSHCSNNGTVHLIC KLDDKDLPSVPPLELSVPADYPAQSPLWIDRQWQYDANPFLQSV HRCMTSRLLQLPDKHSVTALLNTWAQSVHQACLSAA INLGNTCYMNSVI*ALFMATDFRRQVLSLNLNGCNSLMKKLQHL FAFLAHTQREAYAPRIFFEASRPPWFTPRSQQDCSEYLRFLLDR LHEEEKILKVQASHKPSEILECSETSLQEVASKAAVLTETPRTS DGEKTLIEKMFGGKLRTHIRCLNCRSTSQKAEAFTDLSLAFWPS YSLEYMSCPDCSQSPSIQDGGLMQASVPGPSEEPVVYNPTTAAF

SEQ	Predicted	Predicted end	Amino noid gogment containing of the
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1.0.	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
ļ	i	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ŀ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
J	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence		\=possible nucleotide insertion)
			FSSLSESWSVDVDFTDLSENLAKKLKPSGTDEASCTKLVPYLLS
į .	ł	1	SVVVHSGISSESGHYYSYARNITSTDSSYQMYHQSEALALASSQ
1	1	}	SHLLGRDSPSAVFEQDLENKEMSKEWFLFNDSRVTFTSFQSVQK
	1	1	ITSRFPKDTAYVLLYKKQHSTNGLSGNNPTSGLWINGDPPLQKE
1	1	1	LMDAITKDNKLYLQEQELNARARALQAASASCSFRPNGFDDNDP
Í	l.		PGSCGPTGGGGGGGFNTVGRLVF
7018	484	1000	
/010	1 404	1066	SLVFRGNTWSGEAGHHCSALFNLAAYHQLFVGTERIRAPE11FQ
1	1	1	PSLIGEEQAGIAETLQYILDRYPKDVQEMLVQNVFLTGGNTMYP
1	Ĭ	1	GMKARMEKELLEMRPFRSSFQVQLASNPVLDAWYGARDWALNHL
1	1	}	DDNEVWITRKEYEEKGGEYLKEHCASNIYVPIRLPKQASRSSDA
L	L		QASSKGSAAGGGGAGEQA
7019	1048	335	APGGFLVTMVFPAPSPPWMLGCCSHEVTAGPPTLCKDMSALVAA
1		1	RMRHIPLAPGSDWRDLPNIEVRLSDGTMARKLRYTHHDRKNGRS
1		}	SSGALRGVCSCVEAGKACDPAARQFNTLIPWCLPHTGNRHNHWA
i	1	1	GLYGRLEWDGFFSTTVTNPEPMGKQGRVLHPEQHRVVSVRECAR
•	1	(SQGFPDTYRLFGNILDKHRQVGNAVPPPLAKAIGLEIKLCMLAK
l	[ARESASAKIKEEEAAKD
7020	1	2154	FADSKRKSVLLDKIKNLQVALTSKQQSLETAMSFVARNTFKRVR
	-	1	
			NGFLMRKVAVFFSNTPTRASPQLREAVLKLSDAGITPLFLTRQE
	ţ		DRQLINALQINNTAVGHALVLPAGRDLTDFLENVLTCHVCLDIC
1)		NIDPSCGFGSWRPSFRDRRAAGSDVDIDMAFILDSAETTTLFQF
i		į	NEMKKYIAYLVRQLDMSPDPKASQHFARVAVVQHAPSESVDNAS
	1	}	MPPVKVEFSLTDYGSKEKLVDFLSRGMTQLQGTRALGSAIEYTI
1		1	ENVFESAPNPRDLKIVVLMLTGEVPEQQLEEAQRVILQAKCKGY
1	1	i	FFVVLGIGRKVNIKEVYTFASEPNDVFFKLVDKSTELNEEPLMR
			FGRLLPSFVSSENAFYLSPDIRKQCDWFQGDQPTKNLVKFGHKQ
	l	į	VNVPNNVTSSPTSNPVTTTKPVTTTKPVTTTTKPVTTTTKPVTI
}	ł	ł	INQPSVKPAAAKPAPAKPVAAKPVATKTATVRPPVAVKPATAAK
1		ì	PVAAKPAAVRPPAAAAAKPVATKPEVPRPQAAKPAATKPATTKP
ĺ	j		MVKMSREVQVFEITENSAKLHWERPEPPGPYFYDLTVTSAHDQS
{	İ	1	LVLKQNLTVTDRVIGGLLAGQTYHVAVVCYLRSQVRATYHGSFS
	ļ		TKKSQPPPPQPARSASSSTINLMVSTEPLALTETDICKLPKDEG
ł	ł	i	TCRDFILKWYYDPNTKSCARFWYGGCGGNENKFGSQKECEKVCA
			PVLAKPGVISVMGT
7021	2	338	VNAVSFFPNGYAFATGSDDATCRLFDLRADQELLLYSHDNIICG
1] ,,,,	
			ITSVAFSKSGRLLLAGYDDFNCNVWDTLKGDRAGVLAGHDNRVS
7022		0.5.5	CLGVTDDGMAVATGSWDSFLRIWN
1022	2	856	VYIGSFWSHPLLIPDNRKLFEAEEQDLFRDIQSLPRNAALRKLN
İ	·		DLIKRARLAKVHAYIISSLKKEMPSVFGKDNKKKELVNNLAEIY
			GRIEREHQISPGDFPNLKRMQDQLQAQDFSKFQPLKSKLLEVVD
			DMLAHDIAQLMVLVRQEESQRPIQMVKGGAFEGTLHGPFGHGYG
1			EGAGEGIDDAEWVVARDKPMYDEIFYTLSPVDGKITGANAKKEM
1			VRSKLPNSVLGKIWKLADIDKDGMLDDDEFALANHLIKVKLEGH
1			ELPNELPAHLLPPSKRKVAE
7023	2	748	AMVFGGVVPYVPQYRDIRRTQNADGFSTYVCLVLLVANILRILF
		· = =	WFGRRFESPLLWQSAIMILTMLLMLKLCTEVRVANELNARRRSF
			TAADSKDEEVKVAPRRSFLDFDPHHFWQWSSFSDYVQCVLAFTG
1			VAGYITYLSIDSALFVETLGFLAVLTEAMLGVPQLYRNHRHQST
			EGMSIKMVLMWTSGDAFKTAYFLLKGAPLQFSVCGLLQVLVDLA
-			ILGQAYAFARHPQKPAPHAVHPTGTKAL
7024	1207	190	RTGVTGVVAQVWMFGGGGVLSSGEQLQMPVKPERGLGPSDGWLV
			SSRRGSPGTVLGLPFWLLTPVLVSRSIRSMLLLTRSPTAWHRLS
			QLKPPVLPGTLGGQALHLRSWLLSRQGPAETGGQGQPQGPGLRT
1			RLLITGLFGAGLGGAWLALRAEKERLQQQKRTEALRQAAVGQGD
			FHLLDHRGRARCKADFRGQWVLMYFGFTHCPDICPDELEKLVQV
1			VRQLEAEPGLPPVQPVFITVDPERDDVEAMARYVQDFHPRLLGL
			1

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
j	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Ī	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown *=Ston
	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
1			TGSTKQVAQASHSYRVYYNAGPKDEDODYIVDHSIAIYIJNDDG
7025	232		LFTDYYGRSRSAEQISDSVRRHMAAFRSVLS
1023	232	832	ERNSPIGNNENL*K\HSLDCLCFRGDWEGNTQFQTLQDNQEECF
1	İ		KQVIRTCEKRPTFNQHTVFNLHQRLNTGDKLNEFKELGKAFISG
1	1		SDHTQHQLIHTSEKFCGDKECGNTFLPDSEVIQYQTVHTVKKTY
1			ECKECGKSFSLRSSLTGHKRIHTGEKPFKCKDCGKAFRFHSQLS VHKRIHTGEKSYECKECGKAFSCG
7026	328	1146	NPNPSIGDIKDIKKAAKSMLDPAHKSHFHPVTPSLVFLCFIFDG
			LHQALLSVGVSKRSNTVVGNENEERGTPYASRFKDMPNFIALEK
1	ľ		SSVLRHCCDLLIGVAAGSSDKICTSSLQVQRRFKAMMASIGRLS
1		•	HGESADLLISCNAESAIGWISSRPWVGELMFTFLFGDFESPLHK
ĺ			LRKSS*LPRKHR*QPINAVRMFLDQCMDGSIALRAIVSEIPVFE
			EKKNNG*KGIGEIF*VWGCTLPPHYWGAVTTNVPKLSNSGKLLG
7027			QDEQPHIFG
/02/	43	954	GRRLQQQQRPEDAEDGAEGGGKRGEAGWEGGYPEIVKENKLFEH
			YYQELKIVPEGEWGQFMDALREPLPATLRITGYKSHAKEILHCL
1 1			KNKYFKELEDLEMDGQKVEVPQPLSWYPEELAWHTNLSRKILRK
			SPHLEKFHQFLVSETESGNISRQEAVSMIPPLLLNVRPHHKILD
[]			MCAAPGSKTTQLIEMLHADMNVPFPEGFVIANDVDNKRCYLLVH QAKRLSSPCIMVVNHDASSIPRLQIDVDGRKEILFYDRILCDVP
			CSCDGTMRKNIDVWKKWTTLNSLQLHGLQLRIATRGAEQL
7028	189	608	SRPPPEPEPTMVEKGSDSSEKGGVPGTPSTQSLGSKNFIRNS
	1		KKMQSWYSMLSPTYKQRNEDFRKLFSKLPEAERLIVDYSCALQR
i i			EILLQGRLYLSENWICFYSNIFRWETTISIQLKEVTCLKKEKTA
			KLIPNAIQ
7029	1343	40	VLESNTEAKQATGTSSKLRHGTGQEKGREGPRCPSGLAQLRLWG
í l			/PCPHAGRETGPRASAPIPGS*GHGWHW*RKDGRGERSEGPSat.
ĺ			SPHSPSLLNMQQAPTHVGPGMGSQRPRSSVVPEQVGVGSQLSRE
			RWRA*RSLPGAAASERTEMTKERSP/RPCQGYDSSNWFTQPGKK
İ			TRKRNSRRNTMVSRGGGCLLYPLQSIMPE*QLR*GAHASPPTQG R*GKGGPRSPLTKASGTTHIPTPFFGSIP/RPTRDSGPGTDNS\
1 1			AAPGQKRGHREA*QGPEPV/WGRVTTHLQGPAG*TKPLGS\RNW
			VPGPAEGEQGEGAGLEGRP*PLKGCRSTLTFSPQLSIPMVGKKP
			PEGTTASFFP\RSCHSE*RKPPPSCPHAPALSLPHPLPLPPL
			PLPLPGAGT*HSARSGRPGQSETGSLCHNCHHCPPHCPKCSPGG
7030			T
7030	2	521	FVCFSAPGSGQGKRRVNMELSAVGERVFAAEALLKRRIRKGRM
	.		EYLVKWKGWSQKYSTWEPEENILDARLLAAFEEREREMELYGPK
' I	1		KRGPKPKTFLLKAQAKAKAKTYEFRSDSARGIRIPYPGRSPQDL
			ASTSRAREGLRN\RVCPRQRAAPAPAPAP\PRRGPSGPGPRPG*G
7031	960	59	PGLHFPGPGGPSKHGFVPASEQHQHQQHLPRRGPSGPGPRPG
		3,5	HCSVPGAEWPRKPPAQICPQLTSRPHLSSPRSLSPGCGHSFGPG /CKPS/RHCDELHEGPSRTAALPCGKPQPKHGVEECG/PCPCLA
1		İ	PRRLTEPPALTVSPVGRAAPSGAL*PSGRACSACSHRLAPEAAL
			SAAAPRPSLGSGQNASGLPAASLPPQDSSQPHKTVPSPARSVPP
j			LGAQARAAPPRLWCPRALVSG*EASPEAVSVAAGPPVPGPTPST
·			SGSTASHSRRGC*SPR*TPAPPRRDHGRSAAFEVLTAAASAQPC
			ASQGGPRPTGAGRTPSPLGLPFSRGPPAASARPFCRHPSL
7032	1393	2104	RRPGRTEPVEPPPVPPPPRASNSKSRCR*RNLHLAPL*OSPLRK
1			SRQIGTSSLPFGRSAGERPRPAATFCLSRGGSSPVFL*PSSSSL
1			EPWMKRQFGRLHSLFWKSWQKMNSFLLTPKLDTSLMSGWRYROR
1	1		LPRLHTFLKKSLQMASELAPPLPTPAPLASSLPPPPGPPPLL.DV
1	1		PLA*LSRSGILVPPNSGFSLSC\PLGDH*GSSGEVRGSCGSPPP
7033	689		HHCWVLPPPP*LLLPPR
		815	RSRDCLSSSATSNRARRSKCSGPKRATPLDSGPGP*APPGPSSA

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	
1,0.	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
1	l e	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
ł	J	sequence	
	sequence	<u>L</u>	\=possible nucleotide insertion)
		İ	LMMPSSCPWRTGALGPSPAGSRALGRCTSSVGPGSRWLTRTSSP
	i	l .	GCATRTWRTMRMEPRPLRSRMGESAPGIPAELPSAAPSGPSAPS
	İ	1	AAAPSAPTTPAAAGPNTL*SRRTAEWCWPPSCSCCWGWC*SWSA
1	1	ł	WDWRRPPLQVSPAPSSSCRASCCWCLESIT*SSSTARSRATGAS
	ļ	1	
		i	SSSTCPTSRSDRGAAWTP\SPMGAPLLPCSVPLISREEALQDPR
		<u>L</u>	NPSP*GVCSGSSGHAGLALGKPPVACSVP
7034	92	1942	EDTSSMPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYRERV
			KAMFYHAYDSYLENAFPFDELRPLTCDGHDTWGSFSLTLIDALD
	ļ		TLL\TLFYFQILGNVSEFQRVVEVLQDSVDFDIDVNASVFETNI
	1	!	
j	Į	1	RVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKLLPA
1		1	FQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSL
1	1		TGDPVFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWVAQDAG
1	1	1	IGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDW
1		1	YLWVQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTFLNYY
l		1	TVWKQFGGLPEFYNIPQGYTVEKREGYPLRPELIESAMYLYRAT
i		1	
			GDPTLLELGRDAVESIEKISKVECGFATIKDLRDHKLDNRMESF
1			FLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGYI
1	1		FNTEAHPIDPAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQ
		1	KNTVSSGPWEPPARPGTLFSPENHDQARERKPAKQKVPLLSCPS
1		1	QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK
1	1.	i	K
7035	92	1942	<u> </u>
1 ,033	,,,,	1942	EDTSSMPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYRERV
			KAMFYHAYDSYLENAFPFDELRPLTCDGHDTWGSFSLTLIDALD
	•	ļ	TLL\TLFYFQILGNVSEFQRVVEVLQDSVDFDIDVNASVFETNI
1		!	RVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKLLPA
1		1	FQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSL
		i	TGDPVFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWVAODAG
1			IGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDW
		i	
1		· ·	YLWVQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTFLNYY
1	1	ŧ	TVWKQFGGLPEFYNIPQGYTVEKREGYPLRPELIESAMYLYRAT
ì			GDPTLLELGRDAVESIEKISKVECGFATIKDLRDHKLDNRMESF
1	1	1	FLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGYI
	İ	\	FNTEAHPIDPAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFO
1	ļ.	1	KNTVSSGPWEPPARPGTLFSPENHDQARERKPAKQKVPLLSCPS
	ļ	1	
	1	Į.	QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK
		L	K
7036	442	761	CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT
1	1		RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP
1	,		PPPPPPPPPRRPPRNRRPG
7037	442	761	CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT
1	1	1 '31	DWM+EDAY COCODO (DY COLLIAD PROCESSION PROCE
I	1		RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP
		L	PPPPPPPPPRRPPRNRRPG
7038	155	891	GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL
1		I	QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNO
1	1	l	LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM
1	1	1	
1	\	1	QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA
ł	1	i	LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR
			LQEAASPAAERACRSSKGTSTSRTG
7039	155	891	GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL
1		1	QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ
}	Į.	j	LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM
1	1	I	· · · · · · · · · · · · · · · · · · ·
1	1	1	QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA
1	1		LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR
	<u> </u>	L	LQEAASPAAERACRSSKGTSTSRTG
7040	34	789	KITPPRRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS
1			GYESVMRDSEATGSASSAQDSTSENSSSVGGRCRSLKTPKKRSN
		<u> </u>	

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, FaPhenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
Į	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
l	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
-	sequence	Sequence	Codon, /=possible nucleotide deletion,
			\=possible nucleotide insertion)
	1		PGSQRRRLIPALSLDTSSPVRKPPNSTGVRWVDGPLRSSPRGLG
	i	i	EPFEIKVYEIDDVERLQRRRGGASKEAMCFNAKLKILEHRQQRI
			AEVRAKYEWLMKELEATKQYLMLDPNKWLSEFDLEQVWELDSLE
7041	1 1		YLEALECVTERLESRVNFCKAHLMMITCFDIT
7041	1 -	567	SGRVAMGRRRAPAGGSLGRALMRHQTQRSRSHRHTDSWLHTSEL
1		!	NDGYDWGRLNLQSVTEQSSLDDFLATAELAGTEFVAEKI.NIKEV
			PAEARTGLLSFEESQRIKKLHEENKOFLCIPRRPNWNONTTDEE
1			LKQAEKDNFLEWRRQL\VRLEEEQKLILTPFERNLDFWROLWRV
7042			IERSDIVVQIVDA
7042	7	345	PIHMAAAALRADI\ISPLFPHIQGYLLLSASHG\ATSLHTKGAL
1	Ì	,	PLETVTMYTVIPKSKYVLVKPDTOYPYSENLDEFKRLAENSASN
			DDLLMAEVAISDYGDKLTLELREKY
7043	2	2170	ARGMAARDSDSEEDLVSYGTGLEPLEEGERPKKPIPLQDQTVRD
1			EKGRYKRFHGAFSGGFSAGYFNTVGSKEGWTPSTFVSSPONPAD
	1	•	KSVLGPEDFMDEEDLSEFGIAPKAIVTTDDFASKTKDPTPEKAP
1	l i		QLAAATAPIPGATLLDDLITPAKLSVGFELLRKMGWKEGOGVGP
			RVKRRPRRQKPDPGVKIYGCALPPGSSEGSEGEDDDVLDDNDTFF
			APKDVTPVDFTPKDNVHGLAYKGLDPHQALFGTSGEHFNLFSGG
1	ł i		SERAGDLGEIGLNKGRKLGISGQAFGVGALEEEDDDIYATETLS
			KYDTVLKDEEPGDGLYGWTAPRQYKNQKESEKDLRYVGKILDGF
	J		SLASKPLSSKKIYPPPELPRDYRPVHYFRPMVAATSENSHLLQV
İ	i		LSESAGKATPDPGTHSKHQLNASKRAELLGETPIQGSATSVLEF
1	ļ		LSQKDKERIKEMKQATDLKAAQLKARSLAQNAQSSRAQPSPAAA
			AGHCSWNMALGGGTATLKASNFKPFAKDPEKQKRYDEFLVHMKQ
1			GQKDALERCLDPSMTEWERGRERDEFARAALLYASSHSTLSSRF
1	ļ		THAKEEDDSDQVEVPRDQENDVGDKQSAVKMKMFGKLTRDTFEW
1			HPDKLLFQ/RLVGLPRVKRDKYSVFNFLTLPETASLPTTQASSE
			KVSQHRGPDKSRKPSRWDTSKHEKKEDSISEFLRLARSKAEPPK
1 1	}		QQSSPLVNKEEEHAPELSAN
7044	276	734	EVYLTDEFAKGRKVADLYELVQYAGNIIPRLYLLITVGVVYVKS
			FPQSRKDILKDLVEMCRGVQHPLRGLFLRNYLLQCTRNILPDEG
1	1		EDTDEETTCDICDEMCKGVQHPLKGLELKNYLLQCTRNILPDEG
)	1		EPTDEETTGDISDSMDFVLLNFAEMNKLWVRMQHQGHSRDREKR ERERQELRILVGTNLVRLSQV
7045	3	513	I GEVMENT CENCOUNCY THE VOID
		323	LGFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP
1 1	ļ		KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK
l i			DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE
7046	3	513	ETRRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSQG
	-	213	LGFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP
į į			KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK
]			DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE
7047	103	405	ETRRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSQG
1 1	103	486	QMKIEKCGWSEGLTSIKGNCHNFYTAISKDVTYKELKNLLNSKN
	ĺ		IMLIDVREIWEILEYQKIPESINVPLDEVGEALQMNPRDFKEKY
7048			NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGFHSYYER
/ ''*	92	627	FFCLTLLSSWDYRHHATRRVISSPVFTMEDSGKTFSSEREEANV
	ļ		WKDLAMTYKQRAENTQEELREFOEGSREYEAELETOLOOJETRN
ļ İ			RDLLSENNRLRMELETIKEKFEVOHSEGYROISALEDDIAOTKA
	Ì		IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI
			EKKW
7049	393	938	KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL
	İ		VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL
			NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKKREEILEEIAKVT
		1	EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX
		1	ASSLWG
7050	393	938	KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL
			TATABO VAGACOS VGAT PARACTEDEL

SEO	Predicted	I Deceded to	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cvsteine, D=Aspartic Acid R
	location		Glutamic Acid, F=Phenylalanine G-Glucino
1	corresponding	corresponding to first	H=H1Stidine, I=Isoleucine, K=Iscine
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion
	Bequeite		\=possible nucleotide insertion)
1		1	VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL
	1		NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKKRERILERTAKUT
J	1]	EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX
7050			ASSLWG
7051	119	816	KKMNLAEICDNAKKGREYALLGNYDSSMVYYQGVMQQIQRHCQS
1		1	VRDPAIKGKWQQVRQELLEEYEOVKSIVGTLESEKIDKDDDRDV
1	1	1	SCQUEPFRDPAVWPPPVPAEHRAPPOIRR/ROSPSKTSFFDNGD
ĺ	ł	1	SRSPGTCRPST\PISKSEKPSTSRDKDYRARGRDDKGRKNMQDG
ı			ASDGEMPKFDGAGYDKDLVEALERDIVSRNPSIHWDDIADLEEA
	<u> </u>	ļ	KKLLREAGVLPMWM
7052	467	715	SCPGRGKMSKLLNPEEMTSRDYYFDSYAHFGIHEEMLKDEVRTL
			TYRNSMYHNKHVFKDKVVLDVGSGTGILSMFAARQGPRR
7053	467	715	SCPGRGKMSKLLNPEEMTSRDYYFDSYAHFGIHEEMLKDEVRTL
1			TYRNSMYHNKHVFKDKVVLDVGSGTGILSMFAARQGPRR
7054	1	1036	GTSORS RETURN PROCESSION OF THE STATE OF THE
		1 2030	GTSQRSRETDARRRSAGAEPTARLPWPAALEEWPSCPCEPLGPG
}			RRCRWDAMEYDEKLARFRQAHLNPFNKQSGPRQHEQGPGEEVPD
	1		VTPEEALPELPPGEPEFRCPERVMDLGLSEDHFSRPVGLFLASD
1			VQQLRQAIEECKQVILELPEQSEKQKDAVVRLIHLRLKLQELKD
	[PNEDEPNIRVLLEHRFYKEKSKSVKQTCDKCNTIIWGLIQTWYT
			CIGCYYRCHSKCLNLISKPCVSSKVSHOAEVELNICDETGLDGO
ł	1 1	i	DYRCAECRAPI/CS/DGVVPSEAROCDYTGOYYCSHCHWNDIAU
7055			IPARVVHNWDFEPRKVSRCSMRYLALMVSRPVI.RI.DETN
,033	2	527	DSRRVSWRSWLANE/WGKHLCLFIWLSMNVI.I.FWKTELLVNOGD
			EYHYLHQMLG/ALCLSRASASVININCSI.II.I.PMCPTI.I.AVI.PC
1	İ		SQKVPSRRTRRLLDKSRTFHITCGATICTFSGVHVAAHLUMALN
1	[FSVNYSEDFVELNAARYRDEDPRKLLFTTVPGLTGVCMEVVI.FI.
7056			M
1036	2	527	DSRRVSWRSWLANE/WGKHLCLFIWLSMNVLLFWKTFLLYNQGP
			EXHYDHQMLG/ALCLSRASASVININCSI.TI.I.DMCDTTITAVIDG
1	l l		SQKVPSRRTRRLLDKSRTFHITCGATICIFSGVHVAAHIJMAIN
	ļ		FSVNYSEDFVELNAARYRDEDPRKLLFTTVPGLTGVCMEVVLFI.
7057			M
/05/	1368	431	GIYLHVNEKIPRPTCIGDRQENDKENLNLENHRDQELLHASCQA
١.			SGEVPSQASLRGFFTEDEPGCFGEGENLPEALONTODEGTGEOL
[[1		SPQERISEKQLGQHLPNPHSGEMSTMWLEEKRETSOKGODDADM
]			AQKLPTCRECGKTFYRNSOLIFHORTHTGETVFOCTTCKKAFIB
[l l	į	SSDFVKHQRTHTGEKPCKCDYCGKGFSDFSGLRHHEKTHTGEKP
į ([г	YKCPICEKSFIQRSNFNRHORVHTGEKPYKCSHCGKGEGWGGGT
, ,	ł	j	DKHQRSHLGKKPFQ*PVTKLSFPISISQPSHKNTQLHQEELCLR
<u> </u>			GYPC
7058	1	469	FSGFGAVPDALGCRMSDLRITEAFLYMDYLCFRALCCKGPPPAR
			PEYDLVCIGLTGSGKTSLLSKLCSESPDNVVSTTGFSIKAVPFO
;	}		NAILNVKELGGADNIRKYWSRYYQGSQGVIFVLDSASSEDDLEA
			ARN*SCTQLLQHPQLCTLPFLILA
7059	1	1178	WPAFPRQPAAAAMDALLGTGPRRARGCLGAAGPTSSGRAARTPA
ļ			APWARPSAWLECUCAUTEDI EL COLLEGAGETSGRAARTPA
I		Ī	APWARPSAWLECVCVVTFDLELGQALELVYPNDFRLTDKEKSSI
		ļ	CYLSFPDSHSGCLGDTQFSFRMRQCGGQRSPWHADDRHYNSRAP
	,	1	VALQREPAHYFGYVYFRQVKDSSVKRGYFQKSLVLVSRLPFVRL
		1	FQALLSLIAPEYFDKLAPCLEAVCSEIDQWPAPAPGQTLNLPVM
ľ			GVVVQVRIPSRVDKSESSPPKQFDQENLLPAPVVLASVHELDLF
J	}	j	RCFRPVLTHMQTLWELMLLGEPLLVLAPSPDVSSEMVI,AI.TSCT.
1	1		QPLRFCCDFRPYFTIHDSEFKEFTTRTQAPPNVVLGVTNPFFIK
7060			TLQHWPHILRVGEPKMSGDLPKOVKLKKPFKV*RPWDTKP
,000	90	1670	SVNLPPSLWPWEEAMDSTKSEPLKGSPEAEDGNIEYKKLVNPSO
			YRFEHLVTQMKWRLQEGRGEAVYQIGVEDNGLLVGLAEEEMRAS

<u> </u>	T-5		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location	location corresponding	Glutamic Acid, F≈Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
}	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	Doquesice	\=possible nucleotide insertion)
			LKTLHRMAEKVGADITVLREREVDYDSDMPRKITEVLVRKVPDN
			QQFLDLRVAVLGNVDSGKSTLLGVLTQGELDNGRGRARLNLFRH
1		{	LHEIQSGRTSSISFEILGFNSKGEVHGINGTQWGQTLRMGW***
1			RT*DGGRVWRLFEIV*MNALRGL*TSSAPLRKSMGNQLN*IKNG
ĺ	(VKIKRQGHPGNGLGPGNSEGVGRAGRRH*GPWALGQVVNYSDSR
			TAEEICESSSKMITFIDLAGHHKYLHTTIFGLTSYCPDCALLLV
ĺ	1		SANTGIAGTTREHLGLALALKVPFFIVVSKIDLCAKTTVERTVR
ļ	i		QLERVLKQPGCHKVPMLVTSEDDAVTAAQQFAQSPNVTPIFTLS
i		}	SVSGESLDLLKVFLNILPPLTNSKEQEELMQQLTEFQVDEIYTV
1 .			PEVGTVVGGTLSR*IDLLATLPTQPSPIYSKTSWPKGGDPGI
7061	364	710	ARMPSPLGPPCLPVMDPETTLEEPETARLRFRGFCYQEVAGPRE
			ALARLRELCCQWLQPEAHSKEQMLEMLVLEQFLGTLPPEIQAWV
}	j		RGQRPGSPEEAAALVEGLQHDP*ARMPSPLGPPCLPVMDPETTL
]	•		EEPETARLRFRGFCYQEVAGPREALARLRELCCQWLQPEAHSKE
ļ	ļ	ļ	QMLEMLVLEQFLGTLPPEIQAWVRGQRPGSPEEAAALVEGLQHD
<u> </u>			PGQLLG
7062	71	744	AKAGTNLERLHWLSYFFCIPKHKLKSSQKDKVRQFMACTQAGER
			TAIYCLTQNEWRLDEATDSFFQNPDSLHRESMRNAVDKKKLERL
1			YGRYKDPQDENKIGVDGIQQFCDDLSLDPASISVLVIAWKFRAA
]	1		TQCEFSRKEFLDGMTELGCDSMEKLKALLPRLEQELKDTAKFKD
İ	İ	}	FYQFTFTFAKNPGQKGLDL*MAGAYWKLVLSGRFKFLYLWNTFL
7063			менн
/063	2	562	LRTVPDLPGRRFRAMRTGQRR*PELPPDMNSLEQAEDLKAFERR
l	1		LTEYIHCLQPATGRWRMLLIVVSVCTATGAWNWLIDPETQKVSF
ł	ł		FTSLWNHPFFTISCITLIGLFFAGIHKRVVAPSIIAARCRTVLA
İ			EYNMSCDDTGKLILKPRPHVQ*QSSLIVMGLKIAFLRISDTAKS HKGFLLRLDM
7064	300	884	RDTGSDPSSTRRLCSTCCTGH*PAEPIASPHPSRGTCPPASSAS
	1	004	SRRTGCWTCPPESGHAQARRSRRASASRWGARGAVRSAVAARGC
	Ì.		SSRAGRWLETPGRRRGPPACAAAAGRLRGPAP*AAPPTASVPAR
			CRCPAARTGAPAAATWLRRRLSGLRAPALGRRRSPGPSPKSAAP
ļ			PLLTPLGAGRAGGSRANS
7065	1	555	ATTTHSARRSGRGAAAEAAASAAGGRQKGPDRKAWEGRRTTPGG
]		===	RSQSEPKAPPPQKRSEAAFASMAHSPVAVQVPGMQNNIADPEEL
	'		FTKLERIGKGSFGEVFKGIDNRTQQVVAIKIIDLEEAEDEIEDI
	ŀ		QQEITVLSQCDSSYVTKYYGSYLKGSKLWIIMEYLGGGSALDLL
			RAGPFDEFQ
7066	356	676	PGPQRGPWRAREGGHPLDPADHPRAPASLRSNVRAATMMQICDT
			YNQKHSLFNAMNRFIGAVNNMDQTVMVPSLLRDVPLADPGLDND
	<u> </u>		VGVEVGGSGGCLEERTPP
7067	152	973	KENITMATEIGSPPRFFHMPRFQHQAPRQLFYKRPDFAQQQAMQ
			QLTFDGKRMRKAVNRKTIDYNPSVIKYLENRIWQRDQRDMRAIO
			PDAGYYNDLVPPIGMLNNPMNAVTTKFVRTSTNKVKCPVFVVRW
			TPEGRRLVTGASSGEFTLWNGLTFNFETILQAHDSPVRAMTWSH
			NDMWMLTADHGGYVKYWQSNMNNVKMFQAHKEAIREARFIHNIP
]		FSVVPIVMVKLFSKCILGAEMHGLCQFLGNFLHPINTIFFFVFT
70.22			HSPFCWAPF
7068	222	816	DTMKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDD
			DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
	ļ J		VHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLY
			GLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSL
7069			AELRIHENKVKKIQKDTFKKK
7069	1147	1765	FRDHRRYFYVNEQSGESQWEFPDGEEEEESQAQENRDETLAKQ
			TLKDKTGTDSNSTESSETSTGSLCKESFSGQVSSSSLMPLTPFW
L	<u></u>		TLLQSNVPVLQPPLPLEMPPPPPPPPPPESPPPPPPPPPPPPAPKMPPP

686	Throdianad	1 500-31-50-3	
SEQ	Predicted beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location	E .	Glutamic Acid, F=Phenylalanine, G=Glycine,
1		corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid		P=Proline, Q=Glutamine, R=Arginine,
	residue of	residue of	S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	1	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
		1	EKTKKGRKDKAKKSKTKMPSLVKKWQSIQRELDEEDNSSSSEED
7070	 	547	RVSTAQKRIEEWKQQQLVSGMAERNANFEA
1 7070	1	547	DGTMEDSEAVQRATALIEQRLAQEEENEKLRGDARQKLPMDLLV
ſ		İ	LEDEKHHGAQSAALQKVKGQERVRKTSLDLRREIIDVGGIQNLI
	i	1	ELRKKRKQKKRDALAASHEPPPEPEEITGPVDEETFLKAAVEGK
ļ		}	MKVIEKFLADGGSADTCDQFRRTALHRASLEGHMEILEKLLDNG
2052			ATVDFQ
7071	2	921	ARGTLRALETAKKVGKVGANGQKAAGPSADSVTENKIGSPPKTP
ı		1	VSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPAYPPHSENIQY
	1	ł	FQDPRTQIPFEVPQYPQTGYYPPPPTVPAGVAPCVPRFVRSNNV
		1	PESSI.PPASMPYADHYSTFSPRDRMNSSPYQPPPPQPYGPVPPV
1			PSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPMDVMHSSVYQT
		,	SLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQ
7072	 	000	IRRKPDQWAQYHTQKAPLVSSTLPVATQSPTPPSTLNRGEGS
1072	2	921	ARGTLRALETAKKVGKVGANGQKAAGPSADSVTENKIGSPPKTP
1	1	l .	VSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPAYPPHSENIQY
İ		1	FODPRTQIPFEVPQYPQTGYYPPPPTVPAGVAPCVPRFVRSNNV
			PESSLPPASMPYADHYSTFSPRDRMNSSPYQPPPPQPYGPVPPV
1		1	PSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPMDVMHSSVYQT
			SLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQ
7073			IRRKPDQWAQYHTQKAPLVSSTLPVATQSPTPPSTLNRGEGS
7073	50	504	LAHGSFGVSDFPAPAAAPAHTLTSFSGSLSPQFRKPLGRAPAMP
1	1		LVRYRKVVILGYRCVGKTSLAHQFVEGEFSEGYDPTVENTYSKI
	1	1	VTLGKDEFHLHLVDTAGQDEYSILPYSFIIGVHGYVLVYSVTSL
7074	263	1003	HSFQVIESLYQKLHEGHGK
/0/4	263	1003	VCPVLCSTRQEPGHSSLVTYFGKPTRRKEFLLGHCIAAGKMNIS
1	į.]	VDLETNYAELVLDVGRVTLGENSRKKMKDCKLRKKQNERVSRAM
]	}	j	CALLNSGGGVIKAEIENEDYSYTKDGIGLDLENSFSNILLFVPE YLDFMQNGNYFLIFVKSWSLNTSGLRITTLSSNLYKRDITSAKV
	Ì	1	MNATAALEFLKDMKKTRGRLYLRPELLAKRPRVDIQEENNMKAL
j		1	AGVFFDRTELDRKEKLTFTESTHVEI
7075	598	1005	NYINFFFRKEYPPHVQKVEINPVRLSRLQGVERIMKKTEESESQ
]		1005	VEPEIKRKVQQKRHCSTYQPTPPLSPASKKCLTHLEDLQRNCRO
			AITLNESTGPLLRTSIHQNSGGQKSQNTGLTTKKFYGNNVEKVP
	1		IDII (
7076	279	1049	LQSESSNAAEGNEQRHEDEQRSKRGGWSKGRKRKKPLRDSNAPK
1	- · -		SPLTGYVRFMNERREQLRAKRPEVPFPEITRMLGNEWSKLPPEE
1	1	ļ	KQRYLDEADRDKERYMKELEQYQKTEAYKVFSRKTODROKGKSH
1	1	Ì	RQDAARQATHDHEKETEVKERSVFDIPIFTEEFLNHSKAREAEL
1			RQLRKSNMEFEERNAALQKHVESMRTAVEKLEVDVIQERSRNTV
1			LOQHLETLROVLTSSFASMPLPEXGETPTVDTIDSYM
7077	3	1119	SSMGSNSEINGLALRKTDKYGFLGGSQYSGSLKSSIPVDVAROR
1			ELKWLDMFSNWDKWLSRRFQKVKLRCRKGIPSSLRAKAWQYLSN
1			SKELLEQNPRKFEELERAPGDPKWLDVIEKDLHROFPFHEMFAA
1			RGGHGQQDLYRILKAYTIYRPDEGYCQAQAPVAAVLLMHMPAEO
1			AFWCLVQICDKYLPGYYSAGLEAIQLDGEIFFALLRRASPLAHR
1			HLRRQRIDPVLYMTEWFMCIFARTLPWASVLRVWDMFFCEGVKI
1			IFRVALVLLRHTLGSVEKLRSCQGMYETMEQLRNLPQQCMQEDF
[(LVHEVTNLPVTEALIERENAAQLKKWRETRGELQYRPSRRLHGS
İ			RAIHEERRRQQPPLGPSSS
7078	483	767	FQGQRMAGEQKPSSNLLEQFILLAKGTSGSALTALISOVLEAPG
			VYVFGELLELANVOELAEGANAAYLOLLNLFAYGTYPDYIANKE
1	f		SLPELY
7079	2	376	SVVEFKRPKEPSGSDGESDGPIDVGQEGQLSQMARPLSTPSSSQ
j	}	= . •	MQARKKRRGIIEKRRRDRINSSLSELRRLVPTAFEKQGSSKLEK
	<u> </u>	L	1

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
]	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	201	\=possible nucleotide insertion)
	Dequence		LKEOLRGAQELAASSQOKATLLGEELASAAAARDRTIAELHRSR
1	1	ł	LEVAEVNGKLAELGLHLKEEKCOWSKERAGLLQSVEAEKDKILK
		}	LSAEILRLEKAVQEERTQNQVFKTELAREKDSSLVQLSESKREB
ļ	1	}	TELRSALRVLOKEKEOLOEEKOELLEYMRKLEARLEKVADEKWN
1	1	1	
ļ	{	}	EDATTEDEEAAVGLSCPAALTDSEDESPEDMRLHPMAFVSVETQ
		<u></u>	ASLLLGLE
7090	33	1775	SVCWEDRYLKARMEESPLSRAPSRGGVNFLNVARTYIPNTKVEC
į.			HYTLPPGTMPSASDWIGIFKVEAACVRDYHTFVWSSVPESTTDG
1	1	1	SPIHTSVQFQASYLPKPGAQLYQFRYVNRQGQVCGQSPPFQFRE
i		1	PRPMDELVTLEEADGGSDILLVVPKATVLQNQLDESQQERNDLM
1			QLKLQLEGQVTELRSRVQELERALATARQEHTELMEQYKGISRS
1		J	HGEITEERDILSRQQGDHVARILELEDDIQTISEKVLTKEVELD
1			RLRDTVKALTREOEKLLGQLKEVQADKEQSEAELQVAQQENHHL
1			NLDLKEAKSWQEEQSAQAQRLKDKVAQMKDTLGQAQQRVAELEP
			LKEQLRGAQELAASSQQKATLLGEELASAAAARDRTIAELHRSR
			LEVAEVNGKLAELGLHLKEEKCQWSKERAGLLQSVEAEKDKILK
	ĺ	1	LSAEILRLEKAVOEERTONOVFKTELAREKDSSLVQLSESKREL
1	į		
	i	ł	TELRSALRVLQKEKEQLQEEKQELLEYMRKLEARLEKVADEKWN
1	Į.		EDATTEDEEAAVGLSCPAALTDSEDESPEDMRLHPMAFVSVETQ
			ASLLLGLE
7091	186	1076	EGMLTREHRCGRSEEQELEPWPSPKKARSGRWLRNGFKRKMEEP
1		Ì	EEPADSGQSLVPVYIYSPEYVSMCDSLAKIPKRASMVHSLIEAY
1	İ	Į.	ALHKQMRIVKPKVASMEEMATFHTDAYLQHLQKVSQEGDDDHPD
	1	}	SIEYGLGYDCPATEGIFDYAAAIGGATITAAQCLIDGMCKVAIN
1	1	i	WSGGWHHAKKDEASGFCYLNDAVLGILRLRRKFERILYVDLDLH
1			HGDGVEDAFSFTSKVMTVSLHKFSPGFFPGTGDVSDVGLGKGRY
1	}	1	YSVNVPIQDGIQDEKYYQICERYEPPAPNPGL
7092	522	809	KOGINEDOEESOKPRLGEGCEPISKROMKKLIKOKOWEEQRELR
1	1		KOKRKEKRKKKLERQCOMEPNSDGHDRKRVRRDVVHSTLRLII
1			DCSFDXLM
7093	454	655	NFGVSGVELAQQASMVRMSFVIAACQLVLGLLMTSLTESSIQNS
7093	1 234	1 055	ECPOLCVCEIRPWFTPQSTYREA
			FVRSMHWGVGFASSRPCVVDLSWNQSISFFGWWAGSEEPFSFYG
7094	2	508	
1	1	1	DIIAFPLQDYGGIMAGLGSDPWWKKTLYLTGGALLAAAAYLLHE
		1	LLVIRKQQEIDSKDAIILHQFARPNNGVPSLSPFCLKMETYLRM
	<u></u>		ADLPYQNYFGGKLSAQGKMPWIEYNHEKVSGTEFII
7095	1	411	IASSLPKMASLLQSDRVLYLVQGEKKVRAPLSQLYFCRYCSELR
1		1	SLECVSHEVDSHYCPSCLENMPSAEAKLKKNRCANCFDCPGCMH
1			TLSTRATSISTQLPDDPAKTTMKKAYYLACGFCRWTSRDVGMAD
i	1	1	KSVGE
7096	224	2067	ETRSLAVQEKPSQAGRRRSSRISFAGALFLTRFLLQELLLNNFC
1			SAMSPAPDAAPAPASISLFDLSADAPVFQGLSLVSHAPGEALAR
1		1	APRTSCSGSGERESPERKLLQGPMDISEKLFCSTCDQTFQNHQE
			OREHYKLDWHRFNLKORLKDKPLLSALDFEKQSSTGDLSSISGS
1			EDSDSASEEDLOTLDRERATFEKLSRPPGFYPHRVLFQNAQGQF
1			LYAYRCVLGPHODPPEEAELLLQNLQSKGPRDCVVLMAAAGHFA
1			
1			GAIFQGREVVTHKTFHRYTVRAKRGTAQGLRDARGGPSHSAGAN
1			LRRYNEATLYKDVRDLLAGPSWAKALEEAGTILLRAPRSGRSLF
1	1	1	FGGKGAPLQRGDPRLWDIPLATRRPTFQELQRVLHKLTTLHVYE
1			EDPREAVRLHSPQTHWKTVREERKKPTEEEIRKICRDEKEALGQ
1			NEESPKQGSGSEGEDGFQVELELVELTVGTLDLCESEVLPKRRR
		l	RKRNKKEKSRDQEAGAHRTLLQQTQEEEPSTQSSQAVAAPLGPL
			LDEAKAPGOPELWNALLAACRAGDVGVLKLQLAPSPADPRVLSL
		1	LSAPLGSGGFTLLHAAAAAGRGSVVRLLLEAGADPTVQCQDH
7097	256	1228	IRTKSAATWEAWPOCGREGSRIITEPCEANAGSRQELQTERISS
1			FLAAQGDQAFHSGLETNNSNSELPLRVGLKVAQGSPLMGGQVSA
L	_l		

597

-

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID NO:	beginning nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ì	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	554-5	\=possible nucleotide insertion)
7108	1	942	VKVALLLTNLEQPRTESEWENSFTLKMFLFQFVNLNSSTFYIAF
1			FLGRFTGHPGAYLRLINRWRLEECHPSGCLIDLCMOMGIIMVLK
1	ļ	}	QTWNNFMELGYPLIQNWWTRRKVRQEHGPERKISFPQWEKDYNL
1	Ì	İ	QPMNAYGLFDEYLEMILQFGFTTIFVAAFPLAPLLALLNNIIEI
	ļ]	RLDAYKFVTQWRRPLASRAKDIGIWYGILEGIGILSVITNAFVI
}	}]	AITSDFIPRLVYAYKYGPCAGQGEAGQKCMVGYVNASLSVFRIS
	j		DFENRSEPESDGSEFSGTPLKYCRYRDYRDPPHSLVPYGYTLQF
1			WHVLAW
7109	964	102	WDQRKRNSLVPGPAHGPAQEEPWEKKESLGAAQEALSIQLQPKE
	[Į.	TQPFPKSEQVYLHFLSVVTEDGPEPKDKGSLPQPPITEVESQVF
1	1		SEKLATDTSTFEATSEGTLELQQRNPKAERLRWSPAQEESFRQM
1			VVIHKEIPTGKKDHECSECGKTFIYNSHLVVHQRVHSGEKPYKC
		i	SDCGKTFKQSSNLGQHQRIHTGEKPFECNECGKAFRWGAHLVQH
j	1		QRIHSGEKPYECNECGKAFSQSSYLSQHRRIHSGEKPFICKECG
			KAYGWCSELIRHRRVHARKEPSH
7110	96	697	RLDNFSGFLVEVTKEERHIVKPLYDRYRLVKQMLTRASITPVLG
ļ			SPSTKRRGQMLQPIIEGETAHFFEEIKEEEEDGVNLSSELGDML
		İ	KTAVQVQSSLKNSESDVEENQEKLALDLRLSSSRAASMPELLEQ
ì			LWKARAEKKKLRKTLREFEEAFYQQNGRNAQKEDRVPVLEEYRE YKKIKAKLRLLEVLISKQDSSKSI
7111	2	414	GSGLYRGPTPGGOCIWKPNSMPPDHERNFGFTQFALELNELTAE
/ / 111	_	414	LKRSLPSTDTRLRPDORYLEEGNIQAAEAQKRRIEQLQRDRRKV
1		İ	MEENNIVHQARFFRRQTDSSGKEWWVTNNTYWRLRAEPGYGNMD
1		}	GAVLW
7112	103	495	PRCFPVADRGRLIGGLPDVVTIMEGKTLNLTCTVFGNPDPEVIW
1		ļ	FKNDQDIQLSEHFSVKVEQAKYVSMTIKGVTSEDSGKYSINIKN
			KYGGEKIDVTVSVYKHGEKIPDMAPPQQAKPKLIPASASAAGQ
7113	1	824	KCLRQAWHEAPSSLAFTRWCSREERAEGGGNLHRSITRDPKPPG
1			LRPSQRPMDDKKKKRSPKPCLAQPAQAPGTLRRVPVPTSHSGSL
1			ALGLPHLPSPKQRAKFKRVGKEKCRPVLAGGGSGSAGTPLQHSF
1			LTEVTDVYEMEGGLLNLLNDFHSGRLQAFGKECSFEQLEHVREM
1		ĺ	QEKLARLHFSLDVCGEEEDDEEEEDGVTEGLPEEQKKTMADRNL
			DQLLSNLGSCLGALVPGGMRGGEGTYSQSHSWALGEKVGVHGSK
7114	 	1492	SSGPLNLPRR VWEVDEOIDHYKESODKFLWOAAFIGKETLKDESGOECKICRKI
1 /114	3	1492	VWEVDEQIDHYKESQDKFLWQAAFIGKETDKDESGQECKICKKI IYLNTDFVSVKQRLPKYYSWERCSKHHLNFLGQNRSYVRKKDDG
1		1	CKAYWKVCLHYNLHKAQPAERFFDPNQRGKALHQKQALRKSQRS
		}	QTGEKLYKCTECGKVFIQKANLVVHQRTHTGEKPYECCECAKAF
	1		SQKSTLIAHQRTHTGEKPYECSECGKTFIQKSTLIKHQRTHTGE
		1	KPFVCDKCPKAPKSSYHLIRHEKTHIRQAFYKGIKCTTSSLIYQ
1 -			RIHTSEKPQCSEHGKASDEKPSPTKHWRTHTKENIYECSKCGKS
	İ		FRGKSHLSVHQRIHTGEKPYECSICGKTFSGKSHLSVHHRTHTG
		1	EKPYECRRCGKAFGEKSTLIVHQRMHTGEKPYKCNECGKAFSEK
1		1	SPLIKHQRIHTGERPYECTDCKKAFSRKSTLIKHQRIHTGEKPY
1			KCSECGKAFSVKSTLIVHHRTHTGEKPYECRDCGKAFSGKSTLI
L		L	KHQRSHTGDKNL
7115	1	947	NAAHGYNWGLWCMY1IPPQDWLDRGDESAPIRTPAMIGCSFVVD
1			REYFGDIGLLDPGMEVYGGENVKLGMRVWQCGGSMEVLPCSRVA
		j	HIERTRKPYNNDIDYYAKRNALRAAEVWMDDFKSHVYMAWNIPM
			SNPGVDFGDVSERLALRQRLKCRSFKWYLENVYPEMRVYNNTLT
-	1		YGEVRNSKASAYCLDQGAEDGDRAILYPCHGMSSQLVRYSADGL
1			LQLGPLGSTAFLPDSKCLVDDGTGRMPTLKKCEDVARPTQRLWD
	1		FTQSGPIVSRATGRCLEVEMSKDANFGLRLVVQRCSGQKWMIRN
7116	866	95	WIKHARH RVRMRRNAEVIEEKLSMKSWAKFRPGEPWKGYPNIDPETDPYVT
,110	000	75	PGSVINNLSINTVREVDHLRDRNSGSSSSLNTTLPSTSAWSSIR
L		<u> </u>	1.20 A TUMB THE AVEADURE TO TOWN DELICE TO TOWN DELICE

SEQ	Predicted	Predicted end	Amino agid gogment
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Ston
Ì i	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence		\=possible nucleotide insertion)
			ASNYNVPLSSTAQSTSARNSDSKLTWSPGSVTNTSLAHELWKVP
1			LPPKNITAPSRPPPGLTGQKPPLSTWDNSPLRIGGGWGNSDARY
			TPGSSWGESSSGRITNWLVLKNLTPQIDGSTLRTLCMQHGPLIT
7117	695	1261	FHLNLPHGNALVRYSSKEEVVKAQKSLHISDLFLLTL
''	0,7,5	1261	LLISTPGGCHPPPSSIEFTYTGAWGKALPAPHMPCAPGALPQGA
, 1			FVSQAARAIPLLQPSQAAQAEGLSQPARACGALCSLPWPLRNWG
1 1			SPILRLPGGLRTPTNDRKTRTRSAMACWARAQWDTLGPLKLSHR GKVCLRHPRPTGVRGGPGAAGRQGGMGTRRGTFTSGARDPGGL
			RVKHRCQPTGHLP
7118	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE
	-		ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR
			LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI
, !			LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD
		T	NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT
1 1			YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG
			MDISAIDLINIESFSSRVVSLSEYROSLHTYLRSKMSOVAPSLS
]			ALIGEAVGARLIAHAGSLTNLAKYPASTVOILGAEKALFRALKT
į i	·		RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF
1			SEVPTSVFGEKLREQVEERLSFYETGEIPRKNLDVMKRAMVQAE
[[EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE
i i			EMSEKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSFSKEEL
			MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK
7119	49	1863	FSKEEPVSSGPEEAAGKSSSKKKKKFHKASQED PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE
		1005	ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR
]			LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI
i i			LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD
1			NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT
[{			YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG
] }	J		MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSOVAPSLS
			ALIGEAVGARLIAHAGSLTNLAKYPASTVOILGAEKALFRALKT
			RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF
]		,	SEVPTSVFGEKLREQVEERLSFYETGEIPRKNLDVMKEAMVQAE
[ĺ		EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE
1	1		EMSEKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSFSKEEL
	ļ		MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK
7120	1991	64	FSKBEPVSSGPEEAAGKSSSKKKKKFHKASQED
ļ		0.3	QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFAEEMKFSKKLSAISLGQGQGP
	ĺ		RAEAMMRSSIERGKWVFFQNCHLAPSWMPALERLIEHINDDKVH
}	ļ		RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLLKSYSS
	ļ	·	LGEDFLNSCHKVMEFKSLLLSLCLFHGNALERRKFGPLGFNIPY
¦	ì	İ	EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD
J			DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY
			LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIOLOPK
	ļ		SSSAGSQGREEIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES
			MNTVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLELMA
	1		ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIODG
}	J		IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE
j			APSELTQRPQVGCYIHGLFLEGARWDPEAFQLAESQPKELYTEM
)		j	AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI
3		ì	AVEIPTHQPQRHWIKRGVALICALDY
7121			
7121	2	546	RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK
7121	2	546	RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALOEGLRRAV
7121	2	546	RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ŀ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
ĺ	sequence	bodac	\=possible nucleotide insertion)
			ETRQE
7122	2	546	RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK
	_		LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV
i		İ	SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVP
l	ł	{	GAYFNVLINLRDITDEAFKDQIHHRVSSLLQEAKTQAALVLDCL
1	Ì		ETROE
7123	1	1092	KPAVPEARSAGTSEAGRSGAEEVSCGSVSGDGAAMRLTPRALCS
1			AAQAAWRENFPLCGRDVARWFPGHMAKGLKKMQSSLKLVDCIIE
1			VHDARIPLSGRNPLFQETLGLKPHLLVLNKMDLADLTEQQKIMQ
l	,		HLEGEGLKNVIFTNCVKDENVKQIIPMVTELIGRSHRYHRKENL
1	1		EYCIMVIGVPNVGKSSLINSLRRQHLRKGKATRVGGEPGITRAV
1]	1	MSKIQVSERPLMFLLDTPGVLAPRIESVETGLKLALCGTVLDHL
1			VGBETMADYLLYTLNKHQRFGYVQHYGLGSACDNVERVLKSVAV
ì			KLGKTQKVKVLTGTGNVNVIQPNYPAAARDFLQTFRRGLLGSVM
1			LDLDVLRGHPRV
7124	2	382	LPLTLLLAAPFAHLLLPPGHDQSPCWHPGPALSPGTLGPLSWAM
1			ANSGLQLLGYFLALGGWVGIIASTALPQWKQSSYAGDASIQLRS
	}		KVFVLESEWGGDSLGLPRDCGWSCLLHSAVRSEKGFWS
7125	166	1127	NCISEKRNYSFSMQKGKGRTSRIRRRKLCGSSESRGVNESHKSE
1	ļ		FIELRKWLKARKFQDSNLAPACFPGTGRGLMSQTSLQEGQMIIS
1			LPESCLLT\RDTVIRSYLGAYITKWKPPPSPLLALCTFLVSEKH
Í		Í	AGHRSLLEA\YLEILPKAYTCPVCLEPEVVNLLPKSLKAKAEEQ
1 .		i	RAHVQEFFASSRDFFSSLQPLFAEAVDSIFSYSALLWAWCTVNT
			RAVYL\SPGSGNAFLQSRTPVQLAPYLDLLNHSPHVQVKAAFNE
1	1	í	ETHSYEIRTTSRWRKHEEVFICYGPHDNQRLFLEYGFVSVHNPH
			ACVYVSRGWNQLCS
7126	1	733	CRDMAAFIVPSPARRCSQKGSLGHLPTQPWLWAAMSPRGQERGT
1	f .	•	SHSQAREPQRPGRWLLGSLQSSPGTLGQAGTASRRRGCMVQRWV
			QVATGRRAVQVPKGALGLALGETSPGASRGMSGGAGGCWALGWA
			PSPVLPSWLLEGPPPWLSIISDSGTQRPSPRRCPARPSPWGPQC
1		1	WRGGRIASAEASST*TPGSGSRARSGRRSPGSRRRSASAPSPTP
7127	1311	277	PTDACA*SCVARPAGSRSSRPAAA
1 '12'	1311	277	GLPAMCST*KAGYYEETEGDCIPKDR*IEKRPFKEI*RRIPRIF
1	1		AKQKQI+S+NSQKIGASEIDRGRKEADCSDAPAAARIGAVSVFR RSTQEARVSPRSNAKSANLRAVRAD+WEHFVLLFHTPEOFLAEC
1			ICRST**K*WHQLC*PLSSL*TGLKRKLLL*VLFRI*WLKDCDV
1		}	*FCQKIFATNFCNWQNLIQ*EE*KPVEYSVEN*HIMNLLLPM*L
1	1		CQSSLRDQTIVTWRM*RNYSMFRINMISSL*DGSIHIPLKLHFY
1	1	ł	PALIFTLTVPINSCCQRPLPLFAHQSIKTLASSGSPMLACLRFL
1			LVKKRAFIHTPRSPGCSV*CKHVLVKDNKNNCVGSEV
7128	2	5228	GRVDLWTILLGRSALRELSOIEAELNKHWRRLLEGLSYYKPPSP
1	_		SSAEKVKANKOVASPLKELGLRISKFLGLDEEOSVOLLOCYLOE
1			DYRGTRDSVKTVLQDERQSQALILKIADYYYEERTCILRCVLHL
1			LTYFQDERHPYRVEYADCVDKLEKELVSKYRQQFEELYKTEAPT
1	1	1	WETHGNLMTERQVSRWFVQCLREQSMLLEIIFLYYAYFEMAPSD
1	1	}	LLVLTKMFKEQGFGSRQTNRHLVDETMDPFVDRIGYFSALILVE
1		ļ	GMDIESLHKCALDDRRELHQFAQDGLICODMDCLMLTFGDIPHH
1	1	1	APVLLAWALLRHTLNPEETSSVVRKIGGTAIQLNVFQYLTRLLQ
1]		SLASGGNDCTTSTACMCVYGLLSFVLTSLELHTLGNQODIIDTA
1	1	ļ	CEVLADPSLPELFWGTEPTSGLGIILDSVCGMFPHLLSPLLOLL
1	1	1	RALVSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHEDGTLWR
1	1		RQTPKLLYPLGGQTNLRIPQGTVGQVMLDDRAYLVRWEYSYSSW
1	1		TLFTCEIEMLLHVVSTADVIQHCQRVKPIIDLVHKVISTDLSIA
1		l	DCLLPITSRIYMLLQRLTTVISPPVDVIASCVNCLTVLAARNPA
1	!		KVWTDLRHTGFLPFVAHPVSSLSQMISAEGMNAGGYGNLLMNSE
1		ţ	QPQGEYGVTIAFLRLITTLVKGQLGSTQSQGLVPCVMFVLKEML

SEO	Prodict	I D 3:	
ID	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid F-
NO:	location	location	Glutamic Acid, F=Phenylalanine G=Glycine
ļ	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
j	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
į	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	i .	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	sequence	sequence	Codon, /=possible nucleotide deletion,
——	sequence	ļ	\=possible nucleotide insertion)
			PSYHKWRYNSHGVREQIGCLILELIHAILNLCHETDLHSSHTPS
1		Ì	LQFLCICSLAYTEAGQTVINIMGIGVDTIDMVMAAQPRSDGAEG
[QGQGQLLIKTVKLAFSVTNNVIRLKPPSNVVSPLEQALSQHGAH
1	1		GNNLIAVLAKYIYHKHDPALPRLAIQLLKRLATVAPMSVYACLG
į.			NDAAAIRDAFLTRLQSK\IE\DMRIK\VMIL\EFLTVA\VETQP
ł	1		GLIELFLNLEVKDG\SDGSKEFSLGMW\SCLHAV/VWELIDSQQ
Î	1		QDRYWCPPLLHRAAIAFLHALWQDRRDSAMLVLRTKPKFWENLT
			SPLFGTLSPPSETSEPSILETCALIMKIICLEIYYVVKGSLDQP
	Í		LKDTLKKFSIEKRFAYWSGYVKSLAVHVAETEGSSCTSLLEYOM
	·		LVSAWRMLLIIATTHADIMHLTDSVVRRQLFLDVLDGTKALLLV
i			PASVNCLRLGSMKCTLLLILLRQWKRELGSVDEILGPLTEILEG
1	}		VLQADQQLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLVLNV
			CETLQEEVIALFDQTRHSLALGSATEDKDSMETDDCSRSRHRDQ
1 1	}		RDGVCVLGLHLAKELCEVDEDGDSWLQVTRRLPILPTLLTTLEV
			SLRMKQNLHFTEATLHLLLTLARTQQGATAVAGAGITQSICLPL
1			LSVYQLSTNGTAQTPSASRKSLDAPSWPGVYRLSMSLMEQLLKT
			LRYNFLPEALDFVGVHQERTLQCLNAVRTVQSLACLEEADHTVG FILQLSNFMKEWHFHLPQLMRDIQVNLGYLCQACTSFLHSRKML
, I			QHYLQNKNGDGLPSAV\AQRV\QRPPSAASAAPSSSKQPAADTE
1 1			ASEQQALHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSLDLA
			EYNFLFALSFTTPTFDSEVAPSFGTLLATVNVALNMLGELDKKK
i l			EPLTQAVGLSTQAEGTRILKSLLMFTMENCFYLLISQAMRYLRD
) 1			PAVHPRDKQRMKQELSSELSTLLSSLSRYFRRGAPSSPATGVLP
			SPQGKSTSLSKASPESQEPLIQLVQAFVRHMQR
7129	1	1054	FRRFRWRRRLH*AGPASSAGGSPGEASGTMSGELPPNINIKEPR
1			WDQSTFIGRANHFFTVTDPRNILLTNEQLESARKIVHDYRQGIV
1			PPGLTENELWRAKYIYDSAFHPDTGEKMILIGRMSAQVPMNMTI
1			TGCMMTFYRTTPAVLFWQWINQSFNAVVNYTNRSGDAPLTVNEL
1 1		*	GTAYVSATTGAVATALGLNALTKHVSPLIGRFVPFAAVAAANCI
1 1	1		NIPLMRQRELKVGIPVTDENGNRLGESANAAKOAITOVVVSRIL.
1			MAAPGMAIPPFIMNTLEKKAFLKRFPWMSAPIOVGLVGFCLVFA
<u></u>			TPLCCALFPQKSSMSVTSLEAELQAKIOESHPELRRVYFNKGI.
7130	2	780	HEVPSLQTSDPLPGSVQRCSVVVSQPNKENWCODHLYNSLGRKG
1	1		ISAKSQPYHRSQSSSSVLINKSMDSINYPSDVGKOOLLSLHRSS
]	1		RCESHQDLLPDIADSHQQGTEKLSDLTLODSOKVVVVVNRNI.PI.N
1	1		AQIATQNYFSNFKETDGDEDDYVEIKSEEDESELELSHNRRRKS
1 1	1		DSKFVDADFSDNVCSGNTLHSLNSPRTPKKPVNSKI.GI.Spvi.TD
I-7733			YNDSDKLNDYLWRGPSPNQQNIVQSLREKFQCLSSSSFA
7131	805	573	AAAEGHIEVVKFLIEACKVNPFAKDRWGNIPLDDAVOFNHLEVV
7132	1450		KLLQDYQDSYTLSETQAEAAAEALSKENLESMV
1 /132	1420	1087	IDMLLLSGALVSGPYTLITTAVSADLGTHKSLKGNAHALSTVTA
			IIDGTGSVGAALGPLLAGLLSPSGWSNVFYMLMFADACALLFLI
7133			RLIHKELSCPGSATGDQVPFKEQ
'233	2	3648	QQIPGLLPAHGESGDALRKPRLQKPITGHLDDLFFTLYPSLEKF
1 1	j	1	EEELLELHVQDHFQEGCGPLDGGALEILERRLRVGVHNGLGFVO
[ľ	1	RPQVVVLVPEMDVALTRSASFSRKVVSSSKTSSGSOALVI, RSPI.
	1	i	RLPEMVGHPAFAVIFQLEYVFSSPAGVDGNAASVTSLSNLACMH
		1	MVRWAVWNPLLEADSGRVTLPLQGGIQPNPSHCLVYKVPSASMS
1	1	ļ	SEEVKQVESGTLRFQFSLGSEEHLDAPTEPVSGPKVERRPSRKP
			PTSPSSDDADUDDUI AA DOMEDUCDOI GEGOT AR COD GROOT
	İ	ļ	PTSPSSPPAPVPRVLAAPQNSPVGPGLSISQLAASPRSPTQHCL
			ARPTSQLPHGSQASPAQAQEFPLEAGISHLEADLSOTSLVLETS
			ARPTSQLPHGSQASPAQAQEFPLEAGISHLEADLSQTSLVLETS IAEQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLOSSGFP
			ARPTSQLPHGSQASPAQAQEFPLEAGISHLEADLSQTSLVLETS IAEQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSGFP EILDANKQPAEAVSATEPVTFNPQKEESDCLOSNEMVLOFLAFS
			ARPTSQLPHGSQASPAQAQEFPLEAGISHLEADLSQTSLVLETS IAEQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSGFP EILDANKQPAEAVSATEPVTFNPQKEESDCLQSNEMVLQFLAFS RVAQDCRGTSWPKTVYFTFOFYRFPPATTPRLOLVOLDEAGOPS
			ARPTSQLPHGSQASPAQAQEFPLEAGISHLEADLSQTSLVLETS IAEQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSGFP EILDANKQPAEAVSATEPVTFNPQKEESDCLOSNEMVLOFLAFS

Deginning nucleotide location corresponding to first anino acid amino acid residue of amino acid residue of amino acid sequence corresponding to first amino acid amino acid sequence degine for the first amino acid sequence degine for the first amino acid sequence degine for the first amino acid sequence degine for the first control of the first amino acid sequence degine for the first	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Not mucleotide location corresponding to first shino acid residue of shino acid residue of shino acid residue of shino acid sequence sequen	1 -			(A=Alanine, C=Cysteine, D=Aspartic Acid P=
Corresponding Coirespondin	1	, , ,		Glutamic Acid. F=Phenylalanine G-Glycine
Corresponding to first amino acid residue of saino acid residue of saino acid residue of saino acid sequence S-Serine, T-Threenine, V-Valine, S-Serine, T-Threenine, V-Valine, S-Serine, T-Threenine, V-Valine, S-Serine, T-Threenine, V-Valine, S-Serine, T-Threenine, V-Valine, S-Serine, T-Threenine, V-Valine, S-Serine, T-Threenine, V-Valine, S-Serine, T-Threenine, V-Valine, S-Serine, T-Threenine, V-Valine, S-Serine, T-Threenine, V-Valine, S-Serine, T-Threenine, V-Valine, S-Serine, T-Threenine, V-Valine, S-Serine, T-Threenine, V-Valine, S-Serine, V-Valine, V-Va		1	i e	H=Histidine I=Isoleucine K-Lysine
to first amino acid residue of amino acid residue of amino acid sequence ##TYPTOPINE, Y=Tyrosine, X=Usklenown, *=Stop codon, /=postible nucleotide deletion, /-possible nucleotide insertion) LEVWATEYEQDNWYSGOMLIFEGEWYFIGWSYWKGKHLITLAN VGHPCEGKYRGCSTLPFSSRVISNDGASFSGGSLLTTGSSTRRK KHYWQAGKLADUSELAAMLLITHARGGGROPDVSRESDATRRKR KHYWQAGKLADUSELAAMLLITHATGGASFPGTVLKAPPHNYGH TYTYEINDFLSVIVDSGGBRDFKGAGALHTTVGASFFFGTVLKAPPHNYGH TYTYEINDFLSVIVDSGGBRDFKGAGALHTVGEDMFHLKGAG APQLYLRHEINTAWFFKCSFSAGALHTVGASFFFTVLKAPPHNYGH TYTYEINDFLSVIVDSGGBRDFKGAGALHTVGEDMFHLKGAG APQLYLRHEINTAWFFKCSFSAGALHTVGASFFFTVLKAPPHNYGH TYTYEINDFLSVIVDSGGBRDFKGAGALHTVGEDMFHLKGAG APQLYLRHEINTAWFFKCSFSAGALHTVGASFFFTVLKAPPHNYGH TYTYEINDFLSVIVDSGGBRDFKGAGALHTVGASFFFTVLKAPPHNYGH TYTYEINDFLSVIVDSGGBRDFKGAGALHTVGASFFFTVLKAPPHNYGH TYTYEINDFLSVIVDSGGBRDFKGAGALHTVGASFFTVLKAPPHNYGH TYTYEINDFLSVIVDSGGBRDFKGAGALHTVGAGAGAR SPRKSSAVPTKHAKVLFRASGGKFLAVLCLTVELOPHVVDCOPN TYTYEINDFLSVIVDSGGBRDFKGAGALHTVGASFFFTVLKAPPHNYGH TYTYEINDFLSVIVDSGGBRDFKGAGALHTVGAGAGAR SPRKSSAVPTKHAKVLFRASGGKFLAVLCLTVELOPHVVDCOPN TYTYEINDFLSVIVDSGGGAGALHTVGAGAGAR SPRKSSAVPTKHAKVLFRASGGKFLAVLCLTVELOPHVVGCGBFTVLKAPPHNGT TYTYEINDFLSVIVDSGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	ł	l '		LeLeucine Memethionine NeAsparagine
amino acid residue of amino acid sequence salve of amino acid sequence sequ	İ			
residue of amino acid sequence	ì			
amino acid sequence Codon, /-possible nuclectide insertion	1)		
Sequence \ \possible nuclectide insertion	ł	1	ľ.	Codon. /=possible nucleotide deletion
LEVVATEVEQDINVOVSGEMIGFGRVKEPIGVHSVVKGELHHITAN VGHPCGRVKKGCTIPPSRSTVISNGGARS FESTATRER KHVVQAQKLADVDSELAAMILITHARCKKGPODVSRESDATRERK LERMRSVELQBAGGGLGRRGTSVLAQOSVATCHDQVITAYE ERTKAESIASLISLAITTEHTLHATLGVARFFEPVLKNPHNTQH TVTVEIDHPELSVIVIDSGEMRSVLAQOSVATCHLQVITAYE ERTKAESIASLISLAITTEHTLHATLGVARFFEPVLKNPHNTQH TVTVEIDHPELSVIVIDSGEMRSGEPIAVLAQOSVATCHLQVHAVQH SPWKSSAVPTKHKVLFRASGGSPIAVLGVERVEDHVHLOVGH FYHPELSFLKKAIRLPPHTTPGAPVGMIGGEDPVHAVGSP FYHPELSFLKKAIRLPPHTTPGAPVGMIGGEDPVHAVGSP FYHPELSFLKKAIRLPPHTTPGAPVGMIGGEDPVHAVGSP GEGELIVINDHSCHVERVERVERVERVILLIVUND CHGUAVSHLVCLCKQPLISKAFEIMLAAGGKGVMRTTTYND YPERTPHLISDBFQVGGGETFVILLADAGSKGVMRTTTYND YPERTPHLISDBFQVGGGETFVILLADAGSKGVMRTTTYND YPERTPHLISDBFQUSGGETFVILLADAGSKGVMRTTTYND YPERTPHLISDBFQUSGGETFULLADAGSKGVMRTTTYND YPERTPHLISDBFQUSGGETFULLADAGSKGVMRTTTYND YPERTPHLISDBFQUSGGETFULLADAGSKGVMRTTTYND YPERTPHLISDBFQUSGGETFULLADAGSKGVMRTTYND GEGESTYPPHOFULSIGETTLDBFPQUSGGETFULLADAGSKGV GEGESTYPPHOFULSIGETTLDBFTQUSGFGRSV GEGESTYPPHOFULSIGETTLDBFTQUSGFGSSKOTL LAYDDPFDFNQSFQTLKERQTILLBALLAGGGLSFTNIKUL LAYDDPFDFNQSFQTLKERQTILLBALLAGGGLSFTNIKUL LAYDDPFDFNQSFQTLKERQTILLBALLAGGGLSFTNIKUL SLEVNYNCSKTNDAKSSTTDFJDSSFLTPLAGDFTVX SLEVNYNCSKTNDAKSSTTDFJDSSFLTPLAGDFTVX GEGESTSSSSSHHRDFSTSFLTPLAGASSTDGGC VERVTYPSSELGGFKGSSVGSTTOFJDSSFLTPLAGASSTDGGC VERVTYPSSELGGFKGSSVGSTTOFJDSSFLTPLAGASSTDGGC MLDALLALAGCSSLARLDTCKCQGROGFGTSDDASPSSLCLUDA SATVHDDDLIPLDAGSSLENDASSKSTTPPLAGASSTDTTQDBFX KTSSGDOSETPGAPVTRGTTVVEQVQGELGBLGRAGQUTYSSE ENKSLMWTLLKQLARPMLDSFLAGASSTAFPLTGDBFX KTSSGDOSETPGAPVTRGTTVVEQVQGELGBLGRAGQUTYSSE ENKSLMWTLLKQLARPMLDSFLAGASSTAFPLTGDBFX KTSSGDOSETPGAPVTRGTTVVEQVQGELGBLGRAGQUTYSSE ENKSLMWTLLKQLARPMLDSFLAGASTAFTAGA TJ35 2 466 SEKTATGBRYGASTLGGGFGSSVGTASSSSSTPPTGGDSFTST NG SKITAGGEVLASLLGGKFTSTSTQGTVTHELARPTTAFTAGAQ PTPGLLGSPRSFTSGTVTULDAGASTTAFTAGAQ PTPGLLGSPRSFTSGTVTULDAGATTAFTAGAGA PTPGLLGSPRSFTSGTVTULDAGATTAFTAFTAGAAA PTPGLGSPRSFTSGTTAGATTAFTAGATTAFTAGAAA PTPGLGSPRSFTSGTTAGATTAFTAGATTAFTAGAAA GSKTATGATTAGATTAFTAGATTAFTAGAAAATTAFTAGAAAA GSKTATGATTAGATTAGATTAGATTAGAAATTAFTAGAAAAAAAA	ł	i		\=possible nucleotide insertion)
VGHPCGRVRGCSTLPFSRSRVISNDGASRFSGGSLLTTGSSRR KHWVQAOKLADVDSELAMLITHARQCKGPQDVSREDATRRIK LERMSVBLQBAGGDLGRGTSVLAQQSVRTGHLRDLQVIAAYR ERTKASIASLIALITEHTLHARGVSFPEFVLKNPHNYQH TVTVETDHPELSYLVDSGERDPKGAAGLHTFVEEDDFFLKRSL APQLYLRPHSTAVPPKYOSFSAQQLAMVQSLGNEKGMDAV SPKSSAVPTKHAKVLFRASGGKPIAVLCLTVELQPHVVQOVFR FYHPELSFLKKARILPPHHTFDAPVGMLGGDFVAGAMY ICETQMVGEGEPDIFLKVASGPSPEIKDFVIIYSDRVLAFFY OTWQVLHSIGQRDVDSCVAQGITRISLVLRGTYRVVARPSH PQBLKTDBKQVFVLPPRQVQDLHVGVSRDRAGSRRVHLHLDDVD CHQLVASSILVALCCRQPLISKAREPHLAAGGSRRVHLHLDDVD CHQLVASSILVALCCRQPLISKAREPHLAAGGSRRVHLHLDDVD CHQLVASSILVALCCRQPLISKAREPHLAAGGSRRVHLHLDDVD CHQLVASSILVALCCRQPLISKAREPHLAAGGSRRVHLHLDDVD CHQLVASSILVALCCRQPLISKAREPHLAAGGSRRVHLHLDDVD CHQLVASSILVALCCRQPLISKAREPHLAAGGSRRVHLHLDDVD CHQLVASSILVALCCRQPLISKAREPHLAAGGSRRVHLHLDDVD CHQLVASSILVALCCRQPLISKAREPHLAAGGSRRVHLHLDDVD CHQLVASSILVALCCRQPLISKAREPHLAAGGSRRVHLHLDDVD CHQLVASSILVALCCRQPLISKAREPHLAAGGSRRVHLINDVD CHQLVASSILVALCCRQPLISKAREPHLAAGGSRRVHLINDVD CHQLVASSILVALCCRQPLISKAREPHLAAGGSRRVHLINDVD TYSRRPPHLHSDHPELAFRAGGTTYTEQUAGGETYTTGLQCFAPSGRV GEBELLIVINDHEDKNEBEACUMYLIFTALFRADENTERGEMTY TYSRRTPHLATTARP THE STATEMPLATER TO THE STATEMP				LEVVATEYEODNMVVSGDMLGFGRVKPTGVHSVVKGPLHLTLAN
HHVVQAOKLADVDSELAAMILITHARCGKOPDVSRESDATRRRK LERMRSVELGEAGGGILGRRGTVSLQOGSVEPOHTROPUQUTAAYE ERTKAESIASLISLAITEHTLHATLGVARFFEPVLKNPHNTQH TVTVEIDNPELSYVIDSOGRAPDKAAGALHFEDDFHLRGSL APGLILREHETAAVPFKKOSFSAGGLAMVQASPGLSDEKGMDAV SPWKSSAVPTIKHKVLFRASGGSPIAVGLTUPLTVOPVOP FYHPELSFLKKAIRLPPHTTFCAPVGMIGEDPPVHYRCSDBVV ICETONVGGGERDITFLKVASGSPSELKDPFVIJSORNLAPPTI OTMOVYLHSLQRVDVSCVAGQITRLSLVLRGTQTVTREVRAFTSH POELKTDPKGVFVLPRRVQXDJHVVADVPRFSEPVLINLUDVD CHQLVASKILVCLCCRQPLISKAPEIMLAAGEGKGVNRTITYTNP YPERFFFLKHSDBJFDLAGFERDFVAGGETFVLINLUTVG GEBELLYINDHEDKNREAPCVKVIYO GEBELLYINDHEDKNREAPCVKVIXO MCGSTRSMCTALLAHLALARA MCGSTRSMCTALLAHLALARA MCGSTRSMCTALLAHLALARA MCGSTRSMCTALLAHLALARA MCGSTRSMCTALLAHLALARA MCGSTRSMCTALLAHLALARA ANADAY	1		ĺ	
LERMSVRIORAGGOLIGRRGTSVLAQOSVATOHLRIDQVIANYE ERTKASEJALSLAITETHHAHATUGVAEPVULKOPHNYON TVTVETDNPELSVLVDSQENDDYKGAGLHTPVEEDVLKOPHNYON TVTVETDNPELSVLVDSQENDDYKGAGLHTPVEEDVLKOPHNYON APQULKERPETAHVPEKPGSPSAGLANWQASPCLSNEKGMDAV SPKSSAVPTKHAKVLFRASGGKP LAVLCLTVELQEHVVDQVGF FYHPELSSIKKATRLEPHRTPFGAPVMGNOSPCLSNEKGMDAV SPKSSAVPTKHAKVLFRASGGKP LAVLCLTVELQEHVVDQVGF FYHPELSSIKKATRLEPHRTPFGAPVMGNOSPCSPNAVLANWQASPCLSNEKGMDAV SPKSSAVPTKHAKVLFRASGGKP LAVLCLTVELQEHVVDQVGF FYHPELSSIKKATRLEPHRTPGAPVMGNGDFTVLTVSDDRNAVL LCTQNVGRIGHDILVKVASGGSPBIKDFYLLYSDDRNATPSH PQELKTDPKQFFVLPRAGGGRFTVLTGLGAFASGRV LCTQNVGREGHPRULVCLCCROPLISKASE PQELKTDPKQFFVLPRAGGORFTLTTGLQAFASGRV GEBEILLYINDHEDKNEEAFVKVVGGGETYTTGLQAFASGRV GEBEILLYINDHEDKNEEAFVKVVGGGETYTTGLQAFASGRV GEBEILLYINDHEDKNEEAFVKVVGGGETYTTGLQAFASGRV GEBEILLYINDHEDKNEEAFVKVVLTHAAGGGKPAURATTTVD YPSRPPHHGLSICOTFEDPHTVLLEHYDDPTYBEGLIDNSC LREFTYMDIRKYDAGVIRGAGMVSLPHTIPPGMPEFGSGHCTL ECLERALBRAKPSGIHVARVLLAHALGGGRILLHFRKKKEMKL LATDDPFDRRQEFGVILKEGTLIPGDNLTTCCTYNTRORABMT MGCLSTRSEMCLSYLLTYTRINTRCASITPLINGAGTILLHFRKKKEMKL LATDDPFDRRQEFGVILKEGTLIPGDNLTTCCTYNTRORABMT MGCLSTRSEMCLSYLLTYTRINTRCASITPLINGAGTILLHFRKKKEMKL LATDDPFDRRQEFGVILKEGGTLIPGDNLTTCCTYNTRORABMT MGCLSTRSEMCLSYLLTYTRINTRCASITPLINGAGTILTFORMSTRORABMT MGCLSTRSENDLSVCLLLLAGGTTSTLAGGURTLEPTYRAPELVCGTSSS SSLHROFSINLLVCLLLLAGGTTTVLGGURTLEPTYRAPELVCGTSSS SSLHROFSINLLVCLLLLAGGRVTLGCLBFSYLLTFRASESDGRC WLDALELALRCSSLLRLGTCCXPGROEPGTSPDAS PSSLCCLPA ADLLSRAVEDDAYSMKLVLRWLLSGFYKKPKGIKKPYNPILG ETRRCCWFHIPCTDSRTFTJAAGVSHIPPSFLINKLSDYTYTH ADLLSRAVEDDAYSMKLVLRWLLSGFYKKPKGIKKPYNPILG ETRRCCWFHIPCTDSRTFTJAAGVSHIPPSFLINKLSDYTYTH ADLLSRAVEDDAYSMKLVLRWLLSGFYKKPKGIKKPYNPILG GSTNASRFYGNSLSALLLGGRATLTFLINABDTTLTMPYAHCKG GGTAASSFYCNSLSALLEGGRUFTSESGSSSLFFTSGFPLSKTGDYTYTATAG GGTAASSFYCNSLSALLEGGRUFTSGTSTTNOPTHYNSKKGFCTG GSTNASSFYCNSLSALLEGGRUFTSGTSTTNOPTHYNSKCHTGCTG GGTAAGSFTFTGGSFTTGTTVTLLAGATTLEKKPFGGSTSTNOP TAJST 2 466 WASSMSTVFGGSRHSLGGGVGAVARGTFTFLSKPPSFKPMP TINVET PMSCLSDRSFYLLSCLLEPHRANGAVARGTFTFLSKFYTYFT PMSCLS	1	1		
ERTKARSIASILASIATTEHTHAHATUADEPFEPULKUPHNTOGI TUTVEIDHPELSVIUNSGEMBOFRGAGAGHAPVEEDHPHLRIGISL APQLYLREHETAHVPEKOSFSAGGILAMVQASPELSERGMBAN SPRWSSAVPTHHAKULFRASGGRE IANCHEQPHVVDQVER FYHPELSFLKKATRLPPHHTPFGRPVELQPHVVDQVER FYHPELSFLKKATRLPPHHTPFGRPVELQPHVVDQVER FYHPELSFLKKATRLPPHHTPFGRPVELQPHVVDQVER FYHPELSFLKKATRLPPHHTPFGRPVELQPHVVDQVER FYHPELSFLKKATRLPPHHTPFGRPVELQPHVVDQVER CHQUASHLVCLCCRQPLISTAGGERFVILTYDDRIVARSPSPELLARPY OTWQVYLHSLORVDVSCVARGUTRLSLVLRGTGTVRKVRAFTSH POPELKTDPKGVFVULPPRGVQDLHVGVRETARAGSFVUNLATPY CHQUASHLVCLCCRQPLISTAGERGKGVAVRRITTYNN YERRTFHLHSDHPELLKFREDSFQVGGGETYTIGLQFAPSGRV GEBELINI TUNDHBUNNESSFCVKVIVQ GEBELINI TUNDHBUNNESSFCVKVIVQ GEBELINI TUNDHBUNNESSFCVKVIVQ GEBELINI TUNDHBUNNESSFCVKVIVQ LRHFYTMDIRKYDAGVIRGHWSLPHTIPPGMPERGSSGRCTL ECLERALBAREPSGIHVPAVLLHAHLAGGGIRLHFRKKEMKL LAVDDPFOPROPGCFQLKEEGTILPPDHTYLEGYHTKDRAEMT WGGLSTREMCLSYLLYTPRINLTRCASIPPIMEQFGYSTKECHYNTKORAEMT WGGLSTREMCLSYLLYTPRINLTRCASIPPIMEQFTGYHKKEGNSKLVL SLEVNVRCSKTDMASMSIQGHTALPPDIERFYKAEPLVCGTSSS SSLHRPFSINLLVCLLLISCTISTASI 7135 2 2072 FVRVYTPRSLSLGGPKGESVGSTTOPLPSSYLIFRAASESDGRC KTSGSGDOSTFOAPVRRGTCTSPGRDEPSDAPSSSCGLPA SATVHPDQDLEPLNGSSLENDAFSDKSEREPPESSDTPTQDHSR KTSGSGDOSTFTAVSGVOGELGELGEASQVETYSE ENKSLHWTLLKQLRFPMINLSCHLERTYTVEWQVGELGELGEASQVETYSE ENKSLHWTLLKQLRFPMINLSSLLEHGLEGLEGLGEASQVETYSE ENKSLHWTLLKQLRFPMINLSSLLEHGLEGLEGLEGASQVETYSE ENKSLHWTLLKQLRFPMINLSSLLEHGLEGLEGLEGASGVETYSE ENKSLHWTLLKQLRFPMINLSSLLEHGLEGLEGLEGASGVETYSE ENKSLHWTLLKQLRFPMINLSSVLERAFDSFTRYNDE ALDISAAVERDAPSMKLULRAFLSGFKKRIKFNYNPTYH ADDLISAAVERDAPSMKLULRAFLSGFKKRIKFNYNPTYH ADLISAAVERDAPSMKLULRAFLSGFKKRIKFNYNPTYH ADLISAAVERDAPSMKLULRAFLSGFKKRIKFNYNPTYH ADLISAAVERDAPSMKLULRAFLSGFKKKRIKFNYNPTYH ADLISAAVERDAPSMKLULRAFLSGFTYNDEORPTSGESVR QRACHTYPLEEGTELGEGRAAGATERGKFROHDENPTHENGERFTRENGEPORGES GRACHTYPLEEGTELGEGRAAGATERGKKROWPHORGESFGRENGEFDORL RKASGOPSGHGATTSSSSTTESSCFFLSDEGQDGDFYCPGESFG PRCKKARRICALBAHLEM LKMCH BERGRETARAGATARAKTHTHAKAMLSSTTARAAGA PTGGLLGSPRASHLUCVLLACOLFTHHILK SQRKTYGGSSHSGIGVRGGWGTGGEESSLTVPUADTWQA GSFKVATOERNPORAGMRRICAKGVVPFLGDFLTKL	[[
TVTVETDNPELSVIVDSGENRDFKGAGLIHTPVEEDHFLIKGSI APQLILERPRETAHVPFKPSSPSAGLAMVOAS PELSNEKGMDAV SPKKSSAVPTKHAKVLFRASGER IAVLCLTVELOPHVVTOOVER FYHPELSFIKKATRLPPHRTFPGAPVGANOAS PELSNEKGMDAV SPKKSSAVPTKHAKVLFRASGER IAVLCLTVELOPHVVTOOVER FYHPELSFIKKATRLPPHRTFPGAPVGANOAS PELSNEKGMDAV ICETQAVGGEPRDIFLKVASGEPSPIKNFVIIYSDRWLAPPT OTMOVILHSLORUDVSCVAGOLTRLSLVIRGTGYTVRKVRAFTSH PQELKTDPKGVFVLPPRGVQDLHUGVRPLARGSRFVHINLUDVD CHOLVASHLVCLCCRPLISKAE FILLBAAGSGKUWKRITYTINP YERREFHILEBDHFELLERFREDSFQVGGGETYTIGLGFAPSGRV GEBEILIVINDHEDKHERAFCVKVIVQ GEBEILIVINDHEDKHERAFCVKVIVQ GEBEILIVINDHEDKHERAFCVKVIVQ GEBEILIVINDHEDKHERAFCVKVIVQ GEBEILIVINDHEDKHERAFCVKVIVQ GEBEILIVINDHEDKHERAFCVKVIVQ GEBEILIVINDHEDKHERAFCVKVIVQ GEBEILIVINDHEDKHERAFCVKVIVQ GEBEILIVINDHEDKHERAFCVKKUNTQ LRIPTMPIRKSPAGUVRALLHHLAGGGRGUNGTTLPPGMPEGSGHCTL ECLFEALBEREPSGINVFVILHHALGGGKUNDHTPTPGMPEFGSGHCTL ECLFEALBEREPSGINVFVILHINGGAGRIRHPRKKEMKL LAYDDPFDPNOEFGVLKEEGTLIPGDNLITECRYNTKDRABMT WGGLSTRSEMGLSVLLIVYTRINITRCASIGINGULGTKSS SSLHERGESLIVENTUNGTHEN GATTLEFUNGLOFFICKEE TREVETTREFILLOGFICHSEVASTFODLPSSVLIFPAAGSESDGC NEPATVREPSLAGGFGESVASTFODLPSSVLIFPAAGSESDGC NLDALELALRCSSLLBLGTCKGRSVASTFODLPSSVLIFPAAGSESDGC NLDALELALRCSSLLBLGTCKGRSVASTFODLPSSVLIFPAAGSESDGC NLDALELALRCSSLLBLGTCKGRSVASTFODLPSSVLIFPAAGSESDGC NLDALELALRCSSLLBLGTCKGRSVASTFODLPSSVLIFPAAGSESDGC SSLATAKSRFVANDSASLLDGLARGVASTATULARVLSSTTADAGSTSSLOOTH ADLISEAAVENDATAGVASTATULARVLSSTTATAGVSHHPPVSAPHVSKRGGCTIS GSTTAKSRFVANDSASLLDGATTLTILBRADVTLTMPYAHCKG ILVGTINTLELGGKVTIECAKNNEQAGLEFKLKPPFFGSEVTR QRKGTTFDELGSFRYNDLSALLDGATLTILBRADDTILTMPYAHCKG ILVGTINTLELGGKVTIECAKNNEQAGLEFKLKPPFFGSEVTR QRKGTTFDELGGSFRASHLGATLTSSKSTPESPELDSEGSSALFNTPGGSEVTR QRKGTTFDELGGSFRASHLGATLTSSKSTPESPELDSEGSSTSINGT ETTRELGGSFRASHLGATLTAGGAVARGTTFLGSFGSTSINGT GSFKVASCOLASLAGHDRAFVERDERSPRDDCATAGGSTSTSTAGAGATHAGAGAATLTRAGGATTTLTMPYAHCKG LKGTATAGATAGAATAGAATLTGGATAGATAGAATLTGBATAGAAA EERQAGRARGEGSLIMPKGLGFTDFUTGAGATTTLTMPYAHCKG LKGTATAGATAGAATAGAATLTGGATAGAAAAAAAAAAAA	1	1	l	
APOLYLRPHETAHVPRKYOSFSAGOLAMWQASPOLARKGMDAY SPWKSSANPTHAKULFRASGGRI ANLUQASPOLATIVELQPHVVDOVFR FYHPELSFLKKARILPPHHTFGAPVGMLGEDPPUYHCSDPNV ICETONVSGEPRDIPLKVASGSPSPIKDFVILYSDRWLATPT OTMOVYLHSLORVDVSCWAGQLTRLSLVLHGTGYVRVDAFTSH PORLKTDBVGVFVLPPRSQUDLHWGVRPFVILYSDRWLATPT OTMOVYLHSLORVDVSCWAGQLTRLSLVLHGTGYVRVDAFTSH PORLKTDBVGVFVLPPRSQUDLHWGVRPLFSTVLHAVDVD CHQLVASMLVCLCCROPLISKAPEIMLAAGGGKGVNKRITYTND YPEREPTHHLBDHPELLRRERDSRVGGGGTFVILGUAPPSQNV GEBEILIYINDHEDKWEAFCVKVIYQ GEBEILIYINDHEDKWEAFCVKVXIYQ GEBEILIYINDHEDKWEAFCVKVXIYQ GEBEILIYINDHEDKWEAFCVKVXIYQ GEBEILIYINDHEDKWEAFCVKVXIYQ GEBEILIYINDHEDKWEAFCVKVXIXQ GEBEILIYINDHEDKWEAFCXXIXQ GEBEILIYINDHEDKWEAFCXXIXQ GEBEILIYINDHEDKWEAFCXXIXQ GEBEILIYINDHEDKWEAFCXXIXQ GEBEILIYINDHEDKWEAFCXXIXQ GEBEILIYINDHEDKWEAFCXXIXQ GEBEILIYINGHEAFCXXIXQ GEBEILIYINGHEAFCXXIXQ GEBEILIYINGHEAFCXXIXQ GEBEILIYINGHEAFCXXIXQ GEBEILIYINGHEAFCXXIXQ GEBEILIYINGHEAFCXXIXQ GEBEILIYINGHEAFCXXIXQ GEBEILIYINGHEAFCXXIXQ GEBEILIYINGHEAFCXXIXQ GEBEILIYINGHEAFCXXIXQ GEBEILIYINGHEAFCXXIXQ GEBEILIYINGHEAFCXXIXQ GEBEILIYACAFCXXIXQ GEBEILIYACAFCXXIXQ GEBEILIYINGHEAFCXXIXQ GEBEILIYACAFCXXIXQ GEBEILIYACAFCXXIXQ G	i	1	{	
SPWKSSAVPTKHAKULERASGGEVELVALCLITVELQPHVVDOVEK FYHPELSFLKKAIRLIPWHTFFGAPVGMLGEDPVHVRGSDPNV ICETQRVGGGERDIFLKVANSGGSDEI KDIFVI 19DRRLATPT OTTGVVLHSLQRVDVSCVAQGITELSLULGGTYVEKVRAFTSH POELKTDPKGVFVLPPRGVQDLHVGVRPLRAGSRFVHLNILVDVD CHQLVASMLVCLCCRQPILISKAFEIMLAGGGSKGVMKRITTTND POELKTDPKGVFVLPPRGVQDLHVGVRPLRAGSRFVHLNILVDVD CHQLVASMLVCLCCRQPILISKAFEIMLAGGGSKGVMKRITTTND POELKTDPKGVFVLPPRGVQGGETYTIGLQFAFSGRV GEBEILIVINDHBOKNBEAFCVKVIYQ GEBEILIVINDHBOKNBEAFCVKVIYQ GEBEILIVINDHBOKNBEAFCVKVIYQ GEBEILIVYNDAGVIERGLWVSLPHTIPGMPGPGSEGHCTL LRIFYTMDIRKYDAGVIERGLWVSLPHTIPGMPGREGSEGHCTL LAVDDFFDPNCGFTQVLKEEQTILGGONLITECRYMTKDRABMT WGGLSTRSEMCLSYLLYPRINITTGAB PIDHEQLGFIGKEI YRPVTTWPFIIKSPKQYKNLSFMDAMKFRWTKKECLSFNKLOUL SLPVNNVCRSYNDABWSIGGMTALPPDLERPYKAFELVCGTSS SSLHRDFSINLLVCLLLLSCTLSTREPYRAFELVCGTSSS SSLHRDFSINLLVCLLLLSCTLSTREPYRAFELVCGTSSS SSLHRDFSINLLVCLLLLSCTLSTREPYRAFELVCGTSSS SSLHRDFSINLLVCLLLLSCTLSTREPYRAFELVCGTSSS SSLHRDFSINLLVCLLLLSCTLSTREPYRAFELVCGTSSS SSLHRDFSINLLVCLLLLSCTLSTREPYRAFELVCGTSSS SSLHRDFSINLLVCLLLLSCTLSTREPYRAFELVCGTSSS SSLHRDFSINLLVCLLLLSCTLSTREPYRAFELVCGTSSS SSLHRDFSINLLVCLLLLSCTLSTREPYRAFELVCGTSSS SSLHRDFSINLLVCLLLLSCTLSTREPYRAFELVCGTSSS SSLHRDFSINLLVCLLLLSCTLSTREPYRAFELVCGTSSS SSLHRDFSINLLVCLLLLSCTLSTREPYRAFELVCGTSSS SSLHRDFSINLLVCLLLLSCTLSTREPYRAFELVCGTSSS SSLHRDFSINLLVCLLLLSCTLSTREPYRAFELVCGTSSS SSLHRDFSINLLVCLLLLSCTLSTREPYRAFELVCGTSSS SSLHRDFSINLLVCLLLLSCTLSTREPYRAFELVCGTSSS KTESGDQSEPPGAPVRRCTTVLEQVGELGBLGBASQVETVSE ENKSLMWTLLKQLRPGMDLSRVLJETVLBERSPLBSTRINLDDVTLY ADDLLSCTLARPSSLAGGESSSLAFWTPSORRYSTRINLSDTYTHYARCK ILVGTNTLLLGGRVTISCTREPYSERPSESTSINGL STRASFRYNGISSALDGAATLFINRAEDYTLTMRPVSRKHGCTLS STRASFRYNGISSALDGAATLFINRAEDYTLTMRPVSRKHGCTLS GSKTARGERVASLAGGEVLASLSGMBRDPVFILEGRMFSGSSALFWTPSGSVRR QRLGGTTARAFTEN FOR FOR FOR FOR FOR FOR FOR FOR FOR FOR	1			
FYMPELSFLKKAIRLIPBMHTFERAYGMLGEDPPUNTKCSDPNV ICTEGONVEGGBRDILERVANGGSPEILKDFUILTSUPLATPT OTWOVALHSLORVOVSCAGQLIRLSLVLKGTGTVEKVEAFFSH PORLKTDPKGVFVLIPBEGVOLHVGVRPLRAGSRFVHLNLVDVD CHQLVASWLVCLCCROPLISKAFEIMLAGGGKGVNKRITTTINP YESRRIFHHHSDHELLRERBDSROVGGGETYTIGLQFAFSQRV GEBELILIVINDHEDKNEAFCVKAIVY TYPSRRIFHHHSDHELLRERBDSROVGGGETYTIGLQFAFSQRV GEBELILIVINDHEDKNEAFCVKAIVY THE GEBELILIVINDHEDKNEAFCVKAIVY THE GEBELILIVINDHEDKNEAFCVKAIVY THE GEBELILIVINDHEDKNEAFCVKAIVY THE GEBELILIVINDHE GALGAGENTH THE GEBELITH THE GEBE	1		1	
ICETGNVGGGBPRDIFLKVASGGSPELKDFFUTJYSDRWLATPJ CTGWVANBLORDVDSCVAGQITELSLUTGGTTVEKVARFISH POELKTDPKGVEVILPPRGVQDLHVGVRPLERGSRPVHLNLVDVD CHQLVASWLVCLCCRQPLISKAFSIMLAGGGSRGVHKRITTHND YPSRRTPHHHSDHPELLRPREDSRQVGGGETYTIGLQPAFSGRV GEBELILYINDHBUKNBEAFCVKVIYQ GEBELILYINDHBUKNBEAFCVKVIYQ GEBELILYINDHBUKNBEAFCVKVIYQ GEBELILYINDHBUKNBEAFCVKVIYQ GEBELILYINDHBUKNBEAFCVKVIYQ GEBELILYINDHBUKNBEAFCVKVIYQ GEBELILYINDHBUKNBEAFCVKVIYQ GEBERILYINDHBUKNBEAFCVKVIYQ GEBERILYINDHBUKNBEAFCVKVIYQ GEBERILYINDHBUKNBEAFCVKVIYQ GEBERILYINDHBUKNBEAFCVKVIYQ GEBERILYINDHGVLARHALAGGGIRLRHFRKGEMKL LAYDDFPDRYGDFQYLKEBGTILDGDNLITECRYNTKDRABMT WGGLSTRSEMCLSYLLYPRINLTRALGAGGIRLRHFRKGEMKL LAYDDPDRYGDFQYLKEBGTILDGDNLITECRYNTKDRABMT WGGLSTRSEMCLSYLLYPRINLTRALGAGGIRLRHFRKGEMKL LAYDDPDRYGDFQYLKEBGTILDGDNLITECRYNTKDRABMT WGGLSTRSEMCLSYLLYPRINLTRALGAGGIRLRHFRKGEMKLVL ANDADELBARABCASSLINDHAAMISTERDHEYKARFLVCGTSSS SSHENGFSINLLVCLLLLSCTLSTKST TYPVTWPFILKSPKQYKNLSFMDAMNKFKWTKKEGLSFNKLVL SLEWANTCSKTUNABMSIGGMTALDFDIEBFYKARFLVCGTSSS SSHENGFSINLLVCLLLLSCTLSTKAND KARSHEYLLCSSLLRHGTGTCFGGRGGFGSTSDASPSSLCCLPA SATVHPDQDLFPLLAGCSLENDHAFSKSERENPESSTLCCLPA SATVHPDQDLFPLLAGCSLENDHAFSKSERENPESSTLCOLPA SATVHPDQDLFPLLAGCSLENDHAFSKSERENPESSTLTCHOHSR KTSSGBOGSTFGAPVRGTTVLEGVGBEIGBGASQOVETVSE ENKSLMWTLLKQLEPGNDLSRTVLJERTSPKLYBFGGSTSLNKLSDYYPYH ADLLSRAAVEBDAYSRKAVLJERNLSGEBIGBGAGGAGVETVSE ENKSLMWTLLKQLEPGNDLSRTVLJERNLSGEBIGBGAGGAGVETVSE ENKSLMWTLLKGLEPGNTLTSREDSTLRHTPSAGEVIR GSTAKSRTVGNSLSALLDGKATLTFLURFREDSFUTMALAGCE LINGTNTLELGGKVTLECKKENFUTGSTSLNQ SGKKTTSGEBEVLASLLSGRWDRDVFIKEBGSGSSENDEDGDDFVPGGESPG RKATGBAGAAANTARISKGDPAFTARISKGDGHATGEBFAL EEAQRQRARERQESLMPWKPQLFHLDPITGBHYRYEDHSPMDA LKDIAGPFSTRAAGAAATRESSTAPPESCPUTMAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA				
GTMQVYLHSLQRVDVSCVAGOLTRISLVLRGTGTVPKVRAFTSH PQELKTIPRGVVPLIPPRGVVDLIPPRGOSPHULVGVRPLRGSRFVHINLNDVD CHOLVASMLVCLCCRQPLISKAFEIMLAAGEGKGVWKRITYTND YPSRPTPHHISHDHELDRPEDSPQVGGGFTTIGLGFAPSQRV GEBEILIYINDHEDKNERAFCVKIYQ T134	1	1	[
POELKTDPKGVFVLPPRGVODLHVGVRPLRASSRFVHLNLUDVD CHQLVASMLVCLCCORPLISKARF HLAMAGEGKGWINKRITTTND YPSRRTPHHLHSDHPBLLEFREDSFQVGGGETYTIGLQFAPSQRV GEBEILIYINDHEDKNEBAFCVKVIYQ 7134 2115 1111 GGSGFSYPPHVGLSGTFLDPHVYULLEVHYDNPTYEEGLIDNSG LRLFYTMDIRKYDAGVIRAGLWSLFHTIPPMPFFGSEGRCTL ECLEEALEAREKSGIHVAPULLHAHLAGRGIRLRHFRGKEMKL LAYDDPFDRNGEFGYLKEEGTILPGDNLITECRYNTKDRABWT WGGLSTRESMCLSYLLYYPRINTIRCASIPDIMEGLOFIGVKEIT YRPVTWPFIIKSPKQYKNLSFMDANNKFKWYKKSGLSFNKLVL SLPVNVMCSKTDNASWSIQOMTALPDIREPYKAEPLVCGTSSS SSLHRDFSINLUVCLLLSCTLSTKSL 7135 2 2072 FVRVTTPRSLSLQGFKGERSVGSTTGPLPSSYLIFRAASESDGRC WLDALBLARCSSLLRLGTCKPGRGCEPGTSPDASPSSLCGLPA SATVHPDQDLFPLNGSSLENDAFSDKSERENPESDTTTQDHSR KTESGSDOSTTGAPVRGTTYVQCEFLGSLGFSAGVETVSE ENKSLWWTLLKQLRFGMDLSRVVLFTFVLEPRSFLNKLSDYYH ADLISKAAVEDDAYSRMLVLAWYDGEBLGSLGFSAGVETVSE ENKSLWWTLLKQLRFGMDLSRVVLFTFVLEPRSFLNKLSDYYH ADLISKAAVEDDAYSRMLVLAWYDGEBLGSLGFSKYCKFGK KKKFYNFLIG ETFRCCNFHPQTDSRTFYLAGOVSHPPPVSAFHVSNRKDGFCIS GSITASSRFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG ILKGTWTLELGGKVTIECAKNNGQLEFKKKPYNFLGG GSITASSRFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG ILKGTWTLELGGKVTIECAKNNGQLEFKKKPYNFLGE GSITASSRFYGNSLSSLSTBESCPBLSDEGDGDFVPGGESPC RGKRARRICAALHSALISTREAQHAVRATGEKFAL EEAQRQRABERGGSLMPWKFQLFHLDPITQSWHYRYEDHSPWDP LKDIAGPEGDGILFRILGQGAVARGTLGSSPAFWTRSGESPC RKASDQPSGHSOATESSGSTFESCPBLSDEGDGDFVPGGESPC PGCKKRARRICAALHSALISTREAQHAVRATSKGDDHRATQEKFAL EEAQRGNASERGPSLMPWKFQLFHLDPHTQSGPDFHRERSGPDORL RKASDQPSGHSOATESSGSTFESCPBLSDEGDGDFVPGGESPC PGCKKRARRICAALHSALISTREAQHAVRATSKEDDHRATQEKFAL EEAQRGNASENFILCVPLACOLFINHILK 7136 2 418 DFVPSFRFSGNTSGTVULKGALTGATLEKEVAGLEEKIHHLDDMLK SQRKVGMISCLCDNSKAVIQSKOATIGSEESLTVPVADTWQA GSFKVATOERNFGRAMKLRRGKKGVVPPLGDFLTELQRLDSAI PDDLDGNTMKRSKSVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMBQLSDKESYKLSCQLEPENP 7137 2 466 WASGMSTVPGGSRHSLGIQVRGWGVTGGEEESLTVPVADTWQA GSFKVATOERNFGRAMKLRRGKKGVVPPLGDFLTELQRLDSAI PDDLDGNTMKRSKSVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMBQLSDKESYKLSCQLEPENP 7138 2 466 WASGMSTVPGGSRHSLGIQVAGFWYPTGFTELQRLDSAI PDDLDGNTMKRSKSVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMBQLSDKESYKLSCQLEPENP 7139 1 357 SLEN	1			
CHOLVASMILVCLCCROPLISKAPEIMLAAGBGKGVNRKITTYTNP YPSRTPHHHSDHPLAFREDSFOVGGGTYTIGLQFAPSQRV GEBEILIYINDHEDKNEEAFCUKVIYO 7134 2115 1111 GGKSFSYPFHVGLSIGTFLIDPHYLLEVHYDDFYTEEGLIINSG LRIFYFMDIRKYDAGVIFAGLWUSHHTIPPGMPFFGSEGKCTL ECLEEALEAEKPSGTHVBAVLIHAHLAGRGIRLRHFRKGKEMKL LAYDDFDFNFGSFGYLKEEGTLIGNLITECRYNTKDRABMT WGGLSTRSEMCLSYLLYYPRINTTRCASIPDITMEOLOFIGKET YRPYTYPFIIKSPGYKKESTHOPHYNLLHHALAGRGIRLRHFRKGKEMKL LAYDDFDFNFGSFGYLKEEGTLIGNLITECRYNTKDRABMT WGGLSTRSEMCLSYLLYYPRINTTRCASIPDITMEOLOFIGKET YRPYTYPFIIKSPGYKKESTHOPHSSYLIFRAASESDGRC WLDALSLAIRCSKLINLGTCKPGRDGEPGTSPDASPSSLCGLPA SATVHPDOLPFILAGSSLENDAPSGERENDEESDTTODHSS KTESGSDOSETFGAPVRRGTTYVEQVOEBLGBLGBRASOYETVSE ENKSLMWILLKQLRFCMDLSRVVLPTFFVLBFRSFLNKLSDYYH ADLLSRAAVEBDAYSRKKLVLRWYLSGFYKKPKGIKKFYNFILG ETTRCCWFHPGTDSRTTYLAEQUSHHPPVSABHVSNRKDGFCIS GSITAKSRYGNGLSABLLDGKATLTFLNRAEDYTLTMFYAHCKS ILVGTWTLBLGGKYTIBCAKNNFQAQLEFKLKPFFGGSTSINQI SGKITSGEVLASISGHWDRDVFLAGSGSSALPWFSGEVRR QRRGTTVBLEEGTELBSBLWGHVTFRAISKGDGHRATOBEFAL EEAGRORABERGESLMPHKPQLFHLDPITQEWHYRYEDHSPWDP LKDIAQFEQDGILRTLQCRAVARCTFLISSPOPHERSGFDQDFVBGGESPC PRCKKEARRIQALHEALISIREAGQSHHHBLSAMLSSTARAQA PTFGLLQSFRSWFLLCVFLLACOLFINHILK SQCRKVRQMIEDLQNSKAVIGSKDATIGBLKKKAYLBEANLEM HDRMEHLIEKQISHGNGFTVWLLERATIGSKRIKKTYLBEANLEM HDRWEHLIEKQISHGNGFTVWLLERATIGSKRIKTYLBEANLEM HDRWEHLIEKQISHGNGFTVWLGRAKTGVPFLGGFTTELGRIDSAI PDDLDGNTTNKRSKEVRVLOGMQLQVAANNYRLRPLEKFVTYFT RMSGLSDKSSYKLSCQLEPEND 7136 2 466 WASGMSTVPGGSRRSLGIQVRGGWGTGGEEESLTVPVADTWQA GSFKVATGERNPGRAQMELRRQKKGVVPFLGDFLTELGRIDSAI PDDLDGNTTNKRSKEVRVLOGMQLQVAANNYRLRPLEKFVTYFT RMSGLSDKSSYKLSCQLEPEND 7139 1 357 SLENSRAGLKMAASAARGAAALBRSITGGVAPVRRTIPHTAASSQ LKEHFAQFCHVRRCILPPKRTGFHRGLGWVQFSSEEGLRNALQ QKHIIDGVKQWITRRPKLPGTSDDEKKDD 7140 1401 1957 RASSLQVLKANGGLIPSFFQQGTGGYALEELFFDLKYDGFGFF	}			
YPSRRTPHLHISDHPELLERPREDSFQVGGGETTIGLQFAPSQRV GEEEILIYINDHEDREAFCVUVIYO 7134 2115 1111 GGEGFSYPPHVGLSLGTPLDPHYVLLEVHYDNPTYEEGLIDNSC LREFYTMDIRKYDAGVIRGHWSLPHTIPEMPEFGSEGKCTL ECLEEALRERPSGIHVAVLLHAHLAGRGIRLRHFRGKEMKL LAYDDPFDRNFQFFGYLKEEGTILPGDNLITECRYNTKDRABMT WGGLSTRSEMCLSYLLYYPRINLTRCASIPDIMEGLOFIGVKEI YRPVTTWPFIIKSPKQYKNLSFHDANNKFKWYKKSGLSFNKLVL SLPVNVNCSKTDNABWSIQGMTALPPDIERPYKAEPLVCGTSSS SSLHRDPSINLLVCLLLLSCTLSTKSL 7135 2 2072 FVPRVTFRSLSLQBKGESVGSITQPLPSSYLIFRAASESDGRC WLDALBLARCSSLLRLGTCKPGROEPGTSPDASPSSLCGLPA SATVHPDQDLPPLNGSSLENDAFSDKSERENPESDITETQDHSR KATSGSDOSETTGAPVRRGTTYVQCBELGBLGERSQVETVSE ENKSLMWTLLKQLRPGMDLGRVVLPTFVLLERSFLNKLSDYYH ADLISRAAVEBDAYSMKLVLRWYLSGFYKKPKGTKKKFYNPILG ETTRCCWFHPQTDSRTFYLAGVSHPPVSAPHVSNRKDGFCIS GSTAKSAPWEDASYSMKLVLRWYLGFFKKKPYNFLK ETTRCCWFHPQTDSRTFYLAGVSHPPVSAPHVSNRKDGFCIS GSTAKSFYGNGLSALLDGKATLHRAEDYILTMPYAHCKG ILVGTWTLBLIGGKVTIBCAKNNPQAQLEPKLKPPFGGSTSINQI GGKTAKSFYGNGLSALLDGKATLHRAEDYILTMPYAHCKG ILVGTWTLBLIGGKVTIBCAKNNPQAQLEPKLKPPFGGSTSINQI GGKTAKSFYGNGLSALLDGKATLTHRAEDYITLMPYAHCKG ILVGTWTLBLIGGKVTIBCAKNNPQAQLEPKLKPPFGGSTSINQI GGKTAKSFYGNGLSALLDGKATLTHRAEDYITLMPYAHCKG ILVGTWTLBLIGGKVTIBCAKNNPQAQLEPKLKPPFGGSTSINQI GGKTAKSFYGNGLAGLAGVARTASSSTPESCPBLSDEEDGDFVPGGESPC PGRKRARRIQALHBALISTREAQDATTLSSGEDHKTSFTDSPGPHRERSGFDQRI RKASDQPSGHSQATESSGSTFESCPBLSDEEDGDFVPGGESPC PGRKRARRIQALHBALISTREAQDATTLSSGPPHRERSGFDQRI RKASDQPSGHSQATESSGSTFESCPBLSDEEDGDFVPGGESPC PGRKRARRIQALHBALISTREAQDATTLSSGPPHRERSGFDQRI RKASDQPSGHSQATESSGSTFESCPBLSDEEDGDFVPGGESPC PGRKRARRIQALBARALISTREAQDATTLSSGPPHRERSGFDRAL PTPGLLOSPSSWFLLCVPLLAGOLFINHILK 7136 2 418 DFVPSFRPSGNTSGTVWLLRAATLEKEVAGLREKIHHLDMLK SQGRKVRGMISCLQNSKAVIQSKGVAPFLGBEESLTVPVADTWQA GSFKVATOERNPGRAMKLRRGKKGVVPFLGDFLTELQRLDSAI PDDLDCNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7137 2 466 WASGMSTVPGGSRHSLGIQVGGGWGTGGEEESLTVPVADTWQA GSFKVATOERNPGRAMKLRRGKKGVVPFLGDFLTELQRLDSAI PDDLDCNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7139 1 357 SLENSARGLKAMASAARGAAALRESINGGVALEELFFTLKYDCFCSF	1	1		
GEBEILIYINDHEDKNEEAFCUKUIYU GEBESYPPPRUSLGIFTIDPPHYLLEUHYUNDPTYEEGLIDNSC LRLFYTMDIRKYDAGUIRAGLWUSLPHTIPPGMPEFQSEGHCTL ECLEBALBAEKPSGIHVFAVLLHAHLAGGTIRLEHFEKGEMKL LAYDDPDENNEGEFQYLKEEGTJILBGDNLITECKYNTKDRAEMT WGGLSTRSENCLSYLLYVFRINLTRCASIPDIMEQLOFIGVEET TYPVTTWPFIIKSPKOMMNKPKWTKKEGLSFNKLVL SLPVNVRCSRTDNAENSIGGMTALPPDIERPYKAEGLSFNKLVL SLPVNVRCSRTDNAENSIGGMTALPPDIERPYKAEGLSFNKLVL SLPVNVRCSRTDNAENSIGGMTALPPDIERPYKAEGLSFNKLVL SLPVNVRCSRTDNAENSIGGMTALPPDIERPYKAEGLSFNKLVL SLPVNVRCSRTDNAENSIGGMTALPPDIERPYKAEGLSFNKLVL SLPVNVRCSRTDNAENSIGGMTALPPDIERPYKAEGLSFNKLVL SLPVNVRCSRTDNAENSIGGMTALPPDIERPYKAEGLSFNKLVL SLPVNVRCSRTDNAENSIGGMTALPPDIERPYKAEGLSFNKLVL SLPVNVRCSRTDNAENSIGGMTALPPDIERPYKAEGLSFNKLVL SLPVNVRCSRTDNAENSIGGMTALPPGRESTSS SCHLEPS SCHLENGESTENDAENSICCLEPA SATVHPOQLIFFLNGSSLENDAFSNKSERENPEESDTETODHSR KTESGSDOSETPCAPVRRGTTTVEQVQESLGELGEASGVETVSS ENKSLAWTLIKGGLRPMDLISRVULPTFYLEPRSFLINKLSDYYH ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKRKDGIKKRYNFILG ETFRCCWFHPQTDSRTFYLAEQVSHHPVSAFHVSNRKDGFCIS SKITASSRFYGNSLSALLIGKATLTFILNRAEDYTLTMPYAHCKS ILKGTHTLEIGGKVT1EGAKNNFQAQLEFKLKPFFGSSTSINQI SGRITASGEVLALSGHDNDAYDIKEGSGSSALHFWTSGEVRR QRIRGHTVHEEGGLTARTAGAA GSTRKVATGSRNFQRAENSINGHTARISKGDOHRATGEKFAL EEAQRGARAERGSESLMPWKFQLJFHLDPTTQEMHTAYEDHSPWDP LKDJAFPERSGESSESLMPWKFQLJFHLDPTTQEMHTAYEDHSPWDP LKDJAFPERSGESSESLMPWKFQLJFHLDPTTQEMHTAYEDHSPWDP LKDJAFPERSGESSESLMPWKFQLJFHLDNAENSTARAAQA PTROLLQSPRSWFLLCVELACQLFINHLK SQORKVRQMIEQLQNSKAVIGSKDATTQELKEKTAYLEAENLEM PROLLQSPRSWFLLCVELACQLFINHLK SQORKVRQMIEQLQNSKAVIGSKDATTQELKEKTAYLEAENLEM PRECLEDKESSTATGTOTWILLKAAATLEKEVAGLERKIHHLDDMLK SQORKVRQMIEQLQNSKAVIGSKDATTQELKEKTAYLEAENLEM PRECLEDKESSTATGTOTWILLKAAATLEKEVAGLERKIHHLDDMLK SQORKVRQMIEQLQNAKKSVVPFLOGTITELQRILDSAI PROLLDONTNKRSKEVRVLQEMQLLQVAAMMYRLRPLEKFVTYFT RMSQLSDKSSYKLSQLEPENF RASSGLONTARSKRVVLQEMQLLQVAAMMYRLRPLEKFVTYFT RMSQLSDKSSYKLSQLEPENF PWTAASSQ LKBHFAQFGHVRRCILPPDKSTGPHRGLGWVGSSEEGLRNALQ QNHIILDGVKVQVHTRPKLPGTSDDEKWF	ļ			
7134 2115 1111 GGEGFSYPPINGLSLOTPLDPHYVLLEVHYDNPTYEEGLINNSC LRIFYTMDIRKYDAGVIRAGLWVSLIPHTIPPGMPEFQSEGHCTL LCLEEALEAEKPSGIHVRAVLLHARLLAGGIRLEHFRKGKEMKL LAYDDDFDENFQEFQYLKEEQTILGDBLITECKYNTKDRAEWT WGGLSTRSEMCLSYLLYYPRINITRCASIPDIMEQLQFIGYKEI YRPVTTWPFIIKSPKQYKNLLSFMADLATICKYNTKDRAEWT WGGLSTRSEMCLSYLLYYPRINITRCASIPDIMEQLQFIGYKEI YRPVTTWPFIIKSPKQYKNLSFMADMNFKWTKKEGLSFMKLVL SLPVNVRCSKTDNAEWSIQGMTALPPDIERPYKAEPLVCGTSSS SSLHRDFSINLIVCLLLISCTLSTKSL 7135 2 2072 FVERVTPRSISLQGFKGEVGSITQPLESSYLIFPRASESDGRC WLDALELARCSSLKRIGTCKPGRGBEGTSPDASPSSLCGLPA SATVHPDQDLFPLNGSSLENDAFSDKSERNPERSDTETQDHSR KTESGDOSETPLGAPVRGGTTVTVEGVQDELGELGEGASQVETVSE ENKSLMWTLLKQLRPGMDLSRVVLPTFVLEPRSFLNKLSTYYH ADLISRAWEDAYSRMKLVLRWYLSGFYKKPGGIKKYNFILG GSTRAKSRFYGNSLSALLGGKATLTFLNRAEDYTLTMPYAHCKG GSTRAKSRFYGNSLSALLGGKATLTFLNRAEDYTLTMPYAHCKG GGTAKASFFYGNSLSALLGGKATLTFLNRAEDYTLTMPYAHCKG GGTAKASFFYGNSLSALLGGKATLTFLNRAEDYTLTMPYAHCKG GGTAKASFFYGNSLSALLGGKATLTFLNRAEDYTLTMPYAHCKG GGTAKASFFYGNSLSALLGGKATLTFLNRAEDYTLTMPYAHCKG HEAVANGTTELGSFGFRHERSGFDQRI KADLAGFEGGSTALFWTPSGEVRR QRLRQHTVPLEEOTELESERLWQHVTRAISKGDQHRATGEKFLA EEAQRGRAERGESLMPWKPGLFHLDPITGEWHYRYEDHSPWP LKDIAGFEGGSTSINGKGTHTSGEFGFPRHERSGFDQRI KADLAGFTENGAARGTTERSGFFTRHESGFDQRI KADLAGFTENGAARGTTERSGFFTRHESGFDQRI KADLAGFTENGAARGTTERSGFFTRHE				
LRLFYTMDIRKYDAGVIFAGLWVSLFHTIPPGMPEFGSECHCTL ECLEBALBARKPSGIHVPAVLLHARLAGGTRILHFRKGEMML LAYDDPDFDNEFGFGYVLKEGGTJLLFORNLITEGASIPOT WGGLSTRSENCLSYLLYTPRINLTRCASIPOTHROLOFIGVKET YRPVTTWPFIIS BYRGYNLISPMDAMNFKWTKKEGLSFNKLVI SLPVNVRCSKTDNAEWSIQGMTALPPDIERPYKAEPLVCCTSSS SSHRDFSINLLVCLLLLSCTLSTKSL 7135 2 2072 FVPRVYPTRSLSLOGPKGESVGSTOPPLPSSYLIFRAASESDGRC WLDALBLALRCSSLLRLGTCKFGRDGEPGTSPDASPSSLCCLPA SATVHPODLFPLNGSSLENDAFSPKSEREMPEESDTETQDHSR KTESGSDQSETFGAPVRRGTTYVEQVQEELGELGEASQVETVSE ENKSLMWTLLKQLRPEMDLSRVVLPTFVLPERSFLNKLISDTYTH ADLLSRAAVEEDAYSRMKJVLWAWTLSGFYKKPKGIKKFYNFILG ETTRCCWFHPQTDSRTFYIAEQVSHHPPVSAPHVSNRKDGFCIS GSITASRFYGNSLSALLDLGATTLFURRABDYTLTMPYAHCKG ILYGTWTLELGGKVTIECAKNNFQAQLEFKLKPFFGGSTSINQI SGKITSGEBVLAS LSGHUDRDVFIKEGSGSSALFWTPSGEVRR QRLRGHTVPLEBGTDELESBERLDWATRAISKGDQHRATQEKFAL EEAQRQRARERGESLMPWKPQLFHLDFITGBWHTRYEDHSPWDP LKDIAGPEGOGILRTLQCGRAVARQTTPLGSWGPRHERSGPDQRR RKASDQPSGHSQATESSGSTPESCPELSDEEQQDGFVPGGESPC PRCRKEARRLQALHEAILS IREAQQELHRHLSANLSSTARAAQA PTPGLLQSPRSWFLLCVILACQLFINHILK 7136 2 418 DFVPSFRFPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIHAYLBAENLEW HRMEHLIBKQISHMFTQAARATLEKEVAGLREKIHHLDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKITAYLBAENLEW HRMEHLIBKQISHONFSTQARAKTENPGGIRISKFPSPKPMPV IRVUET 7137 2 466 WASSMSTVPGGSRHSLGTQVRGGWGVTGGEESLTVEVADTWQA GSFKVATQERPDQRAQMRLRQKKGVVPFLGDFLTELQRLDSAI PDDLIGNTNKRSKEVRVLQEWQLLQVAAMWYRLRPLEKFVTYPT RMSQLSDKESYKLSCQLEPENP 7138 2 466 WASSMSTVPGGSRHSLGTQVRGGWGVTGGEESLTVEVADTWQA GSFKVATQERNPQRAQMRLRQKKGVVPFLGDFLTELQRLDSAI PDDLIGNTNKRSKEVRVLQEWQLLQVAAMNYRLRPLEKFVTYPT RMSQLSDKESYKLSCQLEPENP 7139 1 357 SLENKSAGLKMASAARGAAALRRSINGPVAFVRRIFWTAASSQ LKEHFAQFGHVRRCILPFDKETGFRGLGWVGFSSEEGLRNALQ QENHILDGVKVQVHTRPKLPDTSDEKKDF 7140 1401 1957 RASSLQVLKANGGLIFSSFQQQHTGQYSLEELEPDLKVYDCFCSF	7134	2115	1111	
ECLEBALBARKPSGIHVFAVLLHAHLAGRGIRLRHFRIGKEMKIL LAYDDDFDFPFGFQYLKEEQTILPGDDLITECRYNTKDRABMT WGGLSTRSEWCLSYLLYYPRINLTRCASIPDIMEQLQFIGVKEI YRPVTTWPFIIKSPKQYKNLSFMDAMKFKWTKKEGLSFMKLVI, SLPVVWRCSKTDNAEMSIGQEMTALPPDIERPYKAEPILVCGTSSS SSLHRDFSINLLVCLLLLSCTLSTKSL 7135 2 2072 FVPRVFPRSISLGGFKGESVGSITOPLPSSYLIFRAASESDGRC WLDALBLAIRCSSLLRHGTCKPGRDGEPGTSPDASPSSLGGLPA SATVHPQDLFPLNGSSLENDAFSDKSERENPESSDTETQDHSR KTESGSDQSSTFFGAPVRRGTTYVEQVQEELGEASQVSTVSE ENKSLMMTLLKQLRPGMDLSRVVLIPFYLSEPSFLNKLSDYYH ADLLSRAVEBDAYSRMKLVLRWYLSGFYKKPKJRIKKPYNPILG ETFRCCWFHPQTDSRTFYIAEQVSHHPPVSAPHVSNRKDGFGIS GSITAKSRFYGNSLSALLDGKATLTFILRREDVITLTMPYAHCKG ILVGTMTLELGGKVITECKARNNQAQLEFKLKFFFGGSTSINQI SGKITSGEEVLASLSGHWDRDVFIKEGGSSSALFWTPSGEVKR QRLRGHTVPLEEGTELSSERLWHVTRAISKGDOHRATQSEKFAL EEAQRQRARERQESLMPWKPQLFHLDPITQEWHYRYEDHSPWDP LKDIAGFEQGILRTLQGRAVARQTTFLGSPGRHERSGFDQRL RKASDQPSGHSQATESSSTPESCPBLSDEEQDGDFVPGGESPC PRCHKEARRIQALHEAILSITERQQGIHRHLSAMLSSTARAAQA PTGCLLQSPRSWFLLCUFLACQLFINHILK 7136 2 418 DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK SQCKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM HDRMEHLIEKGLSHGWFTAGARKKTNPGGSIRTSKFPSPKPMPV IRVVET 7137 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEESSLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAANNYRLRPLEKFVTYFT RMSQLSDKESYKLSCQLEPENP 7138 2 466 WASGMSTVPGSRHSLGIQVRGGWGVTGGEESSLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAANNYRLRPLEKFVTYFT RMSQLSDKESYKLSCQLEPENP 7139 1 357 SLRNSARGLKMAAASAARGAAALBRSINQPVAFVRRIPWTAASSQ LKEHFAQFGHVRRCILPFDKETGFHBGLGWVQFSSEEGLRNALQ QENHILDGVKVQVHTRRPKLPCTSDDEKKDF 7140 1401 1957 RASSLQVLKWGGGIFSSTDQQRTGGYALEELEDLLKVYPCFSF				
LAYDDDEPFREQEPQULKEROTILPGONLITECRYNTKDRAEMT WGGLSTRSEMCLSYLLYYPRINLITRCASIPDIMEQLOFIOVKEI YRPVTWPFIIKSPKOYKNISFMDAMNKFWTKKEGLSFMKLVI. SLEVNVNCSKTDNAEMSIQCMTALPPDIERPYKAEPIVCGTSSS SSLHRDFSINLUVLLLLISCTLSTKSL 7135 2 2072 FVPRVTPSIS.LOGPKGESVGSTTOPLPSSYLIFRAASESDGRC WLDALELARCSSLLRLGTCKYGGRDGEPGTSPDASPSLCGLBG KTESGSDQSSTFGAPVURGTTYVEQVQEELGELGEASQVETVSE ENKSLMMTLLKUKLURSPMOLDSVLTPTVLERPSFILMKLDYYH ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGIKKPYNPILG ETTRCCWFHPQTDSRTFYIAEQVSHHPPVSAPHVSNRKDGFGIS GSITAKSRFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKS ILYGTWTLELGGRVTIECAKNNPQAGLEFKLKPFFGGSTSINQI SGKITSGEVILASLSGHWDRDVFIKEEGGSSALFWPPSGEVRR QRLRQHTVPLEEQTELESBRLWQHVTRAISKGDQHRATQEKFAL EEAQRGRAERGESLMPWKPQLFHLDPITQBWTYREDHSPWDP LKDIAQFEQDGIIRRTLQQEAVARQTTTFLGSPGPRHERSGPDQKL RKASDQPSGHSQATESSGSTPESCPELSDEEQDGDFVPGGGSPC PCCKEARRLQALHEAILSIREAQGELHRHLSAMLSSTARAQA PTBGLLQSPRSWFLLCVFLACQLFINHILK 7136 2 418 DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLEKHHLDDMLK SQOKKVRQMIEGLQNSKAVIOKDATIQLEKEKIAYLEABNLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET 7137 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATOERNPQRAQMGLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7138 2 466 WASGMSTVPGGSRHSLGIQVRGGWGTGGEEESLTVPVADTWQA GSFKVATOERNPQRAQMGRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7138 1 357 SLENSRAGLKMAAASAARGAAALERSINQPVAFVRRIPWTAASSQ LKEHFAQFGHVRRCILPFDKETGPHRGLGWVQFSSEEGLRNALQ QENHIIDGVKVQVHTRRPKLPQTSDDEKKDF 7140 1401 1957 RASSLQVLKWGGGIFFSTQQORTGGYALEELFDLKVYDCFCSF		1	[
WGGLSTRSEMCLSYLLYYPRINLTRCASIPDIMEQLQFIGVKET YRPVTTWPFIIKSPKQYKNLSFMDAMMKPKWTKKEGLSFNKUJL SLEVNVRCSKTDNAEWSIQGMTALPPDIERPYKAEPLVCGTSSS SSLHRDFSINLLVCLLLLSCTLSTKSL 7135 2 2072 FVPRVTPSLSLQGPKGEVGSITOPLPSSYLIFRAASESDGRC WLDALELALRCSSLLRLGTCKPGRDGEPGTSPDASPSSLCGLPA SATVHPDQDLFPLMGSSLENDAFSKSERENPEESDTETQDHER KTEGSBOOSETPGAPVRRGTTYVEQVQEDEIGLGEASQVETVGS ENKSLMWTLLKQLRPGMDLSRVVLPTPVLEPRSFLMKLSDYYH ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGIKKPYNPILG ETTRCCMFHPQTDSRTTFYIAEQUSHHPPVSAPHVSNRKDGFCIS GSITAKSRFYGNSLSALLDGKATITFINRAEDYTLTMPYAHCKG LLYGTMTLELGGKVTIECKHLRPFFGSSTSINQI GGSITAKSRFYGNSLSALLDGKATITFINRAEDYTLTMPYAHCKG LLYGTMTLELGGKVTIECKHLRPFFGSSTSINQI GGKITSGEEVLASLSGHWDRDVFIKEEGSGSSALFWTPSGEVRR QRLRQHTVPLEEQTELESERLWQRVTTRAISKGDHRATQEKFAL EEAQRGAARERQESLIMPMCLFHLDPTTQEMHYRYEDHSPWDP LKDIAQPEQDGILRTLQQBAVARQTTFLGSPGPRHERSGPDQRL RKASDQPSGHSQATESSGSTPSCELSDEEQDGFVPGGESSC PRCKEARRLQALHEAILS IREAQQELHRHLSAMLSSTARAAQA PTFGLLQSPRSWFLLCVFLACQLFINHILK 7136 2 418 DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMLEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM HDRMEHLIERQISHGNFSTQARAKTENPGSIRISKFPSPKPMPV IRVVET 7137 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSQLEPENP 7138 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSQLEPENP 7139 1 357 SLENSARGLKMAASAARGAALRRSINQPVAFVRRIPWTAASSQ LKEHFAQFGHVRRCILPPDKSTGPHRGLGWVQFSSEEGLRNALQ QENHIIDGVKVQVHTRRPKLPQTSDDEKKDF 7140 1401 1957 RASSLQVLKAWGGLIFFSFQQQHTGQVALEELFDLKVYYDCFCSF	1	i		
YRPVTMPFIIKSPKQYKNLSFMDAMNKFKWTKKEGLSPNKLUL SLPVNVRCSKTDNAEWSIQGMTALPPDIERPYKAEDLVCGTSSS SSLHRPFSINLLVCLLLLSCTLSTKSL 7135 2 2072 FVPRVTPRSLSLGGPKGESVGSITOPLPSYNLFRASESDGRC WLDALELALRCSLLKILGTCKPGRDGEPGTSPDASPSSLCGLPA SATVHPDQDLFPLNGSSLENDAFSDKSERNPESDTETQDHSR KTESGSDQSETPGAPVRRGTTYVEQVQEELGEBASQVETVSE ENKSLMMTLLKQLRPGMDLSRVULFTFVLEPRSFLNKLSDYYHH ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGIKKPYNPILG ETRCCHPHPQTDSRTFYLAEQVSHHPPVSAFHVSNRKDGFCIS GSITAKSR FYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG ILVGTWTLELGGKVTIECAKNNFQAQLEFKLKPFFGGSTSINQI SGKITAGSEVLASLSGHWDDFYIKEEGSSSALFWTPSGEVRR QRLRQHTVPLECOTELESBRLWQHVTRAISKGDQHRATQEKFAL EEAQRQRARERQESLMPWKPQLFHLDPITQEWHYRYEDHSPWDP LKDIAGFEQDGILRTLQQEAVARQTTFLGSPGPRHERSGPPDQRL RKASDQPSGHSQATESSGSTFESCPELSDEEQDGFVPGGESSC PRCKEARRIQALHEAILS IREAQQELHEHLSAMLSSTARAAQA PTPGLLQSPRSWFLLCVFLACQLFINHILK 7136 2 418 DFVPSFRRPSGNTSQTWULLRAATLEKEVAGLREKIHHLDDMLK SQQKVKVRQMIEQLQNSKAVIQSKDATIQELKEKIHYLBABNLEM HDRWEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET 7137 2 466 WASSMSTVPGGSRHSLGIQVRGGWGVTGGEESSLTVPVADTWQA GSFKVATQERNFQRAQWRLRRQKKGVVPFLGGFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7138 2 466 WASSMSTVPGGSRHSLGIQVRGGWVTGGEEESLTVPVADTWQA GSFKVATQERNFQRAQWRLRRQKKGVVPFLGFFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7139 1 357 SLRNSARGLKMAASAARGAALRRSINQPVAFVRRIFWTAASSQ LKEHFAQFGHVRRCILPFDKSTGPHRGLGWVQFSSEEGLRNALQ QENHIJDGVKVQVHTRRPKLPQTSDDEKKDF 7140 1401 1401 1957 RASSLQVLKANGGLIFSSFQQQHTGQVALEELFFDLKVYDCFCSF				
SLEVNVRCSKTDNAEWSIQGMTALEPDIERPYKAEPLVCGTSSS SSLHRDFSINLUVCLLLLSCTLSTKSL 7135 2 2072 FVERVTPRSISIQGPKGESVGSITQPLESYLIFRAASESDGRC WLDALBLALRCSSLLRLGTCKPGRDGEPGTSPDASPSSLCGLPA SATVHPDQDLFPLNGSSLENDAFSDKSERENPEESDTETQDHSR KTESGSDQSETPGAPVRRGTTYVEQVQEELGELGEBASQVETVSE ENKSLMMTLLKQLRPGMDLSRVVLDFTVLEPRSFLNKLSDYYYH ADLLSRAAVEBDAYSRMKIVLRWYLSGFYKKPKG KKPYNPILG ETFRCCWFHPQTDSRTFYIAEQVSHHPPVSAPHVSNRKDGFCIS GSITAKSRFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG ILVGTMTLELGGKVTIECAKNNFQAQLEFKLKPFFGGSTSINGI SGKITSGEVLASLSGHWDRDVFIKEGGGSSALFWTPSGEVRR QRLRQHTVPLEEQTELESERLWQHVTRAISKGDQHRATQEKFAL EEAQRGRARERQESLMWKFQLFHLDPITQEWHYRYEDHSPWDP LKDIAGFEQDGILRTLQQEAVAROTFFLGSPGPRHERSGFDQBL KRSADQPSGRSQATESSSTBSCPELSDEEQDGDFVPGGESPC PRCRKEARRLQALHEAILSIREAQGELHRHLSAMLSSTRRAAQA PTFGLLGSPRSWFLLCVFLACQLFINHILK 7136 2 418 DFVPSFRFBSGNTSGTVMLRAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM HDRMEHLIERQISHGNFSTQARAKTENPGSIRISKPPSFKPMPV IRVVET 7137 2 466 WASGMSTVPGGSRHSLGTQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSQQLEPENP 7138 2 466 WASGMSTVPGGSRHSLGTQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSQLEPENP 7139 1 357 SLRNSARGLKMAASAARGAALRRSINGPVAFVRRIPWTAASSQ LKEHFAQFGMYRRCILPPDKSTGFHRGLGWVQFSSEEGLRNALQ QENHIIGGVKVQVHTRRPKLPOTSDDEKKDF 7140 1401 1401 1957 RASSLQVLKANGGLIFSSFQQQHTGQVALEELFDLKVYDCFCSF				
SSLHRDFSINLLVCLLLLSCTLSTKSL 7135 2 2072 FVPRVTPRSLSLQGFKGESVGSITQFLDFSSYLIFRAASESDGRC WLDALELALRCSSLLRLGTCKPGRDGEPGTSPDASPSSLCGLPA SATVHPDQDLFPLNGSSLENDAFSDKSERRMPEESDTFTQDHSR KTESGDQSETPGAPVRRGTTYVEQVQEELGELGEASQVETVSE ENKSLMMTLLKQLRPGMDLSRVVLPTFVLBERSFLNKLSDYYHH ADLLSRAAVEBDAYSRMKLVLRWYLSGFYKKPKGIKKPVNPILG ETFRCCWFHPQTDSRTFY1AEQVSHHPPVSAFHVSNRKDGFCIS GSITAKSRFYGNSLSALLDGKATLITFLNRAEDYTLTMPYAHCKG ILYGTMTLELGGKVTIECAKNNROAQLEFKLKPFFGGSTSINQI SGKITSGEVLASLSGHWDRDVFIKEEGSGSSALFWTPSGEVRR QRLRQHTVPLEEQTELESERLWGHVTRAISKGDQHRATQEKFAL EEAQRQRARERQESLMPWRPQLFHLDPITQEWHYRYEDHSPWDP LKDIAQFPQDGILRTLQAVAAAQTTFLGSFGPRHERSGPDQRL RKASDQPSGHSQATESSGSTPESCPELSDEDQXDDFVPGGESPC PRCRKEARRLQALHEAILSIREAQGEHRHLSANLSSTARAAQA PTFGLLGSPSSWFLLCLALACQLFINHILK 7136 2 418 DFVPSFRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK SQORKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLBEANLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET 7137 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEESSLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFITELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQULQVAAMNYRLRPLEKKVTTYFT RMSQLSDKESYKLSQLEPENP 7138 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEESSLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQULQVAAMNYRLRPLEKKVTTYFT RMSQLSDKESYKLSQLEPENP 7139 1 357 SLRNSARGLKMAASAARGAALRRSINQPVAFVRRIPWTAASSQ LKEHFAQFGHVRRCILPFDKETGFHRGLGWVGFSSEEGLRNALQ QENHIIOGVKVQVHTRGLPGTDDEKKDF 7140 1401 1957 RASSLQVLKAWGGLIPSSFQQRHTGGYALEELFDLKVYDCPCSF	1	1		
7135 2 2072 FVPRVTPRSLSLQGPKGESVGSITQPLPSSYLIFRAASESDGRC WLDALBLALRCSSLRURGTCKPGROEEPGTSPDASPSSLCGLPA SATVHPDQDLFPLNGSSLENDAFSDKSERNPEESBJTETQDHSR KTESGSDQSETYGEPGNEGSPURGESDJTETQDHSR KTESGSDQSETYGEPGNEGSVETVSE ENKSLMWTLLKGPLSRVVLPTFVLEPRSFLNKLSDYYH ADLLSRAAVEBDAYSMKLVLRWYLSGFYKCPKGIKKPYNPILG ETRCCWFHPQTDGSRTFYTAEQWSHHPPVSAFHVSNRKDGFCIS GSITAKSFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG ILKGTWTLELGGKVTILECAKNNFQAQLEFKLKPFFGGSTSINQI SGKITSGEVLRA QRENQHTVPLEFOTELESRRLWGHVTRAISKGDHRATQEKFAL EEAQRQRARERQESLMPWKPQLFFLDPITQEWHYRYEDHSPWDP LKDIAGFEQDGILRRLQQBAVARQTTFLGSPGPHRESGPDQRL RKASQQPSGHSQATESSTPSSCPELISDEEQQGDFVPGGESSP PRCRKEARRLQALHEALISIREAQQBLHRHLSAMLSSTARAAQA PTPGLLQSPSKSTPSSCPBLISDEEQGDFVPGGESSP PRCRKEARRLDALHEALISIREAQQBLHRHLSAMLSSTARAAQA PTPGLLQSPSKSTPSSCPBLISDEEQGDFVPGGESSP PRCRKEARRLDALHEALISIREAQQBLHRHLSAMLSSTARAAQA PTPGLLQSPSKSTPSSCPBLISDEEQGDFVPGGSSP PRCRKEARRLDALHEALISIREAQQBLHRHLSAMLSSTARAAQA PTPGLLQSPSKSTPSCPBLISDEEQGDFVPGGSSP PRCRKEARRLDALHEALISIREAQQBLHRHLSAMLSSTARAAQA PTPGLLQSPSKSPLLCVFLACQLFINHILK SQCRKVRQMIBQLGNSKAVIQSKDATIQELKEKIAYLRAENLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMFV IRVET IRVET RMSCLSDKSWSVLQCMGGGEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGMTNKRSKEVRVLQEMQLLQVAAMYRIRPLEKFVTYFT RMSCLSDKSSYKLSCQLEPENP ASSMSTVPGGSRHSLGIQVRGGWGVTGGEESSLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGMTNKRSKEVRVLQEMQLLQVAAMYRIRPLEKFVTYFT RMSCLSDKSSYKLSCQLEPENP SLENGARGAARRAANTRIRPLEKFVTYFT RMSCLSDKSSYKLSCQLEPENP SLENGARGAARRAANTRIRPLEKFVTYFT RMSCLSDKSSYKLSCALEPENP SLENGARGAARRAANTRIRPLEKFVTYFT RMSCLSDKSSYKLSCALEPENP SLENGARGAARRAANTRIRPLEKFVTYFT RMSCLSDKSSYKLSCALEPENP SLENGARGAARRAANTRIRPLEKFVTYFT RMSCLSDKSSYKLSCALEPENP SLENGARGAARAARAARAARAARAARAARAARAAARAAARAAA			1	
### WIDALELALRCTSLIRIGTCKPGRDGEPGTSPDASPSSLCGLPA SATVHPDQDLFPINGSSLENDAFSDKSERNPESSTDTTQDH9A KTESGSDQSETFGAPVRRGTTYVEQVQEELGELGEASQVETVSE ENKSLMWTLLKQLRPGMDLSRVVLPTFVLDPRSFLNKLSDYYYH ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGIKKPYNPILG ETFRCCWFHPQTDSRTFYIAEQVSHHPPVSAFHVSNRKDGFCIS GSITAKSRFYGNSLSALLDGKATLTFLNRREDYTLTMPYAHCKG ILYGTMTLELGGKVTIECAKNNFQAQLEPKLKPFFGGSTSINQI SGKITSGEVLASLSGHWDRDVFIKEEGSGSSALFWTPSGEVRR QRLRQHTVPLEEQTELESERLWQHVTRAISKGDQHRATQEKFAL EEAQRQRARERQESLMPWKPQLFHLDPITQEWHYRYEDHSPWDP LKDIAQFEQDGILRTLQQEAVARQTTFLGSPGPRHERSGPDQRL RKASDQPSGHSQATESSGSTPESCPELSDEEQDGDFVPGGESPC PRCRKEARRLQALHEAILSIREAQQELHRHLSAMLSSTARAAQA PTFGLLQSPRSWFLLCVFLACQLEFINHILK 7136 2 418 DFVPSFRRPSGNTSQTWWLLFAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIHHLDDMLK HDRMEHLIEKQISHGMFSTQARAKTENPGSIRISKPPSPPKPMPV IRVUET 7137 2 466 WASGMSTVPGGSRHSLGJQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7138 2 466 WASGMSTVPGGSRHSLGJQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7139 1 357 SLRNSARGLKMAASAARGAAALRRSINQPVAFVRRIPWTAASSQ LKEHFAQFGHVRCILPFDKETGFHRGLGWVQFSSEEGLRNALQ QSNHIILOKVVQVTHTRPKLPQTSDEKKDF 7140 1401 1957 RASSLQVLKAWGGLIFSSFQQQHTGQYALEELFDLKVYDCPCSF	7135	2	2072	FVPRVTPRSLSLQGPKGESVGSITQPLPSSYLIFRAASESDGRC
SATYHPDQDLFPLNGSSLENDAFSDKSERENPEESDTETQDHSR KTESGSDQSETPGAPVRGGTTYDEQVEEGGELGEASQVETVSE ENKSLMWTLLKQLRPGMDLSRVVLPTFYULEPGSFLNKLSDYYHH ADLLSRAAVEBDAYSRMKLVLRWYLSGFYKKPKGIKKPYNPILG ETFRCCWFHPQTDSRTFY1LAEQVSHHPPVSAFHVSNRRDGFGIS GSTTAKSRPYGNSLSALLDGKATLTFLNRAEDVTLTMPYAHCKG ILYGTMTLELGGKVTIECAKNNFQAQLEFKLKPFFGGSTSINQI SGKITSGEEVLASLSGHWDRDVFIKEEGGSSALFWTPSGEVRR QRLRQHTVPLEEDGTELESERLWQHVTRAISKGDQHRATQEKFAL EEAQRQRARERQESLMPWKPQLFHLDPITQEMHYRYEDHSPWDP LKDIAQFEQDGIIRTLQQEAVARQTTFLGSPGPRHERSGPDQRL RKASDQPSGHSQATESSGSTPESCPELSDEEQDGDFVPGGESPC PRCKKEARRLQALHEAILSIREAQQELHRHLSAMISSTARAAQA PTFGLLQSPRSWFLLCVFLACQLFINHILK 7136 2 418 DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK SQORKVRQMIBQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM HDRWEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET 357 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCDLEPENP 7138 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCOLEPENP 7139 1 357 SLRNSARGLKMAASAARGAAALRRSINQPVAFVRRIPWTAASSQ LKEHFAQFGHVRCILPFDKETGFHGGLGWVQFSSEECLRNALQ QENHIILOVKVQVTHTRPPKLPQTSDDEKKDF 7140 1401 1957 RASSLQVLKAWGGLIFSSFQQQRTGQYALEELFDLKVYDCPCSF	1	l		
ENKSLMWTLLKQLRPGMDLSRVVLPTFVLEPRSFLMKLSDYYH ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGIKKPYNPILG ETTRCCWFIPQTDSRTFYIAEQVSHHPPVSAFHVSNRKDGFCIS GSITAKSRFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG ILYGTMTLEELGGKVTIECAKNNFQAQLEFKLKPFFGGSTSINQI SGKITSGEFVLASLSGHWDRDVFIKEEGSGSSALFMTPSGEVRR QRLRQHTVPLEEQTELESERLWQHVTRAISKGDQHRATQEKFAL EEAQRQRARERQESLMPWKPQLFHLDPITQEWHYRYEDHSPWDP LKDIAQFEQDGILRTLQQEAVARQTTFLGSPGPRHERSGPDQRL RKASDQPSGHSQATESSGSTPESCPELSDEEQDGDFVPGGESPC PRCKKEARRLQALHEAILSIREAQQBLHRHLSAMLSSTARAAQA PTPGLLQSPRSWFLCVFLACQLFINHILK 7136 2 418 DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVUET 7137 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATOENPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7138 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATOENPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7139 1 357 SLRNSAGLKMAASAARGAALRRSINQPVAFVRRIPWTAASSQ LKEHFAQGFWRRCILPPKETGFHRGLGWVQFSSEEGLRNALQ QENHIIDGVKVQVHTRRPKLPQTSDDEKKPF 7140 1401 1957 RASSLQVLKAWGGLIPSSFQQQHTGQYALEELFDLKVYDCFCSF				SATVHPDQDLFPLNGSSLENDAFSDKSERENPEESDTETQDHSR
ENKSLMWTLLKQLRPGMDLSRVVLPTFVLEPRSFLMKLSDYYH ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGIKKPYNPILG ETTRCCWFIPQTDSRTFYIAEQVSHHPPVSAFHVSNRKDGFCIS GSITAKSRFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG ILYGTMTLEELGGKVTIECAKNNFQAQLEFKLKPFFGGSTSINQI SGKITSGEFVLASLSGHWDRDVFIKEEGSGSSALFMTPSGEVRR QRLRQHTVPLEEQTELESERLWQHVTRAISKGDQHRATQEKFAL EEAQRQRARERQESLMPWKPQLFHLDPITQEWHYRYEDHSPWDP LKDIAQFEQDGILRTLQQEAVARQTTFLGSPGPRHERSGPDQRL RKASDQPSGHSQATESSGSTPESCPELSDEEQDGDFVPGGESPC PRCKKEARRLQALHEAILSIREAQQBLHRHLSAMLSSTARAAQA PTPGLLQSPRSWFLCVFLACQLFINHILK 7136 2 418 DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVUET 7137 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATOENPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7138 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATOENPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7139 1 357 SLRNSAGLKMAASAARGAALRRSINQPVAFVRRIPWTAASSQ LKEHFAQGFWRRCILPPKETGFHRGLGWVQFSSEEGLRNALQ QENHIIDGVKVQVHTRRPKLPQTSDDEKKPF 7140 1401 1957 RASSLQVLKAWGGLIPSSFQQQHTGQYALEELFDLKVYDCFCSF	1	}	ļ	KTESGSDQSETPGAPVRRGTTYVEQVQEELGELGEASQVETVSE
### ETFRCCWFHPQTDSRTFY1AEQVSHHPPVSAPHVSNRKDGFCIS GSITAKSRFYGNSLSALLDGKATLTFILMRAEDYTLTMPYAHCKG GSITAKSRFYGNSLSALLDGKATLTFILMRAEDYTLTMPYAHCKG ILVGTMTLELIGGKVTTECAKNNFQAQLEFKLKPFFGGSTSINQI SGKITSGEEVLASLSGHWDRDVFIKEEGSGSSALFWTPSGEVRR QRLRQHTVPLEEQTELESERLWQHVTRAISKGDQHRATQEKFAL EEAQRQRARERQESLMPWKPQLFHLDPITQEWHYRYEDHSPWDDP LKDIAQFFQDGILRTLQQEAVARQTTFILGSPGFRHERSGFDQRL RKASDQPSGHSQATESSGSTPESCPELSDEEQDGDFVPGGESPC PRCRKEARRLQALHEAILSIREAQQBLHRHLSANLSSTARAAQA PTPGLLQSPRSWFLLCVFLACQLFINHILK 7136 2 418 DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKITAYLEAENLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET 7137 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQWRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7138 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQWRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7139 1 357 SLRNSARGLKMAASAARGAAALRRSINGPVAFVRRIPWTAASSQ LKEHFAQFGHVRRCILPFDKETGFHRGLGWVQFSSEEGLRNALQ QENHILIDGVKQVHTRRPKLPQTSDDEKKDF 7140 1401 1957 RASSLQVLKAWGGLIFSSFQQQHTGQYALEELFDLKVYDCFCSF	Ī	1		ENKSLMWTLLKQLRPGMDLSRVVLPTFVLEPRSFLNKLSDYYYH
GSITAKSRFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG ILYGTMTLELGGKVTITECAKNNFQQLEFKLKPFFGGSTSINQI SGKITSGEEVLASLSGHWDRDVFIKEEGGSSSALFWTPSGEVRR QRLRQHTVPLEEQTELESERLWQHVTRAISKGDQHRATQEKFAL EEAQRQRARERQESLMPWKPQLFHLDPITQEWHYRYEDHSPWDP LKDIAQFEQDGILRTLQEAVARQTTFIGSPGPRHERSGPDQRL RKASDQPSGGSQATESSGSTPESCPELSDEEQDGDFVPGGESPC PRCRKEARLQALHEAILSIREAQQBLHRHLSANLSSTARAAQA PTFGLLQSPRSWFLLCUFLACQLFINHILK 7136 2 418 DFVPSFRPSGNTSQTVWLLERAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVUET 7137 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7138 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7139 1 357 SLRNSARGLKMAASAARGAAALRRSINGPVAFVRRIPWTAASSQ LKEHFAQFGHVRRCILPFDKETGFHRGLGWVGFSSEEGLRNALQ QENHIIDGVKVQVHTRRPKLPCTSDDEKKDF 7140 1401 1957 RASSLQVLKAWGGLIPSSFQQQHTGQYALEELFDLKVYDCFCSF	1	l .	}	ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGIKKPYNPILG
ILYGTMTLELGGKVTIECAKNNFQAQLEFKLKPFFGGSTSINQI SGKITSGEEVLASLSGHWDRDVFIKEEGSGSSALFWTPSGEVRR QRLRQHTVPLEEQTELESERLWQHVTRAISKGDQHRATQEKFAL EEAQRQRARERQESLMPWKPQLFHLDPITQEWHYRYEDHSPWDP LKDIAQFEQDGILRTLQQEAVARQTTFLGSPGPRHERSGPDQRL RKASDQPSGHSQATESSGSTPESCPELSDEEQDGDFVPGGESPC PRCRKEARRLQALHEAILSIREAQQBLHRHLSAMLSSTARAAQA PTPGLLQSPRSWFLLCVFLACQLFINHILK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM HDRWEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7138 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7139 1 357 SLRNSARGLKMAASAARGAAALRRSINQPVAFVRRIPWTAASSQ LKEHFAQFGHVRRCILPFDKETGFHRGLGWVQFSSEEGLRNALQ QENHILDGVKVQVHTRRPKLPQTSDDEKKDF 7140 1401 1957 RASSLQVLKAWGGLIPSSFQQQHTGQYALEELFDLKVYDCFCSF	1	ļ.		
SGKITSGEEVLASLSGHWDRDVFIKEEGSGSSALFWTPSGEVRR QRIRQHTVPLEEQTELESBELWQHVTRAISKGDQHRATQEKFAL EEAQRQRARERQESLMPWKPQLFHLDPITQEWHYRYEDHSPWDP LKDIAQFEQDGILRTLQQEAVARQTTFLGSPGPRHERSGPDQRL RKASDQPSGHSQATESSGSTPESCPELSDEEQDGDFVPGGESPC PRCKKEARRLQALHEAILSIREAQQBLHRHLSAMLSSTARAAQA PTPGLLQSPRSWFLLCVFLACQLFINHILK 7136 2 418 DFVPSFRPSGNTSQTVWLLEAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET 7137 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7138 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7139 1 357 SLRNSARGLKMAASAARGAAALRRSINQPVAFVRRIPWTAASSQ LKEHFAQFGHVRRCILPFDKETGFHRGLGWVQFSSEEGLRNALQ QSNHILDGVKVQVHTRPRKLPQTSDDEKKDF 7140 1401 1957 RASSLQVLKAWGGLIPSSFQQQHTGQYALEELFDLKVYDCFCSF	1)		GSITAKSRFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG
QRLRQHTVPLEEQTELESERLWQHVTRAISKGDQHRATQEKFAL EEAQRQRARERQESLMPWKPQLFHLDPITQEWHYRYEDHSPWDP LKDIAQFEQDGILRTLQQEAVARQTTFLGSPGPRHERSGPDQRL RKASDQPSGHSQATESSGSTPESCPELSDEEQDGDFVPGGESPC PRCRKEARRLQALHEAILSIREAQQBLHRHLSAMLSSTARAAQA PTPGLLQSPRSWFLLCVFLACQLFINHILK 7136 2 418 DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET 7137 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7138 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7139 1 357 SLRNSARGLKMAASAARGAALRRSINQPVAFVRRIPWTAASSQ LKEHFAQFGHVRRCILPFDKETGFHRGLGWVQFSSEEGLRNALQ QENHIIDGVKVQVHTRRPKLPQTSDDEKKDF 7140 1401 1957 RASSLQVLKAWGGLIPSSFQQQHTGQYALEELFDLKVYDCFCSF	Ì			
EEAQRQRARERQESLMPWKPQLFHLDPITQEWHYRYEDHSPWDP LKDIAQFEQDGILRTLQQEAVARQTTFLGSPGPRHERSGPDQRL RKASDQPSGHSQATESSGSTPESCPELSDEEQDGDFVPGGESPC PRCRKEARRLQALHEAILSIREAQQELHRHLSAMLSSTARAAQA PTFGLLQSPRSWFLLCVFLACQLFINHILK 7136 2 418 DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET 7137 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7138 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7139 1 357 SLRNSARGLKMAASAARGAAALRRSINQPVAFVRRIPWTAASSQ LKEHFAQFGHVRRCILPFDKETGFHRGLGWVQFSSEEGLRNALQ QENHIIDGVKVQVHTRRPKLPQTSDDEKKDF 7140 1401 1957 RASSLQVLKAWGGLIPSSFQQQHTGQYALEELFDLKVYDCFCSF	Ì	1		
LKDIAQFEQDGILRTLQQEAVARQTTFLGSPGPRHERSGPDQRL RKASDQPSGHSQATESSGSTPESCPELSDEEQDGDFVPGGESPC PRCKKEARRLQALHEAILS IREAQQELHRHLSAMLSSTARAAQA PTPGLLQSPRSWFLLCVFLACQLFINHILK 7136 2 418 DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET 7137 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7138 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7139 1 357 SLRNSARGLKMASSAARGAAALRRSINQPVAFVRRIPWTAASSQ LKEHFAQFGHVRRCILPFDKETGFHRGLGWVQFSSEEGLRNALQ QENHIIDGVKVQVHTRRPKLPQTSDDEKKDF 7140 1401 1957 RASSLQVLKAWGGLIPSSFQQQHTGQYALEELFDLKVYDCFCSF				
RKASDQPSGHSQATESSGSTPESCPELSDEEQDGDFVPGGESPC PRCRKEARRLQALHEAILSIREAQQELHRHLSAMLSSTARAAQA PTPGLLQSPRSWFLLCVFLACQLFINHILK 7136 2 418 DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET 7137 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7138 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQULQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7139 1 357 SLRNSARGLKMAASAARGAAALRRSINQPVAFVRRIPWTAASSQ LKEHFAQFGHVRRCILPFDKETGFHRGLGWVQFSSEEGLRNALQ QENHIIDGVKVQVHTRRPKLPQTSDDEKKDF 7140 1401 1957 RASSLQVLKAWGGLIPSSFQQQHTGQYALEELFDLKVYDCFCSF	Í	j		
PRCRKEARRLQALHEAILSIREAQQELHRHLSAMLSSTARAAQA PTPGLLQSPRSWFLLCVFLACQLFINHILK 7136 2 418 DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET 7137 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7138 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7139 1 357 SLRNSARGLKMAASAARGAAALRRSINQPVAFVRRIPWTAASSQ LKEHFAQFGHVRRCILPFDKETGFHRGLGWVQFSSEEGLRNALQ QENHIIDGVKVQVHTRRPKLPQTSDDEKKDF 7140 1401 1957 RASSLQVLKAWGGLIPSSFQQQHTGQYALEELFDLKVYDCFCSF	ŀ	!		
PTPGLLQSPRSWFLLCVFLACQLFINHILK 7136 2 418 DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET 7137 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7138 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7139 1 357 SLRNSARGLKMAASAARGAAALRRSINQPVAFVRRIPWTAASSQ LKEHFAQFGHVRRCILPFDKETGFHRGLGWVQFSSEEGLRNALQ QENHIIDGVKVQVHTRRPKLPQTSDDEKKDF 7140 1401 1957 RASSLQVLKAWGGLIPSSFQQQHTGQYALEELFDLKVYDCFCSF	ł	1		
7136 2 418 DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMLK SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM HDRWEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET 7137 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7138 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7139 1 357 SLRNSARGLKMAASAARGAAALRRSINQPVAFVRRIPWTAASSQ LKEHFAQFGHVRCILPFDKETGFHRGLGWVQFSSEEGLRNALQ QENHIIDGVKVQVHTRRPKLPQTSDDEKKDF 7140 1401 1957 RASSLQVLKAWGGLIPSSFQQQHTGQYALEELFDLKVYDCFCSF	Į.			
SQQRKVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET 7137 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7138 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7139 1 357 SLRNSARGLKMAASAARGAAALRRSINQPVAFVRRIPWTAASSQ LKEHFAQFGHVRRCILPFDKETGFHRGLGWVQFSSEEGLRNALQ QENHILDGVKVQVHTRRPKLPQTSDDEKKDF 7140 1401 1957 RASSLQVLKAWGGLIPSSFQQQHTGQYALEELFDLKVYDCFCSF	<u> </u>			
HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV IRVVET 7137 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7138 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7139 1 357 SLRNSARGLKMAASAARGAAALRRSINQPVAFVRRIPWTAASSQ LKEHFAQFGHVRRCILPFDKETGFHRGLGWVQFSSEEGLRNALQ QENHIIDGVKVQVHTRRPKLPQTSDDEKKDF 7140 1401 1957 RASSLQVLKAWGGLIPSSFQQQHTGQYALEELFDLKVYDCFCSF	7136	2	418	
7137 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7138 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7139 1 357 SLRNSARGLKMAASAARGAAALRRSINQPVAFVRRIPWTAASSQ LKEHFAQFGHVRRCILPFDKETGFHRGLGWVQFSSEEGLRNALQ QENHIIDGVKVQVHTRRPKLPQTSDDEKKDF 7140 1401 1957 RASSLQVLKAWGGLIPSSFQQQHTGQYALEELFDLKVYDCFCSF	1	}		
7137 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7138 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7139 1 357 SLRMSARGLKMAASAARGAAALRRSINQPVAFVRRIPWTAASSQ LKEHFAQFGHVRRCILPFDKETGFHRGLGWVQFSSEEGLRNALQ QENHIIDGVKVQVHTRRPKLPQTSDDEKKDF 7140 1401 1957 RASSLQVLKAWGGLIPSSFQQQHTGQYALEELFDLKVYDCFCSF	1			
GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7138 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7139 1 357 SLRNSARGLKMAASAARGAAALRRSINQPVAFVRRIPWTAASSQ LKEHFAQFGHVRCILPFDKETGFHRGLGWVQFSSEEGLRNALQ QENHILDGVKVQVHTRRPKLPQTSDDEKKDF 7140 1401 1957 RASSLQVLKAWGGLIPSSFQQQHTGQYALEELFDLKVYDCFCSF	<u></u>	ļ		<u> </u>
PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7138 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7139 1 357 SLRNSARGLKMAASAARGAAALRRSINQPVAFVRRIPWTAASSQ LKEHFAQFGHVRRCILPFDKETGFHRGLGWVQFSSEEGLRNALQ QENHIIDGVKVQVHTRRPKLPQTSDDEKKDF 7140 1401 1957 RASSLQVLKAWGGLIPSSFQQQHTGQYALEELFDLKVYDCFCSF	7137	2	466	
RMEQLSDKESYKLSCQLEPENP 7138 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7139 1 357 SLRNSARGLKMAASAARGAAALRRSINQPVAFVRRIPWTAASSQ LKEHFAQFGHVRRCILPFDKETGFHRGLGWVQFSSEEGLRNALQ QENHILDGVKVQVHTRRPKLPQTSDDEKKDF 7140 1401 1957 RASSLQVLKAWGGLIPSSFQQQHTGQYALEELFDLKVYDCFCSF	ļ	}		
7138 2 466 WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7139 1 357 SLRNSARGLKMAASAARGAAALRRSINQPVAFVRRIPWTAASSQ LKEHFAQFGHVRRCILPFDKETGFHRGLGWVQFSSEEGLRNALQ QENHIIDGVKVQVHTRRPKLPQTSDDEKKDF 7140 1401 1957 RASSLQVLKAWGGLIPSSFQQQHTGQYALEELFDLKVYDCFCSF	i .	[
GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7139 1 357 SLRNSARGLKMAASAARGAAALRRSINQPVAFVRRIPWTAASSQ LKEHFAQFGHVRRCILPFDKETGFHRGLGWVQFSSEEGLRNALQ QENHILDGVKVQVHTRRPKLPQTSDDEKKDF 7140 1401 1957 RASSLQVLKAWGGLIPSSFQQQHTGQYALEELFDLKVYDCFCSF				
PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP 7139 1 357 SLRNSARGLKMAASAARGAAALRRSINQPVAFVRRIPWTAASSQ LKEHFAQFGHVRRCILPFDKETGFHRGLGWVQFSSEEGLRNALQ QENHIIDGVKVQVHTRRPKLPQTSDDEKKDF 7140 1401 1957 RASSLQVLKAWGGLIPSSFQQQHTGQYALEELFDLKVYDCFCSF	7138	2	466	
RMEQLSDKESYKLSCQLEPENP 7139 1 357 SLRNSARGLKMAASAARGAAALRRSINGPVAFVRRIPWTAASSQ LKEHFAQFGHVRRCILPFDKETGFHRGLGWVQFSSEEGLRNALQ QENHIIDGVKVQVHTRRPKLPQTSDDEKKDF 7140 1401 1957 RASSLQVLKAWGGLIPSSFQQQHTGQYALEELFDLKVYDCFCSF	1			GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI
RMEQLSDKESYKLSCQLEPENP 7139 1 357 SLRNSARGLKMAASAARGAAALRRSINGPVAFVRRIPWTAASSQ LKEHFAQFGHVRRCILPFDKETGFHRGLGWVQFSSEEGLRNALQ QENHIIDGVKVQVHTRRPKLPQTSDDEKKDF 7140 1401 1957 RASSLQVLKAWGGLIPSSFQQQHTGQYALEELFDLKVYDCFCSF				
LKEHFAQFGHVRRCILPFDKETGFHRGLGWVQFSSEEGLRNALQ QENHIIDGVKVQVHTRRPKLPQTSDDEKKDF 7140 1401 1957 RASSLQVLKAWGGLIPSSFQQQHTGQYALEELFDLKVYDCFCSF				RMEQLSDKESYKLSCQLEPENP
QENHIIDGVKVQVHTRRPKLPQTSDDEKKDF 7140 1401 1957 RASSLQVLKAWGGLIPSSFQQQHTGQYALEELFDLKVYDCFCSF	7139	1	357	
7140 1401 1957 RASSLQVLKAWGGLIPSSFQQQHTGQYALEELFDLKVYDCFCSF	}			LKEHFAQFGHVRRCILPFDKETGFHRGLGWVQFSSEEGLRNALQ
The state of the s				QENHIIDGVKVQVHTRRPKLPQTSDDEKKDF
NMNVSLEKQLRPSQPWPRGKCRKTPGWEEARPKAQDLRGDLGKT	7140	1401	1957	
	<u>L</u>			NMNVSLEKQLRPSQPWPRGKCRKTPGWEEARPKAQDLRGDLGKT

ID beginning nucleotide location corresponding to first amino acid residue of amino acid sequence s	SEO	Predicted	Predicted end	
NO: nucleotide location corresponding to first amino acid residue of amino acid sequence sequ	~			Amino acid segment containing signal peptide
location corresponding to first amino acid residue of amino acid sequence Sequence	NO:		-	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
To first amino acid residue of amino acid residue of amino acid sequence se				Grutamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of amino acid residue of amino acid sequence se	į.	corresponding		H=Histidine, I=Isoleucine, K=Lysine,
amino acid residue of amino acid sequence Seserine, TeThreonine, VeValine, w=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,	1			Debeucine, M=Methionine, N=Asparagine,
residue of amino acid sequence Sequence	1			P=Proline, Q=Glutamine, R=Arginine,
amino acid sequence Codon, /=possible nucleotide deletion, =possible nucleotide insertion -possible nucleotice -possible nucleotice -possible nucleotice -possibl	Í			S=Serine, T=Threonine, V=Valine,
sequence \ \ \ \ \ \ \ \ \ \ \ \ \	İ			W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
OAGPAEATRGPPRLPAATGCPPHLPGLLSGISVDIDPTGLQSQ WTPKSQDPPLMFSEDYQKSLLEQYHLGLDQKLRKYVVGELIUMF ADFMTNQCG LDSRSCWLDMEDLEEDVRFIVDETLDFGGLSPSDSREEEDITVL VTPEKPLRRGLSHRSDPNAVAPAPQGVRLSLGPLSPEKLEEILD EANRLAAQLEQCALQDRESAGEGLGPRRVKPSPRRETFVLKDSP VRDLLPTVNSLTRSTPS/LKQPDASTPE***EGVSQGSFGYIWK EALQHEEGVTHLQSVPCIQKPSIFSS\SRSTPPVRGRAGPSGRA AASEETRAAKLRGAAAKSSCQLFIPSAIPRPASRMPLTSRSVPP GATRSNLQPP 7142 658 839 LIFLMLHMELKMLSSVTLHIRAFLYWICLKPTSCLIFQNVLNLL KK*SRAVGVVVVMCRT/YSSDLQVGVIKPWLLLGSQDAAHDLDT LKKNKVTHILNVAYGVENAFLSDFTYKSISILDLPETNILSYFP ECFEFIEEAKRKDGVVLVHCNA SLEMSSDGEPLSRMDSEDSISSTIMDVDSTISSGRSTPAMMNGQ GSTTSSSKNIAYNCCWDQCQACFNSSPDLADHIRSIHVDGQRGG VFVCLMKGCKVVNTPSTSQSWLQRHMLTHSGDKPFKCVVGGCNA SFASQGGILARHVPTHFSQQNSSKVSSQPKAKEESPSKAGMNKRR KLKNKRRRSLARPHDFFDAQTLDAIRHRAICFNLSAHIESLGKG HSVVFHSTVSILLFFQIKYKTLQKNISTIISKSLKI 7144 1 988 FRVMMQDGGPSPAEHSKAEESAGMEARFIGLPDAAGSSGPTPAR RCPAPRPAGVSYVIRDEVEKYNRNGVNALQLDPALNRLFTAGRD SIIRIMSVNQHKQDPYIASMEHHTDWWNDIVLCCMSKTLISASG			sequence	Codon, /=possible nucleotide deletion,
##PRGQDPPLMFSEDYQKSLLEQYHLGLDQKLRKYVVGELIWNF ADFMTNQCG 1DSRSCWLDMEDLEEDVRFIVDETLDFGGLSPSDREEEDITVL VTPEKPLRRGLSHRSDPNAVAPAPQGVRLSLGPLSPEKLEEILD EANRLAAQLEQCALQDRESAGEGLGPRRVKPSPRRETFVLKDSP VRDLLPTVNSLTRSTPS/LKQPDASTPE***EGVSQGSPGYIWK EALQHEEGVTHLQSVPCIQKPSIFSS\SRSTPPVRGRAGPSGRA AASEETRAAKLRGAAAKSSCQLPIPSAIPRPASRMPLTSRSVPP GRGALPPDSLSTRKGLPRPSTAGHRVRESGHKVPVSQRLNLPVM GATRSNLQPP 1142 658 839 LIFIMLHMELKMLSSVTLHIRAFLYWICLKPTSCLIFQNVLNLL KK*SRAVGVVVVMCRT/YSSDLQVGVIKPWLLLGSQDAAHDLDT LKKNKVTHILNVAYGVENAFLSDFTYKSISILDLPETNILSYFP ECFEFIEEAKRKDGVVLVHCNA 1 3 773 SLEMSSDGEPLSRMDSEDSISTIMDVDSTISSGRSTPAMMNGQ GSTTSSSKNIAYNCCWDQCQACFNSSPDLADHIRSIHVDGQRGG VFVCLWKGCKVYNTPSTSQSWLQRHMLTHSGDKPFKCVVGGCNA SFASQGGLARHVPTHFSQONSSKVSSQPKAKEESPSKAGMNKRR KLKNKRRRSLARPHDFFDAQTLDAIRHRAICFNLSAHIESLGKG HSVVFHSTVSILLFFQIKYKTLQKNISTIISKSLKI 7144 1 988 FRVMPDGGSPAEHSKAEESAGMEARFLGIPDAAGSSGPTPAR RCPAPRPAGVSYVIRDEVEKYNRNGVNALQLDPALNRIFTAGRD SIIRIWSVNQHKQDPYIASMEHHTDWVNDIVLCCNGKTLLSASS	 	Joquenee		\=possible nucleotide insertion)
##PRGQDPPLMFSEDYQKSLLEQYHLGLDQKLRKYVVGELIWNF ADFMTNQCG 1DSRSCWLDMEDLEEDVRFIVDETLDFGGLSPSDREEEDITVL VTPEKPLRRGLSHRSDPNAVAPAPQCGVRLSLGPLSPEKLEEILD EANRLAAQLEQCALQDRESAGEGLGPRRVKPSPRRETFVLKDSP VRDLLPTVNSLTRSTPS/LKQPDASTPE***EGVSQGSPGYIWK EALQHEEGVTHLQSVPCIQKPSIFSS\SRSTPPVRGRAGPSGRA AASEETRAAKLRGAAAKSSCQLPIPSAIPRPASRMPLTSRSVPP GRGALPPDSLSTRKGLPRPSTAGHRVRESGHKVPVSQRLNLPVM GATRSNLQPP 1142 658 839 LIFIMLHMELKMLSSVTLHIRAFLYWICLKPTSCLIFQNVLNLL KK*SRAVGVVVVMCRT/YSSDLQVGVIKPWLLLGSQDAAHDLDT LKKNKVTHILNVAYGVENAFLSDFTYKSISILDLPETNILSYFP ECFEFIEEAKRKDGVVLVHCNA 1 3 773 SLEMSSDGEPLSRMDSEDSISTIMDVDSTISSGRSTPAMMNGQ GSTTSSSKNIAYNCCWDQCQACFNSSPDLADHIRSIHVDGQRGG VFVCLWKGCKVYNTPSTSQSWLQRHMLTHSGDKPFKCVVGGCNA SFASQGGLARHVPTHFSQONSSKVSSQPKAKEESPSKAGMNKRR KLKNKRRRSLARPHDFFDAQTLDAIRHRAICFNLSAHIESLGKG HSVVFHSTVSILLFFQIKYKTLQKNISTIISKSLKI 7144 1 988 FRVMPDGGSPAEHSKAEESAGMEARFLGLPDAAGSSGPTPAR RCPAPRPAGSVSYVIRDEVEKYNRNGVNALQLDPALNRIFTAGRD SIIRIWSVNQHKQDPYIASMEHHTDWVNDIVLCCNGKTLLSASS			ţ	QAGPAEAHTRGPPRLPAATGCPPHLPGLLSGISVDIDPTGLQSO
7141 124 1073 LDRRCWLDMEDLEEDVRFIVDETLDFGGLSPSDSREEEDITVL VTPEKPLRRGLSHRSDPNAVAPAPQGVRLSLGPLSPEKLEEILD VTPEKPLRRGLSHRSDPNAVAPAPQGVRLSLGPLSPEKLEEILD VTPEKPLRRGLSHRSDPNAVAPAPQGVRLSLGPLSPEKLEEILD VRDLLPTVNSLTRSTPS/LKQPDASTPE***EGVSQGSPGYIWK EALQHEEGVTHLQSVPCIQKPSIFSS\SRSTPPVRGRAGPSGRA AASEETRAAKLRGAAAKSSCQLPIPSAIPRPASRMPLTSRSVPP GRGALPPDSLSTRKGLPRPSTAGHRVRESGHKVPVSQRLNLPVM GATRSNLQPP 7142 658 839 LIFLMLHMELKMLSSVTLHIRAFLYWICLKPTSCLIFQNVLNLL KK*SRAVGVVVVMCRT/YSSDLQVGVIKPWLLLGSQDAAHDLDT LKKNKVTHILNVAYGVENAFLSDFTYKSISILDLPETNILSYFP ECFEFIEEAKRKDGVVLVHCNA 7143 3 773 SLEMSSDGEPLSRMDSEDSISSTIMDVDSTISSGRSTPAMMNGQ GSTTSSSKNIAYNCCWDQCQACFNSSPDLADHIRSIHVDGGRGG VFVCLWKGCKVVNTPSTSQSWLQRHMLTHSGDKPFKCVVGGCNA SFASQGGLARHVPTHFSQQNSKVSSQPKAKEESPSKAGNNKRR KLKNKRRRSLARPHDFFDAQTLDAIRHRAICFNLSAHIESLGKG HSVVFHSTVSILLFFQIKYKTLQKNISTIISKSLKI 7144 1 988 FRVNMQDGGPSPAEHSKAEESAGMEARFLGLPDAAGSSGFTPAR RCPAPRPAGUSYVIRDEVEKYNRNGVNALQLDPALNRLFTAGRS SIIRIWSVNQHKQDPYIASMEHHTDWVNDIVLCCNGKTLISASS		ľ	ł	WIPKGQDPPLMFSEDYQKSLLEQYHLGLDOKLRKYVVGELTWMF
LDSRSCWLDMEDLEEDVRFIVDETLDFGGLSPSDSREEEDITVL VTPEKPLRRGLSHRSDPNAVAPAPQGQRLSLGPLSPEKLEEILD EANRLAAQLEQCALQDRESAGEGLGPRVKPSPRRETFVLKDSP VRDLLPTVNSLTRSTPS/LKQPDASTPE***EGVSQGSPGYIWK EALQHEEGVTHLQSVPCIQKPSIFSS\SRSTPPVRGRAGPSGRA AASEETRAAKLRGAAAKSSCQLPIPSAIPRPASRMPLTSRSVPP GRGALPPDSLSTRKGLPRPSTAGHRVRESGHKVPVSQRLNLPVM GATRSNLQPP 7142 658 839 LIFLMLHMELKMLSSVTLHIRAFLYWICLKPTSCLIFQNVLNLL KK*SRAVGVVVVMCRT/YSSDLQVGVIKPWLLLGSQDAAHDLDT LKKNKVTHILNVAYGVENAFLSDFTYKSISILDLPETNILSYFP ECFEFIEEAKRKDGVVLVHCNA 7143 3 773 SLEMSSDGEPLSRMDSEDSISSTIMDVDSTISSGRSTPAMMNGQ GSTTSSKNIAYNCCWDQCQACFNSSPDLADHIRSIHVDGQRGG VFVCLWKGCKVYNTPSTSQSWLQRHMLTHSGDKPFKCVVGGCNA SFASQGGLARHVPTHFSQQNSKVSSQPKAKEESPSKAGMNKRR KLKNKRRRSLARPHDFFDAQTLDAIRHRAICFNLSAHIESLGKG HSVVFHSTVSILLFFGIKYKTLQKNISTIISKSLKI 7144 1 988 FRVMQDGGPSPAEHSKAEESAGMEARFLGLPDAAGSSGPTPAR RCPAPRPAGVSYVIRDEVEKYNRNGVNALQLDPALNRLFTAGRD SIIRIWSVNQHKQDPYLASMEHHTDWVNDIVLCCNGKTLLSAGS	7141	124		ADFMINGCG
VTPEKPERGLSHRSDPNAVAPAPQGVRLSLGPLSPEKLEEILD EANRLAAQLEQCALQDRESAGEGLGPRRVKPSPRRETFVLKDSP VRDLLPTVNSLTRSTPS/LKQPDASTPE***EGVSQGSPGYIWK EALQHEEGVTHLQSVPCIQKPSIFSS\SRSTPPVRGRAGPSGRA AASEETRAAKLRGAAAKSSCQLPIPSAIPRPASRMPLTSRSVPP GRGALPPDSLSTRKGLPRPSTAGHRVRESGHKVPVSQRLNLPVM GATRSNLQPP 7142 658 839 LIFIMLHMELKMLSSVTLHIRAFLYWICLKPTSCLIFQNVLNLL KK*SRAVGVVVVMCRT/YSSDLQVGVIKPWLLLGSQDAAHDLDT LKKNKVTHILNVAYGVENAFLSDFTYKSISILDLPETNILSYFP ECFEFIEEAKRKDGVVLVHCNA 7143 3 773 SLEMSSDGEPLSRMDSEDSISSTIMDVDSTISSGRSTPAMMNGQ GSTTSSSKNIAYNCCWDQCQACFNSSPDLADHIRSIHVDGQRGG VFVCLWKGCKVYNTPSTSQSWLQRHMLTHSGDKPFKCVVGGCNA SFASQGGLARHVPTHFSQQNSSKVSSQPKAKEESPSKAGMNKRR KLKNKRRRSLARPHDFFDAQTLDAIRHRAICFNLSAHIESLGKG HSVVFHSTVSILLFFQIKYKTLQKNISTIISKSLKI 7144 1 988 FRVMMQDGGPSPAEHSKAEESAGMEARFLGLPDAAGSSGPTPAR RCPAPRPAGVSYVIRDEVEKYNRNGVNALQLDPALNRLFTAGSS	, 111	124	1073	LDSRSCWLDMEDLEEDVRFIVDETLDFGGLSPSDSREEEDITVL
PARALAQLEQCALQDRESAGEGLGPRRVKPSPRRETFVLKDSP VRDLLPTVNSLTRSTPS/LKQPDASTPE***EGVSQGSPGYIWK EALQHEEGVTHLQSVPCIQKPSIFSS\SRSTPPVRGRAGPSGRA AASEETRAAKLRGAAAKSSCQLFIPSAIPRPASRMPLTSRSVPP GRGALPPDSLSTRKGLPRPSTAGHRVRESGHKVPVSQRLNLPVM GATRSNLQPP 1142 658 839 LIFLMLHMELKMLSSVTLHIRAFLYWICLKPTSCLIFQNVLNLL KK*SRAVGVVVVMCRT/YSSDLQVGVIKPWLLLGSQDAAHDLDT LKKNKVTHILNVAYGVENAFLSDFTYKSISILDLPETNILSYFP ECFEFIEEAKRKDGVVLVHCNA GSTTSSKNIAYNCCWDQCQACFNSSPDLADHIRSIHVDGQRGG VFVCLWKGCKVYNTPSTSQSWLQRHMLTHSGDKPFKCVVGGCNA SFASQGGLARHVPTHFSQQNSSKVSSQPKAKEESPSKAGMNKRR KLKNKRRRSLARPHDFFDAQTLDAIRHRAICFNLSAHIESLGKG HSVVFHSTVSILLFFQIKYKTLQKNISTIISKSLKI FRVNMQDGGFSPAEHSKAEESAGMEARFLGLPDAAGSSGPTPAR RCPAPRPAGVSYVIRDEVEKYNRNGVNALQLDPALNRLFTAGRD SIIRIWSVNQHKQDPYIASMEHHTDWVNDIVLCCNGKTLISASE			•	VTPEKPLRRGLSHRSDPNAVAPAPOGVRLSLGPLSPEKLEFILD
VRDLEPTVSLTRSTPS/LKQPDASTPE***EGVSQGSPGYIWK EALQHEEGVTHLQSVPCIQKPSIFSS\SRSTPPVRGRAGPSGRA AASEETRAAKLRGAAAKSSCQLPIPSAIPRPASRMPLTSRSVPP GRGALPPDSLSTRKGLPRPSTAGHRVRESGHKVPVSQRLNLPVM GATRSNLQPP 7142 658 839 LIFLMLHMELKMLSSVTLHIRAFLYWICLKPTSCLIFQNVLNLL KK*SRAVGVVVVMCRT/YSSDLQVGVIKPWLLLGSQDAAHDLDT LKKNKVTHILNVAYGVENAFLSDFTYKSISILDLPETNILSYFP ECFEFIEEAKRKDGVVLVHCNA 7143 3 773 SLEMSSDGEPLSRMDSEDSISSTIMDVDSTISSGRSTPAMMNGQ GSTTSSSKNIAYNCCWDQCQACFNSSPDLADHIRSIHVDGQRGG VFVCLWKGCKVYNTPSTSQSWLQRHMLTHSGDKPFKCVVGGCNA SFASQGGLARHVPTHFSQQNSSKVSSQPKAKEESPSKAGMNKRR KLKNKRRRSLARPHDFFDAQTLDAIRHRAICFNLSAHIESLGKG HSVVFHSTVSILLFFQIKYKTLQKNISTIISKSLKI 7144 1 988 FRVNMQDGGPSPAEHSKAEESAGMEARFLGLPDAAGSSGPTPAR RCPAPRPAGVSYVIRDEVEKYNRNGVNALQLDPALNRLFTAGRD SIIRIWSVNQHKQDPYIASMEHHTDWVNDIVLCCNGKTLISASS	1	1		EANKLAAQLEQCALQDRESAGEGLGPRRVKPSPRRETEVLKDgp
AASEETRAKLRGAAAKSSCQLPIPSAIPRPASRMPLTSRSVPP GRGALPPDSLSTRKGLPRPSTAGHRVRESGHKVPVSQRLNLPVM GATRSNLQPP 7142 658 839 LIFLMLHMELKMLSSVTLHIRAFLYWICLKPTSCLIFQNVLNLL KK*SRAVGVVVVMCRT/YSSDLQVGVIKPWLLLGSQDAAHDLDT LKKNKVTHILNVAYGVENAFLSDFTYKSISILDLPETNILSYFP ECFEFIEEAKRKDGVVLVHCNA 7143 3 773 SLEMSSDGEPLSRMDSEDSISSTIMDVDSTISSGRSTPAMMNGQ GSTTSSSKNIAYNCCWDQCQACFNSSPDLADHIRSIHVDGQRGG VFVCLWKGCKVYNTPSTSQSWLQRHMLTHSGDKPFKCVVGGCNA SFASQGGLARHVPTHFSQQNSSKVSSQPKAKEESPSKAGMNKRR KLKNKRRRSLARPHDFFDAQTLDAIRHRAICFNLSAHIESLGKG HSVVFHSTVSILLFFQIKYKTLQKNISTIISKSLKI 7144 1 988 FRVNWQDGGPSPAEHSKAEESAGMEARFLGLPDAAGSSGPTPAR RCPAPRPAGVSYVIRDEVEKYNRNGVNALQLDPALNRLFTAGRD SIIRIWSVNQHKQDPYIASMEHHTDWVNDIVLCCNGKTLISASS	Í			VRDLLPTVNSLTRSTPS/LKQPDASTPE***EGVSQGSPGVTWK
AASEETRAAKLRGAAAKSSCQLPIPSAIPRPASRMPLTSRSVPP GRGALPPDSLSTRKGLPRPSTAGHRVRESGHKVPVSQRLNLPVM GATRSNLQPP 7142 658 839 LIFLMLHMELKMLSSVTLHIRAFLYWICLKPTSCLIFQNVLNLL KK*SRAVGVVVVMCRT/YSSDLQVGVIKPWLLLGSQDAAHDLDT LKKNKVTHILNVAYGVENAFLSDFTYKSISILDLPETNILSYFP ECFEFIEEAKRKDGVVLVHCNA 7143 3 773 SLEMSSDGEPLSRMDSEDSISSTIMDVDSTISSGRSTPAMMNGQ GSTTSSSKNIAYNCCWDQCQACFNSSPDLADHIRSIHVDGQRGG VFVCLWKGCKVYNTPSTSQSWLQRHMLTHSGDKPFKCVVGGCNA SFASQGGLARHVPTHFSQQNSSKVSSQPKAKEESPSKAGMNKRR KLKNKRRRSLARPHDFFDAQTLDAIRHRAICFNLSAHIESLGKG HSVVFHSTVSILLFFQIKYKTLQKNISTIISKSLKI 7144 1 988 FRVNMQDGGPSPAEHSKAEESAGMEARFLGLPDAAGSSGPTPAR RCPAPRPAGVSYVIRDEVEKYNRNGVNALQLDPALNRLFTAGRD SIIRIWSVNQHKQDPYIASMEHHTDWVNDIVLCCNGKTLISASS	J			EALQHEEGVTHLQSVPCIOKPSIFSS\SRSTPPVPGPAGPGGDA
7142 658 839 LIFLMLHMELKMLSSVTLHIRAFLYWICLKPTSCLIFQNVLNLL KK*SRAVGVVVVMCRT/YSSDLQVGVIKPWLLLGSQDAAHDLDT LKKNKVTHILNVAYGVENAFLSDFTYKSISILDLPETNILSYFP ECFEFIEEAKRKDGVVLVHCNA 7143 3 773 SLEMSSDGEPLSRMDSEDSISSTIMDVDSTISSGRSTPAMMNGQ GSTTSSSKNIAYNCCWDQCQACFNSSPDLADHIRSIHVDGQRGG VFVCLWKGCKVYNTPSTSQSWLQRHMLTHSGDKPFKCVVGGCNA SFASQGGLARHVPTHFSQQNSSKVSSQPKAKEESPSKAGMNKRR KLKNKRRRSLARPHDFFDAQTLDAIRHRAICFNLSAHIESLGKG HSVVFHSTVSILLFFQIKYKTLQKNISTIISKSLKI 7144 1 988 FRVNMQDGGPSPAEHSKAEESAGMEARFLGLPDAAGSSGPTPAR RCPAPRPAGVSYVIRDEVEKYNRNGVNALQLDPALNRLFTAGRD SIIRIWSVNQHKQDPYIASMEHHTDWVNDIVLCCNGKTLISASS	1			AASEETRAAKLRGAAAKSSCQLPIPSAIPRPASRMPLTSRSVDD
7142 658 839 LIFLMLHMELKMLSSVTLHIRAFLYWICLKPTSCLIFQNVLNLL KK*SRAVGVVVVMCRT/YSSDLQVGVIKPWLLLGSQDAAHDLDT LKKNKVTHILNVAYGVENAFLSDFTYKSISILDLPETNILSYFP ECFEFIEEAKRKDGVVLVHCNA 7143 3 773 SLEMSSDGEPLSRMDSEDSISSTIMDVDSTISSGRSTPAMMNGQ GSTTSSSKNIAYNCCWDQCQACFNSSPDLADHIRSIHVDGQRGG VFVCLWKGCKVYNTPSTSQSWLQRHMLTHSGDKPFKCVVGGCNA SFASQGGLARHVPTHFSQQNSSKVSSQPKAKEESPSKAGMNKRR KLKNKKRRSLARPHDFFDAQTLDAIRHRAICFNLSAHIESLGKG HSVVFHSTVSILLFFQIKYKTLQKNISTIISKSLKI 7144 1 988 FRVNMQDGGPSPAEHSKAEESAGMEARFLGLPDAAGSSGPTPAR RCPAPRPAGVSYVIRDEVEKYNRNGVNALQLDPALNRLFTAGRD SIIRIWSVNQHKQDPYIASMEHHTDWVNDIVLCCNGKTLISASS	Ī			GRUALPPUSLSTRKGLPRPSTAGHRVRESGHKVPVSOPT.NI.DVM
TIFIMIMELKMLSSVTLHIRAFLYWICLKPTSCLIFQNVLNLL KK*SRAVGVVVVMCRT/YSSDLQVGVIKPWLLLGSQDAAHDLDT LKKNKVTHILNVAYGVENAFLSDFTYKSISILDLPETNILSYFP ECFEFIEEAKRKDGVVLVHCNA 3 773 SLEMSSDGEPLSRMDSEDSISSTIMDVDSTISSGRSTPAMMNGQ GSTTSSSKNIAYNCCWDQCQACFNSSPDLADHIRSIHVDGQRGG VFVCLWKGCKVYNTPSTSQSWLQRHMLTHSGDKPFKCVVGGCNA SFASQGGLARHVPTHFSQQNSSKVSSQPKAKEESPSKAGMNKRR KLKNKRRSLARPHDFFDAQTLDAIRHRAICFNLSAHIESLGKG HSVVFHSTVSILLFFQIKYKTLQKNISTIISKSLKI 7144 1 988 FRVNMQDGGPSPAEHSKAEESAGMEARFLGLPDAAGSSGPTPAR RCPAPRPAGVSYVIRDEVEKYNRNGVNALQLDPALNRLFTAGRD SIIRIWSVNQHKQDPYIASMEHHTDWVNDIVLCCNGKTLISASS	7747			GATRSNLQPP
7143 3 773 SLEMSSDGEPLSRMDSEDSISSTIMDVDSTISSGRSTPAMMNGQ GSTTSSSKNIAYNCCWDQCQACFNSSPDLADHIRSIHVDGQRGG VFVCLWKGCKVYNTPSTSQSWLQRHMLTHSGDKPFKCVVGGCNA SFASQGGLARHVPTHFSQQNSSKVSSQPKAKESPSKAGMNKRR KLKNKRRSLARPHDFFDAQTLDAIRHRAICFNLSAHIESLGKG HSVVFHSTVSILLFFQIKYKTLQKNISTIISKSLKI 7144 1 988 FRVNMQDGGPSPAEHSKAEESAGMEARFLGLPDAAGSSGPTPAR RCPAPRPAGVSYVIRDEVEKYNRNGVNALQLDPALNRLFTAGRD SIIRIWSVNQHKQDPYIASMEHHTDWVNDIVLCCNGKTLISASS	/142	658	839	LIFLMLHMELKMLSSVTLHIRAFLYWICLKPTSCLIFONVLNLL
7143 3 773 SLEMSSDGEPLSRMDSEDSISSTIMDVDSTISSGRSTPAMMNGQ GSTTSSSKNIAYNCCWDQCQACFNSSPDLADHIRSIHVDGQRGG VFVCLWKGCKVYNTPSTSQSWLQRHMLTHSGDKPFKCVVGGCNA SFASQGGLARHVPTHFSQQNSSKVSSQPKAKEESPSKAGMNKRR KLKNKRRSLARPHDFFDAQTLDAIRHRAICFNLSAHIESLGKG HSVVFHSTVSILLFFQIKYKTLQKNISTIISKSLKI 7144 1 988 FRVNMQDGGPSPAEHSKAEESAGMEARFLGLPDAAGSSGPTPAR RCPAPRPAGVSYVIRDEVEKYNRNGVNALQLDPALNRLFTAGRD SIIRIWSVNQHKQDPYIASMEHHTDWVNDIVLCCNGKTLISASS	1			KK*SRAVGVVVVMCRT/YSSDLOVGVIKPWLLLGSODAAHDLDT
7143 3 773 SLEMSSDGEPLSRMDSEDSISSTIMDVDSTISSGRSTPAMMIGQ GSTTSSSKNIAYNCCWDQCQACFNSSPDLADHIRSIHVDGQRGG VFVCLWKGCKVYNTPSTSQSWLQRHMLTHSGDKPFKCVVGGCNA SFASQGGLARHVPTHFSQQNSSKVSSQPKAKEESPSKAGMNKRR KLKNKRRRSLARPHDFFDAQTLDAIRHRAICFNLSAHIESLGKG HSVVFHSTVSILLFFQIKYKTLQKNISTIISKSLKI 7144 1 988 FRVNMQDGGPSPAEHSKAEESAGMEARFLGLPDAAGSSGPTPAR RCPAPRPAGVSYVIRDEVEKYNRNGVNALQLDPALNRLFTAGRD SIIRIWSVNQHKQDPYIASMEHHTDWVNDIVLCCNGKTLISASS	1	i		LKKNKVTHILNVAYGVENAFLSDFTYKSISILDI,DETNII,SVED
SLEMSSDGEPLSRMDSEDSISSTIMDVDSTISSGRSTPAMMINGQ GSTTSSSKNIAYNCCWDQCQACFNSSPDLADHIRSIHVDGQRGG VFVCLWKGCKVYNTPSTSQSWLQRHMLTHSGDKPFKCVVGGCNA SFASQGGLARHVPTHFSQQNSSKVSSQPKAKEESPSKAGMNKRR KLKNKRRRSLARPHDFFDAQTLDAIRHRAICFNLSAHIESLGKG HSVVFHSTVSILLFFQIKYKTLQKNISTIISKSLKI 1 988 FRVNMQDGGPSPAEHSKAEESAGMEARFLGLPDAAGSSGPTPAR RCPAPRPAGVSYVIRDEVEKYNRNGVNALQLDPALNRLFTAGRD SIIRIWSVNQHKQDPYIASMEHHTDWVNDIVLCCNGKTLISASS	7143			ECFEFIEEAKRKDGVVLVHCNA
GSTTSSSKNTAYNCCWDQCQACFNSSPDLADHIRSIHVDGQRGG VFVCLWKGCKVYNTPSTSQSWLQRHMLTHSGDKPFKCVVGGCNA SFASQGGLARHVPTHFSQQNSSKVSSQPKAKEESPSKAGMNKRR KLKNKRRRSLARPHDFFDAQTLDAIRHRAICFNLSAHIESLGKG HSVVFHSTVSILLFFQIKYKTLQKNISTIISKSLKI 1 988 FRVNMQDGGPSPAEHSKAEESAGMEARFLGLPDAAGSSGPTPAR RCPAPRPAGVSYVIRDEVEKYNRNGVNALQLDPALNRLFTAGRD SIIRIWSVNQHKQDPYIASMEHHTDWVNDIVLCCNGKTLISASS	/143	J	773	SLEMSSDGEPLSRMDSEDSISSTIMDVDSTISSGRSTPAMMNGO
VFVCLWKGCKVYNTPSTSQSWLQRHMLTHSGDKPFKCVVGGCNA SFASQGGLARHVPTHFSQQNSSKVSSQPKAKEESPSKAGMNKRR KLKNKRRRSLARPHDFFDAQTLDAIRHRAICFINLSAHIESLGKG HSVVFHSTVSILLFFQIKYKTLQKNISTIISKSLKI 1 988 FRVNMQDGGPSPAEHSKAEESAGMEARFLGLPDAAGSSGPTPAR RCPAPRPAGVSYVIRDEVEKYNRNGVNALQLDPALNRLFTAGRD SIIRIWSVNQHKQDPYIASMEHHTDWVNDIVLCCNGKTLISASS	1			GSTTSSSKNIAYNCCWDQCQACFNSSPDLADHIRSTHVDGOPGG
SFASQGLARHVPTHFSQQNSSKVSSQPKAKEESPSKAGMNKRR KLKNKRRRSLARPHDFFDAQTLDAIRHRAICFNLSAHIESLGKG HSVVFHSTVSILLFFQIKYKTLQKNISTIISKSLKI 1 988 FRVNMQDGGPSPAEHSKAEESAGMEARFLGLPDAAGSSGPTPAR RCPAPRPAGVSYVIRDEVEKYNRNGVNALQLDPALNRLFTAGRD SIIRIWSVNQHKQDPYIASMEHHTDWVNDIVLCCNGKTLISASS	į .			VFVCLWKGCKVYNTPSTSQSWLORHMLTHSGDKPFKCVJGGCNA
RLKNKRRRSLARPHDFFDAQTLDAIRHRAICFNLSAHIESLGKG HSVVFHSTVSILLFFQIKYKTLQKNISTIISKSLKI 1 988 FRVNMQDGGPSPAEHSKAEESAGMEARFLGLPDAAGSSGPTPAR RCPAPRPAGVSYVIRDEVEKYNRNGVNALQLDPALNRLFTAGRD SIIRIWSVNQHKQDPYIASMEHHTDWVNDIVLCCNGKTLISASS	[SFASQGGLARHVPTHFSQQNSSKVSSOPKAKESPSKAGMNKDD
7144 1 988 FRVNMQDGGPSPAEHSKAEESAGMEARFLGLPDAAGSSGPTPAR RCPAPRPAGVSYVIRDEVEKYNRNGVNALQLDPALNRLFTAGRD SIIRIWSVNQHKQDPYIASMEHHTDWVNDIVLCCNGKTLISASS			İ	KLKNKRRRSLARPHDFFDAQTLDAIRHRAICFNLSAHTESLGVG
FRVNMQDGGPSPAEHSKAEESAGMEARFLGLPDAAGSSGPTPAR RCPAPRPAGVSYVIRDEVEKYNRNGVNALQLDPALNRLFTAGRD SIIRIWSVNQHKQDPYIASMEHHTDWVNDIVLCCNGKTLISASS	77744			HSVVFHSTVSILLFFQIKYKTLQKNISTIISKSLKT
RCPAPRPAGVSYVIRDEVEKYNRNGVNALQLDPALNRLFTAGRD SIIRIWSVNQHKQDPYIASMEHHTDWVNDIVLCCNGKTLISAGG	1 '144	1	988	FRVNMQDGGPSPAEHSKAEESAGMEARFLGLPDAAGSSGPTDAD
SIIRIWSVNQHKQDPYIASMEHHTDWVNDIVLCCNGKTLICAGG				RCPAPRPAGVSYVIRDEVEKYNRNGVNALOLDPALNRLETACRD
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	j			SIIRIWSVNQHKQDPYIASMEHHTDWVNDIVLCCNGKTLTCAGG
DITVKVWNAHKGFCMSTLRTHKDYVKALAYAKDKET,VASAGLDR	, ,	}		DITVKVWNAHKGFCMSTLRTHKDYVKALAYAKDKELVAGAGLDB
QIFLWDVNTLTALTASNNTVTTSSLSGNKDSIYSLAMNOLGTI	1	1		QIFLWDVNTLTALTASNNTVTTSSLSGNKDSIYSLAMNOLGTII
VSGSTEKVLRVWDPRTCAKLMKLKGHTDNVKALLINRDGTOCLS] [j	ł	VSGSTEKVLRVWDPRTCAKLMKLKGHTDNVKALLIJNRDGTOCLS
GSSDGTIRLWSLGQQRCIATYRVHDEGVWALOVNDAFTHVVSGG		į	1	GSSDGTIRLWSLGQQRCIATYRVHDEGVWALOVNDAFTHVVSGG
RDRKIYCTDLRNPDIRVLICE	<u></u>			RDRKIYCTDLRNPDIRVLICE

TRADOCS:1416260.1(%CSK01!.DOC)

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:1-1786 and 3573-5358, a mature protein coding portion of SEQ ID NO:1-1786 and 3573-5358, an active domain of SEQ ID NO:1-1786 and 3573-5358, and complementary sequences thereof.

- 2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
- 3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
- 4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
- 5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
- 6. A vector comprising the polynucleotide of claim 1.
- 7. An expression vector comprising the polynucleotide of claim 1.
- 8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
- 9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
- 10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:

(a) a polypeptide encoded by any one of the polynucleotides of claim 1; and

- (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO:1-1786 and 3573-5358.
- 11. A composition comprising the polypeptide of claim 10 and a carrier.
- 12. An antibody directed against the polypeptide of claim 10.
- ·13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
- b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
- 14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
- b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
- c) detecting said product and thereby the polynucleotide of claim 1 in the sample.
- 15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
- 16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

 a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and

- b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.
- 17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
- a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and
- b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
- 18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
- a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and
- b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
- 19. A method of producing the polypeptide of claim 10, comprising,
- a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO:1-1786 and 3573-5358, a mature protein coding portion of SEQ ID NO:1-1786 and 3573-5358, an active domain of SEQ ID NO:1-1786 and 3573-5358, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO:1-1786 and 3573-5358, under conditions sufficient to express the polypeptide in said cell; and
 - b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of any one of the polypeptides SEQ ID NO:1787 -3572 and 5359-7144, the mature protein portion thereof, or the active domain thereof.

- 21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.
- 22. A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO:1-1786 and 3573-5358.
- 23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.
- 24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.
- 25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.
- 26. The collection of claim 22, wherein the collection is provided in a computer-readable format.
- 27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.
- 28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

International application No.

PCT/US00/34263

	SIFICATION OF SUBJECT MATTER	15/95, COTK 14/00		
IPC(7) : C07H 21/04; C12N 15/11, 15/63, 15/70, 15/82, 15/85; C07K 14/00 US CL : 536/23.1; 435/320.1, 455, 468, 530/300, 350				
US CL : 536/23.1; 435/320.1, 455, 468, 530/300, 530 According to International Patent Classification (IPC) or to both national classification and IPC				
B. FIELL	S SEARCHED			
Minimum doc U.S.: 53	umentation searched (classification system followed by 6/23.1; 435/320.1, 455, 468, 530/300, 350	classification symbols)		
Documentatio	n searched other than minimum documentation to the e	xtent that such documents are included in	the fields searched	
Electronic dat MEDLINE, I	a base consulted during the international search (name	of data base and, where practicable, sear	ch terms used)	
C. DOC	IMENTS CONSIDERED TO BE RELEVANT			
Category *	Citation of document, with indication, where app	propriate, of the relevant passages	Relevant to claim No.	
A	WAJIMA et al. The cDNA cloning and transient expr hydroxysteroid dehydrogenase of chickens. Gene. 195	99, Vol.233, pages 75-82	1-11, 13-16, and 19-26	
A	US 5,175,095 A (MARTINEAU et al) 29 December columns 3-18.	1992 (29.12.1992), see especially	1-11, 13-16, and 19-26	
A	Database PubMed, ID No. 2393392, FREUDENSTE inhibitor of metalloproteinase: sequence and expression Biophys. Res. Commun. August 1990. Vol.171. No.	on in bovine ovarian tissue. Biochem.	1-11, 13-16, and 19-26	
A,P	Database PubMed, ID No. 10919256, HENNEBOLI generation and characterization of an ovary-selective library. Endocrinology. August 2000. Vol.141. No.8	complementary deoxyribonucleic acid	1-11, 13-16, and 19-26	
A	Database PubMed, ID No. 2760883, BEIL et al. Synthe baboon (Papio anubis). J. Reprod. Fertil. July 198 Abstract.	thesis of polypeptides by the cervix of 89, Vol.86. No.2. pages 535-544, see	1-11, 13-16, and 19-26	
A,P	Database PubMed, ID No. 10830289, HINSHELWO upstream of the human CYP19 (aromatase) gene med transgenic mice. Endocrinology. June 2000. Vol.141.	liates ovary-specific expression in	1-11, 13-16, and 19-26	
Furthe	r documents are listed in the continuation of Box C.	See patent family annex.		
1	pecial categories of cited documents:	"T" later document published after the int date and not in conflict with the appli principle of theory underlying the inv	cation but cited to understand the	
of partic	of particular relevance "X" document of particular relevance; the claimed invention cannot be considered to involve an invention.		claimed invention cannot be	
"L" documer establish specified	which may throw doubts on priority claim(s) or which is cited to the publication date of another citation or other special reason (as)	"Y" document of particular relevance; the considered to involve an inventive ste	p when the document is	
"O" documen	combined with one or more other such documents, such combined obvious '2 a person skilled in the art.			
	As a decimal manches of the enter material family		t family	
Date of the	actual completion of the international search	Date of mailing of the international sea	rch report	
Co	nailing address of the ISA/US mmissioner of Palents and Trademarks	Authorizachofficer Ali Marsh Michael Woodward	to Isha for	
w	x PCT ashington, D.C. 20231	Telephone No. (703) 308-0196	<i>[</i>]	
Facsimile No. (703)305-3230		Leichitotic 140. (103)-300-0130	1/	

Facsimile No. (703)305-3230
Form PCT/ISA/210 (second sheet) (July 1998)

International application No.
PCT/US00/34263

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)	
This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:	
Claim Nos.: because they relate to subject matter not required to be searched by this Authority, namely:	
2. Claim Nos.: because they relate to parts of the international application that do not comply with the prescribed requirements to suc an extent that no meaningful international search can be carried out, specifically:	h
3. Claim Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a	ı).
Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)	
This International Searching Authority found multiple inventions in this international application, as follows: This includes 4 invention Groups and 3572 sequence species	
 As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.: 	
4. No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.; Remark on Protest The additional search fees were accompanied by the applicant's protest. No protest accompanied the payment of additional search fees.	

Form PCT/ISA/210 (continuation of first sheet(1)) (July 1998)

International application No.

PCT/US00/34263

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional serch fees must be paid. Group I, claims 1-11, 13-16, and 19-26, drawn to nucleic acid molecules, vector molecules and host cells containing said nucleic acids, polypeptides, methods of making said polypeptides and method of detection using said nucleic acids and polypeptides. Group II, claim 12 and 28, drawn to antibodies and method of treatment using composition comprising said antibodies. Group III, claims 17-18, drawn to methods of indentifying a binding partner to a polypeptides. Group IV, claim 27, drawn to method of treatment using composition comprising polypeptides.

The inventions listed as Groups I-IV do not relate to a single inventive concept under PCT Rule 13.1 because, udner PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Group I encompasses nucleic acids, polypeptides expressed thereby, vectors and host cells containg same, respectively, and methods of making as well as the first method of use of this jubject matter. Groups II-V all are directed to different special technical features as summarized as follows: Group II is directed to an antibody and method of treatment using same, which antibody undergoes recognition and binding reactions wherein what is bound is different from what is bound by the compositions of Group I. For example, the polypeptides of Group I do not bind the polypeptides of Group I as the antibody of Group II does. Identification of binding partner and treatment are clearly different special technical features from detection. Group III is directed to the identification of a binding partner of a polypeptide, which is not identified in any of the other Groups and thus clearly contains its own special technical feature. Group IV is directed to treatment, which is a clearly different methods than the methods in the other Groups. Thus, in summary, each of Groups I-IV are directed to different special technical features and thus support this lack of unity.

Additionally, each of the claims is directed to more than one species of the generic invention. These species are deemed to lack unity of invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be searched, the appropriate additional search fees must be paid. The species are as follows: The claims include a series of polynucleotides and the polypeptides encoded thereby as represented by the sequences of SEQ ID Nos: 1-1786, and 3573-5358. Each of these polynucleotide sequences encodes a separate polypeptide and thus represent a separate gene. Therefore, each of these genes defines its own special technical feature. In summary, one species is a gene represented by one polynucleotide sequence and one polypeptide sequence encoded thereby.

Form PCT/ISA/210 (extra sheet) (July 1998)

CORRECTED VERSION

(19) World Intellectual Property Organization International Bureau



(43) International Publication Date 26 July 2001 (26.07.2001)

PCT

(10) International Publication Number WO 01/53312 A1

- (51) International Patent Classification⁷: C07H 21/04, C12N 15/11, 15/63, 15/70, 15/82, 15/85, C07K 14/00
- (21) International Application Number: PCT/US00/34263
- (22) International Filing Date:

26 December 2000 (26.12.2000)

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

,	I HOLLY Date.		
	09/471,275	23 December 1999 (23.12.1999)	US
	09/488,725	21 January 2000 (21.01.2000)	US
	09/552,317	25 April 2000 (25.04.2000)	US
	09/598,042	9 July 2000 (09.07.2000)	US
	09/620,312	19 July 2000 (19.07.2000)	US
	09/653,450	3 August 2000 (03.08.2000)	US
	09/662,191	14 September 2000 (14.09.2000)	US
	09/693,036	19 October 2000 (19.10.2000)	US
	09/727,344	29 November 2000 (29.11.2000)	US

(63) Related by continuation (CON) or continuation-in-part (CIP) to earlier applications:

	09/488,725 (CIP)
	21 January 2000 (21.01.2000)
	09/552,317 (CIP)
	25 April 2000 (25.04.2000)
	09/598,042 (CIP)
	9 July 2000 (09.07.2000)
_	09/620,312 (CIP)
	19 July 2000 (19.07.2000)
	09/653,450 (CIP)
	3 August 2000 (03.08.2000)
	09/662,191 (CIP)
	14 September 2000 (14.09.2000)
	09/693,036 (CIP)
	19 October 2000 (19.10.2000)
	09/727,344 (CIP)
	29 November 2000 (29.11.2000)

(71) Applicant (for all designated States except US): HYSEQ, INC. [US/US]; 670 Almanor Avenue, Sunnyvale, CA 94086 (US).

- (72) Inventors; and
- (75) Inventors/Applicants (for US only): TANG, Y., Tom [US/US]; 4230 Ranwick Court, San Jose, CA 95118 (US).

LIU, Chenghua [CN/US]; 1125 Ranchero Way #14, San Jose, CA 95117 (US). ASUNDI, Vinod [US/US]; 709 Foster City Boulevard, Foster City, CA 94404 (US). CHEN, Rui-hong [US/US]; 1031 Flying Fish Street, Foster City, CA 94404 (US). MA, Yunging [CN/US]: 280 W. California Avenue #206, Sunnyvale, CA 94086 (US). QIAN, Xiaohong, B. [CN/US]; 3662 Tumble Way, San Jose, CA 95132 (US). REN, Feiyan [US/US]; 7703 Oak Meadow Court, Cupertino, CA 95014 (US). WANG, Dunrui [CN/US]; 932 La Palma, Milpitas, CA 95035 (US). WANG, Jian-Rui [CN/US]; 744 Stendhal Lane, Cupertino, CA 95014 (US). WANG, Zhiwei [CN/US]; 836 Alturas Avenue, B36, Sunnyvale, CA 94085 (US). WEHRMAN, Tom [US/US]; 3210 CCSR Mol Pharm. 269 W. Campus Drive, Stanford, CA 94305 (US). XU, Chongjun [CN/US]; 4918 Manitoba Drive, San Jose, CA 95130 (US). XUE, Aidong, J. [CN/US]; 1621 S. Mary Avenue, Sunnyvale, CA 94087 (US). YANG, Yonghong [CN/US]; 4230 Ranwick Court, San Jose, CA 95118 (US). ZHANG, Jie [CN/US]; 4930 Poplar Terrace, Campbell, CA 95008 (US). ZHAO, Qing, A. [CN/US]; 1556 Kooser Road, San Jose, CA 95118 (US). ZHOU, Ping [CN/US]; 1461 Japaul Lane, San Jose, CA 95132 (US). GOODRICH, Ryle [US/US]; 4896 Sandy Lane, San Jose, CA 95124 (US). DRMANAC, Radoje, T. [YU/US]: 850 East Greenwich Place, Palo Alto, CA 94303 (US).

- (74) Agent: ELRIFI, Ivor, R.; Mintz, Levin, Cohn, Ferris, Glovsky, and Popeo, P.C., One Financial Center, Boston, MA 02111 (US).
- (81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.
- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:

with international search report

[Continued on next page]

(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.

WO 01/53312 A1



(48) Date of publication of this corrected version:

1 November 2001

(15) Information about Correction:
see PCT Gazette No. 44/2001 of 1 November 2001, Section

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

REVISED VERSION

(19) World Intellectual Property Organization International Bureau



T TODIO BINIDRIR AT DIRINI REGER ILBA I IN ROME ANNO ANNO INCLUDIO NELLA REGERMA ILBA ANNO ILBA

(43) International Publication Date 26 July 2001 (26.07.2001)

PCT

(10) International Publication Number WO 01/53312 A1

(51) International Patent Classification⁷: C07H 21/04. C12N 15/11, 15/63, 15/70, 15/82, 15/85, C07K 14/00

(21) International Application Number: PCT/US00/34263

(22) International Filing Date:

26 December 2000 (26.12.2000)

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

09/471,275	23 December 1999 (23.12.1999)	US
09/488,725	21 January 2000 (21.01.2000)	US
09/552,317	25 April 2000 (25.04.2000)	US
09/598,042	9 July 2000 (09.07.2000)	US
09/620.312	19 July 2000 (19.07.2000)	US
09/653.450	3 August 2000 (03.08.2000)	US
09/662,191	14 September 2000 (14.09.2000)	US
09/693,036	19 October 2000 (19.10.2000)	US
09/727,344	29 November 2000 (29.11.2000)	US

(63) Related by continuation (CON) or continuation-in-part (CIP) to earlier applications:

09/488,725 (CIP)
21 January 2000 (21.01.2000)
09/552,317 (CIP)
25 April 2000 (25.04.2000)
09/598.042 (CIP)
9 July 2000 (09.07.2000)
09/620,312 (CIP)
19 July 2000 (19.07.2000)
09/653,450 (CIP)
3 August 2000 (03.08.2000)
09/662,191 (CIP)
14 September 2000 (14.09.2000)
09/693,036 (CIP)
19 October 2000 (19.10.2000)
09/727,344 (CIP)
29 November 2000 (29.11.2000)

(71) Applicant (for all designated States except US): HYSEQ, INC. [US/US]; 670 Almanor Avenue. Sunnyvale. CA 94086 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): TANG, Y., Tom [US/US]: 4230 Ranwick Court, San Jose, CA 95118 (US).

LIU, Chenghua [CN/US]; 1125 Ranchero Way #14. San Jose, CA 95117 (US). ASUNDI, Vinod [US/US]; 709 Foster City Boulevard, Foster City, CA 94404 (US). CHEN, Rui-hong [US/US]; 1031 Flying Fish Street, Foster City, CA 94404 (US). MA, Yunqing [CN/US]; 280 W. California Avenue #206, Sunnyvale, CA 94086 (US). QIAN, Xiaohong, B. [CN/US]: 3662 Tumble Way, San Jose, CA 95132 (US). REN, Feiyan [US/US]; 7703 Oak Meadow Court, Cupertino, CA 95014 (US). WANG, Dunrui [CN/US]: 932 La Palma, Milpitas. CA 95035 (US). WANG, Jian-Rui [CN/US]; 744 Stendhal Lane, Cupertino, CA 95014 (US). WANG, Zhiwei [CN/US]; 836 Alturas Avenue, B36, Sunnyvale, CA 94085 (US). WEHRMAN, Tom [US/US]: 3210 CCSR Mol Pharm, 269 W. Campus Drive, Stanford, CA 94305 (US). XU, Chongjun [CN/US]; 4918 Manitoba Drive, San Jose, CA 95130 (US). XUE, Aidong, J. [CN/US]: 1621 S. Mary Avenue, Sunnyvale, CA 94087 (US). YANG, Yonghong [CN/US]; 4230 Ranwick Court, San Jose, CA 95118 (US). ZHANG, Jie [CN/US]; 4930 Poplar Terrace, Campbell. CA 95008 (US). ZHAO, Qing, A. [CN/US]; 1556 Kooser Road, San Jose, CA 95118 (US). ZHOU, Ping [CN/US]: 1461 Japaul Lane, San Jose, CA 95132 (US). GOODRICH, Ryle [US/US]; 4896 Sandy Lane. San Jose, CA 95124 (US). DRMANAC, Radoje, T. [YU/US]; 850 East Greenwich Place, Palo Alto, CA 94303 (US).

- (74) Agent: ELRIFI, Ivor, R.; Mintz. Levin. Cohn. Ferris, Glovsky, and Popeo, P.C., One Financial Center, Boston, MA 02111 (US).
- (81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.
- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, Fl, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:

with international search report

[Continued on next page]

(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.

(

WO 01/53312 A1



(88) Date of publication of the revised international search report: 20 June 2002

(15) Information about Corrections:

see PCT Gazette No. 25/2002 of 20 June 2002, Section II Previous Correction:

see PCT Gazette No. 44/2001 of 1 November 2001, Section II

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

BNSDOCID: <WO_____0153312A1_IB>

REVISED VERSION

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/34263

					
CLASSIFICATION OF SUBJECT MATTER IPC(7) : C07H 21/04; C12N 15/11, 15/63, 15/70, 15/82, 15/85; C07K 14/00 US CL : 536/23.1; 435/320.1, 455, 468, 530/300, 350					
According to	International Patent Classification (IPC) or to both national	onal classification and IPC			
	DS SEARCHED				
Minimum dos	umentation searched (classification system followed by	classification symbols)			
	6/23.1; 435/320.1, 455, 468, 530/300, 350	Classification dymodis,			
Documentatio	Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched				
Electronic dat MEDLINE, E	a base consulted during the international search (name	of data base and, where practicable, sear	ch terms used)		
	JMENTS CONSIDERED TO BE RELEVANT				
Category *	Citation of document, with indication, where ap		Relevant to claim No.		
^	WAJIMA et al. The cDNA cloning and transient expr hydroxysteroid dehydrogenase of chickens. Gene. 199		1-11, 13-16, and 19-26		
A	US 5,175,095 A (MARTINEAU et al) 29 December columns 3-18.	1992 (29.12.1992), see especially	1-11, 13-16, and 19-26		
A	Database PubMed, ID No. 2393392, FREUDENSTE inhibitor of metalloproteinase: sequence and expression Biophys. Res. Commun. August 1990. Vol.171. No.	on in bovine ovarian tissue. Biochem.	1-11, 13-16, and 19-26		
A,P	Database PubMed, ID No. 10919256, HENNEBOLI generation and characterization of an ovary-selective library. Endocrinology. August 2000. Vol.141. No.8	complementary deoxyribonucleic acid	1-11, 13-16, and 19-26		
Α	Database PubMed, ID No. 2760883, BEIL et al. Synthesis of polypeptides by the cervix of the baboon (Papio anubis). J. Reprod. Fertil. July 1989. Vol.86. No.2. pages 535-544, see Abstract.		1-11, 13-16, and 19-26		
A,P	Database PubMed, ID No. 10830289, HINSHELWO upstream of the human CYP19 (aromatase) gene med transgenic mice. Endocrinology. June 2000. Vol. 141	liates ovary-specific expression in	1-11, 13-16, and 19-26		
Further	r documents are listed in the continuation of Box C.	See patent family annex.			
• 5	special categories of cited documents:	"T" later document published after the inte date and not in conflict with the applie			
	a defining the general state of the art which is not considered to be ular relevance	principle or theory underlying the invi	ention		
"E" earlier application or patent published on or after the international filing date		considered novel or cannot be considered when the document is taken alone			
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another criation or other special reason (as specified)		"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination			
"O" document referring to an oral disclosure, use, exhibition or other means		being obvious to a person skilled in the	ne art		
priority	nt published prior to the international filing date but later than the date claimed	"&" document member of the same patent			
Date of the a	actual completion of the international search	Date of mailing of the international sear	rch report		
		0.5 SEP 2001			
Name and m	nailing address of the ISA/US	Authorized officer			
Co	mmissioner of Patents and Trademarks	Michael Woodward	Allen La		
	x PCT sshington, D.C. 20231				
· ·	o. (703)305-3230	Telephone No. (703)/308-0196	[]		

Form PCT/ISA/210 (second sheet) (July 1998)

international application No.

PCT/US00/34263

	Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)		
This	internation	onal report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:	
1.		Claim Nos.: because they relate to subject matter not required to be searched by this Authority, namely:	
2.		Claim Nos.: because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:	
3.		Claim Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).	
Box	II Ot	oservations where unity of invention is lacking (Continuation of Item 2 of first sheet)	
		ional Searching Authority found multiple inventions in this international application, as follows: s 4 invention Groups and 3572 sequence species	
1. 2. 3.		As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:	
4.	emark on	No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims: it is covered by claims Nos.: 1-11, 13-16; and 14-26 Protest The additional search fees were accompanied by the applicant's protest. No protest accompanied the payment of additional search fees.	

Form PCT/ISA/210 (continuation of first sheet(1)) (July 1998)

This Page is Inserted by IFW Indexing and Scanning Operations and is not part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:
D BLACK BORDERS
☐ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES
FADED TEXT OR DRAWING
☐ BLURRED OR ILLEGIBLE TEXT OR DRAWING
☐ SKEWED/SLANTED IMAGES
☐ COLOR OR BLACK AND WHITE PHOTOGRAPHS
☐ GRAY SCALE DOCUMENTS
LINES OR MARKS ON ORIGINAL DOCUMENT
\square REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY
OTHER.

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.

THIS PAGE BLANK (USPTO)